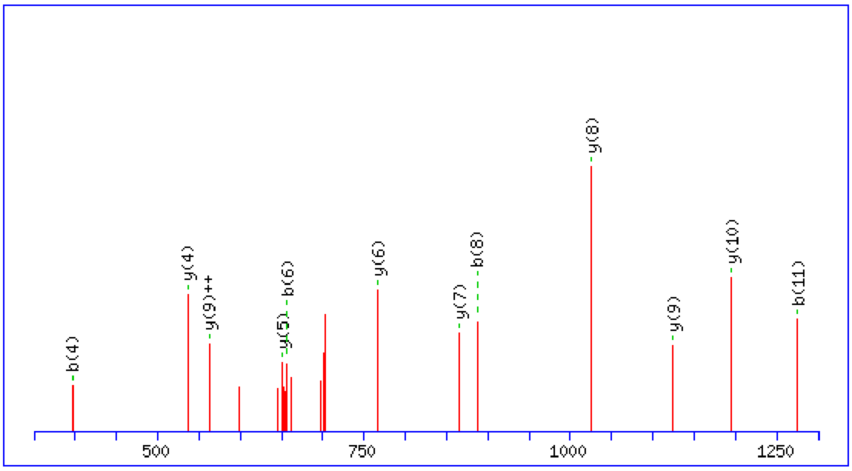
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIAVCVDDPEYK**
Found in **AT1G01050.1** in **TAIR_Arabidopsis**, Symbols: ATPPA1 | ATPPA1 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 1); inorganic diphosphatase/ pyrophosphatase | chr1:31382-32670 REVERSE

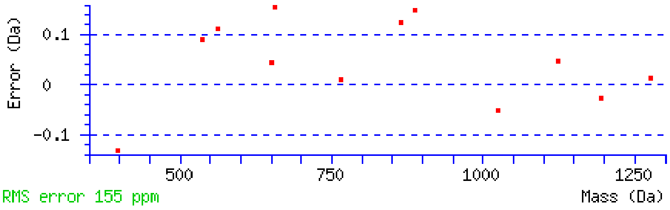
Match to Query 5491: 1420.689784 from(711.352168,2+) index(4906)
Title: Elution from: 43.024 to 43.024 scan no 6142 cid35.00 polarity:+
Data file D1d-3_3.mgf

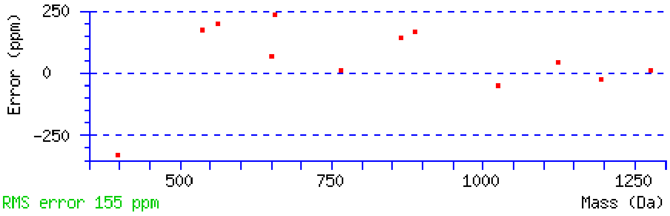
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1420.6908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 7e-007
Matches : 12/94 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							12
2	227.1754	114.0913			I	1308.6140	654.8107	1291.5875	646.2974	1290.6035	645.8054	11
3	298.2125	149.6099			A	***1195.5300***	598.2686	1178.5034	589.7553	1177.5194	589.2633	10
4	**397.2809**	199.1441			V	***1124.4929***	562.7501	1107.4663	554.2368	1106.4823	553.7448	9
5	557.3116	279.1594			C	***1025.4244***	513.2159	1008.3979	504.7026	1007.4139	504.2106	8
6	**656.3800**	328.6936			V	***865.3938***	433.2005	848.3672	424.6873	847.3832	424.1953	7
7	771.4069	386.2071	753.3964	377.2018	D	***766.3254***	383.6663	749.2988	375.1531	748.3148	374.6610	6
8	**886.4339**	443.7206	868.4233	434.7153	D	***651.2984***	326.1529	634.2719	317.6396	633.2879	317.1476	5
9	983.4866	492.2470	965.4761	483.2417	P	***536.2715***	268.6394	519.2449	260.1261	518.2609	259.6341	4
10	1112.5292	556.7683	1094.5187	547.7630	E	439.2187	220.1130	422.1922	211.5997	421.2082	211.1077	3
11	**1275.5926**	638.2999	1257.5820	629.2946	Y	310.1761	155.5917	293.1496	147.0784			2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IIAVCVDDPEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G01050.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.8	1420.6908	-0.0010	IIAVCVDDPEYK
6.8	1420.6868	0.0030	LEPGCSVSSLSTGK

AT1G01090.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVMSELFGK**
Found in **AT1G01090.1** in **TAIR_Arabidopsis**, Symbols: PDH-E1 ALPHA | PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring) | chr1:47705-49166 REVERSE

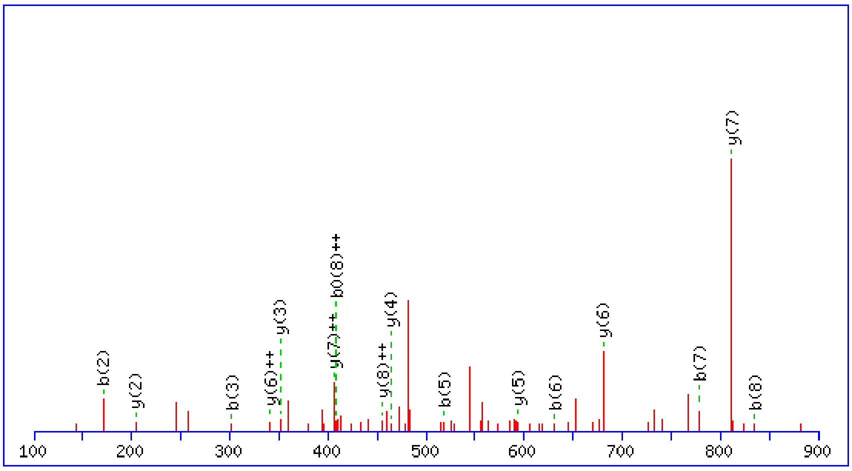
Match to Query 2427: 980.501622 from(491.258087,2+) index(6218)
Title: Elution from: 54.897 to 54.897 scan no 7874 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 900 Da Full range

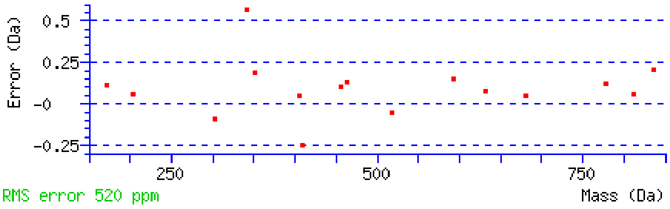
Label all possible matches ○ Label matches used for scoring ●

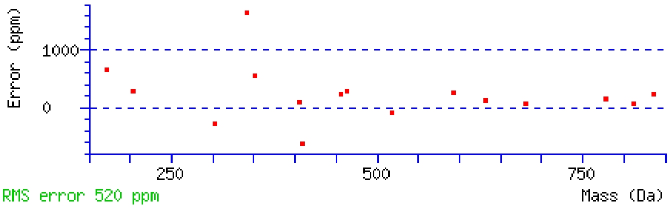
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 980.5001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.015
Matches : 16/66 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			**A**							9
2	***171.1128***	86.0600			**V**	910.4703	455.7388	893.4437	447.2255	892.4597	446.7335	8
3	***302.1533***	151.5803			**M**	***811.4019***	406.2046	794.3753	397.6913	793.3913	397.1993	7
4	389.1853	195.0963	371.1748	186.0910	**S**	***680.3614***	340.6843	663.3348	332.1710	662.3508	331.6790	6
5	***518.2279***	259.6176	500.2173	250.6123	**E**	***593.3293***	297.1683	576.3028	288.6550	575.3188	288.1630	5
6	***631.3120***	316.1596	613.3014	307.1543	**L**	***464.2867***	232.6470	447.2602	224.1337			4
7	***778.3804***	389.6938	760.3698	380.6885	**F**	***351.2027***	176.1050	334.1761	167.5917			3
8	***835.4019***	418.2046	817.3913	409.1993	**G**	***204.1343***	102.5708	187.1077	94.0575			2
9					**K**	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AVMSELFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G01090.1

25.6	980.5001	0.0015	AVMSELFGK
3.2	980.5001	0.0015	AAVYLEMGK

AT1G01100.1

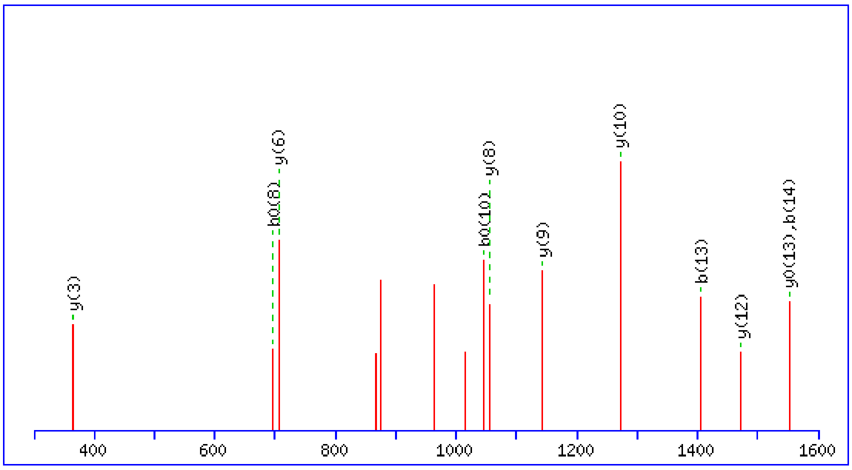
Mascot Search Results

Peptide View

MS/MS Fragmentation of AAGVSIESYWPMLFAK
Found in AT1G01100.1 in TAIR_Arabidopsis, Symbols: | 60S acidic ribosomal protein P1 (RPP1A) | chr1:50284-50954 REVERSE

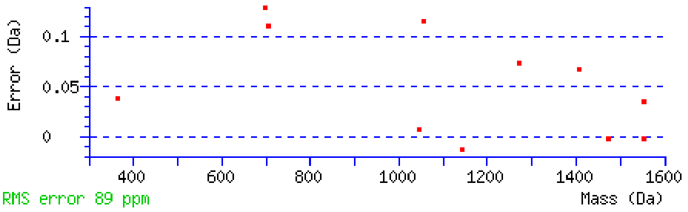
Match to Query 8255: 1768.889628 from(885.452090,2+) index(10498)
Title: Elution from: 103.942 to 103.942 scan no 15310 cid35.00 polarity:+
Data file D12h-1_3.mgf

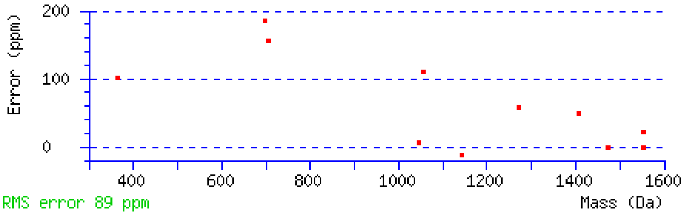
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1768.8858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 6e-005
Matches : 11/126 fragment ions using 12 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258			A							16
2	143.0815	72.0444			A	1698.8560	849.9316	1681.8294	841.4184	1680.8454	840.9264	15
3	200.1030	100.5551			G	1627.8189	814.4131	1610.7923	805.8998	1609.8083	805.4078	14
4	299.1714	150.0893			V	1570.7974	785.9023	1553.7709	777.3891	1552.7868	776.8971	13
5	386.2034	193.6053	368.1928	184.6001	S	***1471.7290***	736.3681	1454.7025	727.8549	1453.7184	727.3629	12
6	499.2875	250.1474	481.2769	241.1421	I	1384.6970	692.8521	1367.6704	684.3388	1366.6864	683.8468	11
7	628.3301	314.6687	610.3195	305.6634	E	***1271.6129***	636.3101	1254.5864	627.7968	1253.6023	627.3048	10
8	715.3621	358.1847	697.3515	349.1794	S	***1142.5703***	571.7888	1125.5438	563.2755	1124.5597	562.7835	9
9	878.4254	439.7164	860.4149	430.7111	Y	***1055.5383***	528.2728	1038.5117	519.7595			8
10	1064.5047	532.7560	1046.4942	523.7507	W	892.4750	446.7411	875.4484	438.2278			7
11	1161.5575	581.2824	1143.5469	572.2771	P	***706.3956***	353.7015	689.3691	345.1882			6
12	1292.5980	646.8026	1274.5874	637.7973	M	609.3429	305.1751	592.3163	296.6618			5
13	**1405.6820**	703.3447	1387.6715	694.3394	L	478.3024	239.6548	461.2758	231.1416			4
14	**1552.7505**	776.8789	1534.7399	767.8736	F	***365.2183***	183.1128	348.1918	174.5995			3
15	1623.7876	812.3974	1605.7770	803.3921	A	218.1499	109.5786	201.1234	101.0653			2
16					K	147.1128	74.0600	130.0863	65.5468			1





AT1G01100.1

NCBI **BLAST** search of AAGVSIESYWPMLFAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.4	1768.8858	0.0038	AAGVSIESYWPMLFAK

Mascot: http://www.matrixscience.com/

AT1G01320.1

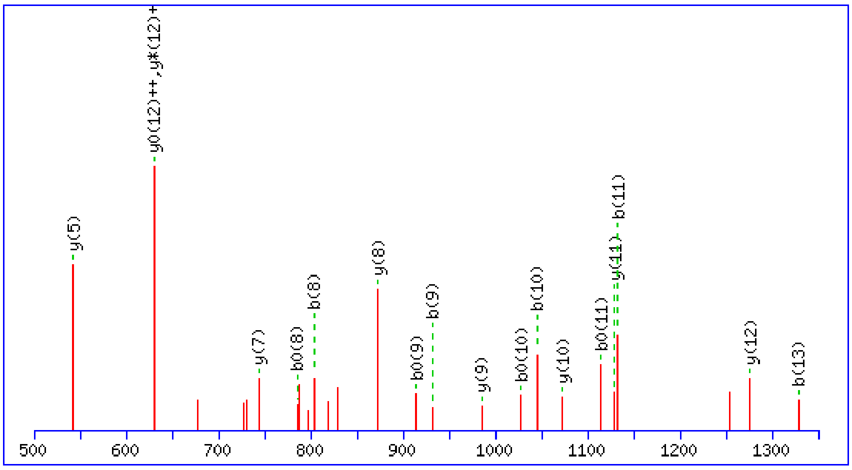
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVADFGSLELSPVDGR**
Found in **AT1G01320.1** in **TAIR_Arabidopsis**, Symbols: | tetratricopeptide repeat (TPR)-containing protein | chr1:121582-130099 REVERSE

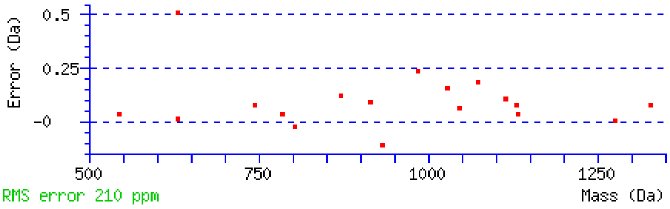
Match to Query 7790: 1673.861286 from(837.937919,2+) index(8664)
Title: Elution from: 77.245 to 77.245 scan no 11584 cid35.00 polarity:+
Data file 0-3_2.mgf

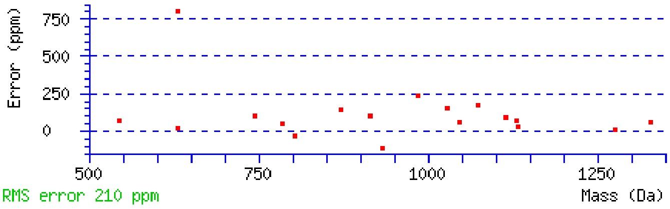
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1673.8625
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 1.6e-006
Matches : 19/140 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							16
2	213.1598	107.0835			V	1561.7857	781.3965	1544.7591	772.8832	1543.7751	772.3912	15
3	284.1969	142.6021			A	1462.7172	731.8623	1445.6907	723.3490	1444.7067	722.8570	14
4	399.2238	200.1155	381.2132	191.1103	D	1391.6801	696.3437	1374.6536	687.8304	1373.6696	687.3384	13
5	546.2922	273.6498	528.2817	264.6445	F	***1276.6532***	638.8302	1259.6266	630.3170	1258.6426	629.8250	12
6	603.3137	302.1605	585.3031	293.1552	G	***1129.5848***	565.2960	1112.5582	556.7828	1111.5742	556.2907	11
7	690.3457	345.6765	672.3352	336.6712	S	***1072.5633***	536.7853	1055.5368	528.2720	1054.5527	527.7800	10
8	**803.4298**	402.2185	785.4192	393.2132	L	***985.5313***	493.2693	968.5047	484.7560	967.5207	484.2640	9
9	**932.4724**	466.7398	914.4618	457.7345	E	***872.4472***	436.7272	855.4207	428.2140	854.4367	427.7220	8
10	**1045.5564**	523.2819	1027.5459	514.2766	L	***743.4046***	372.2060	726.3781	363.6927	725.3941	363.2007	7
11	**1132.5885**	566.7979	1114.5779	557.7926	S	***630.3206***	315.6639	613.2940	307.1506	612.3100	306.6586	6
12	1229.6412	615.3243	1211.6307	606.3190	P	***543.2885***	272.1479	526.2620	263.6346	525.2780	263.1426	5
13	**1328.7096**	664.8585	1310.6991	655.8532	V	446.2358	223.6215	429.2092	215.1083	428.2252	214.6162	4
14	1443.7366	722.3719	1425.7260	713.3666	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
15	1500.7581	750.8827	1482.7475	741.8774	G	232.1404	116.5738	215.1139	108.0606			2
16					R	175.1190	88.0631	158.0924	79.5498			1





AT1G01320.1

NCBI **BLAST** search of LVADFGSLELSPVDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.7	1673.8625	-0.0012	LVADFGSLELSPVDGR
3.0	1673.8584	0.0029	TDERQILKEANTEK

AT1G01800.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDEVINEYLK**
Found in **AT1G01800.1** in **TAIR_Arabidopsis**, Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr1:293396-294888 FORWARD

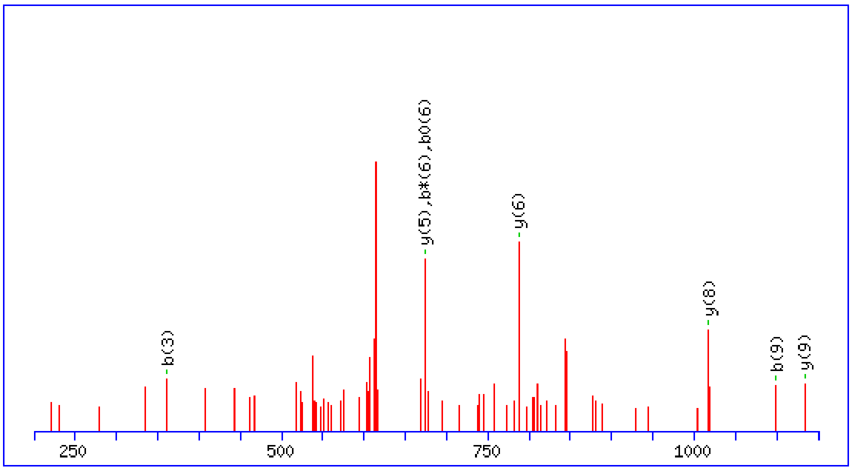
Match to Query 4319: 1246.610802 from(624.312677,2+) index(6509)
Title: Elution from: 58.152 to 58.152 scan no 8414 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, [Plot from] [200] to [1150] Da [Full range]

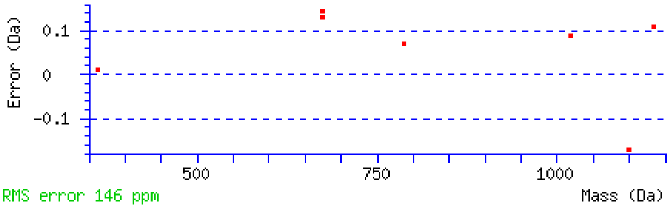
Label all possible matches ○ Label matches used for scoring ●

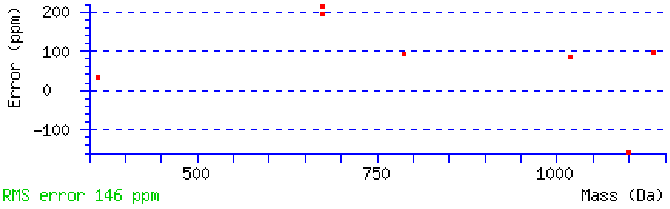
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.6089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.025
Matches : 8/90 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							10
2	231.1124	116.0598			213.1018	107.0545	D	*1133.5351*	567.2712	1115.5115	558.2594	1115.5246	558.2659	9
3	*361.1520*	181.0796			343.1414	172.0743	E	*1017.5111*	509.2592	999.4876	500.2474	999.5006	500.2539	8
4	461.2174	231.1124			443.2069	222.1071	V	887.4715	444.2394	869.4479	435.2276	869.4609	435.2341	7
5	575.2985	288.1529			557.2880	279.1476	I	*787.4061*	394.2067	769.3825	385.1949	769.3955	385.2014	6
6	691.3355	346.1714	673.3119	337.1596	673.3250	337.1661	N	*673.3250*	337.1661	655.3014	328.1543	655.3144	328.1608	5
7	821.3752	411.1912	803.3516	402.1794	803.3646	402.1859	E	557.2880	279.1476	539.2644	270.1358	539.2774	270.1423	4
8	985.4355	493.2214	967.4119	484.2096	967.4250	484.2161	Y	427.2483	214.1278	409.2248	205.1160			3
9	*1099.5166*	550.2619	1081.4930	541.2502	1081.5061	541.2567	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IDEVINEYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G01800.1

Score	Mr(calc)	Delta	Sequence
26.2	1246.6089	0.0019	IDEVINEYLK
8.2	1246.6116	-0.0008	IGGGNVTITSWK
7.3	1246.6120	-0.0012	LREERNNVAK
7.0	1246.6089	0.0019	YIVEEAEALAK
6.7	1246.6116	-0.0008	IGNAFGNIIDAK
6.4	1246.6094	0.0014	EIDKNSEIRK
4.2	1246.6120	-0.0012	EAQARAGIREK
3.7	1246.6132	-0.0024	MMVIGLLMAPK
2.7	1246.6089	0.0019	EVSFEAALIEK
2.3	1246.6089	0.0019	LELAYAIADEK

AT1G01990.1

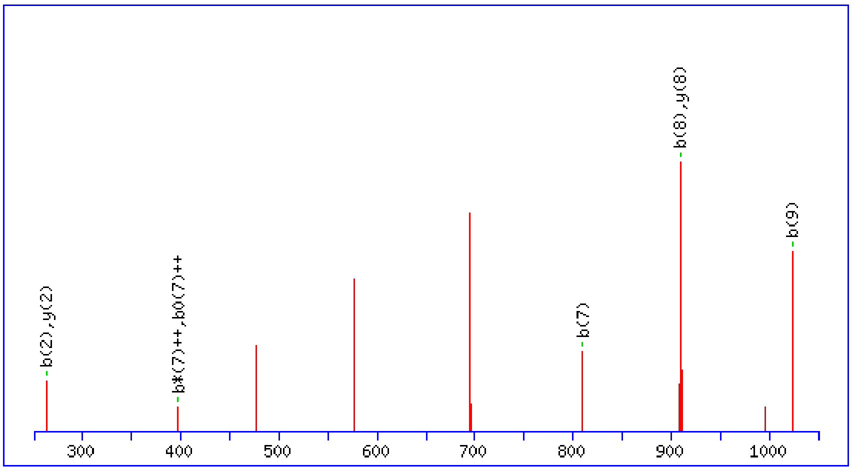
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEAQILNVLK**
Found in **AT1G01990.1** in **TAIR_Arabidopsis**, Symbols: | similar to chloroplast lumen common family protein [Arabidopsis thaliana] (TAIR:AT2G37400.1) | chr1:343462-344199 REVERSE

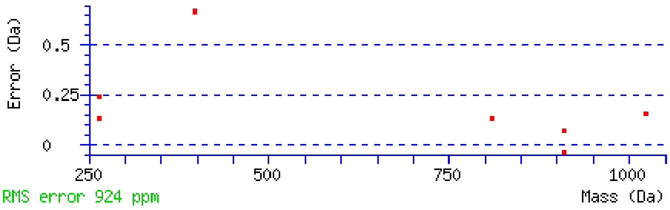
Match to Query 3485: 1170.612624 from(586.313588,2+) index(4133)
Title: Elution from: 39.675 to 39.675 scan no 5307 cid35.00 polarity:+
Data file D1d-2_3.mgf

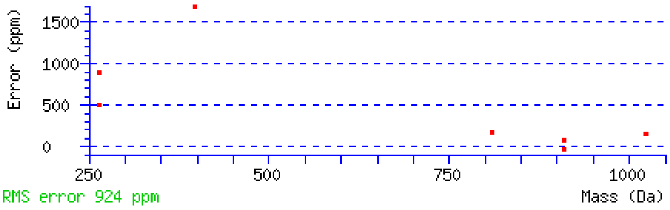
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1170.6093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0032
Matches : 8/84 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					**M**							**10**
2	***263.0844***	132.0458			245.0739	123.0406	**E**	1039.5790	520.2932	1021.5555	511.2814	1021.5685	511.2879	**9**
3	335.1186	168.0629			317.1080	159.0576	**A**	**909.5394**	455.2733	891.5158	446.2616			**8**
4	465.1712	233.0892	447.1476	224.0775	447.1607	224.0840	**Q**	837.5053	419.2563	819.4817	410.2445			**7**
5	579.2523	290.1298	561.2287	281.1180	561.2418	281.1245	**I**	707.4526	354.2299	689.4290	345.2182			**6**
6	693.3334	347.1703	675.3098	338.1586	675.3229	338.1651	**L**	593.3715	297.1894	575.3479	288.1776			**5**
7	***809.3704***	405.1888	791.3468	396.1771	791.3599	396.1836	**N**	479.2904	240.1488	461.2668	231.1371			**4**
8	***909.4359***	455.2216	891.4123	446.2098	891.4253	446.2163	**V**	363.2534	182.1303	345.2298	173.1186			**3**
9	***1023.5170***	512.2621	1005.4934	503.2503	1005.5064	503.2568	**L**	**263.1880**	132.0976	245.1644	123.0858			**2**
10							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MEAQILNVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G01990.1

Score	Mr(calc)	Delta	Sequence
29.6	1170.6093	0.0033	MEAQILNVLK
7.3	1170.6120	0.0007	MKIVHRDLK
4.1	1170.6140	-0.0014	SELKAELELK
3.8	1170.6093	0.0033	MQIPDSLKVK
3.6	1170.6120	0.0007	AHKKICGTIK
3.6	1170.6120	0.0007	ASKKLHACIK
3.6	1170.6140	-0.0014	ELEADKLTIK
3.6	1170.6140	-0.0014	IVQLSETEIK
3.6	1170.6093	0.0033	SCPVKVVEIK
3.6	1170.6140	-0.0014	SLSEQELLLK

AT1G02500.1

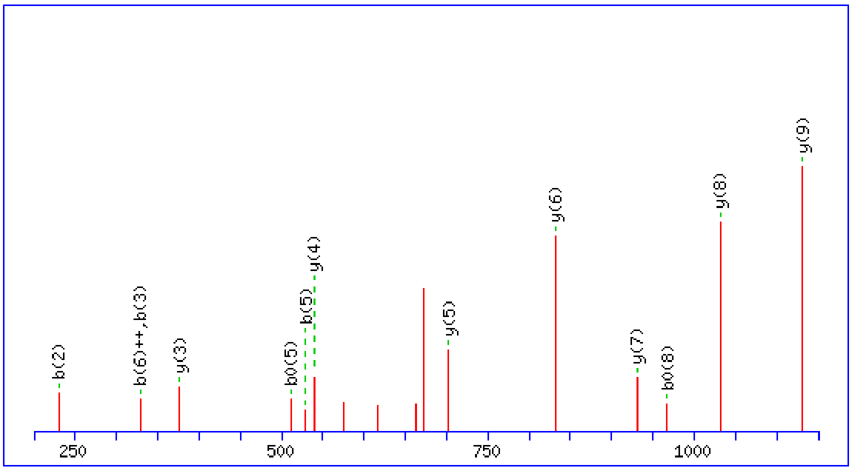
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVTVEYYNDK**
Found in **AT1G02500.1** in **TAIR_Arabidopsis**, Symbols: SAM-1, MAT1, SAM1 | SAM1 (S-adenosylmethionine synthetase 1); methionine adenosyltransferase | chr1:519037-520218 FORWARD

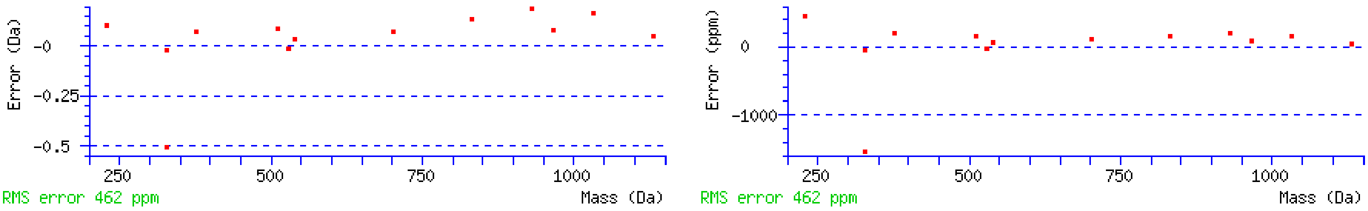
Match to Query 4983: 1358.636682 from(680.325617,2+) index(2565)
Title: Elution from: 26.315 to 26.315 scan no 3208 cid35.00 polarity:+
Data file D12h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1358.6354
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 3e-007
Matches : 13/116 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							11
2	**230.1135**	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1258.5950	629.8011	1241.5685	621.2879	1240.5844	620.7959	10
3	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	V	***1130.5364***	565.7719	1113.5099	557.2586	1112.5259	556.7666	9
4	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	T	***1031.4680***	516.2376	1014.4415	507.7244	1013.4575	507.2324	8
5	**529.2980**	265.1527	512.2715	256.6394	511.2875	256.1474	V	***930.4203***	465.7138	913.3938	457.2005	912.4098	456.7085	7
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	E	***831.3519***	416.1796	814.3254	407.6663	813.3414	407.1743	6
7	821.4040	411.2056	804.3774	402.6923	803.3934	402.2003	Y	***702.3093***	351.6583	685.2828	343.1450	684.2988	342.6530	5
8	984.4673	492.7373	967.4407	484.2240	966.4567	483.7320	Y	***539.2460***	270.1266	522.2195	261.6134	521.2354	261.1214	4
9	1098.5102	549.7587	1081.4837	541.2455	1080.4997	540.7535	N	***376.1827***	188.5950	359.1561	180.0817	358.1721	179.5897	3
10	1213.5372	607.2722	1196.5106	598.7589	1195.5266	598.2669	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of TQVTVEYYNDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G02500.1

Score	Mr(calc)	Delta	Sequence
68.5	1358.6354	0.0013	TQVTVEYYNDK
4.9	1358.6361	0.0006	ERVDREDMGPR

Mascot: http://www.matrixscience.com/

AT1G02560.1

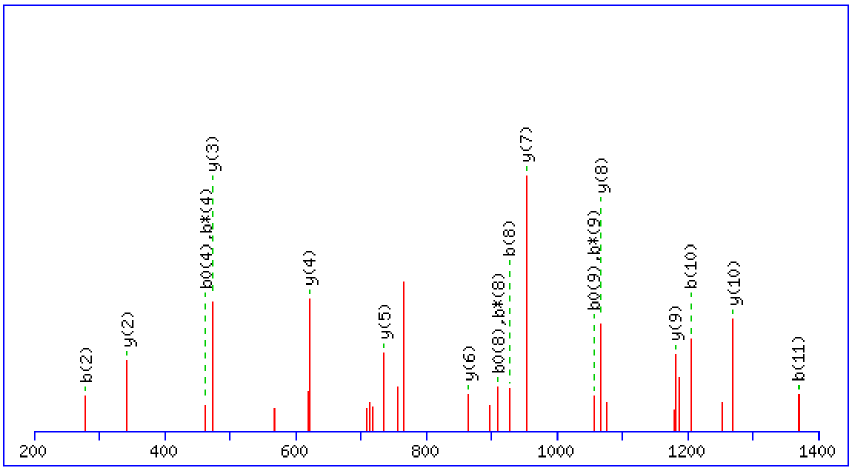
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQSIISQLFQYR**
Found in **AT1G02560.1** in **TAIR_Arabidopsis**, Symbols: NCLPP1, NCLPP5, CLPP5 | CLPP5 (NUCLEAR ENCODED CLP PROTEASE 1); endopeptidase Clp | chr1:538000-539805 FORWARD

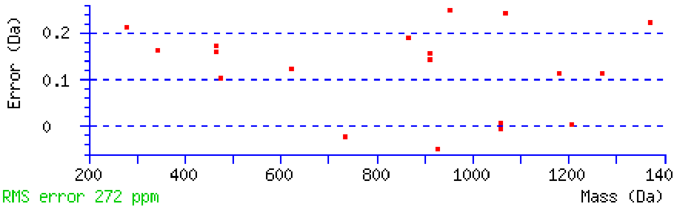
Match to Query 6818: 1546.753580 from(774.384066,2+) index(10657)
Title: Elution from: 102.636 to 102.636 scan no 15209 cid35.00 polarity:+
Data file D6h-2_1.mgf

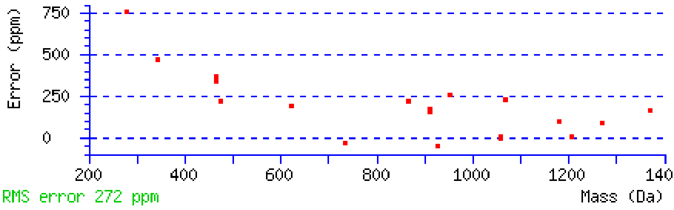
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1546.7504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 93 **Expect:** 4.1e-009
Matches : 19/114 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					F							12
2	**279.1254**	140.0663	261.1018	131.0545			Q	1399.6923	700.3498	1381.6687	691.3380	1381.6817	691.3445	11
3	367.1544	184.0809	349.1309	175.0691	349.1439	175.0756	S	***1269.6396***	635.3234	1251.6160	626.3117	1251.6291	626.3182	10
4	481.2355	241.1214	463.2120	232.1096	463.2250	232.1161	I	***1181.6106***	591.3089	1163.5870	582.2971	1163.6000	582.3036	9
5	595.3166	298.1620	577.2930	289.1502	577.3061	289.1567	I	***1067.5295***	534.2684	1049.5059	525.2566	1049.5189	525.2631	8
6	683.3457	342.1765	665.3221	333.1647	665.3351	333.1712	S	***953.4484***	477.2278	935.4248	468.2160	935.4378	468.2225	7
7	813.3983	407.2028	795.3748	398.1910	795.3878	398.1975	Q	***865.4193***	433.2133	847.3957	424.2015			6
8	**927.4794**	464.2434	909.4559	455.2316	909.4689	455.2381	L	***735.3667***	368.1870	717.3431	359.1752			5
9	1075.5449	538.2761	1057.5213	529.2643	1057.5343	529.2708	F	***621.2856***	311.1464	603.2620	302.1346			4
10	**1205.5975**	603.3024	1187.5740	594.2906	1187.5870	594.2971	Q	***473.2201***	237.1137	455.1965	228.1019			3
11	**1369.6579**	685.3326	1351.6343	676.3208	1351.6473	676.3273	Y	***343.1675***	172.0874	325.1439	163.0756			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FQSIISQLFQYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G02560.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.0	1546.7504	0.0032	FQSIISQLFQYR
27.1	1546.7516	0.0020	EMEPLQQALGKLR
10.0	1546.7538	-0.0002	GCGLTFPLPEALVR
4.7	1546.7561	-0.0025	NQIPWMILFPQK
3.4	1546.7516	0.0020	IVVMANQEGPTITR
3.4	1546.7560	-0.0024	YATLVKTWMFVR
2.6	1546.7516	0.0020	DRPAIAMIADAEKK
1.6	1546.7563	-0.0027	IDLGALEETLNSVR
0.7	1546.7563	-0.0027	LEEDLGSAKGEILR
0.5	1546.7542	-0.0007	VTSNRILMGEIHR

AT1G02730.1

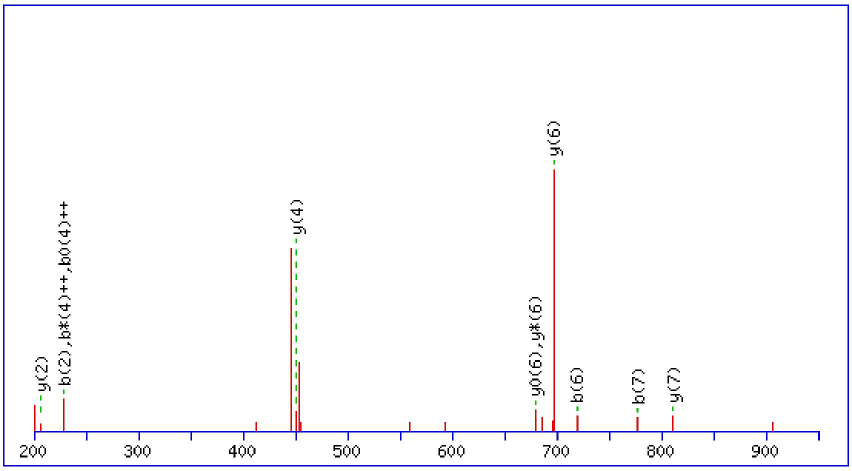
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIQDLQGK**
Found in **AT1G02730.1** in **TAIR_Arabidopsis**, Symbols: CSLD5, ATCSLD5 | ATCSLD5 (CELLULOSE SYNTHASE-LIKE D5); 1,4-beta-D-xylan synthase/ cellulose synthase | chr1:594697-598473 REVERSE

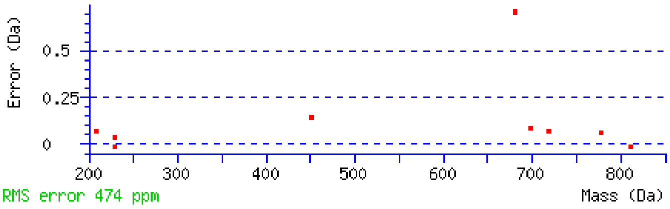
Match to Query 1712: 924.490540 from(463.252546,2+) index(1164)
Title: Elution from: 17.991 to 17.991 scan no 1638 cid35.00 polarity:+
Data file C7-1_3.mgf

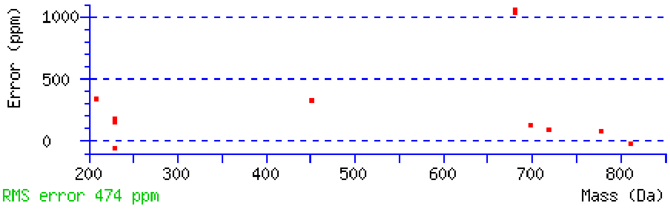
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 924.4906
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0053
Matches : 11/66 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							8
2	***229.1695***	115.0884					I	***811.4168***	406.2121	793.3933	397.2003	793.4063	397.2068	7
3	359.2221	180.1147	341.1985	171.1029			Q	***697.3357***	349.1715	679.3122	340.1597	679.3252	340.1662	6
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	D	567.2831	284.1452	549.2595	275.1334	549.2725	275.1399	5
5	589.3272	295.1672	571.3036	286.1554	571.3166	286.1620	L	***451.2591***	226.1332	433.2355	217.1214			4
6	***719.3798***	360.1936	701.3563	351.1818	701.3693	351.1883	Q	337.1780	169.0926	319.1544	160.0809			3
7	***777.3983***	389.2028	759.3748	380.1910	759.3878	380.1975	G	***207.1254***	104.0663	189.1018	95.0545			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LIQDLQGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	924.4907	-0.0001	IINEQLGK

AT1G02730.1

28.8	924.4906	-0.0001	LIQDLQGK
13.6	924.4907	-0.0001	LLITDPSR
11.3	924.4907	-0.0001	ILDLAQNK
10.0	924.4906	-0.0001	LLEDLVGR
7.8	924.4907	-0.0001	NQELLLGK
3.6	924.4907	-0.0001	KPAEDKVK
2.7	924.4906	-0.0001	LLLAVDDR
2.7	924.4907	-0.0001	LLPTSDLR
0.6	924.4907	-0.0001	ALELAVNGK

AT1G02780.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGFIIR**
Found in **AT1G02780.1** in **TAIR_Arabidopsis**, Symbols: EMB2386 | EMB2386 (EMBRYO DEFECTIVE 2386); structural constituent of ribosome | chr1:608120-609391 REVERSE

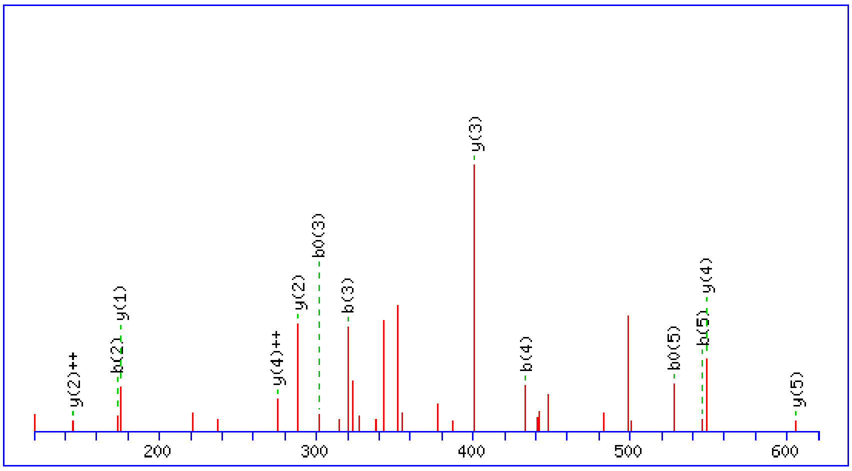
Match to Query 663: 719.396338 from(360.705445,2+) index(3975)
Title: Elution from: 38.274 to 38.274 scan no 5043 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 120 to 620 Da Full range

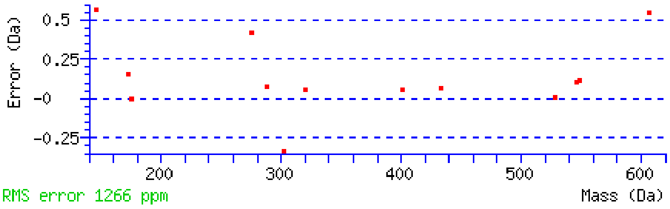
Label all possible matches ○ Label matches used for scoring ●

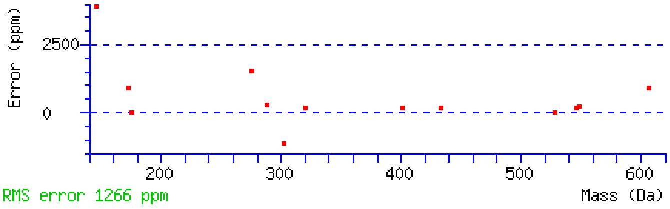
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 719.3966
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.001
Matches : 13/40 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	116.0342	58.5207	98.0237	49.5155	D					6
2	**173.0557**	87.0315	155.0451	78.0262	G	***605.3770***	303.1921	588.3504	294.6788	5
3	**320.1241**	160.5657	302.1135	151.5604	F	***548.3555***	274.6814	531.3289	266.1681	4
4	**433.2082**	217.1077	415.1976	208.1024	I	***401.2871***	201.1472	384.2605	192.6339	3
5	**546.2922**	273.6498	528.2817	264.6445	I	***288.2030***	144.6051	271.1765	136.0919	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of DGFIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.9	719.3966	-0.0003	DGFIIR
22.7	719.3966	-0.0003	GFDLLR
11.3	719.3966	-0.0003	DFLGLR

AT1G02780.1

7.6	719.3966	-0.0003	DAFVLR
6.8	719.3966	-0.0003	LGFDLR
4.7	719.3966	-0.0003	YPATLR
3.6	719.3966	-0.0003	TAIPYR
2.2	719.3966	-0.0003	FSPTLR
2.2	719.3966	-0.0003	GEVFIR
2.2	719.3966	-0.0003	GEVFLR

AT1G02920.1

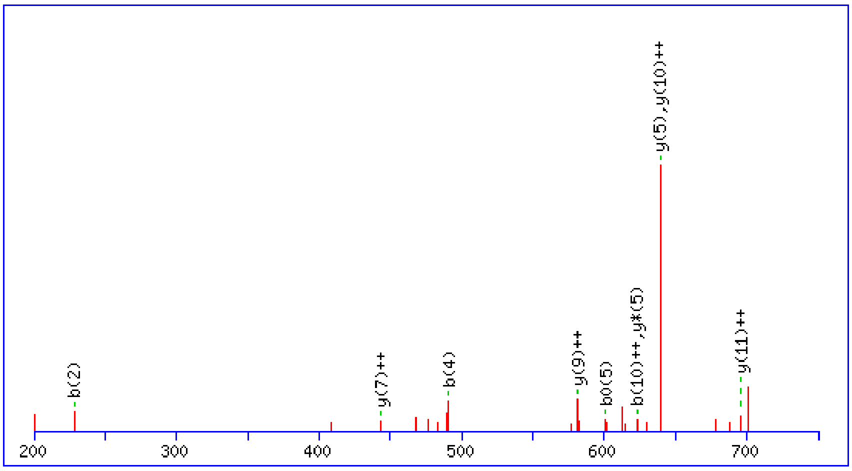
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLDFEFVHIELK**
Found in **AT1G02920.1** in **TAIR_Arabidopsis**, Symbols: GST11, ATGSTF8, GSTF7, ATGSTF7 | ATGSTF7 (GLUTATHIONE S-TRANSFERASE 11); glutathione transferase | chr1:658886-659705 REVERSE

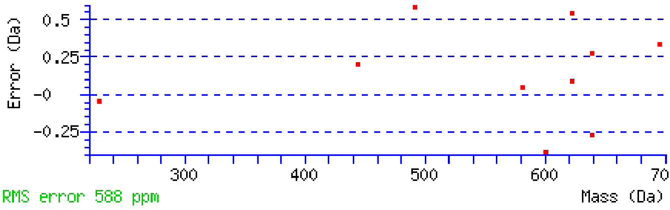
Match to Query 5836: 1502.776074 from(501.932634,3+) index(8977)
Title: Elution from: 85.595 to 85.595 scan no 12470 cid35.00 polarity:+
Data file D1d-1-2.mgf

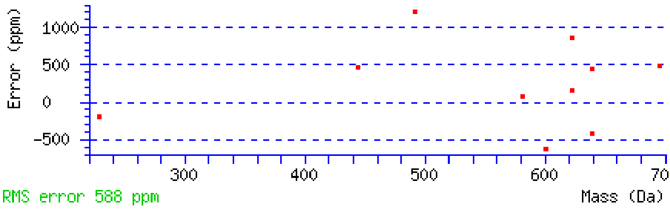
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1502.7769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.044
Matches : 10/124 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	228.1343	114.5708	211.1077	106.0575			L	1389.7413	695.3743	1372.7147	686.8610	1371.7307	686.3690	11
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	D	1276.6572	638.8322	1259.6307	630.3190	1258.6466	629.8270	10
4	490.2296	245.6185	473.2031	237.1052	472.2191	236.6132	F	1161.6303	581.3188	1144.6037	572.8055	1143.6197	572.3135	9
5	619.2722	310.1397	602.2457	301.6265	601.2617	301.1345	E	1014.5619	507.7846	997.5353	499.2713	996.5513	498.7793	8
6	766.3406	383.6740	749.3141	375.1607	748.3301	374.6687	F	885.5193	443.2633	868.4927	434.7500	867.5087	434.2580	7
7	865.4090	433.2082	848.3825	424.6949	847.3985	424.2029	V	738.4509	369.7291	721.4243	361.2158	720.4403	360.7238	6
8	1002.4680	501.7376	985.4414	493.2243	984.4574	492.7323	H	639.3824	320.1949	622.3559	311.6816	621.3719	311.1896	5
9	1115.5520	558.2796	1098.5255	549.7664	1097.5415	549.2744	I	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
10	1244.5946	622.8009	1227.5681	614.2877	1226.5840	613.7957	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	1357.6787	679.3430	1340.6521	670.8297	1339.6681	670.3377	L	260.1969	130.6021	243.1703	122.0888			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NLDFEFVHIELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G02920.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.2	1502.7769	-0.0008	NLDFEFVHIELK
6.0	1502.7803	-0.0042	IVMKEVWGADVEK
6.0	1502.7801	-0.0040	LNIGAESSSSNRLR
5.8	1502.7742	0.0018	KPDPHLWDRSPR
5.6	1502.7778	-0.0017	LMPFTVMPPWIR
2.1	1502.7762	-0.0002	LGGAAITCKNELEK
1.9	1502.7769	-0.0008	NLVDWAIPYLGDK
1.9	1502.7769	-0.0008	EIFVTKFATEYR

AT1G02930.1

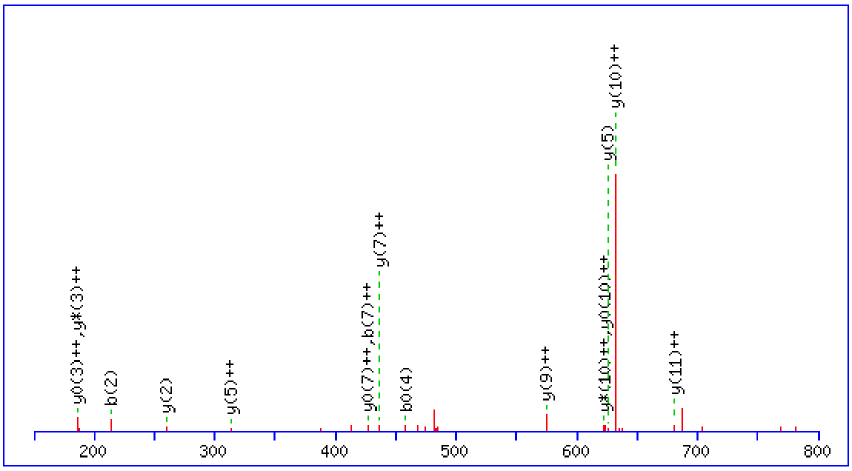
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVDFEFVHVELK**
Found in **AT1G02930.1** in **TAIR_Arabidopsis**, Symbols: GST1, ERD11, ATGSTF3, GSTF6, ATGSTF6 | ATGSTF6 (EARLY RESPONSIVE TO DEHYDRATION 11); glutathione transferase | chr1:661363-662191 REVERSE

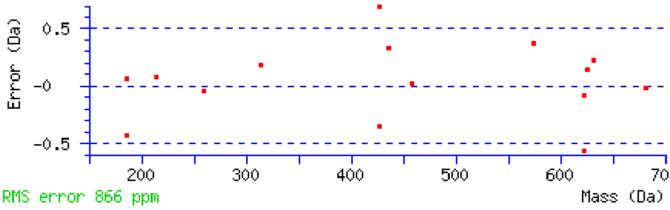
Match to Query 6049: 1474.746573 from(492.589467,3+) index(8057)
Title: Elution from: 71.956 to 71.956 scan no 10673 cid35.00 polarity:+
Data file D6h-1_2.mgf

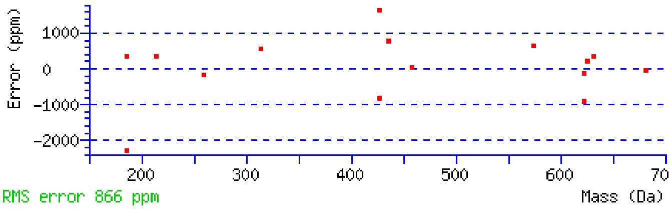
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1474.7456
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0072
Matches : 15/124 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	214.1186	107.5629	197.0921	99.0497			V	1361.7100	681.3586	1344.6834	672.8454	1343.6994	672.3533	11
3	329.1456	165.0764	312.1190	156.5631	311.1350	156.0711	D	1262.6416	631.8244	1245.6150	623.3111	1244.6310	622.8191	10
4	476.2140	238.6106	459.1874	230.0974	458.2034	229.6053	F	1147.6146	574.3109	1130.5881	565.7977	1129.6041	565.3057	9
5	605.2566	303.1319	588.2300	294.6186	587.2460	294.1266	E	1000.5462	500.7767	983.5197	492.2635	982.5356	491.7715	8
6	752.3250	376.6661	735.2984	368.1529	734.3144	367.6608	F	871.5036	436.2554	854.4771	427.7422	853.4930	427.2502	7
7	851.3934	426.2003	834.3668	417.6871	833.3828	417.1951	V	724.4352	362.7212	707.4087	354.2080	706.4246	353.7160	6
8	988.4523	494.7298	971.4258	486.2165	970.4417	485.7245	H	**625.3668**	313.1870	608.3402	304.6738	607.3562	304.1817	5
9	1087.5207	544.2640	1070.4942	535.7507	1069.5102	535.2587	V	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
10	1216.5633	608.7853	1199.5368	600.2720	1198.5527	599.7800	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	1329.6474	665.3273	1312.6208	656.8141	1311.6368	656.3220	L	**260.1969**	130.6021	243.1703	122.0888			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NVDFEFVHVELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G02930.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.3	1474.7456	0.0009	NVDFEFVHVELK
5.5	1474.7450	0.0016	DVLMEEGGDKVRK
5.5	1474.7463	0.0003	MRILQWGEDRR
4.4	1474.7450	0.0016	LTMRTEAQDSVPK
3.9	1474.7450	0.0016	MGAVDVLTGSAGEIR
2.9	1474.7449	0.0017	AAMVAEEAAEKSLR
1.7	1474.7490	-0.0024	DPKPTSMWSSIVK

AT1G03020.1

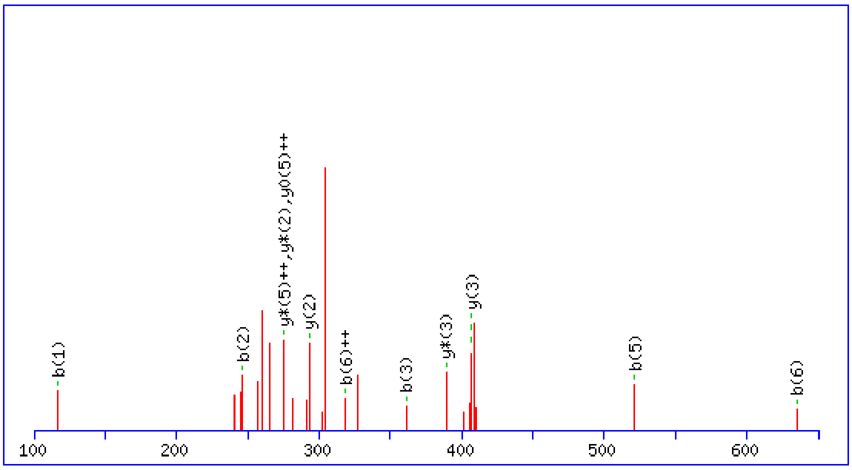
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQLASLLR**
Found in **AT1G03020.1** in **TAIR_Arabidopsis**, Symbols: | glutaredoxin family protein | chr1:698207-698515 REVERSE

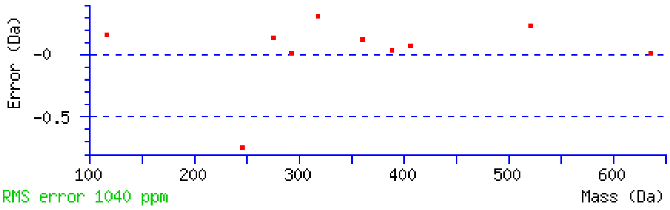
Match to Query 1805: 926.495682 from(309.839170,3+) index(3304)
Title: Elution from: 32.216 to 32.216 scan no 4084 cid35.00 polarity:+
Data file D12h-3_2.mgf

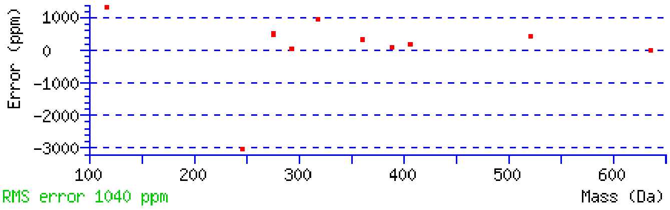
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 926.4960
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.036
Matches : 12/70 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***117.0443***	59.0258	99.0207	50.0140			N							8
2	***247.0969***	124.0521	229.0733	115.0403			Q	811.4662	406.2368	793.4427	397.2250	793.4557	397.2315	7
3	***361.1780***	181.0926	343.1544	172.0809			L	681.4136	341.2104	663.3900	332.1986	663.4030	332.2052	6
4	433.2122	217.1097	415.1886	208.0979			A	567.3325	284.1699	549.3089	275.1581	549.3219	275.1646	5
5	***521.2412***	261.1243	503.2176	252.1125	503.2307	252.1190	S	495.2984	248.1528	477.2748	239.1410	477.2878	239.1475	4
6	***635.3223***	318.1648	617.2987	309.1530	617.3118	309.1595	L	**407.2693**	204.1383	389.2457	195.1265			3
7	749.4034	375.2054	731.3798	366.1936	731.3929	366.2001	L	**293.1882**	147.0977	275.1646	138.0859			2
8							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NQLASLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.1	926.4960	-0.0003	NQLASLLR
16.3	926.4960	-0.0003	RLLEDLR

AT1G03020.1

15.6	926.4960	-0.0003	AGLNSAIIR
12.4	926.4982	-0.0025	ALSGWLLR
9.4	926.4982	-0.0025	LWSQLLR
8.4	926.4960	-0.0003	LREEVIR
7.4	926.4933	0.0024	TSTLSALPK
6.8	926.4960	-0.0003	GTQLLNLR
6.8	926.4982	-0.0025	EAWKLLR
6.8	926.4960	-0.0003	IDREILR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPLVPASVVFDLGGR**
Found in **AT1G03220.1** in **TAIR_Arabidopsis**, Symbols: | extracellular dermal glycoprotein, putative / EDGP, putative | chr1:787143-788444 FORWARD

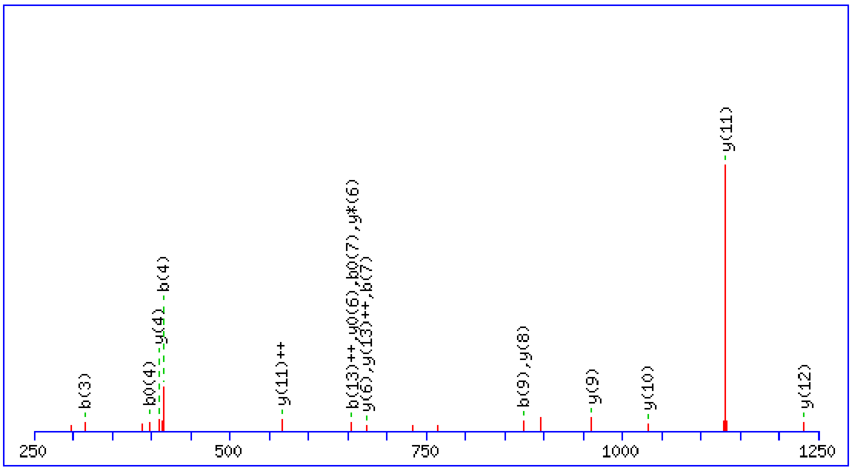
Match to Query 6784: 1544.787674 from(773.401113,2+) index(9587)
Title: Elution from: 86.709 to 86.709 scan no 13135 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1250 Da Full range

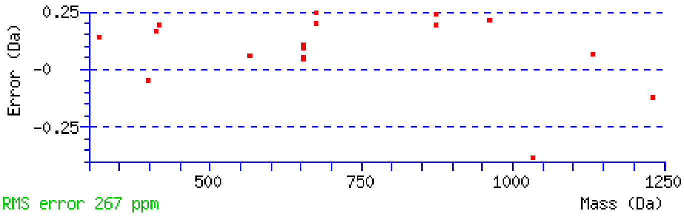
Label all possible matches ○ Label matches used for scoring ●

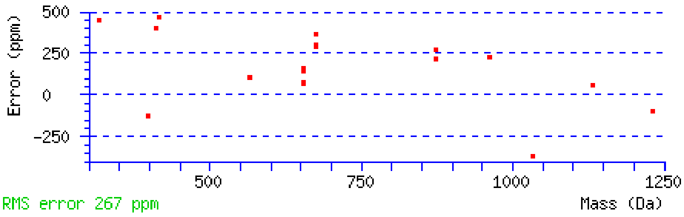
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1544.7923
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 9.3e-006
Matches : 18/132 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							15
2	201.1018	101.0545	183.0912	92.0492	P	1443.7549	722.3811	1425.7313	713.3693	1425.7443	713.3758	14
3	**315.1829**	158.0951	297.1723	149.0898	L	1345.7051	673.3562	1327.6815	664.3444	1327.6945	664.3509	13
4	**415.2483**	208.1278	397.2378	199.1225	V	***1231.6240***	616.3156	1213.6004	607.3038	1213.6134	607.3103	12
5	513.2981	257.1527	495.2876	248.1474	P	***1131.5585***	566.2829	1113.5349	557.2711	1113.5480	557.2776	11
6	585.3323	293.1698	567.3217	284.1645	A	***1033.5087***	517.2580	1015.4851	508.2462	1015.4982	508.2527	10
7	**673.3613**	337.1843	655.3508	328.1790	S	***961.4746***	481.2409	943.4510	472.2291	943.4640	472.2356	9
8	773.4268	387.2170	755.4162	378.2118	V	***873.4455***	437.2264	855.4219	428.2146	855.4349	428.2211	8
9	**873.4922**	437.2498	855.4817	428.2445	V	773.3801	387.1937	755.3565	378.1819	755.3695	378.1884	7
10	1021.5577	511.2825	1003.5471	502.2772	F	***673.3146***	337.1609	655.2910	328.1492	655.3041	328.1557	6
11	1137.5817	569.2945	1119.5711	560.2892	D	525.2492	263.1282	507.2256	254.1164	507.2386	254.1229	5
12	1251.6628	626.3350	1233.6522	617.3297	L	***409.2252***	205.1162	391.2016	196.1044			4
13	1309.6813	655.3443	1291.6707	646.3390	G	295.1441	148.0757	277.1205	139.0639			3
14	1367.6998	684.3535	1349.6892	675.3482	G	237.1256	119.0664	219.1020	110.0546			2
15					R	179.1071	90.0572	161.0835	81.0454			1





AT1G03220.1

NCBI **BLAST** search of TPLVPASVVFDLGGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.4	1544.7923	-0.0046	TPLVPASVVFDLGGR
10.0	1544.7880	-0.0003	AQKMHRLPLSVAR
5.0	1544.7923	-0.0046	LLPSNVPEGSFIVR
2.4	1544.7883	-0.0006	ESPPMIIMPVKKK

AT1G03475.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLQDGNVFEK**
Found in **AT1G03475.1** in **TAIR_Arabidopsis**, Symbols: HEMF1, ATCPO-I, LIN2 | LIN2 (LESION INITIATION 2); coproporphyrinogen oxidase | chr1:869458-871176 REVERSE

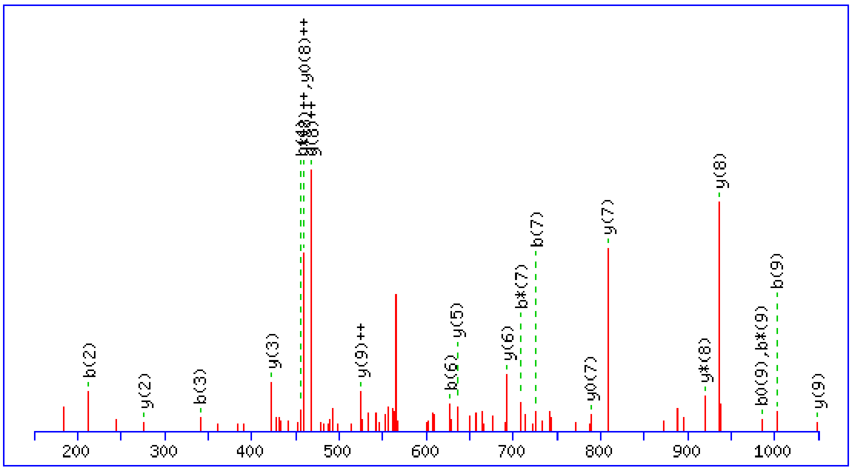
Match to Query 3507: 1147.584486 from(574.799519,2+) index(3242)
Title: Elution from: 34.022 to 34.022 scan no 4111 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1050 Da Full range

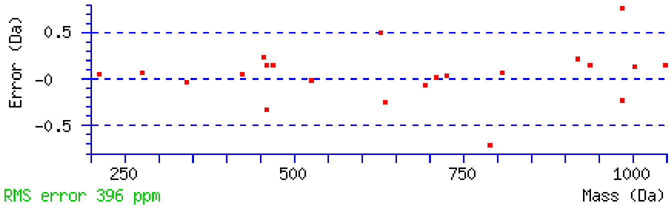
Label all possible matches ○ Label matches used for scoring ●

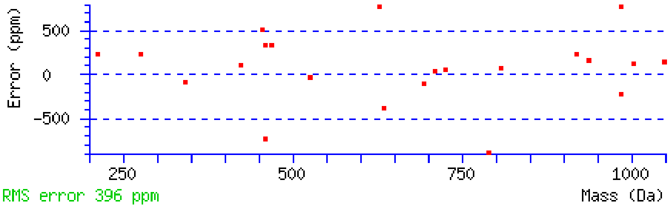
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1147.5873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 4.1e-005
Matches : 22/96 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**10**
2	***213.1598***	107.0835					**L**	***1049.5262***	525.2667	1032.4997	516.7535	1031.5156	516.2615	**9**
3	***341.2183***	171.1128	324.1918	162.5995			**Q**	***936.4421***	468.7247	919.4156	460.2114	918.4316	459.7194	**8**
4	***456.2453***	228.6263	439.2187	220.1130	438.2347	219.6210	**D**	***808.3836***	404.6954	791.3570	396.1821	790.3730	395.6901	**7**
5	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	**G**	***693.3566***	347.1819	676.3301	338.6687	675.3461	338.1767	**6**
6	***627.3097***	314.1585	610.2831	305.6452	609.2991	305.1532	**N**	***636.3352***	318.6712	619.3086	310.1579	618.3246	309.6659	**5**
7	***726.3781***	363.6927	709.3515	355.1794	708.3675	354.6874	**V**	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	**4**
8	873.4465	437.2269	856.4199	428.7136	855.4359	428.2216	**F**	***423.2238***	212.1155	406.1973	203.6023	405.2132	203.1103	**3**
9	***1002.4891***	501.7482	985.4625	493.2349	984.4785	492.7429	**E**	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
10							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VLQDGNVFEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G03475.1

Score	Mr(calc)	Delta	Sequence
50.6	1147.5873	-0.0029	VLQDGNVFEK

Mascot: http://www.matrixscience.com/

AT1G03600.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

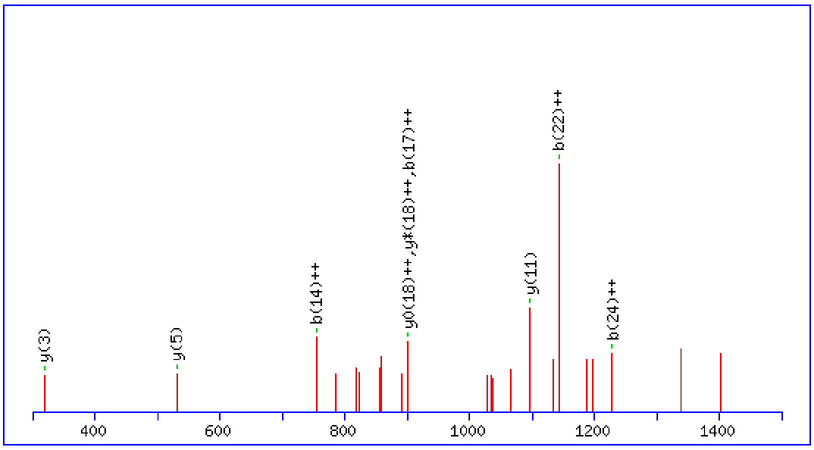
MS/MS Fragmentation of **DIYSALNAVSGHYVSFGPTAPIPAK**
Found in **AT1G03600.1** in **TAIR_Arabidopsis**, Symbols: | photosystem II family protein | chr1:898915-899439 FORWARD

Match to Query 10313: 2603.228754 from(868.750194,3+) index(9913)
Title: Elution from: 93.536 to 93.536 scan no 14004 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, [Plot from] [300] to [1500] Da [Full range]

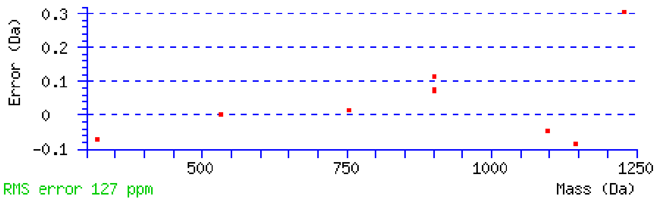
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

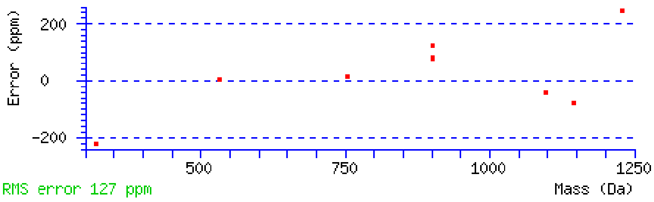


Monoisotopic mass of neutral peptide Mr(calc): 2603.2259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.011
Matches : 9/264 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							25
2	231.1124	116.0598			213.1018	107.0545	I	2488.2092	1244.6082	2470.1856	1235.5964	2470.1986	1235.6029	24
3	395.1727	198.0900			377.1622	189.0847	Y	2374.1281	1187.5677	2356.1045	1178.5559	2356.1175	1178.5624	23
4	483.2018	242.1045			465.1912	233.0992	S	2210.0677	1105.5375	2192.0441	1096.5257	2192.0571	1096.5322	22
5	555.2359	278.1216			537.2254	269.1163	A	2122.0386	1061.5230	2104.0150	1052.5112	2104.0281	1052.5177	21
6	669.3170	335.1622			651.3065	326.1569	L	2050.0045	1025.5059	2031.9809	1016.4941	2031.9939	1016.5006	20
7	785.3540	393.1807	767.3304	384.1689	767.3435	384.1754	N	1935.9234	968.4653	1917.8998	959.4535	1917.9128	959.4600	19
8	857.3882	429.1977	839.3646	420.1859	839.3776	420.1924	A	1819.8864	910.4468	1801.8628	901.4350	1801.8758	901.4415	18
9	957.4536	479.2304	939.4300	470.2187	939.4431	470.2252	V	1747.8522	874.4298	1729.8286	865.4180	1729.8417	865.4245	17
10	1045.4827	523.2450	1027.4591	514.2332	1027.4721	514.2397	S	1647.7868	824.3970	1629.7632	815.3852	1629.7762	815.3917	16
11	1103.5012	552.2542	1085.4776	543.2424	1085.4906	543.2489	G	1559.7577	780.3825	1541.7341	771.3707	1541.7472	771.3772	15
12	1243.5512	622.2792	1225.5276	613.2674	1225.5406	613.2740	H	1501.7392	751.3732	1483.7156	742.3615	1483.7287	742.3680	14
13	1407.6116	704.3094	1389.5880	695.2976	1389.6010	695.3041	Y	1361.6892	681.3482	1343.6656	672.3364	1343.6786	672.3430	13
14	1507.6770	***754.3421***	1489.6534	745.3304	1489.6664	745.3369	V	1197.6288	599.3181	1179.6053	590.3063	1179.6183	590.3128	12
15	1595.7061	798.3567	1577.6825	789.3449	1577.6955	789.3514	S	***1097.5634***	549.2853	1079.5398	540.2735	1079.5528	540.2801	11
16	1743.7715	872.3894	1725.7479	863.3776	1725.7610	863.3841	F	1009.5343	505.2708	991.5107	496.2590	991.5238	496.2655	10
17	1801.7900	***901.3987***	1783.7664	892.3869	1783.7795	892.3934	G	861.4689	431.2381	843.4453	422.2263	843.4583	422.2328	9
18	1899.8398	950.4236	1881.8162	941.4118	1881.8293	941.4183	P	803.4504	402.2288	785.4268	393.2170	785.4398	393.2235	8
19	2001.8845	1001.4459	1983.8610	992.4341	1983.8740	992.4406	T	705.4006	353.2039	687.3770	344.1921	687.3900	344.1986	7
20	2073.9187	1037.4630	2055.8951	1028.4512	2055.9081	1028.4577	A	603.3559	302.1816	585.3323	293.1698			6
21	2171.9685	1086.4879	2153.9449	1077.4761	2153.9579	1077.4826	P	***531.3217***	266.1645	513.2981	257.1527			5
22	2286.0496	***1143.5284***	2268.0260	1134.5166	2268.0390	1134.5231	I	433.2719	217.1396	415.2483	208.1278			4
23	2384.0994	1192.5533	2366.0758	1183.5415	2366.0888	1183.5480	P	***319.1908***	160.0990	301.1672	151.0873			3
24	2456.1335	***1228.5704***	2438.1099	1219.5586	2438.1230	1219.5651	A	221.1410	111.0741	203.1174	102.0624			2
25							K	149.1069	75.0571	131.0833	66.0453			1

AT1G03600.1





NCBI **BLAST** search of DIYSALNAVSGHYVSFGPTAPIPAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.5	2603.2259	0.0029	DIYSALNAVSGHYVSFGPTAPIPAK
13.8	2603.2333	-0.0045	APLDLITVLDVSGSMDGVKMELMK
8.0	2603.2323	-0.0036	EMERLQKPIYNSLRQAAEVHR
7.2	2603.2346	-0.0058	IAQGAAKGLLYLHEGCDPHILHR
3.8	2603.2305	-0.0017	SIGGILGKWSMLVLVGDMHRDMR
1.5	2603.2333	-0.0045	APLDLITVLDVSGSMDGVKMELMK

Mascot: http://www.matrixscience.com/

AT1G03680.1

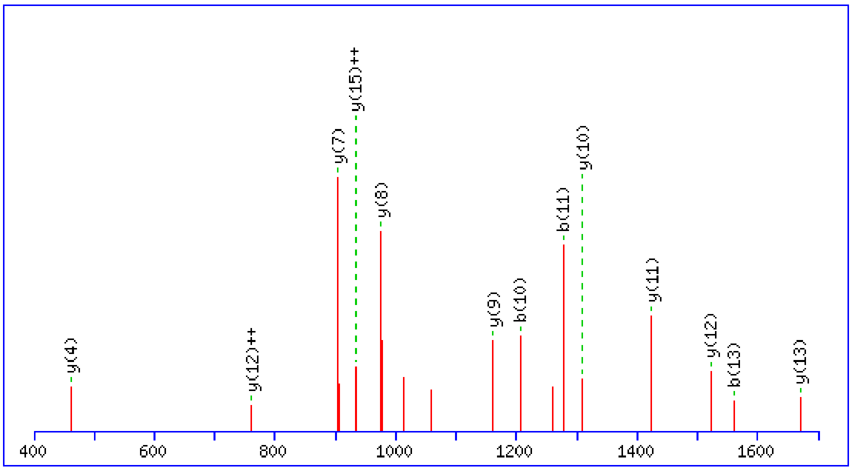
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADEPVFVDFWAPWCGPCK**
Found in **AT1G03680.1** in **TAIR_Arabidopsis**, Symbols: ATM1, TRX-M1, ATHM1 | ATHM1 (Arabidopsis thioredoxin M-type 1); thiol-disulfide exchange intermediate | chr1:916989-917864 REVERSE

Match to Query 9813: 2179.952354 from(1090.983453,2+) index(10805)
Title: Elution from: 110.381 to 110.381 scan no 15798 cid35.00 polarity:+
Data file C7-3_2.mgf

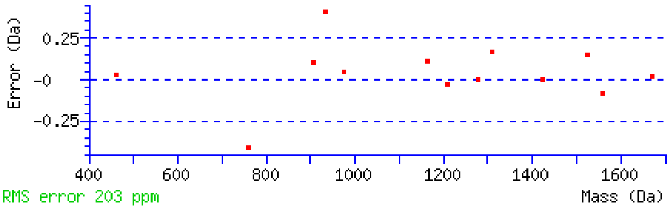
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

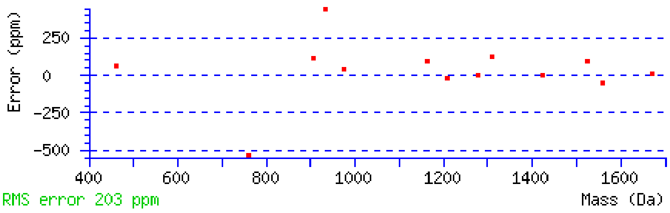


Monoisotopic mass of neutral peptide Mr(calc): 2179.9496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.9e-007
Matches : 13/148 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							18
2	187.0713	94.0393	169.0608	85.0340	D	2109.9197	1055.4635	2092.8932	1046.9502	2091.9092	1046.4582	17
3	316.1139	158.5606	298.1034	149.5553	E	1994.8928	997.9500	1977.8662	989.4368	1976.8822	988.9448	16
4	413.1667	207.0870	395.1561	198.0817	P	1865.8502	933.4287	1848.8236	924.9155	1847.8396	924.4235	15
5	512.2351	256.6212	494.2245	247.6159	V	1768.7974	884.9024	1751.7709	876.3891	1750.7869	875.8971	14
6	659.3035	330.1554	641.2930	321.1501	F	***1669.7290***	835.3681	1652.7025	826.8549	1651.7185	826.3629	13
7	758.3719	379.6896	740.3614	370.6843	V	***1522.6606***	761.8339	1505.6341	753.3207	1504.6500	752.8287	12
8	873.3989	437.2031	855.3883	428.1978	D	***1423.5922***	712.2997	1406.5656	703.7865	1405.5816	703.2945	11
9	1020.4673	510.7373	1002.4567	501.7320	F	***1308.5652***	654.7863	1291.5387	646.2730			10
10	**1206.5466**	603.7769	1188.5360	594.7717	W	***1161.4968***	581.2521	1144.4703	572.7388			9
11	**1277.5837**	639.2955	1259.5732	630.2902	A	***975.4175***	488.2124	958.3910	479.6991			8
12	1374.6365	687.8219	1356.6259	678.8166	P	***904.3804***	452.6938	887.3539	444.1806			7
13	**1560.7158**	780.8615	1542.7052	771.8563	W	807.3276	404.1675	790.3011	395.6542			6
14	1720.7464	860.8769	1702.7359	851.8716	C	621.2483	311.1278	604.2218	302.6145			5
15	1777.7679	889.3876	1759.7573	880.3823	G	***461.2177***	231.1125	444.1911	222.5992			4
16	1874.8207	937.9140	1856.8101	928.9087	P	404.1962	202.6017	387.1697	194.0885			3
17	2034.8513	1017.9293	2016.8408	1008.9240	C	307.1435	154.0754	290.1169	145.5621			2
18					K	147.1128	74.0600	130.0863	65.5468			1

AT1G03680.1





NCBI **BLAST** search of ADEPVFVDFWAPWCGPCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.1	2179.9496	0.0028	ADEPVFVDFWAPWCGPCK

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYSMDDLLSVSNPVR**
Found in **AT1G03870.1** in **TAIR_Arabidopsis**, Symbols: FLA9 | FLA9 | chr1:982624-983367 REVERSE

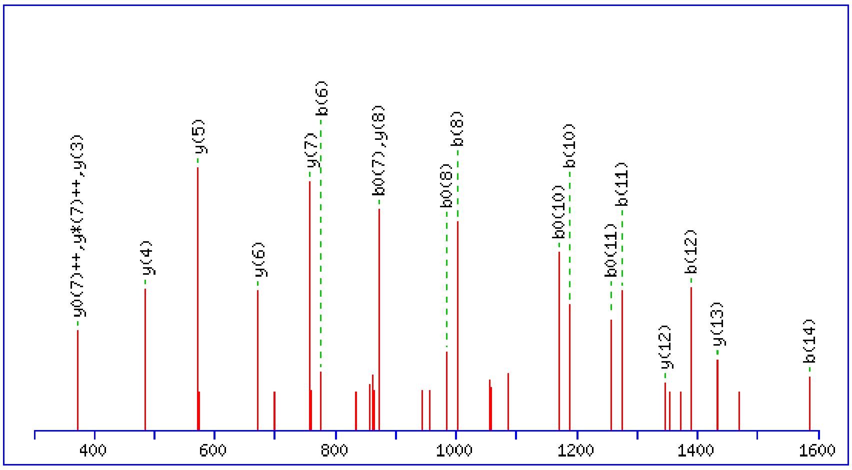
Match to Query 8694: 1757.827458 from(879.921005,2+) index(9508)
Title: Elution from: 85.028 to 85.028 scan no 12795 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1600 Da Full range

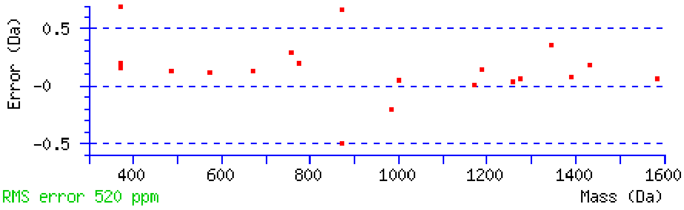
Label all possible matches ○ Label matches used for scoring ●

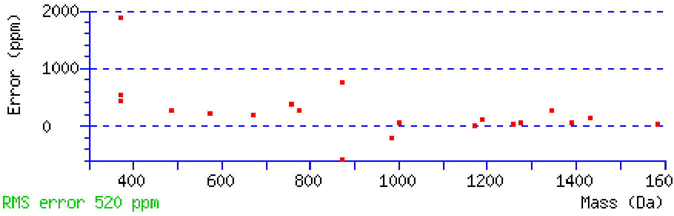
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1757.8294
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 1.2e-007
Matches : 20/134 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					**Y**							**15**
2	327.1339	164.0706					**Y**	1595.7734	798.3903	1578.7468	789.8771	1577.7628	789.3850	**14**
3	414.1660	207.5866			396.1554	198.5813	**S**	***1432.7101***	716.8587	1415.6835	708.3454	1414.6995	707.8534	**13**
4	545.2064	273.1069			527.1959	264.1016	**M**	***1345.6780***	673.3427	1328.6515	664.8294	1327.6675	664.3374	**12**
5	660.2334	330.6203			642.2228	321.6151	**D**	1214.6375	607.8224	1197.6110	599.3091	1196.6270	598.8171	**11**
6	***775.2603***	388.1338			757.2498	379.1285	**D**	1099.6106	550.3089	1082.5840	541.7957	1081.6000	541.3037	**10**
7	888.3444	444.6758			870.3338	435.6706	**L**	984.5837	492.7955	967.5571	484.2822	966.5731	483.7902	**9**
8	***1001.4285***	501.2179			983.4179	492.2126	**L**	***871.4996***	436.2534	854.4730	427.7402	853.4890	427.2482	**8**
9	1088.4605	544.7339			1070.4499	535.7286	**S**	***758.4155***	379.7114	741.3890	371.1981	740.4050	370.7061	**7**
10	***1187.5289***	594.2681			1169.5183	585.2628	**V**	***671.3835***	336.1954	654.3570	327.6821	653.3729	327.1901	**6**
11	***1274.5609***	637.7841			1256.5504	628.7788	**S**	***572.3151***	286.6612	555.2885	278.1479	554.3045	277.6559	**5**
12	***1388.6039***	694.8056	1371.5773	686.2923	1370.5933	685.8003	**N**	***485.2831***	243.1452	468.2565	234.6319			**4**
13	1485.6566	743.3319	1468.6301	734.8187	1467.6461	734.3267	**P**	***371.2401***	186.1237	354.2136	177.6104			**3**
14	***1584.7250***	792.8662	1567.6985	784.3529	1566.7145	783.8609	**V**	274.1874	137.5973	257.1608	129.0840			**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of YYSMDDLLSVSNPVR

AT1G03870.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.4	1757.8294	-0.0020	YYSMDDLLSVSNPVR
1.9	1757.8254	0.0021	ENASMGYTSKLLSDAR

AT1G03990.1

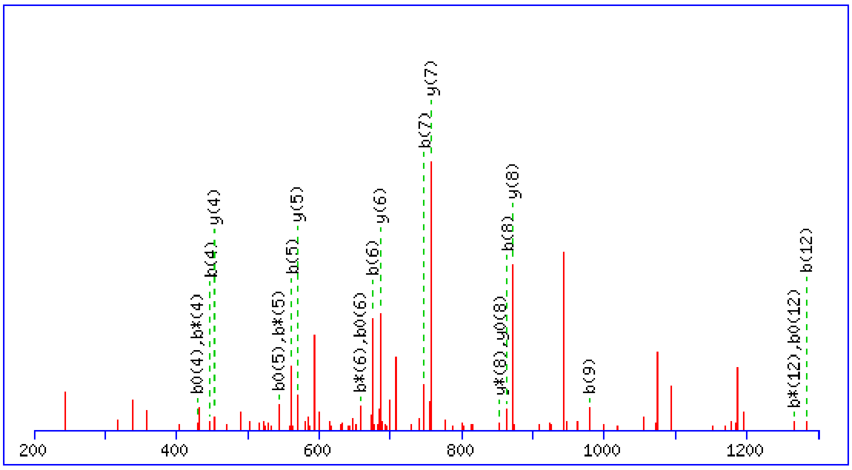
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEKLILADNDANK**
Found in **AT1G03990.1** in **TAIR_Arabidopsis**, Symbols: | alcohol oxidase-related | chr1:1024846-1027615 FORWARD

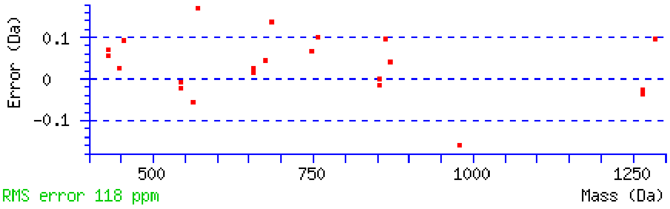
Match to Query 5867: 1430.697286 from(716.355919,2+) index(8297)
Title: Elution from: 73.071 to 73.071 scan no 10850 cid35.00 polarity:+
Data file C7-3_1.mgf

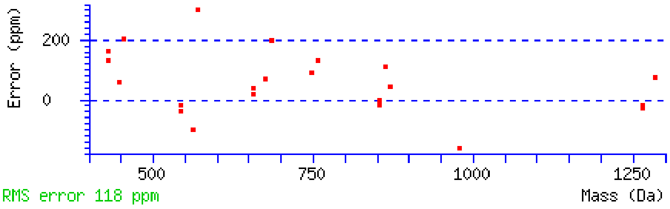
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1430.6960
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.01
Matches : 22/132 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							13
2	203.0811	102.0442			185.0705	93.0389	E	1359.6691	680.3382	1341.6455	671.3264	1341.6585	671.3329	12
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	K	1229.6295	615.3184	1211.6059	606.3066	1211.6189	606.3131	11
4	***447.2512***	224.1292	429.2276	215.1174	429.2406	215.1239	L	1099.5404	550.2738	1081.5168	541.2621	1081.5299	541.2686	10
5	***561.3323***	281.1698	543.3087	272.1580	543.3217	272.1645	I	985.4593	493.2333	967.4357	484.2215	967.4488	484.2280	9
6	***675.4134***	338.2103	657.3898	329.1985	657.4028	329.2050	L	**871.3782**	436.1927	853.3546	427.1810	853.3677	427.1875	8
7	***747.4475***	374.2274	729.4239	365.2156	729.4370	365.2221	A	**757.2971**	379.1522	739.2735	370.1404	739.2866	370.1469	7
8	***863.4715***	432.2394	845.4479	423.2276	845.4609	423.2341	D	**685.2630**	343.1351	667.2394	334.1233	667.2524	334.1298	6
9	***979.5085***	490.2579	961.4849	481.2461	961.4979	481.2526	N	**569.2390**	285.1231	551.2154	276.1113	551.2284	276.1179	5
10	1095.5325	548.2699	1077.5089	539.2581	1077.5219	539.2646	D	**453.2020**	227.1046	435.1784	218.0928	435.1914	218.0994	4
11	1167.5666	584.2870	1149.5431	575.2752	1149.5561	575.2817	A	337.1780	169.0926	319.1544	160.0809			3
12	***1283.6036***	642.3055	1265.5800	633.2937	1265.5931	633.3002	N	265.1439	133.0756	247.1203	124.0638			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AEKLILADNDANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G03990.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	1430.6960	0.0013	AEKLILADNDANK
0.0	1430.6982	-0.0009	KALQLPDYPDQK

AT1G04090.1

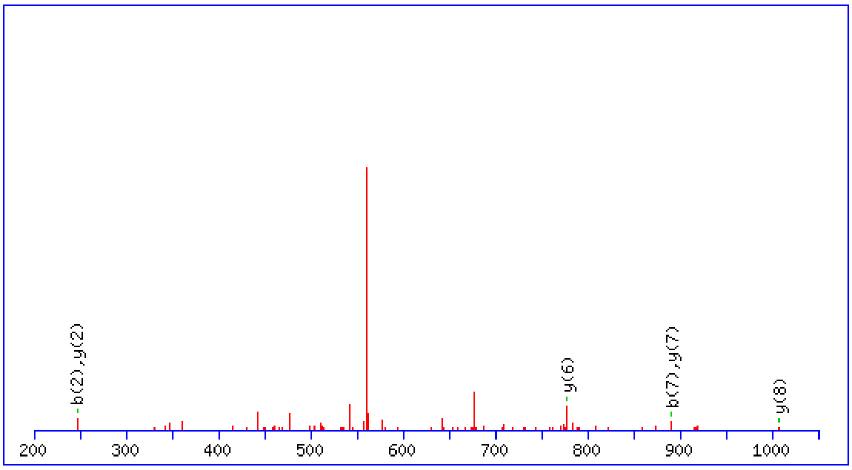
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KNISFYKPK**
Found in **AT1G04090.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G18490.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G43950.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04350.1); similar to hypothetical pr

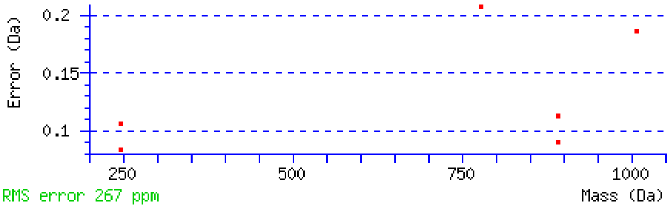
Match to Query 3940: 1136.601326 from(569.307939,2+) index(5500)
Title: Elution from: 48.777 to 48.777 scan no 6807 cid35.00 polarity:+
Data file 0-1_1.mgf

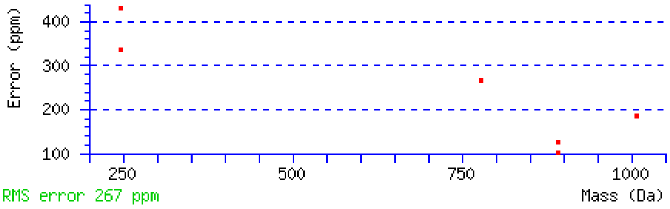
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1136.6004
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.0098
Matches : 6/80 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							9
2	**247.1333**	124.0703	229.1097	115.0585			N	***1007.5187***	504.2630	989.4951	495.2512	989.5081	495.2577	8
3	361.2144	181.1108	343.1908	172.0990			I	***891.4817***	446.2445	873.4581	437.2327	873.4711	437.2392	7
4	449.2435	225.1254	431.2199	216.1136	431.2329	216.1201	S	***777.4006***	389.2039	759.3770	380.1921	759.3900	380.1986	6
5	597.3089	299.1581	579.2853	290.1463	579.2984	290.1528	F	689.3715	345.1894	671.3479	336.1776			5
6	761.3693	381.1883	743.3457	372.1765	743.3587	372.1830	Y	541.3061	271.1567	523.2825	262.1449			4
7	**891.4583**	446.2328	873.4347	437.2210	873.4477	437.2275	K	377.2457	189.1265	359.2221	180.1147			3
8	989.5081	495.2577	971.4845	486.2459	971.4975	486.2524	P	***247.1567***	124.0820	229.1331	115.0702			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KNISFYKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G04090.1

Score	Mr(calc)	Delta	Sequence
25.7	1136.6004	0.0009	KNISFYKPK
12.4	1136.6004	0.0009	AGKWEVPLPK
7.6	1136.6004	0.0009	FPDPLPILGR
5.5	1136.5982	0.0032	TVVGDVAPIPR
3.3	1136.6004	0.0009	HWIVSEIIK
3.1	1136.5982	0.0031	VKELGELAHK
1.4	1136.6004	0.0009	AVERVIFYK
1.2	1136.6009	0.0005	VKNLRTFSR
0.9	1136.6004	0.0009	KALPIYTYR

AT1G04300.1

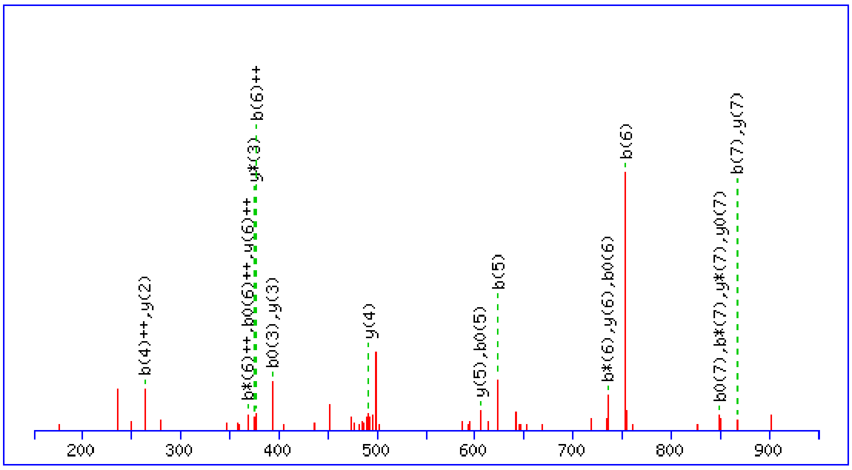
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FMELPKLK**
Found in **AT1G04300.1** in **TAIR_Arabidopsis**, Symbols: | similar to meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] (TAIR:AT5G43560.1); similar to meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Ar

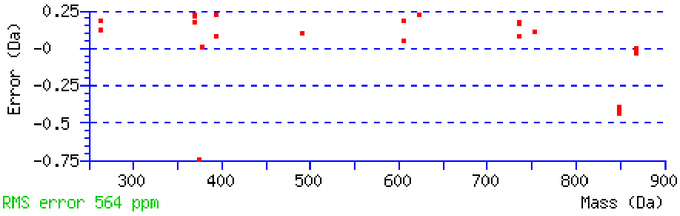
Match to Query 2817: 1014.541144 from(508.277848,2+) index(6541)
Title: Elution from: 56.531 to 56.531 scan no 8268 cid35.00 polarity:+
Data file D1d-3_1.mgf

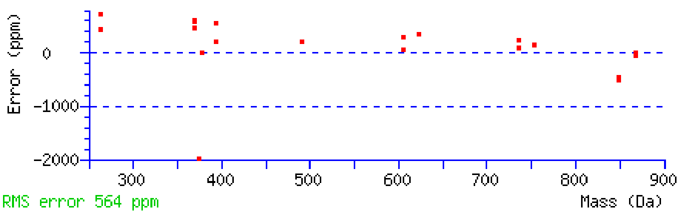
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1014.5432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0004
Matches : 23/60 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							8
2	281.1102	141.0588					M	***867.4851***	434.2462	849.4615	425.2344	849.4745	425.2409	7
3	411.1499	206.0786			393.1393	197.0733	E	***735.4475***	368.2274	717.4239	359.2156	717.4370	359.2221	6
4	525.2310	**263.1191**			507.2204	254.1138	L	***605.4079***	303.2076	587.3843	294.1958			5
5	**623.2808**	312.1440			605.2702	303.1387	P	***491.3268***	246.1670	473.3032	237.1552			4
6	**753.3698**	**377.1885**	735.3462	368.1767	735.3592	368.1833	K	***393.2770***	197.1421	375.2534	188.1303			3
7	**867.4509**	434.2291	849.4273	425.2173	849.4403	425.2238	L	***263.1880***	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FMELPKLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G04300.1

41.8	1014.5432	-0.0021	FMELPKLK
29.9	1014.5410	0.0002	KMLEVQLK
24.7	1014.5403	0.0009	RTFLSHIK
20.3	1014.5403	0.0008	LFNNPRIK
19.8	1014.5410	0.0002	LSGKVLEMK
19.5	1014.5432	-0.0021	LLYCVPLK
14.5	1014.5410	0.0002	KVMEKEIK
11.4	1014.5410	0.0002	KMQDLLIK
10.8	1014.5403	0.0009	FLPKANGVR
10.5	1014.5410	0.0002	LMKIEDKK

Mascot: http://www.matrixscience.com/

AT1G04410.1

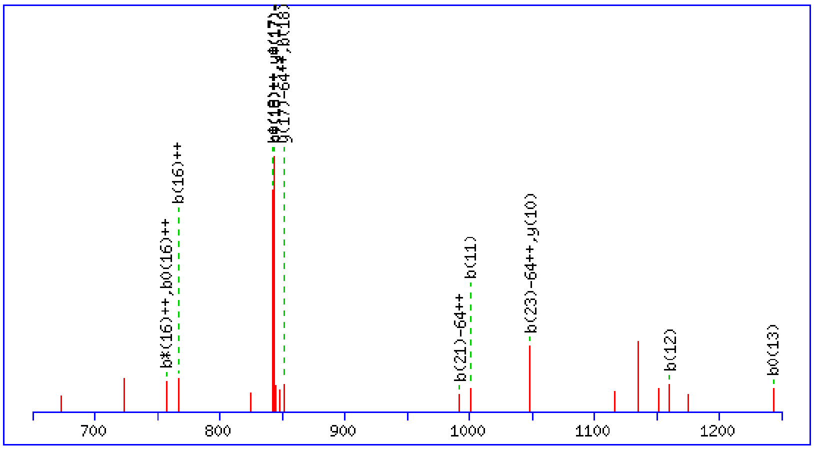
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVVATTDAVEGCTGVNVAVMVGGFPR**
Found in **AT1G04410.1** in **TAIR_Arabidopsis**, Symbols: | malate dehydrogenase, cytosolic, putative | chr1:1189417-1191266 REVERSE

Match to Query 10296: 2578.252845 from(860.424891,3+) index(4693)
Title: Elution from: 43.192 to 43.192 scan no 5910 cid35.00 polarity:+
Data file C7-1_3.mgf

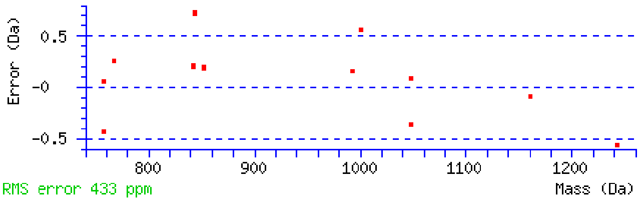
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

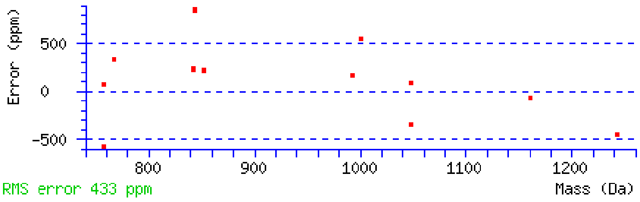


Monoisotopic mass of neutral peptide Mr(calc): 2578.2520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M20 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.022
Matches : 15/372 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							26
2	157.0972	79.0522					V	2458.2395	1229.6234	2441.2129	1221.1101	2440.2289	1220.6181	25
3	256.1656	128.5864					V	2359.1711	1180.0892	2342.1445	1171.5759	2341.1605	1171.0839	24
4	327.2027	164.1050					A	2260.1027	1130.5550	2243.0761	1122.0417	2242.0921	1121.5497	23
5	428.2504	214.6288			410.2398	205.6235	T	2189.0655	1095.0364	2172.0390	1086.5231	2171.0550	1086.0311	22
6	529.2980	265.1527			511.2875	256.1474	T	2088.0179	1044.5126	2070.9913	1035.9993	2070.0073	1035.5073	21
7	644.3250	322.6661			626.3144	313.6608	D	1986.9702	993.9887	1969.9436	985.4755	1968.9596	984.9835	20
8	715.3621	358.1847			697.3515	349.1794	A	1871.9432	936.4753	1854.9167	927.9620	1853.9327	927.4700	19
9	814.4305	407.7189			796.4199	398.7136	V	1800.9061	900.9567	1783.8796	892.4434	1782.8956	891.9514	18
10	943.4731	472.2402			925.4625	463.2349	E	1701.8377	851.4225	1684.8112	842.9092	1683.8272	842.4172	17
11	***1000.4946***	500.7509			982.4840	491.7456	G	1572.7951	786.9012	1555.7686	778.3879	1554.7846	777.8959	16
12	***1160.5252***	580.7662			1142.5147	571.7610	C	1515.7737	758.3905	1498.7471	749.8772	1497.7631	749.3852	15
13	1261.5729	631.2901			1243.5623	622.2848	T	1355.7430	678.3751	1338.7165	669.8619	1337.7324	669.3699	14
14	1318.5944	659.8008			1300.5838	650.7955	G	1254.6953	627.8513	1237.6688	619.3380			13
15	1417.6628	709.3350			1399.6522	700.3297	V	1197.6739	599.3406	1180.6473	590.8273			12
16	1531.7057	***766.3565***	1514.6792	757.8432	1513.6951	757.3512	N	1098.6055	549.8064	1081.5789	541.2931			11
17	1630.7741	815.8907	1613.7476	807.3774	1612.7636	806.8854	V	984.5625	492.7849	967.5360	484.2716			10
18	1701.8112	***851.4093***	1684.7847	842.8960	1683.8007	842.4040	A	885.4941	443.2507	868.4676	434.7374			9
19	1800.8796	900.9435	1783.8531	892.4302	1782.8691	891.9382	V	814.4570	407.7321	797.4305	399.2189			8
20	1883.9168	942.4620	1866.8902	933.9487	1865.9062	933.4567	M	715.3886	358.1979	698.3620	349.6847			7
21	1982.9852	***991.9962***	1965.9586	983.4829	1964.9746	982.9909	V	632.3515	316.6794	615.3249	308.1661			6
22	2040.0066	1020.5070	2022.9801	1011.9937	2021.9961	1011.5017	G	533.2831	267.1452	516.2565	258.6319			5
23	2097.0281	***1049.0177***	2080.0016	1040.5044	2079.0175	1040.0124	G	476.2616	238.6344	459.2350	230.1212			4
24	2244.0965	1122.5519	2227.0700	1114.0386	2226.0859	1113.5466	F	419.2401	210.1237	402.2136	201.6104			3

25	2341.1493	1171.0783	2324.1227	1162.5650	2323.1387	1162.0730	**P**	272.1717	136.5895	255.1452	128.0762			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GVVATTDAVEGCTGVNVAVMVGGFPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.0	2578.2520	0.0008	GVVATTDAVEGCTGVNVAVMVGGFPR
2.1	2578.2499	0.0029	QALSRFGGVPQMQNIGQDFGSWR
1.2	2578.2558	-0.0030	SPHGSMDANGVPATAPAAVGGGGTLSRK

Mascot: http://www.matrixscience.com/

AT1G04420.1

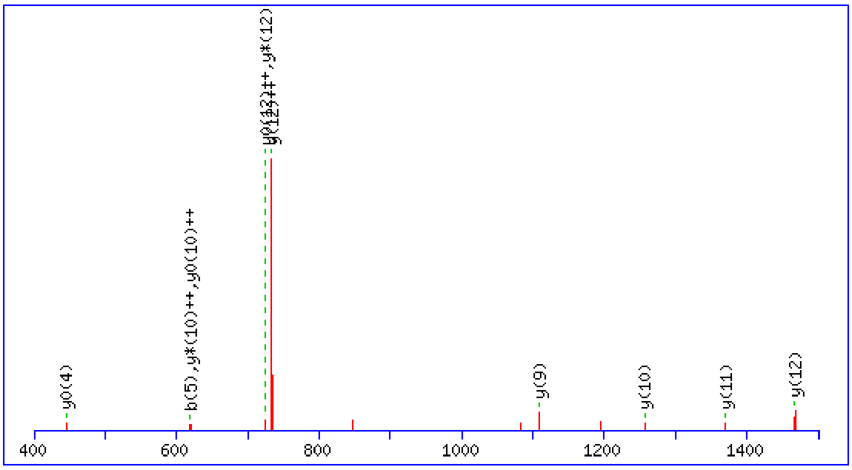
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVPLFGDFYYETSK**
Found in **AT1G04420.1** in **TAIR_Arabidopsis**, Symbols: | aldo/keto reductase family protein | chr1:1191633-1193698 FORWARD

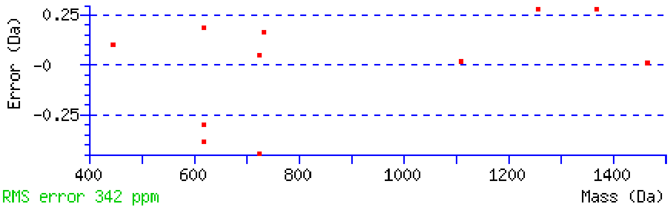
Match to Query 8593: 1727.808112 from(864.911332,2+) index(10099)
Title: Elution from: 91.710 to 91.710 scan no 13884 cid35.00 polarity:+
Data file D1d-3_1.mgf

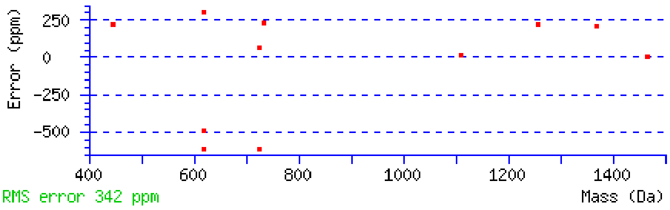
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1727.8083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.027
Matches : 11/116 fragment ions using 14 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389			Y							14
2	263.1390	132.0731			V	1565.7522	783.3798	1548.7257	774.8665	1547.7417	774.3745	13
3	360.1918	180.5995			P	***1466.6838***	733.8456	1449.6573	725.3323	1448.6733	724.8403	12
4	473.2758	237.1416			L	***1369.6311***	685.3192	1352.6045	676.8059	1351.6205	676.3139	11
5	620.3443	310.6758			F	***1256.5470***	628.7771	1239.5204	620.2639	1238.5364	619.7719	10
6	677.3657	339.1865			G	***1109.4786***	555.2429	1092.4520	546.7297	1091.4680	546.2376	9
7	792.3927	396.7000	774.3821	387.6947	D	1052.4571	526.7322	1035.4306	518.2189	1034.4466	517.7269	8
8	939.4611	470.2342	921.4505	461.2289	F	937.4302	469.2187	920.4036	460.7055	919.4196	460.2134	7
9	1102.5244	551.7658	1084.5138	542.7606	Y	790.3618	395.6845	773.3352	387.1712	772.3512	386.6792	6
10	1265.5877	633.2975	1247.5772	624.2922	Y	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	5
11	1394.6303	697.8188	1376.6198	688.8135	E	464.2351	232.6212	447.2086	224.1079	446.2245	223.6159	4
12	1495.6780	748.3426	1477.6674	739.3374	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
13	1582.7100	791.8587	1564.6995	782.8534	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YVPLFGDFYYETSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G04420.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.2	1727.8083	-0.0002	YVPLFGDFYYETSK
9.8	1727.8036	0.0045	ATMEDAHAAILDLDDK
9.8	1727.8121	-0.0040	RNNDHSMNANSIISR
4.3	1727.8110	-0.0029	DMIPILNKMDSEYK

AT1G04430.1

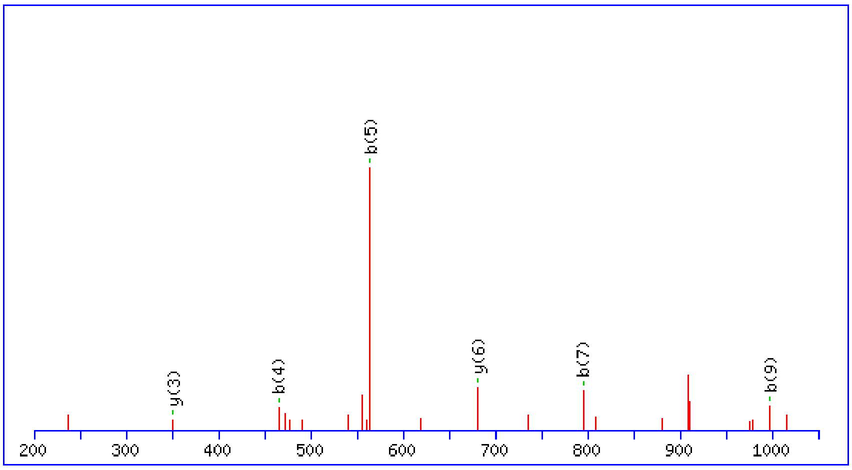
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKQSVVESIK**
Found in **AT1G04430.1** in **TAIR_Arabidopsis**, Symbols: | dehydration-responsive protein-related | chr1:1198859-1201300 FORWARD

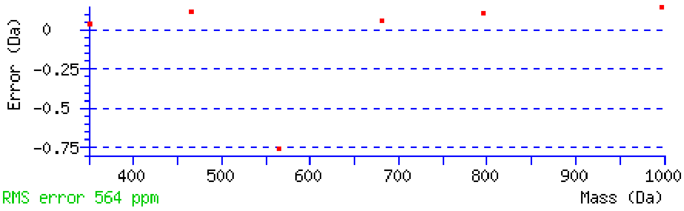
Match to Query 3629: 1144.574276 from(573.294414,2+) index(1335)
Title: Elution from: 19.310 to 19.310 scan no 1834 cid35.00 polarity:+
Data file C7-1_3.mgf

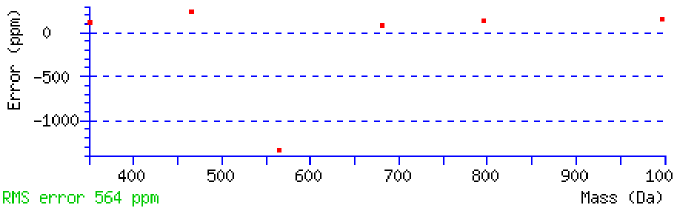
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.5750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.011
Matches : 6/102 fragment ions using 8 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0313	59.0193			99.0207	50.0140	D							10
2	247.1203	124.0638	229.0967	115.0520	229.1097	115.0585	K	1029.5583	515.2828	1011.5347	506.2710	1011.5477	506.2775	9
3	377.1729	189.0901	359.1494	180.0783	359.1624	180.0848	Q	899.4693	450.2383	881.4457	441.2265	881.4587	441.2330	8
4	***465.2020***	233.1046	447.1784	224.0928	447.1914	224.0994	S	769.4166	385.2120	751.3930	376.2002	751.4061	376.2067	7
5	***565.2674***	283.1374	547.2439	274.1256	547.2569	274.1321	V	**681.3876**	341.1974	663.3640	332.1856	663.3770	332.1921	6
6	665.3329	333.1701	647.3093	324.1583	647.3223	324.1648	V	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	5
7	***795.3725***	398.1899	777.3489	389.1781	777.3620	389.1846	E	481.2567	241.1320	463.2331	232.1202	463.2461	232.1267	4
8	883.4016	442.2044	865.3780	433.1926	865.3910	433.1991	S	**351.2170**	176.1122	333.1935	167.1004	333.2065	167.1069	3
9	***997.4827***	499.2450	979.4591	490.2332	979.4721	490.2397	I	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DKQSVVESIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G04430.1

29.2	1144.5750	-0.0007	DKQSVVESIK
19.6	1144.5773	-0.0030	KPSPTFELSK
19.6	1144.5730	0.0013	MSLSHLLRR
14.6	1144.5777	-0.0034	ARAEEKLANK
12.4	1144.5750	-0.0007	TQKSLDEIAK
10.7	1144.5750	-0.0007	QSELESALKK
10.7	1144.5777	-0.0034	GKDGQLSVLGR
10.0	1144.5750	-0.0007	QLETTNVSLK
9.0	1144.5777	-0.0034	GKLEGRGVEGK
8.6	1144.5772	-0.0030	LGIQPYEVSK

AT1G04480.1

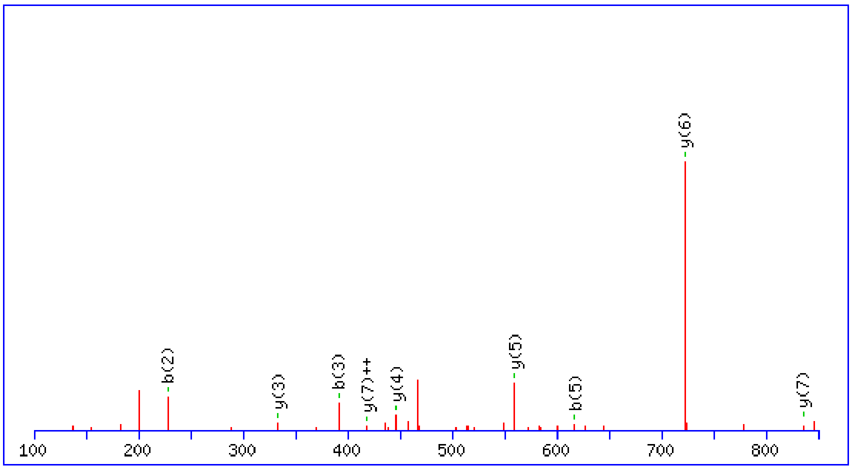
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLYIISVK**
Found in **AT1G04480.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L23 (RPL23A) | chr1:1216109-1217256 FORWARD

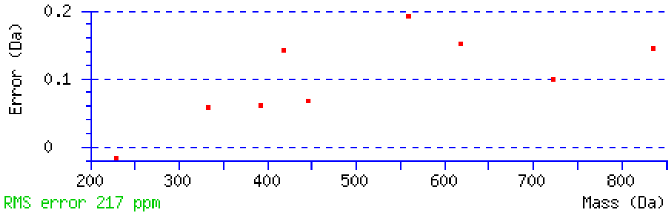
Match to Query 2208: 948.564186 from(475.289369,2+) index(5867)
Title: Elution from: 50.928 to 50.928 scan no 7334 cid35.00 polarity:+
Data file D1d-3_1.mgf

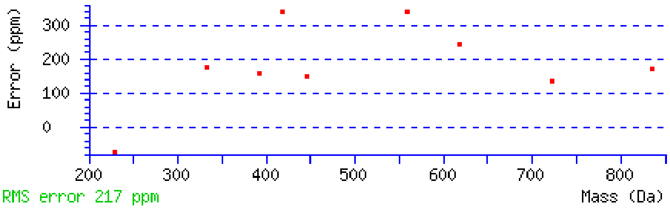
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 948.5644
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0031
Matches : 9/70 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	**228.1343**	114.5708	211.1077	106.0575			L	***835.5288***	418.2680	818.5022	409.7547	817.5182	409.2627	7
3	**391.1976**	196.1024	374.1710	187.5892			Y	***722.4447***	361.7260	705.4182	353.2127	704.4341	352.7207	6
4	504.2817	252.6445	487.2551	244.1312			I	***559.3814***	280.1943	542.3548	271.6811	541.3708	271.1890	5
5	**617.3657**	309.1865	600.3392	300.6732			I	***446.2973***	223.6523	429.2708	215.1390	428.2867	214.6470	4
6	704.3978	352.7025	687.3712	344.1892	686.3872	343.6972	S	***333.2132***	167.1103	316.1867	158.5970	315.2027	158.1050	3
7	803.4662	402.2367	786.4396	393.7234	785.4556	393.2314	V	246.1812	123.5942	229.1547	115.0810			2
8							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NLYIISVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.8	948.5644	-0.0002	NLYIISVK

AT1G04620.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KIVEMYNK**
Found in **AT1G04620.1** in **TAIR_Arabidopsis**, Symbols: | coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family | chr1:1282868-1286491 REVERSE

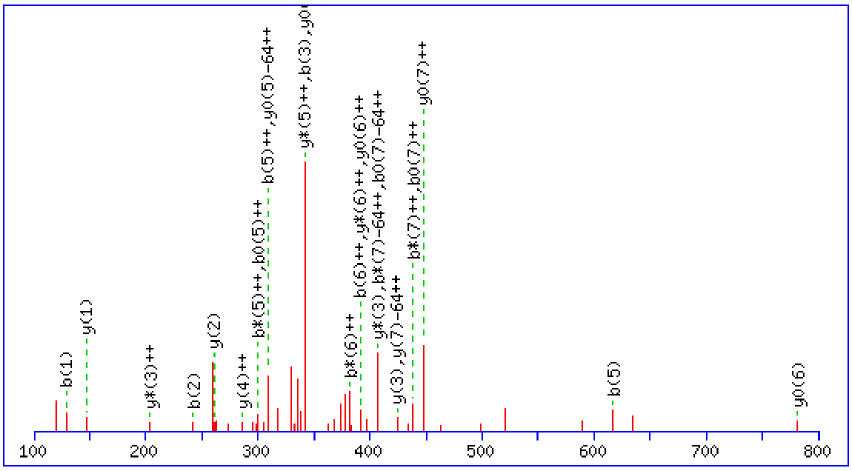
Match to Query 2720: 1039.534440 from(347.518756,3+) index(2125)
Title: Elution from: 23.926 to 23.926 scan no 2702 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

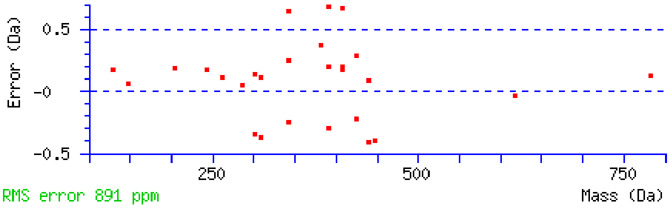
Label all possible matches ○ Label matches used for scoring ●

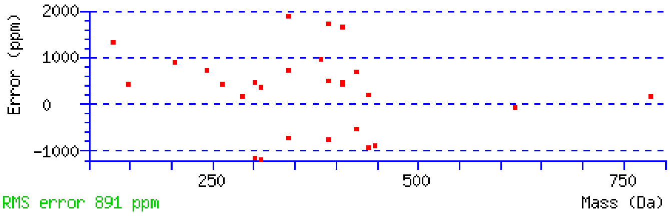
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1039.5372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 19 **Expect:** 0.035
Matches : 28/110 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.1022***	65.0548	112.0757	56.5415			K							8
2	***242.1863***	121.5968	225.1598	113.0835			I	912.4495	456.7284	895.4230	448.2151	894.4390	447.7231	7
3	***341.2547***	171.1310	324.2282	162.6177			V	799.3655	400.1864	782.3389	391.6731	781.3549	391.1811	6
4	470.2973	235.6523	453.2708	227.1390	452.2867	226.6470	E	700.2971	350.6522	683.2705	342.1389	682.2865	341.6469	5
5	***617.3327***	**309.1700**	600.3062	300.6567	599.3221	300.1647	M	571.2545	286.1309	554.2279	277.6176			4
6	780.3960	**390.7017**	763.3695	382.1884	762.3855	381.6964	Y	***424.2191***	212.6132	407.1925	204.0999			3
7	894.4390	**447.7231**	877.4124	439.2098	876.4284	438.7178	N	***261.1557***	131.0815	244.1292	122.5682			2
8							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KIVEMYNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G04620.1

19.0	1039.5372	-0.0027	KIVEMYNK
17.8	1039.5372	-0.0027	KSAMEAIFK
17.6	1039.5338	0.0006	FKDENFIK
14.6	1039.5338	0.0006	STFPSLNFK
7.9	1039.5338	0.0006	YIFDKNQL
7.1	1039.5372	-0.0028	SALSYLCVK
5.8	1039.5338	0.0006	FDLQNYLK
2.8	1039.5372	-0.0028	FQLEKTMK
2.2	1039.5338	0.0006	NELKDFFK
1.5	1039.5372	-0.0028	MSSVTQLFK

AT1G04690.1

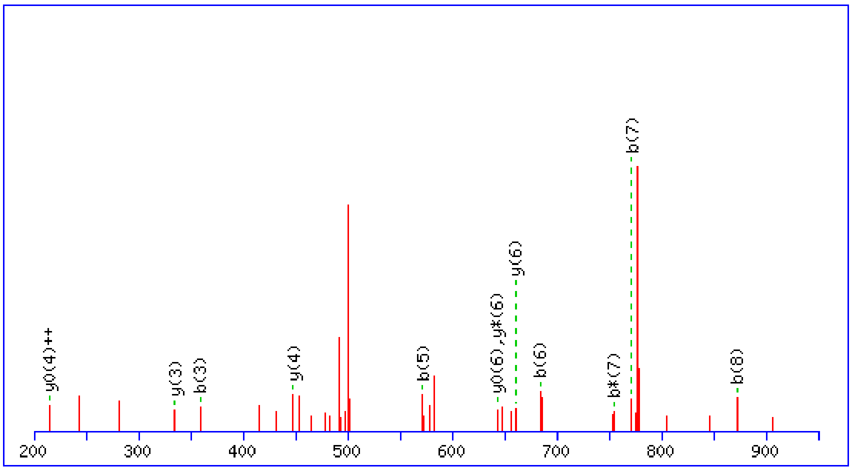
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RSDIVISTK**
Found in **AT1G04690.1** in **TAIR_Arabidopsis**, Symbols: KV-BETA1, KAB1 | KAB1 (POTASSIUM CHANNEL BETA SUBUNIT); potassium channel | chr1:1313661-1315419 FORWARD

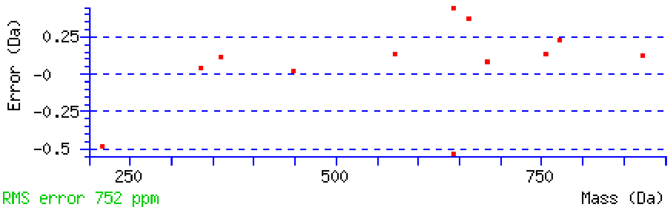
Match to Query 2653: 1017.582502 from(509.798527,2+) index(791)
Title: Elution from: 13.685 to 13.685 scan no 1146 cid35.00 polarity:+
Data file D12h-1_2.mgf

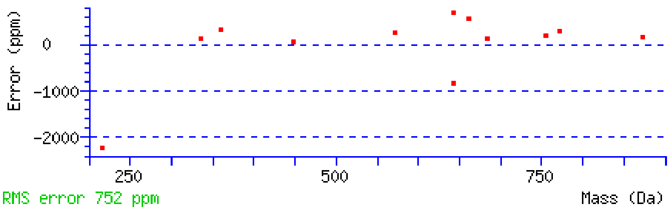
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1017.5818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.0099
Matches : 12/92 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							9
2	244.1404	122.5738	227.1139	114.0606	226.1298	113.5686	S	862.4880	431.7477	845.4615	423.2344	844.4775	422.7424	8
3	***359.1674***	180.0873	342.1408	171.5740	341.1568	171.0820	D	775.4560	388.2316	758.4294	379.7184	757.4454	379.2264	7
4	472.2514	236.6293	455.2249	228.1161	454.2409	227.6241	I	**660.4291**	330.7182	643.4025	322.2049	642.4185	321.7129	6
5	***571.3198***	286.1636	554.2933	277.6503	553.3093	277.1583	V	547.3450	274.1761	530.3184	265.6629	529.3344	265.1709	5
6	***684.4039***	342.7056	667.3774	334.1923	666.3933	333.7003	I	**448.2766**	224.6419	431.2500	216.1287	430.2660	215.6366	4
7	***771.4359***	386.2216	754.4094	377.7083	753.4254	377.2163	S	**335.1925**	168.0999	318.1660	159.5866	317.1819	159.0946	3
8	***872.4836***	436.7454	855.4571	428.2322	854.4730	427.7402	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RSDIVISTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G04690.1

24.4	1017.5818	0.0007	RSDIVISTK
1.8	1017.5818	0.0007	QLKSGKETK
0.3	1017.5818	0.0007	KNLKESATK

Mascot: http://www.matrixscience.com/

AT1G04820.1

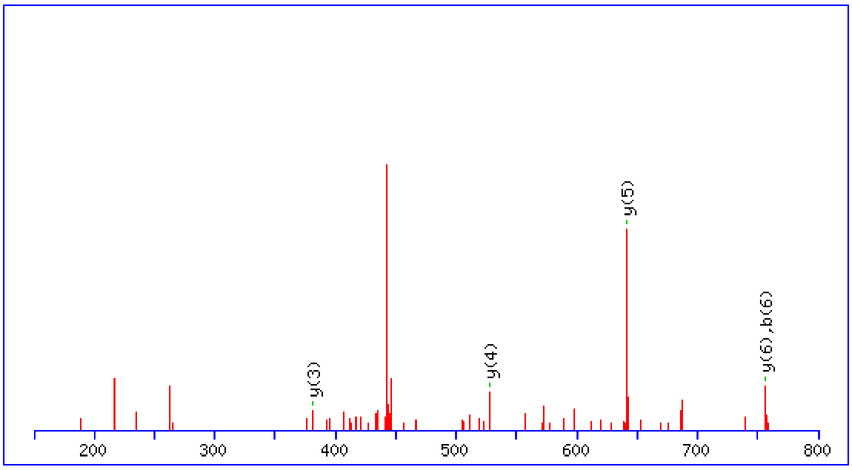
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDLMYAK**
Found in **AT1G04820.1** in **TAIR_Arabidopsis**, Symbols: TUA4 | TUA4 (tubulin alpha-4 chain) | chr1:1356420-1358265 REVERSE

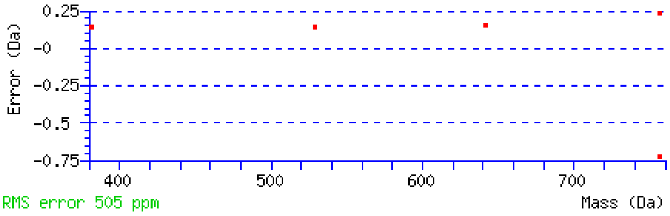
Match to Query 1635: 902.423104 from(452.218828,2+) index(3629)
Title: Elution from: 34.592 to 34.592 scan no 4524 cid35.00 polarity:+
Data file 0-1_3.mgf

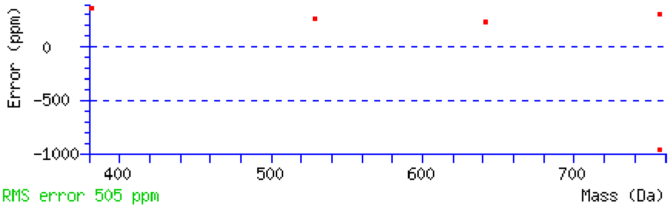
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 902.4208
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 **Expect:** 0.0009
Matches : 5/74 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							7
2	263.1026	132.0550	245.0921	123.0497	D	***756.3597***	378.6835	739.3331	370.1702	738.3491	369.6782	6
3	376.1867	188.5970	358.1761	179.5917	L	***641.3327***	321.1700	624.3062	312.6567			5
4	523.2221	262.1147	505.2115	253.1094	M	***528.2486***	264.6280	511.2221	256.1147			4
5	686.2854	343.6464	668.2749	334.6411	Y	***381.2132***	191.1103	364.1867	182.5970			3
6	757.3225	379.1649	739.3120	370.1596	A	218.1499	109.5786	201.1234	101.0653			2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FDLMYAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.2	902.4208	0.0023	FDLMYAK
22.5	902.4208	0.0023	FDLMYSK

AT1G04820.1

8.1	902.4208	0.0023	MDAIYFK
6.5	902.4208	0.0023	FFMDSIK
1.0	902.4246	-0.0015	HSDNGFVK
0.3	902.4246	-0.0015	HNKDFDK
0.1	902.4208	0.0023	ISMFYDK

AT1G04920.1

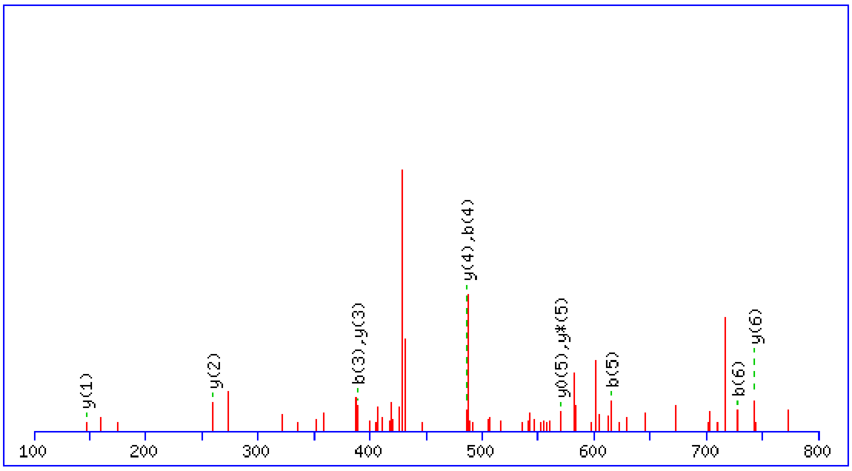
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MRTPEIK**
Found in **AT1G04920.1** in **TAIR_Arabidopsis**, Symbols: ATSPS3F | ATSPS3F (sucrose phosphate synthase 3F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | chr1:1391673-1395755 REVERSE

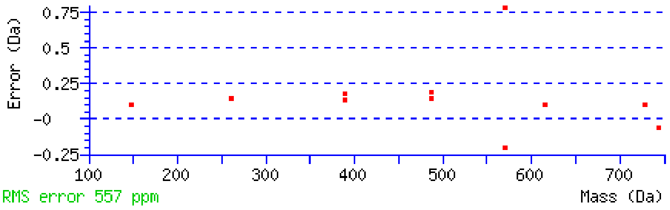
Match to Query 1402: 873.475162 from(437.744857,2+) index(2354)
Title: Elution from: 26.603 to 26.603 scan no 3026 cid35.00 polarity:+
Data file 0-1_2.mgf

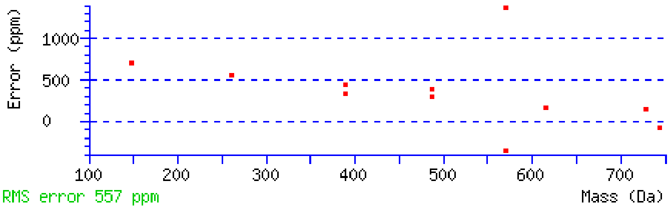
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 873.4742
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.04
Matches : 11/62 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							7
2	288.1489	144.5781	271.1223	136.0648			R	***743.4410***	372.2241	726.4145	363.7109	725.4305	363.2189	6
3	**389.1966**	195.1019	372.1700	186.5886	371.1860	186.0966	T	587.3399	294.1736	570.3134	285.6603	569.3293	285.1683	5
4	**486.2493**	243.6283	469.2228	235.1150	468.2387	234.6230	P	***486.2922***	243.6498	469.2657	235.1365	468.2817	234.6445	4
5	**615.2919**	308.1496	598.2654	299.6363	597.2813	299.1443	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
6	**728.3760**	364.6916	711.3494	356.1783	710.3654	355.6863	I	***260.1969***	130.6021	243.1703	122.0888			2
7							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of MRTPEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.7	873.4742	0.0010	MRTPEIK
10.2	873.4742	0.0009	GVAMELVR

AT1G04920.1

8.6	873.4742	0.0010	MKNPEKK
4.3	873.4742	0.0009	MIQDVLR

Mascot: http://www.matrixscience.com/

AT1G05010.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSGLQLLK**
Found in **AT1G05010.1** in **TAIR_Arabidopsis**, Symbols: ACO4, EAT1, EFE | EFE (ETHYLENE FORMING ENZYME) | chr1:1431418-1432694 REVERSE

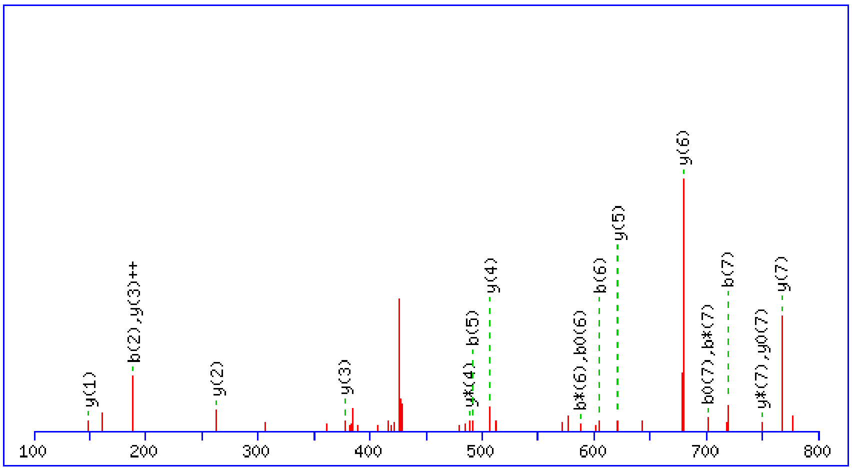
Match to Query 1467: 866.508486 from(434.261519,2+) index(4776)
Title: Elution from: 43.781 to 43.781 scan no 5995 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

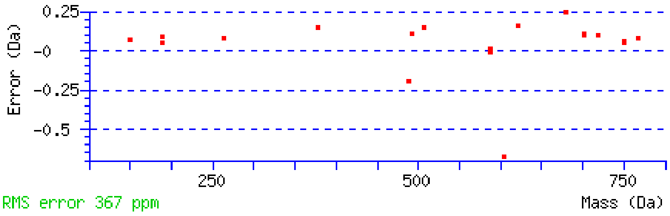
Label all possible matches ○ Label matches used for scoring ●

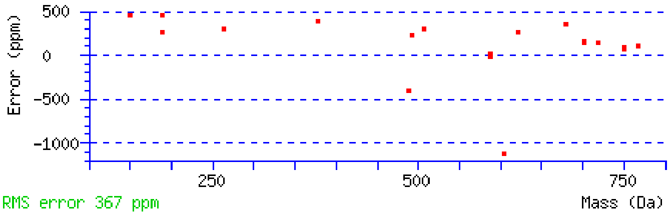
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 866.5085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 2.1e-005
Matches : 19/62 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							8
2	**189.1018**	95.0545			171.0912	86.0492	S	***767.4504***	384.2288	749.4268	375.2170	749.4398	375.2235	7
3	247.1203	124.0638			229.1097	115.0585	G	***679.4213***	340.2143	661.3977	331.2025			6
4	361.2014	181.1043			343.1908	172.0990	L	***621.4028***	311.2050	603.3792	302.1933			5
5	**491.2540**	246.1307	473.2304	237.1189	473.2435	237.1254	Q	***507.3217***	254.1645	489.2981	245.1527			4
6	**605.3351**	303.1712	587.3115	294.1594	587.3246	294.1659	L	***377.2691***	189.1382	359.2455	180.1264			3
7	**719.4162**	360.2118	701.3926	351.2000	701.4057	351.2065	L	***263.1880***	132.0976	245.1644	123.0858			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VSGLQLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.6	866.5085	-0.0001	VSGLQLLK

38.2	866.5085	-0.0001	GEGLKLLK
31.4	866.5108	-0.0023	FLLQLPK
28.2	866.5085	-0.0001	ADVAKLLK
22.2	866.5085	-0.0001	DKLQLLK
21.5	866.5085	-0.0001	VSLAQVIK
14.3	866.5108	-0.0023	VLSWLLK
14.2	866.5085	-0.0001	KDLLQIK
13.3	866.5085	-0.0001	QKVEILK
11.3	866.5085	-0.0001	GEALVKLK

AT1G05190.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEIGQFAATVR**
Found in **AT1G05190.1** in **TAIR_Arabidopsis**, Symbols: EMB2394 | EMB2394 (EMBRYO DEFECTIVE 2394); structural constituent of ribosome | chr1:1502514-1503737 REVERSE

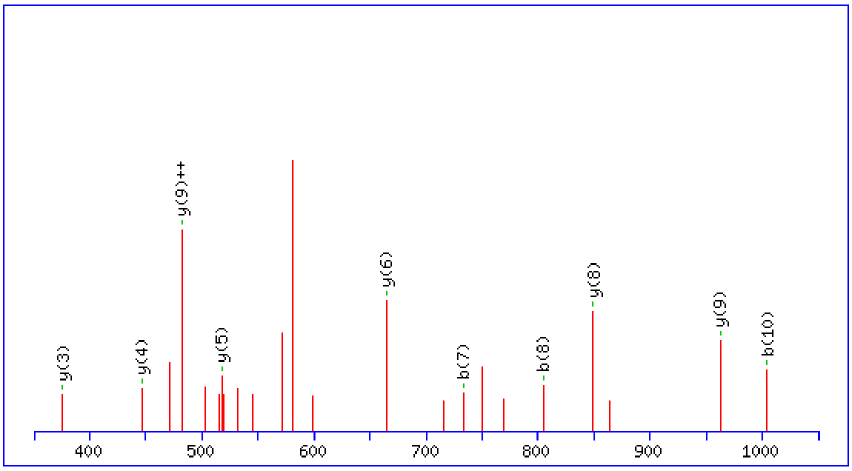
Match to Query 4269: 1177.606228 from(589.810390,2+) index(5064)
Title: Elution from: 45.354 to 45.354 scan no 6275 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1050 Da Full range

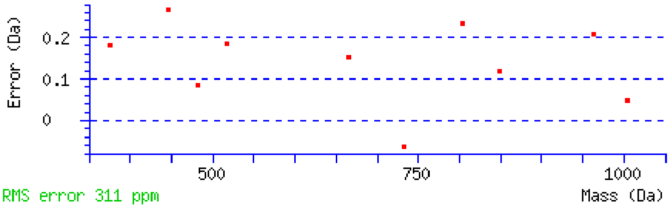
Label all possible matches ○ Label matches used for scoring ●

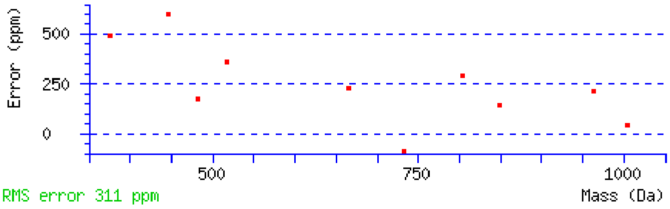
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1177.6091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00034
Matches : 10/108 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	217.0819	109.0446			199.0713	100.0393	E	1091.5844	546.2958	1074.5578	537.7826	1073.5738	537.2905	10
3	330.1660	165.5866			312.1554	156.5813	I	***962.5418***	481.7745	945.5152	473.2613	944.5312	472.7693	9
4	387.1874	194.0974			369.1769	185.0921	G	***849.4577***	425.2325	832.4312	416.7192	831.4472	416.2272	8
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	Q	792.4363	396.7218	775.4097	388.2085	774.4257	387.7165	7
6	662.3144	331.6608	645.2879	323.1476	644.3039	322.6556	F	***664.3777***	332.6925	647.3511	324.1792	646.3671	323.6872	6
7	**733.3515**	367.1794	716.3250	358.6661	715.3410	358.1741	A	***517.3093***	259.1583	500.2827	250.6450	499.2987	250.1530	5
8	**804.3886**	402.6980	787.3621	394.1847	786.3781	393.6927	A	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
9	905.4363	453.2218	888.4098	444.7085	887.4258	444.2165	T	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	**1004.5047**	502.7560	987.4782	494.2427	986.4942	493.7507	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SEIGQFAATVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G05190.1

Score	Mr(calc)	Delta	Sequence
41.4	1177.6091	-0.0029	SEIGQFAATVR
9.5	1177.6091	-0.0029	HPGTKIDDPAK
7.2	1177.6051	0.0011	KSTRSDELSR
4.8	1177.6091	-0.0029	KFEEAQGTIR
3.4	1177.6091	-0.0029	VELNNSFSLR
3.3	1177.6033	0.0030	WLYFHGLSR
2.4	1177.6091	-0.0029	EDNFRSLVAK
1.8	1177.6067	-0.0004	TLVHFVCFR

Mascot: http://www.matrixscience.com/

AT1G05490.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTSTLK**
Found in **AT1G05490.1** in **TAIR_Arabidopsis**, Symbols: CHR31 | CHR31 (chromatin remodeling 31); ATP binding / DNA binding / helicase/ nucleic acid binding | chr1:1618794-1623194 REVERSE

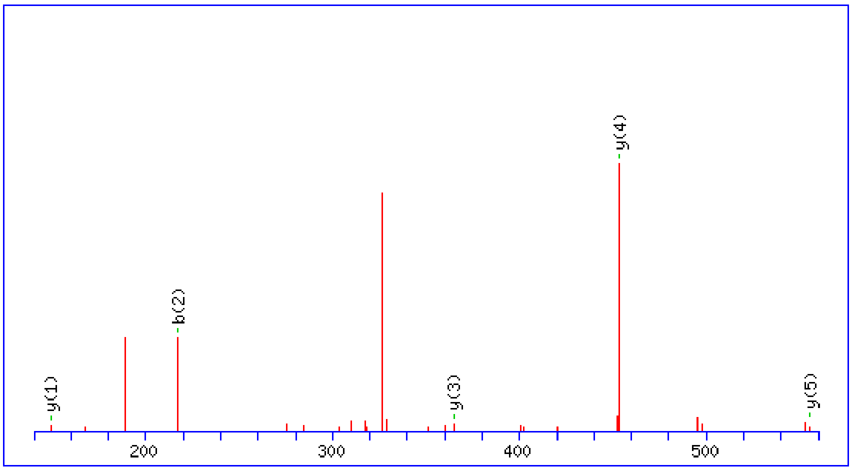
Match to Query 550: 668.378332 from(335.196442,2+) index(636)
Title: Elution from: 12.991 to 12.991 scan no 984 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 140 to 560 Da Full range

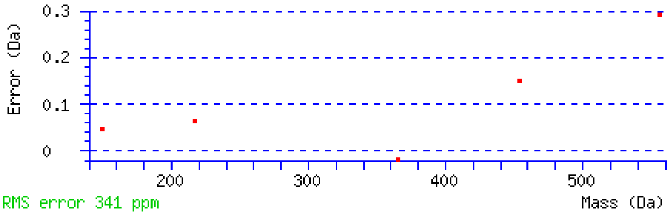
Label all possible matches ○ Label matches used for scoring ●

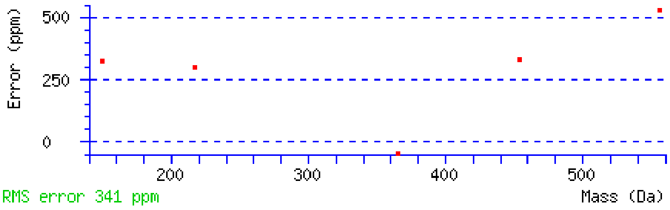
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 668.3803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.012
Matches : 5/44 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			L							6
2	217.1331	109.0702	199.1225	100.0649	T	***555.3065***	278.1569	537.2829	269.1451	537.2959	269.1516	5
3	305.1622	153.0847	287.1516	144.0794	S	***453.2617***	227.1345	435.2382	218.1227	435.2512	218.1292	4
4	407.2069	204.1071	389.1963	195.1018	T	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
5	521.2880	261.1476	503.2774	252.1423	L	263.1880	132.0976	245.1644	123.0858			2
6					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LTSTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.2	668.3803	-0.0019	LTSLTK
21.2	668.3803	-0.0019	LTSTLK
19.0	668.3803	-0.0019	ITTISK

AT1G05490.1

19.0	668.3803	-0.0019	ITTVTK
11.9	668.3803	-0.0019	LTLSTK
10.8	668.3803	-0.0019	TITVTK
10.8	668.3803	-0.0019	TLTLSK
10.8	668.3803	-0.0019	TLTSLK
10.7	668.3803	-0.0019	LTTSKL
3.3	668.3803	-0.0019	TLITSK

AT1G06500.1

{MATRIX SCIENCE} Mascot Search Results

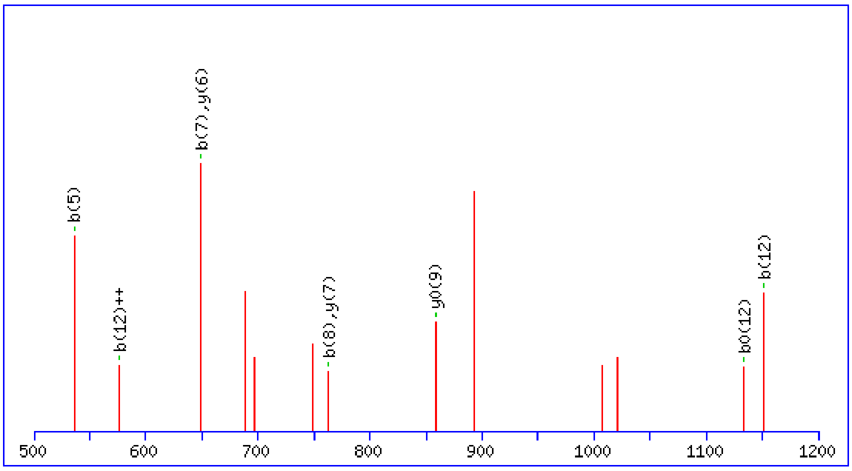
Peptide View

MS/MS Fragmentation of **FGFPSGGLTTVSNK**
Found in **AT1G06500.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96557.1) | chr1:1990175-1990585 FORWARD

Match to Query 5406: 1410.710640 from(706.362596,2+) index(6742)
Title: Elution from: 60.065 to 60.065 scan no 8750 cid35.00 polarity:+
Data file D6h-1_3.mgf

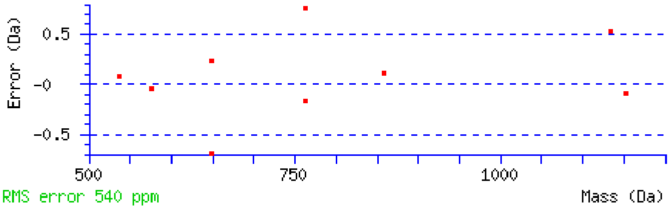
Click mouse within plot area to zoom in by factor of two about that point

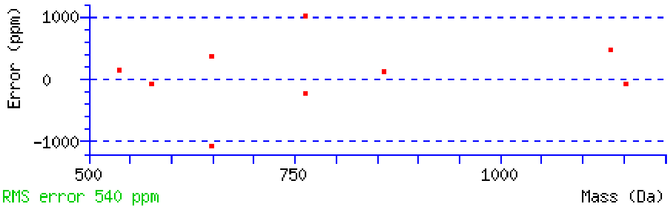
Or, Plot from 500 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1410.7144
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.028
Matches : 9/120 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							14
2	205.0972	103.0522					G	1264.6532	632.8302	1247.6266	624.3170	1246.6426	623.8250	13
3	352.1656	176.5864					F	1207.6317	604.3195	1190.6052	595.8062	1189.6212	595.3142	12
4	449.2183	225.1128					P	1060.5633	530.7853	1043.5368	522.2720	1042.5528	521.7800	11
5	***536.2504***	268.6288			518.2398	259.6235	S	963.5106	482.2589	946.4840	473.7456	945.5000	473.2536	10
6	593.2718	297.1396			575.2613	288.1343	G	876.4785	438.7429	859.4520	430.2296	858.4680	429.7376	9
7	***650.2933***	325.6503			632.2827	316.6450	G	819.4571	410.2322	802.4305	401.7189	801.4465	401.2269	8
8	***763.3774***	382.1923			745.3668	373.1870	L	**762.4356**	381.7214	745.4090	373.2082	744.4250	372.7162	7
9	864.4250	432.7162			846.4145	423.7109	T	**649.3515**	325.1794	632.3250	316.6661	631.3410	316.1741	6
10	965.4727	483.2400			947.4621	474.2347	T	548.3039	274.6556	531.2773	266.1423	530.2933	265.6503	5
11	1064.5411	532.7742			1046.5306	523.7689	V	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
12	***1151.5732***	576.2902			1133.5626	567.2849	S	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	3
13	1265.6161	633.3117	1248.5895	624.7984	1247.6055	624.3064	N	261.1557	131.0815	244.1292	122.5682			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FGFPSGGLTTVSNK

AT1G06500.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.6	1410.7144	-0.0037	FGFPSGGLTTVSNK
2.8	1410.7064	0.0042	LYDEVKAGELMK
1.5	1410.7116	-0.0010	NILLEDHHHQR
1.4	1410.7143	-0.0037	FITGEAKEFDVR
0.8	1410.7143	-0.0037	LFPEIEEEHIR
0.6	1410.7064	0.0042	DQVLEYIKMEK

AT1G06530.1

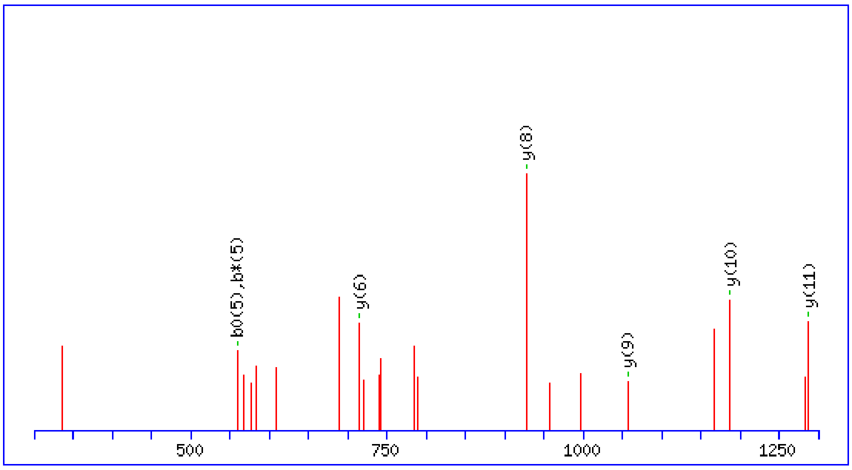
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVVEEPLNGIEFK**
Found in **AT1G06530.1** in **TAIR_Arabidopsis**, Symbols: | myosin heavy chain-related | chr1:2001624-2002595 FORWARD

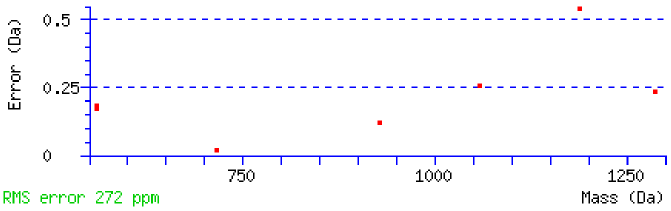
Match to Query 6570: 1502.714958 from(752.364755,2+) index(7194)
Title: Elution from: 63.088 to 63.088 scan no 9223 cid35.00 polarity:+
Data file C7-3_1.mgf

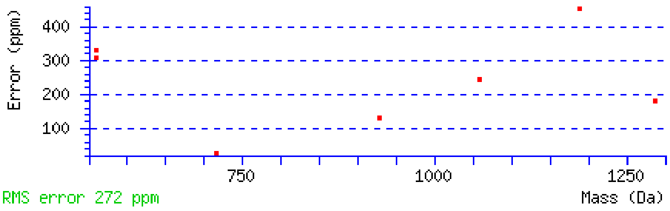
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1502.7193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.041
Matches : 7/134 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							13
2	217.1097	109.0585	199.0861	100.0467			V	1387.6896	694.3484	1369.6660	685.3366	1369.6790	685.3432	12
3	317.1752	159.0912	299.1516	150.0794			V	***1287.6241***	644.3157	1269.6006	635.3039	1269.6136	635.3104	11
4	447.2148	224.1110	429.1912	215.0992	429.2042	215.1058	E	***1187.5587***	594.2830	1169.5351	585.2712	1169.5481	585.2777	10
5	577.2544	289.1309	559.2308	280.1191	559.2439	280.1256	E	***1057.5191***	529.2632	1039.4955	520.2514	1039.5085	520.2579	9
6	675.3042	338.1558	657.2806	329.1440	657.2937	329.1505	P	***927.4794***	464.2434	909.4559	455.2316	909.4689	455.2381	8
7	789.3853	395.1963	771.3617	386.1845	771.3748	386.1910	L	829.4296	415.2185	811.4061	406.2067	811.4191	406.2132	7
8	905.4223	453.2148	887.3987	444.2030	887.4118	444.2095	N	***715.3485***	358.1779	697.3250	349.1661	697.3380	349.1726	6
9	963.4408	482.2240	945.4172	473.2123	945.4303	473.2188	G	599.3115	300.1594	581.2880	291.1476	581.3010	291.1541	5
10	1077.5219	539.2646	1059.4983	530.2528	1059.5114	530.2593	I	541.2930	271.1502	523.2695	262.1384	523.2825	262.1449	4
11	1207.5615	604.2844	1189.5380	595.2726	1189.5510	595.2791	E	427.2120	214.1096	409.1884	205.0978	409.2014	205.1043	3
12	1355.6270	678.3171	1337.6034	669.3053	1337.6164	669.3119	F	297.1723	149.0898	279.1487	140.0780			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NVVEEPLNGIEFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G06530.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.4	1502.7193	-0.0044	NVVEEPLNGIEFK
2.8	1502.7171	-0.0021	LTVGPEITSEEVGR
1.9	1502.7171	-0.0021	ESELIEENVLGVR

AT1G06670.1

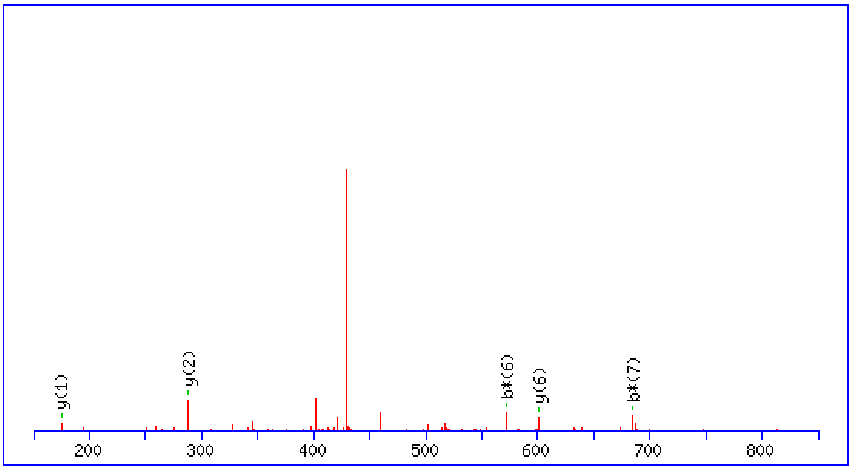
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQKAGGIR**
Found in **AT1G06670.1** in **TAIR_Arabidopsis**, Symbols: NIH | NIH (NUCLEAR DEIH-BOXHELICASE) | chr1:2040566-2047332 FORWARD

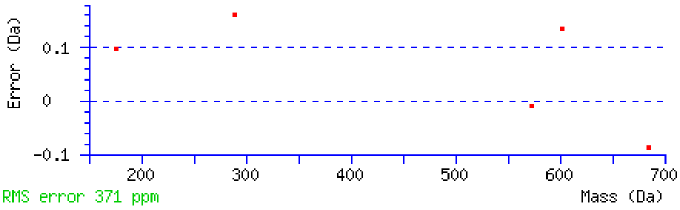
Match to Query 1402: 875.495614 from(438.755083,2+) index(2838)
Title: Elution from: 29.662 to 29.662 scan no 3584 cid35.00 polarity:+
Data file D6h-1_2.mgf

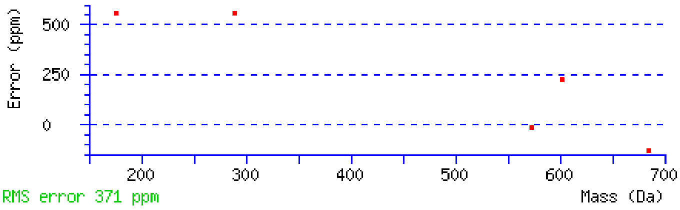
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 875.4977
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.045
Matches : 5/54 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	148.0757	74.5415			F					8
2	276.1343	138.5708	259.1077	130.0575	Q	729.4366	365.2219	712.4101	356.7087	7
3	404.2292	202.6183	387.2027	194.1050	K	***601.3780***	301.1926	584.3515	292.6794	6
4	475.2663	238.1368	458.2398	229.6235	A	473.2831	237.1452	456.2565	228.6319	5
5	532.2878	266.6475	515.2613	258.1343	G	402.2459	201.6266	385.2194	193.1133	4
6	589.3093	295.1583	572.2827	286.6450	G	345.2245	173.1159	328.1979	164.6026	3
7	702.3933	351.7003	685.3668	343.1870	I	***288.2030***	144.6051	271.1765	136.0919	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of FQKAGGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	875.4977	-0.0021	FKGQQLR
18.9	875.4977	-0.0021	FQKAGGIR

AT1G06670.1

10.7	875.4977	-0.0021	TWTKRGK
8.8	875.4977	-0.0021	VKFNVNR
5.7	875.4977	-0.0021	FVLERGR
2.7	875.4964	-0.0008	TSVLESIK
2.5	875.4964	-0.0008	TLVSSIEK
2.1	875.4977	-0.0021	FGRGPSKK
2.1	875.4937	0.0019	VSGKRSSR
1.1	875.4977	-0.0021	HDHKVLK

AT1G06680.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEDNFDATSNLNVMVTPTDKK**
Found in **AT1G06680.1** in **TAIR_Arabidopsis**, Symbols: OEE2, PSII-P, PSBP-1 | PSBP-1 (OXYGEN-EVOLVING ENHANCER PROTEIN 2); poly(U) binding | chr1:2047939-2049185 FORWARD

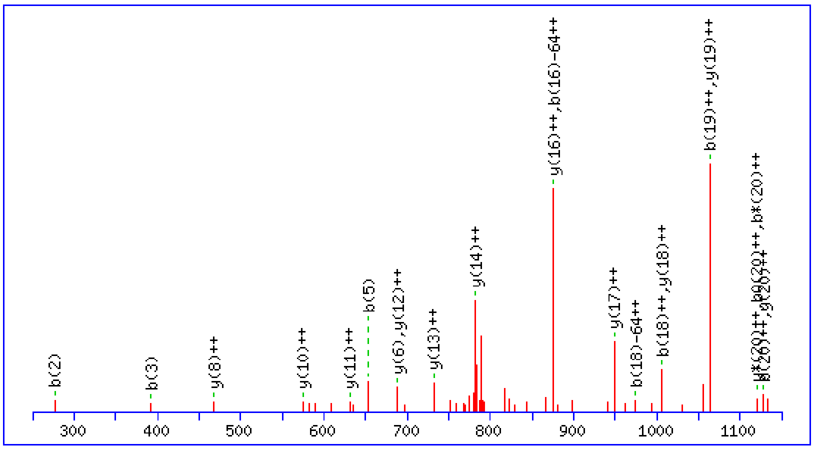
Match to Query 10269: 2401.112205 from(801.378011,3+) index(5914)
Title: Elution from: 53.024 to 53.024 scan no 7559 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1150 Da Full range

Label all possible matches ○ Label matches used for scoring ●

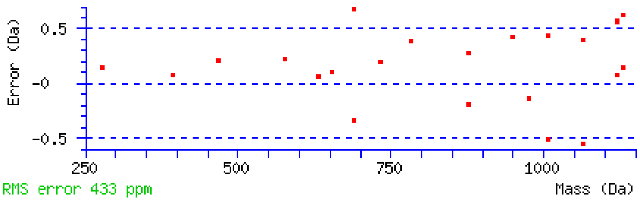
Show Y-axis ☐

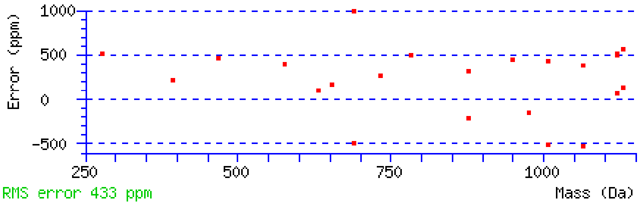


```
Monoisotopic mass of neutral peptide Mr(calc): 2401.1108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M14     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 111  Expect: 1.8e-011
Matches : 23/348 fragment ions using 16 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							21
2	**277.1183**	139.0628			259.1077	130.0575	E	2255.0496	1128.0284	2238.0231	1119.5152	2237.0391	1119.0232	20
3	**392.1452**	196.5763			374.1347	187.5710	D	2126.0070	1063.5072	2108.9805	1054.9939	2107.9965	1054.5019	19
4	506.1882	253.5977	489.1616	245.0844	488.1776	244.5924	N	2010.9801	1005.9937	1993.9535	997.4804	1992.9695	996.9884	18
5	**653.2566**	327.1319	636.2300	318.6186	635.2460	318.1266	F	1896.9372	948.9722	1879.9106	940.4589	1878.9266	939.9669	17
6	768.2835	384.6454	751.2570	376.1321	750.2729	375.6401	D	1749.8687	875.4380	1732.8422	866.9247	1731.8582	866.4327	16
7	839.3206	420.1640	822.2941	411.6507	821.3101	411.1587	A	1634.8418	817.9245	1617.8153	809.4113	1616.8312	808.9193	15
8	940.3683	470.6878	923.3418	462.1745	922.3577	461.6825	T	1563.8047	782.4060	1546.7781	773.8927	1545.7941	773.4007	14
9	1027.4003	514.2038	1010.3738	505.6905	1009.3898	505.1985	S	1462.7570	731.8821	1445.7305	723.3689	1444.7464	722.8769	13
10	1141.4433	571.2253	1124.4167	562.7120	1123.4327	562.2200	N	1375.7250	688.3661	1358.6984	679.8529	1357.7144	679.3608	12
11	1254.5273	627.7673	1237.5008	619.2540	1236.5168	618.7620	L	1261.6821	631.3447	1244.6555	622.8314	1243.6715	622.3394	11
12	1368.5702	684.7888	1351.5437	676.2755	1350.5597	675.7835	N	1148.5980	574.8026	1131.5714	566.2894	1130.5874	565.7973	10
13	1467.6387	734.3230	1450.6121	725.8097	1449.6281	725.3177	V	1034.5551	517.7812	1017.5285	509.2679	1016.5445	508.7759	9
14	1614.6741	807.8407	1597.6475	799.3274	1596.6635	798.8354	M	935.4866	468.2470	918.4601	459.7337	917.4761	459.2417	8
15	1713.7425	857.3749	1696.7159	848.8616	1695.7319	848.3696	V	788.4512	394.7293	771.4247	386.2160	770.4407	385.7240	7
16	1814.7902	907.8987	1797.7636	899.3854	1796.7796	898.8934	T	689.3828	345.1951	672.3563	336.6818	671.3723	336.1898	6
17	1911.8429	956.4251	1894.8164	947.9118	1893.8324	947.4198	P	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
18	2012.8906	**1006.9489**	1995.8641	998.4357	1994.8800	997.9437	T	491.2824	246.1448	474.2558	237.6316	473.2718	237.1395	4
19	2127.9175	**1064.4624**	2110.8910	1055.9491	2109.9070	1055.4571	D	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
20	2256.0125	**1128.5099**	2238.9860	1119.9966	2238.0019	1119.5046	K	275.2078	138.1075	258.1812	129.5942			2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT1G06680.1





NCBI **BLAST** search of FEDNFDATSNLNVMVTPTDKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
111.5	2401.1108	0.0014	FEDNFDATSNLNVMVTPTDKK
13.7	2401.1089	0.0033	CRSFTGHFNMVDRSLMTAQK
7.1	2401.1132	-0.0010	KKPDDVAVPESTEGDDEAEDKK
2.4	2401.1067	0.0055	LNMVSATSFDSSSPSVSPSSDKR
1.7	2401.1141	-0.0019	VKGNGEEADIMTTFKLDNEMK
1.6	2401.1089	0.0033	CRSFTGHFNMVDRSLMTAQK
0.8	2401.1121	0.0001	YLAMLARDNDWASKEFGDQR
0.4	2401.1076	0.0046	MIPMDNHCLPTVDASGSVAAGVK

Mascot: http://www.matrixscience.com/

AT1G06690.1

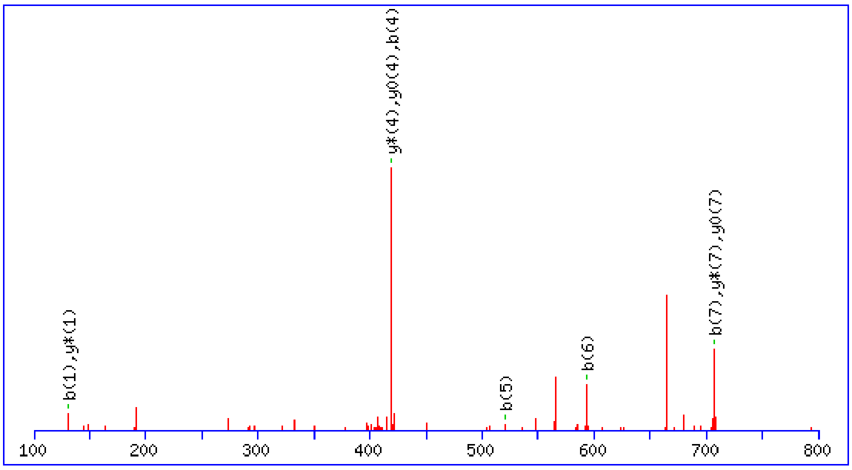
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESVVTALK**
Found in **AT1G06690.1** in **TAIR_Arabidopsis**, Symbols: | aldo/keto reductase family protein | chr1:2049741-2052038 REVERSE

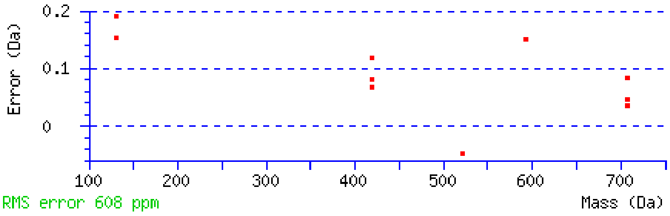
Match to Query 1328: 854.458772 from(428.236662,2+) index(2983)
Title: Elution from: 28.883 to 28.883 scan no 3679 cid35.00 polarity:+
Data file C7-2_3.mgf

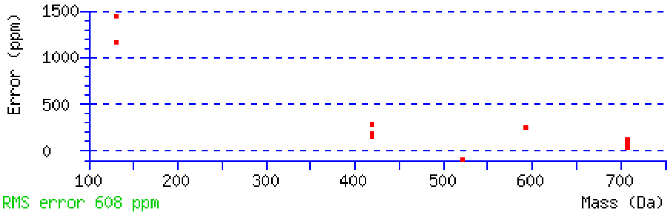
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 854.4591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0035
Matches : 10/64 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	***131.0469***	66.0271	113.0363	57.0218	E							8
2	219.0760	110.0416	201.0654	101.0363	S	725.4268	363.2170	707.4032	354.2052	707.4162	354.2118	7
3	319.1414	160.0743	301.1309	151.0691	V	637.3977	319.2025	619.3741	310.1907	619.3872	310.1972	6
4	***419.2069***	210.1071	401.1963	201.1018	V	537.3323	269.1698	519.3087	260.1580	519.3217	260.1645	5
5	***521.2516***	261.1294	503.2410	252.1241	T	437.2668	219.1371	419.2433	210.1253	419.2563	210.1318	4
6	***593.2857***	297.1465	575.2752	288.1412	A	335.2221	168.1147	317.1985	159.1029			3
7	***707.3668***	354.1871	689.3563	345.1818	L	263.1880	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ESVVTALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.6	854.4591	-0.0004	ESVVTALK
29.8	854.4592	-0.0004	SSILEVAK

AT1G06690.1

21.2	854.4591	-0.0004	TSEIVAVK
12.5	854.4592	-0.0004	EALSSVIK
11.4	854.4592	-0.0004	EESIKIK
11.4	854.4592	-0.0004	ESELKLK
10.4	854.4591	-0.0004	SIVDTLAK
9.3	854.4591	-0.0004	LVGDTTLK
9.3	854.4592	-0.0004	EAVSSLIK
9.3	854.4592	-0.0004	EEIKSLK

AT1G06720.1

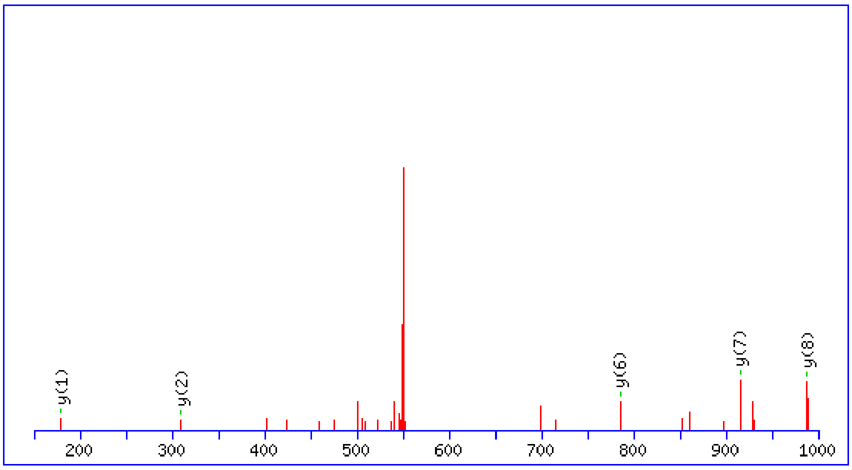
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQEITKQR**
Found in **AT1G06720.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G42440.1); similar to hypothetical protein OsJ_010296 [Oryza sativa (japonica cultivar-group)] (GB:EAZ26813.1); similar to hypothetical protein OsI_011117 [Oryza sativa (indica

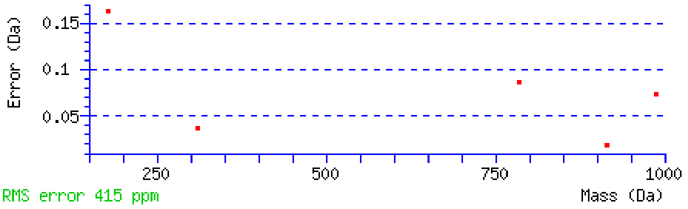
Match to Query 3422: 1116.532332 from(559.273442,2+) index(1597)
Title: Elution from: 19.631 to 19.631 scan no 2082 cid35.00 polarity:+
Data file 0-2_3.mgf

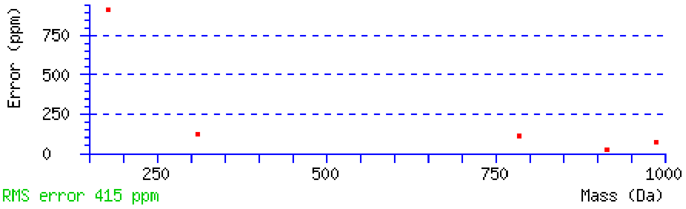
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5333
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0012
Matches : 5/86 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							9
2	203.0811	102.0442			185.0705	93.0389	A	***987.5010***	494.2541	969.4774	485.2423	969.4904	485.2489	8
3	333.1337	167.0705	315.1101	158.0587	315.1231	158.0652	Q	***915.4669***	458.2371	897.4433	449.2253	897.4563	449.2318	7
4	463.1733	232.0903	445.1497	223.0785	445.1628	223.0850	E	***785.4142***	393.2107	767.3906	384.1990	767.4036	384.2055	6
5	577.2544	289.1309	559.2308	280.1191	559.2439	280.1256	I	655.3746	328.1909	637.3510	319.1791	637.3640	319.1856	5
6	679.2991	340.1532	661.2756	331.1414	661.2886	331.1479	T	541.2935	271.1504	523.2699	262.1386	523.2829	262.1451	4
7	809.3882	405.1977	791.3646	396.1859	791.3776	396.1924	K	439.2488	220.1280	421.2252	211.1162			3
8	939.4408	470.2240	921.4172	461.2123	921.4303	461.2188	Q	***309.1597***	155.0835	291.1362	146.0717			2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EAQEITKQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G06720.1

Score	Mr(calc)	Delta	Sequence
39.1	1116.5333	-0.0010	EAQEITKQR
14.1	1116.5333	-0.0010	KAKEQQDQK
13.4	1116.5334	-0.0010	LSNEELNKR
13.4	1116.5334	-0.0010	EDLKKANER
13.4	1116.5356	-0.0033	EPSLTWSKR
13.4	1116.5334	-0.0010	EVNSLKQER
13.4	1116.5333	-0.0010	QQEVVESKR
10.2	1116.5334	-0.0010	KAAEEREAAK
10.0	1116.5333	-0.0010	LSVVEEDRR
9.4	1116.5356	-0.0033	IWTAQSIER

AT1G06820.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAADIGLEK**
Found in **AT1G06820.1** in **TAIR_Arabidopsis**, Symbols: CCR2, CRTISO | CRTISO (CAROTENOID ISOMERASE); carotenoid isomerase | chr1:2093144-2096219 REVERSE

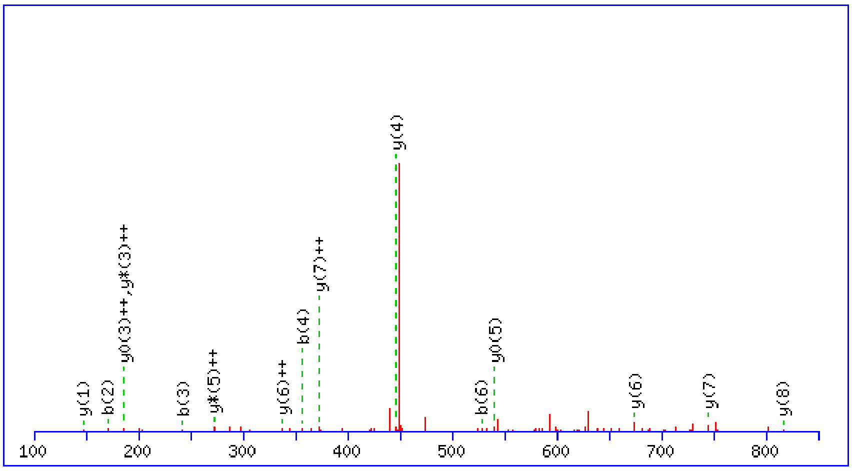
Match to Query 1620: 914.505272 from(458.259912,2+) index(3009)
Title: Elution from: 29.239 to 29.239 scan no 3720 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 850 Da Full range

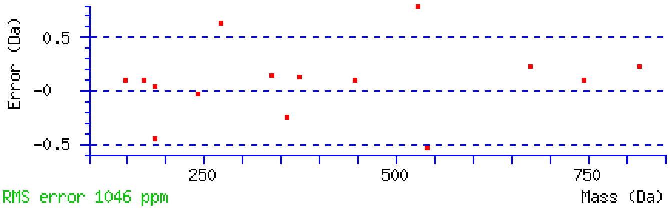
Label all possible matches ○ Label matches used for scoring ●

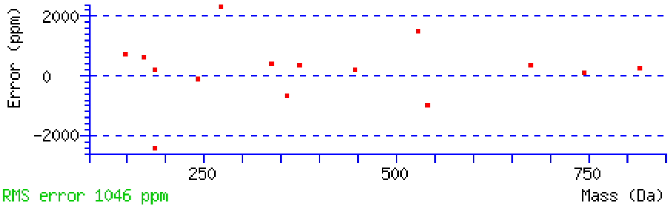
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 914.5073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.018
Matches : 15/72 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							9
2	***171.1128***	86.0600			A	***816.4462***	408.7267	799.4196	400.2134	798.4356	399.7214	8
3	***242.1499***	121.5786			A	***745.4090***	373.2082	728.3825	364.6949	727.3985	364.2029	7
4	***357.1769***	179.0921	339.1663	170.0868	D	***674.3719***	337.6896	657.3454	329.1763	656.3614	328.6843	6
5	470.2609	235.6341	452.2504	226.6288	I	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	***527.2824***	264.1448	509.2718	255.1396	G	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
7	640.3665	320.6869	622.3559	311.6816	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
8	769.4090	385.2082	751.3985	376.2029	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VAADIGLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G06820.1

24.3	914.5073	-0.0020	VAADIGLEK
12.3	914.5073	-0.0020	LQIDDAIK
5.5	914.5046	0.0007	GKTPNSRR
5.2	914.5073	-0.0020	AIGEGDLIK
2.7	914.5073	-0.0020	LQPLSTEK
2.7	914.5073	-0.0020	DEKPIVSK
2.6	914.5073	-0.0020	ILNEEGLK
2.6	914.5073	-0.0020	LQELGDLK
2.5	914.5046	0.0007	QGQRSALR
2.5	914.5073	-0.0020	LVQEALDK

AT1G06950.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVGPISLIGDESDFER**
Found in **AT1G06950.1** in **TAIR_Arabidopsis**, Symbols: ATTIC110, TIC110 | ATTIC110/TIC110 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110) | chr1:2130302-2135562 REVERSE

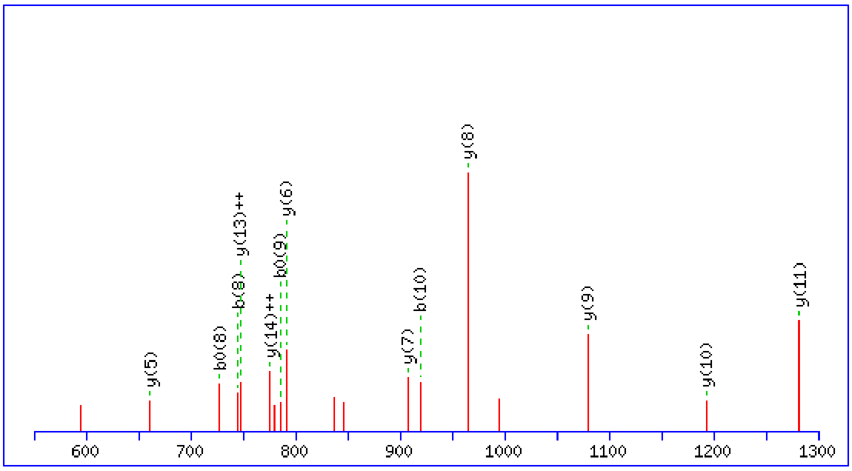
Match to Query 7801: 1708.763110 from(855.388831,2+) index(8277)
Title: Elution from: 73.662 to 73.662 scan no 11100 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

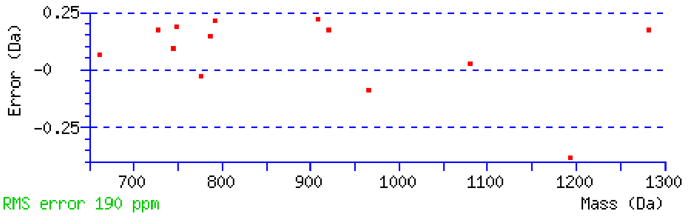
Show Y-axis ☐

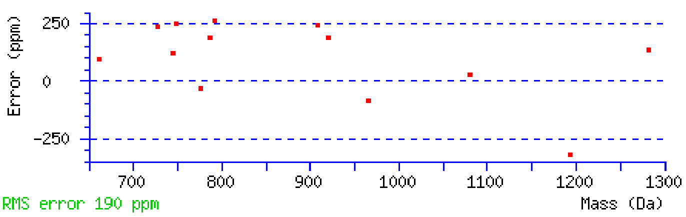


Monoisotopic mass of neutral peptide Mr(calc): 1708.7646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 6e-006
Matches : 13/138 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			**G**							**16**
2	159.0912	80.0492			**V**	1651.7534	826.3803	1633.7298	817.3686	1633.7429	817.3751	**15**
3	217.1097	109.0585			**G**	1551.6880	776.3476	1533.6644	767.3358	1533.6774	767.3423	**14**
4	315.1595	158.0834			**P**	1493.6695	747.3384	1475.6459	738.3266	1475.6589	738.3331	**13**
5	429.2406	215.1239			**I**	1395.6197	698.3135	1377.5961	689.3017	1377.6091	689.3082	**12**
6	517.2697	259.1385	499.2591	250.1332	**S**	***1281.5386***	641.2729	1263.5150	632.2611	1263.5280	632.2676	**11**
7	631.3508	316.1790	613.3402	307.1737	**L**	***1193.5095***	597.2584	1175.4859	588.2466	1175.4989	588.2531	**10**
8	**745.4319**	373.2196	727.4213	364.2143	**I**	***1079.4284***	540.2178	1061.4048	531.2061	1061.4178	531.2126	**9**
9	803.4504	402.2288	785.4398	393.2235	**G**	***965.3473***	483.1773	947.3237	474.1655	947.3367	474.1720	**8**
10	**919.4744**	460.2408	901.4638	451.2355	**D**	***907.3288***	454.1680	889.3052	445.1563	889.3183	445.1628	**7**
11	1049.5140	525.2606	1031.5034	516.2553	**E**	***791.3048***	396.1561	773.2813	387.1443	773.2943	387.1508	**6**
12	1137.5431	569.2752	1119.5325	560.2699	**S**	***661.2652***	331.1362	643.2416	322.1245	643.2546	322.1310	**5**
13	1253.5670	627.2872	1235.5565	618.2819	**D**	573.2361	287.1217	555.2126	278.1099	555.2256	278.1164	**4**
14	1401.6325	701.3199	1383.6219	692.3146	**F**	457.2122	229.1097	439.1886	220.0979	439.2016	220.1044	**3**
15	1531.6721	766.3397	1513.6615	757.3344	**E**	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	**2**
16					**R**	179.1071	90.0572	161.0835	81.0454			**1**

AT1G06950.1





NCBI **BLAST** search of GVGPISLIGDESDFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.1	1708.7646	-0.0015	GVGPISLIGDESDFER
2.5	1708.7633	-0.0001	MEIPDEALGCGLTRK

Mascot: http://www.matrixscience.com/

AT1G07140.1

MATRIX SCIENCE Mascot Search Results

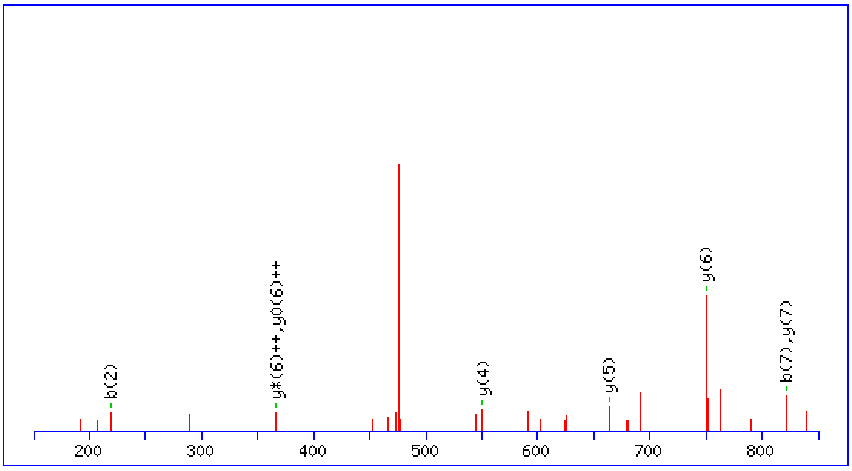
Peptide View

MS/MS Fragmentation of **FASIENCK**
Found in **AT1G07140.1** in **TAIR_Arabidopsis**, Symbols: SIRANBP | SIRANBP (Ran-binding protein 1a); Ran GTPase binding | chr1:2192359-2193687 REVERSE

Match to Query 2312: 967.443388 from(484.728970,2+) index(1185)
Title: Elution from: 18.268 to 18.268 scan no 1675 cid35.00 polarity:+
Data file C7-3_1.mgf

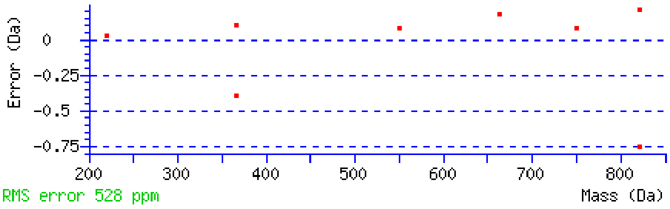
Click mouse within plot area to zoom in by factor of two about that point

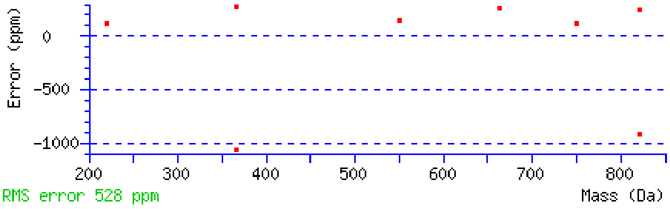
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 967.4433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00027
Matches : 8/64 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							8
2	**219.1128**	110.0600					A	***821.3822***	411.1947	804.3556	402.6815	803.3716	402.1894	7
3	306.1448	153.5761			288.1343	144.5708	S	***750.3451***	375.6762	733.3185	367.1629	732.3345	366.6709	6
4	419.2289	210.1181			401.2183	201.1128	I	***663.3130***	332.1602	646.2865	323.6469	645.3025	323.1549	5
5	548.2715	274.6394			530.2609	265.6341	E	***550.2290***	275.6181	533.2024	267.1049	532.2184	266.6128	4
6	662.3144	331.6608	645.2879	323.1476	644.3039	322.6556	N	421.1864	211.0968	404.1598	202.5836			3
7	**822.3451**	411.6762	805.3185	403.1629	804.3345	402.6709	C	307.1435	154.0754	290.1169	145.5621			2
8							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FASIENCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.3	967.4433	0.0001	FASIENCK

AT1G07140.1

0.8	967.4433	0.0001	IGGFNSDMK
0.2	967.4433	0.0001	ELGMAEYR

Mascot: http://www.matrixscience.com/

AT1G07180.1

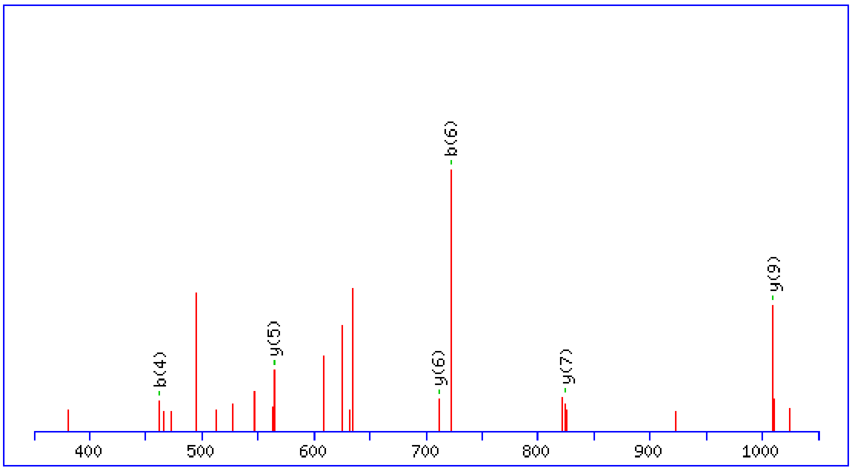
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLANLFNVMGK**
Found in **AT1G07180.1** in **TAIR_Arabidopsis**, Symbols: ATNDI1, NDA1 | ATNDI1/NDA1 (ALTERNATIVE NAD(P)H DEHYDROGENASE 1); NADH dehydrogenase | chr1:2204413-2206772 FORWARD

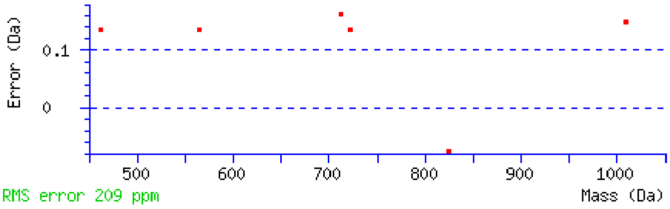
Match to Query 4703: 1284.654132 from(643.334342,2+) index(7436)
Title: Elution from: 65.622 to 65.622 scan no 9699 cid35.00 polarity:+
Data file D12h-1_2.mgf

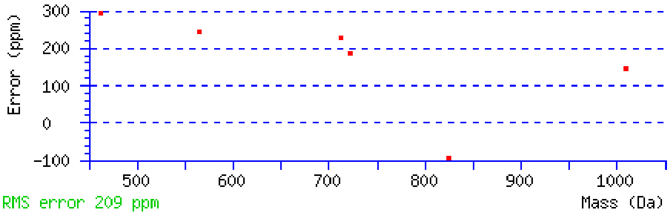
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1284.6536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.013
Matches : 6/114 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	164.0706	82.5389			Y					11
2	277.1547	139.0810			L	1122.5976	561.8024	1105.5710	553.2892	10
3	348.1918	174.5995			A	***1009.5135***	505.2604	992.4870	496.7471	9
4	**462.2347**	231.6210	445.2082	223.1077	N	938.4764	469.7418	921.4499	461.2286	8
5	575.3188	288.1630	558.2922	279.6498	L	***824.4335***	412.7204	807.4069	404.2071	7
6	**722.3872**	361.6972	705.3606	353.1840	F	***711.3494***	356.1783	694.3229	347.6651	6
7	836.4301	418.7187	819.4036	410.2054	N	***564.2810***	282.6441	547.2545	274.1309	5
8	935.4985	468.2529	918.4720	459.7396	V	450.2381	225.6227	433.2115	217.1094	4
9	1082.5339	541.7706	1065.5074	533.2573	M	351.1697	176.0885	334.1431	167.5752	3
10	1139.5554	570.2813	1122.5288	561.7681	G	204.1343	102.5708	187.1077	94.0575	2
11					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of YLANLFNVMGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G07180.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.9	1284.6536	0.0005	YLANLFNVMGK
1.1	1284.6575	-0.0034	SVFHPGSNIATR

Mascot: http://www.matrixscience.com/

AT1G07320.1

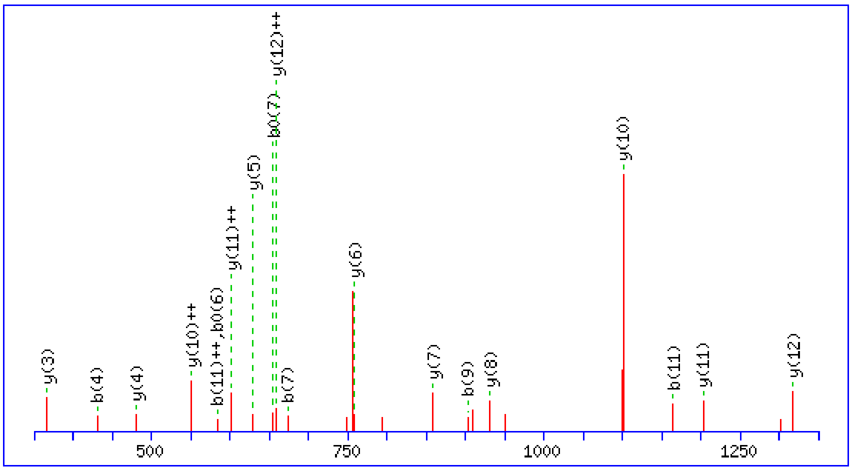
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLTPAAVEFLNAR**
Found in **AT1G07320.1** in **TAIR_Arabidopsis**, Symbols: RPL4 | RPL4 (ribosomal protein L4); poly(U) binding / structural constituent of ribosome | chr1:2249189-2250188 FORWARD

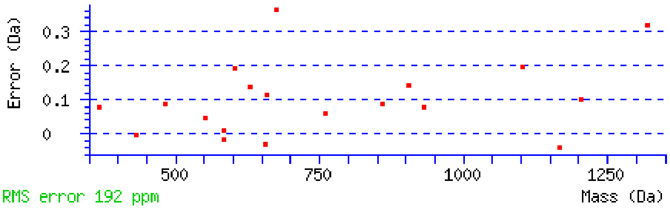
Match to Query 6617: 1530.809084 from(766.411818,2+) index(9324)
Title: Elution from: 83.903 to 83.903 scan no 12641 cid35.00 polarity:+
Data file D12h-1_2.mgf

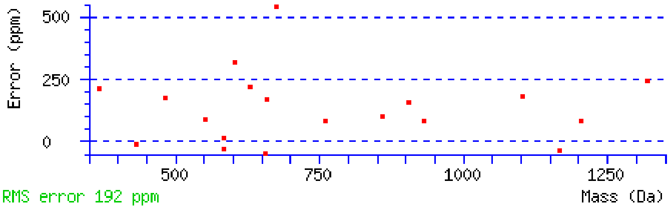
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1530.8130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 82 **Expect:** 2.1e-008
Matches : 19/118 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					**L**							**14**
2	215.1538	108.0805					**V**	1417.7392	709.3732	1399.7156	700.3615	1399.7287	700.3680	**13**
3	329.2349	165.1211					**L**	***1317.6738***	659.3405	1299.6502	650.3287	1299.6632	650.3352	**12**
4	**431.2796**	216.1435			413.2691	207.1382	**T**	***1203.5927***	602.3000	1185.5691	593.2882	1185.5821	593.2947	**11**
5	529.3294	265.1684			511.3189	256.1631	**P**	***1101.5480***	551.2776	1083.5244	542.2658	1083.5374	542.2723	**10**
6	601.3636	301.1854			583.3530	292.1801	**A**	1003.4982	502.2527	985.4746	493.2409	985.4876	493.2474	**9**
7	**673.3977**	337.2025			655.3872	328.1972	**A**	***931.4640***	466.2356	913.4404	457.2239	913.4534	457.2304	**8**
8	773.4632	387.2352			755.4526	378.2299	**V**	***859.4299***	430.2186	841.4063	421.2068	841.4193	421.2133	**7**
9	**903.5028**	452.2550			885.4922	443.2498	**E**	***759.3644***	380.1858	741.3408	371.1741	741.3538	371.1806	**6**
10	1051.5683	526.2878			1033.5577	517.2825	**F**	***629.3248***	315.1660	611.3012	306.1542			**5**
11	**1165.6494**	583.3283			1147.6388	574.3230	**L**	***481.2593***	241.1333	463.2358	232.1215			**4**
12	1281.6864	641.3468	1263.6628	632.3350	1263.6758	632.3415	**N**	***367.1782***	184.0928	349.1547	175.0810			**3**
13	1353.7205	677.3639	1335.6969	668.3521	1335.7099	668.3586	**A**	251.1412	126.0743	233.1177	117.0625			**2**
14							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of LVLTPAAVEFLNAR

AT1G07320.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
82.4	1530.8130	-0.0040	LVLTPAAVEFLNAR
2.9	1530.8108	-0.0017	VTILGDGNAKAVINK
0.8	1530.8061	0.0030	NPLQRKLAEIMAK

AT1G07380.1

MATRIX SCIENCE

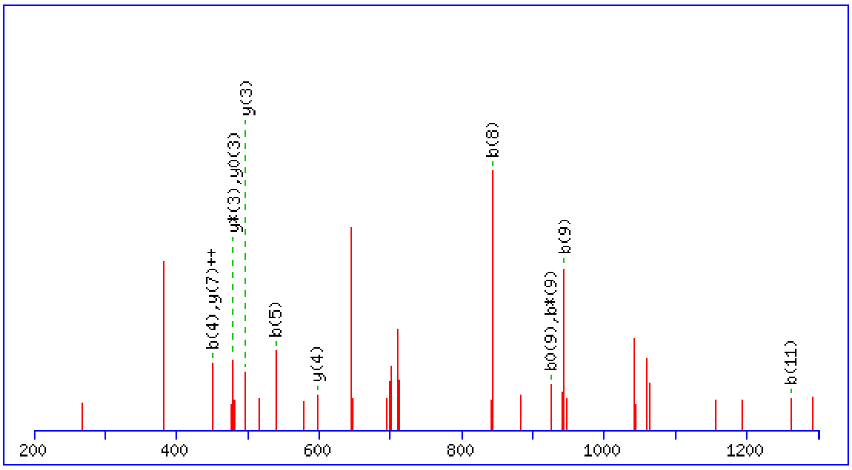
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSRSQATVEWR**
Found in **AT1G07380.1** in **TAIR_Arabidopsis**, Symbols: | ceramidase family protein | chr1:2264827-2268304 REVERSE

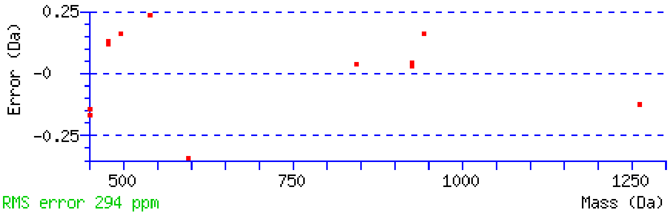
Match to Query 5661: 1438.667850 from(720.341201,2+) index(5195)
Title: Elution from: 47.614 to 47.614 scan no 6515 cid35.00 polarity:+
Data file D6h-2_2.mgf

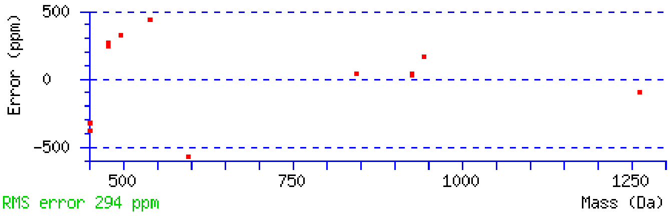
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1438.6673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.031
Matches : 12/120 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							12
2	203.1174	102.0624			185.1069	93.0571	S	1325.5935	663.3004	1307.5699	654.2886	1307.5829	654.2951	11
3	291.1465	146.0769			273.1359	137.0716	S	1237.5644	619.2859	1219.5409	610.2741	1219.5539	610.2806	10
4	***451.2358***	226.1215	433.2122	217.1097	433.2252	217.1162	R	1149.5354	575.2713	1131.5118	566.2595	1131.5248	566.2660	9
5	***539.2648***	270.1360	521.2412	261.1243	521.2542	261.1308	S	989.4461	495.2267	971.4225	486.2149	971.4356	486.2214	8
6	669.3175	335.1624	651.2939	326.1506	651.3069	326.1571	Q	901.4171	451.2122	883.3935	442.2004	883.4065	442.2069	7
7	741.3516	371.1794	723.3280	362.1677	723.3410	362.1742	A	771.3644	386.1858	753.3408	377.1741	753.3538	377.1806	6
8	***843.3963***	422.2018	825.3727	413.1900	825.3858	413.1965	T	699.3303	350.1688	681.3067	341.1570	681.3197	341.1635	5
9	***943.4618***	472.2345	925.4382	463.2227	925.4512	463.2292	V	**597.2856**	299.1464	579.2620	290.1346	579.2750	290.1411	4
10	1073.5014	537.2543	1055.4778	528.2425	1055.4908	528.2491	E	**497.2201**	249.1137	479.1965	240.1019	479.2095	240.1084	3
11	***1261.5748***	631.2910	1243.5512	622.2792	1243.5642	622.2857	W	367.1805	184.0939	349.1569	175.0821			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LSSRSQATVEWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G07380.1

Score	Mr(calc)	Delta	Sequence
25.1	1438.6673	0.0005	LSSRSQATVEWR
15.9	1438.6646	0.0032	KFESVEGVDIGSR
14.9	1438.6695	-0.0017	QDAEFKVNWKR
13.2	1438.6703	-0.0024	GTIGYIAPEMISR
13.2	1438.6673	0.0005	HHQVIVSEDLSR
11.1	1438.6646	0.0032	LGFQSKASDLDNK
9.3	1438.6680	-0.0002	KADKENSGTLTMK
9.3	1438.6646	0.0032	ENQFGVEKESKK
7.4	1438.6707	-0.0028	DTQSRIMTQALR
4.9	1438.6669	0.0010	EDGLNYIKWASK

Mascot: http://www.matrixscience.com/

AT1G07660.1

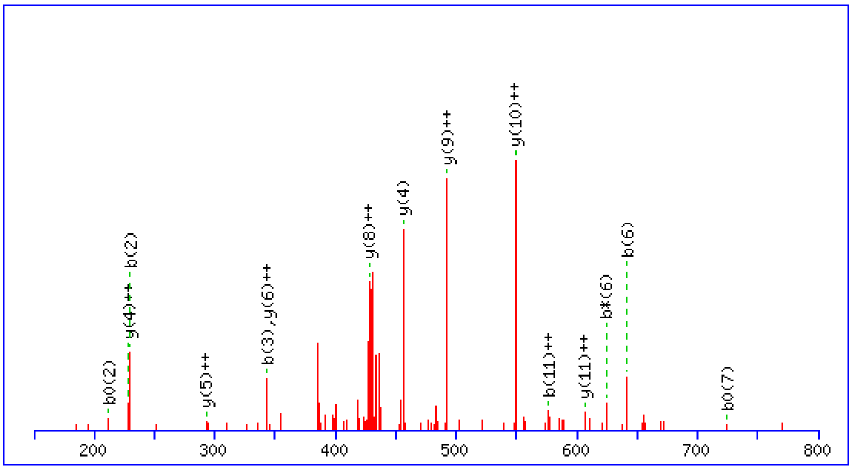
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNIQGITKPAIR**
Found in **AT1G07660.1** in **TAIR_Arabidopsis**, Symbols: | histone H4 | chr1:2369209-2369520 FORWARD

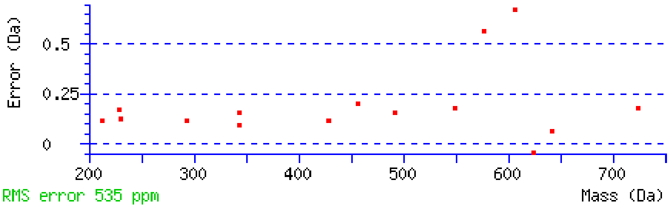
Match to Query 4971: 1324.746651 from(442.589493,3+) index(2719)
Title: Elution from: 28.360 to 28.360 scan no 3400 cid35.00 polarity:+
Data file D6h-3_1.mgf

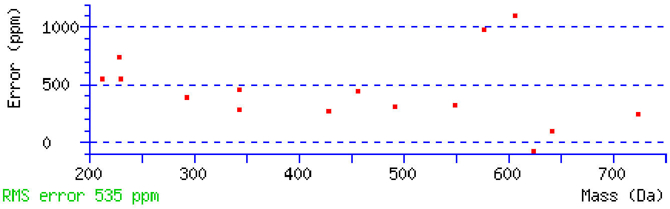
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1324.7463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.1e-005
Matches : 15/120 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	**230.0771**	115.5422	213.0506	107.0289	212.0666	106.5369	N	1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	11
3	**343.1612**	172.0842	326.1347	163.5710	325.1506	163.0790	I	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	10
4	471.2198	236.1135	454.1932	227.6003	453.2092	227.1082	Q	983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	9
5	528.2413	264.6243	511.2147	256.1110	510.2307	255.6190	G	855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	8
6	**641.3253**	321.1663	624.2988	312.6530	623.3148	312.1610	I	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	7
7	742.3730	371.6901	725.3464	363.1769	724.3624	362.6849	T	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	6
8	870.4680	435.7376	853.4414	427.2243	852.4574	426.7323	K	584.3879	292.6976	567.3613	284.1843			5
9	967.5207	484.2640	950.4942	475.7507	949.5102	475.2587	P	456.2929	228.6501	439.2663	220.1368			4
10	1038.5578	519.7826	1021.5313	511.2693	1020.5473	510.7773	A	359.2401	180.1237	342.2136	171.6104			3
11	1151.6419	576.3246	1134.6154	567.8113	1133.6313	567.3193	I	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DNIQGITKPAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G07660.1

Score	Mr(calc)	Delta	Sequence
54.5	1324.7463	0.0004	DNIQGITKPAIR
5.9	1324.7462	0.0004	NIKNKPEINQK
0.6	1324.7463	0.0004	NLPLLREEVSR
0.2	1324.7463	0.0004	NLRSPVPEKTGK
0.2	1324.7463	0.0004	ENVDILRLPTR

AT1G07660.2

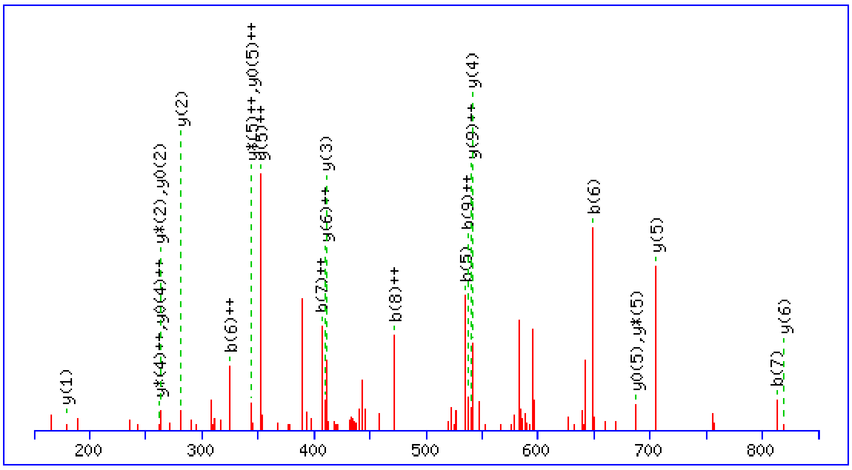
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RISGLIYEETR**
Found in **AT1G07660.2** in **TAIR_Arabidopsis**, Symbols: | histone H4 | chr1:2369209-2369520 FORWARD

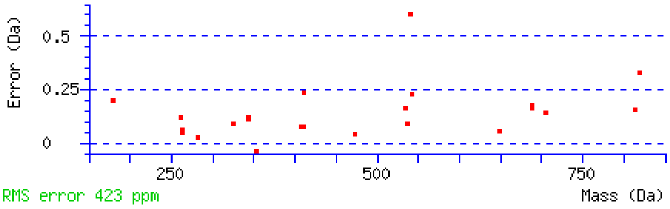
Match to Query 4938: 1352.663982 from(451.895270,3+) index(3146)
Title: Elution from: 30.385 to 30.385 scan no 3912 cid35.00 polarity:+
Data file D12h-3_3.mgf

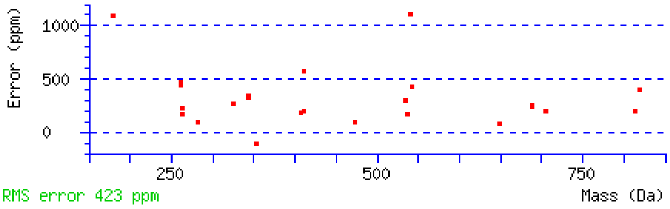
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1352.6642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0054
Matches : 24/114 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			**R**							**11**
2	275.1776	138.0925	257.1540	129.0807			**I**	1193.5823	597.2948	1175.5587	588.2830	1175.5717	588.2895	**10**
3	363.2067	182.1070	345.1831	173.0952	345.1961	173.1017	**S**	1079.5012	540.2542	1061.4776	531.2424	1061.4906	531.2489	**9**
4	421.2252	211.1162	403.2016	202.1044	403.2146	202.1109	**G**	991.4721	496.2397	973.4485	487.2279	973.4616	487.2344	**8**
5	**535.3063**	268.1568	517.2827	259.1450	517.2957	259.1515	**L**	933.4536	467.2304	915.4300	458.2187	915.4431	458.2252	**7**
6	**649.3874**	**325.1973**	631.3638	316.1855	631.3768	316.1920	**I**	***819.3725***	410.1899	801.3489	401.1781	801.3620	401.1846	**6**
7	**813.4478**	**407.2275**	795.4242	398.2157	795.4372	398.2222	**Y**	***705.2914***	353.1494	687.2678	344.1376	687.2809	344.1441	**5**
8	943.4874	**472.2473**	925.4638	463.2355	925.4768	463.2420	**E**	***541.2311***	271.1192	523.2075	262.1074	523.2205	262.1139	**4**
9	1073.5270	**537.2671**	1055.5034	528.2553	1055.5164	528.2619	**E**	***411.1914***	206.0994	393.1678	197.0876	393.1809	197.0941	**3**
10	1175.5717	588.2895	1157.5481	579.2777	1157.5612	579.2842	**T**	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	**2**
11							**R**	***179.1071***	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of RISGLIYEETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G07660.2

Score	Mr(calc)	Delta	Sequence
31.9	1352.6642	-0.0003	RISGLIYEETR
11.8	1352.6642	-0.0003	YILEKREETR
5.5	1352.6665	-0.0025	FGPPKDAPNPLGK
4.7	1352.6616	0.0024	KYDKESTVELK
4.7	1352.6616	0.0024	YGKVDIETSSLK
3.3	1352.6642	-0.0003	GKDGSFLLSVSAR
1.8	1352.6643	-0.0003	LANNNLPPDIQK
1.7	1352.6642	-0.0003	VSGVELGAARSYK
0.9	1352.6616	0.0024	EFSITDLKSATK
0.4	1352.6642	-0.0002	KGSQEGFTVQKK

Mascot: http://www.matrixscience.com/

AT1G07770.1

Mascot Search Results

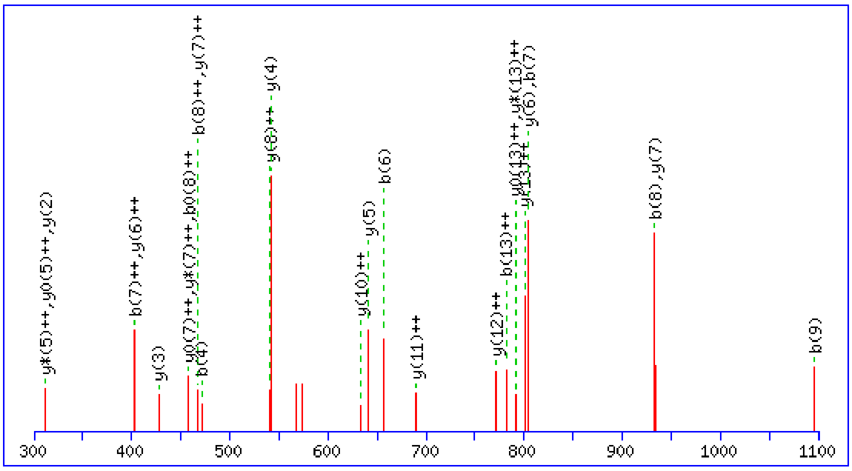
Peptide View

MS/MS Fragmentation of **HGYIGEFEYVDDHR**
Found in **AT1G07770.1** in **TAIR_Arabidopsis**, Symbols: RPS15A | RPS15A (RIBOSOMAL PROTEIN S15A); structural constituent of ribosome | chr1:2408410-2409062 REVERSE

Match to Query 8296: 1735.763808 from(579.595212,3+) index(4438)
Title: Elution from: 40.793 to 40.793 scan no 5554 cid35.00 polarity:+
Data file D12h-1_2.mgf

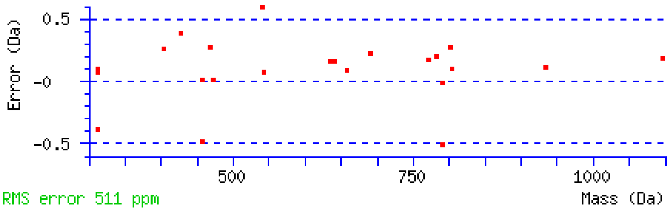
Click mouse within plot area to zoom in by factor of two about that point

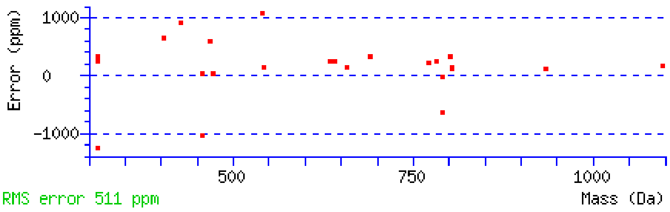
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1735.7590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 1.5e-007
Matches : 28/116 fragment ions using 22 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367			H							14
2	195.0877	98.0475			G	1599.7074	800.3573	1582.6809	791.8441	1581.6968	791.3521	13
3	358.1510	179.5791			Y	1542.6860	771.8466	1525.6594	763.3333	1524.6754	762.8413	12
4	**471.2350**	236.1212			I	1379.6226	690.3149	1362.5961	681.8017	1361.6121	681.3097	11
5	528.2565	264.6319			G	1266.5386	633.7729	1249.5120	625.2596	1248.5280	624.7676	10
6	**657.2991**	329.1532	639.2885	320.1479	E	1209.5171	605.2622	1192.4905	596.7489	1191.5065	596.2569	9
7	**804.3675**	**402.6874**	786.3570	393.6821	F	1080.4745	540.7409	1063.4480	532.2276	1062.4639	531.7356	8
8	**933.4101**	**467.2087**	915.3995	458.2034	E	***933.4061***	467.2067	916.3795	458.6934	915.3955	458.2014	7
9	**1096.4734**	548.7404	1078.4629	539.7351	Y	***804.3635***	402.6854	787.3369	394.1721	786.3529	393.6801	6
10	1195.5419	598.2746	1177.5313	589.2693	V	***641.3002***	321.1537	624.2736	312.6404	623.2896	312.1484	5
11	1310.5688	655.7880	1292.5582	646.7828	D	***542.2318***	271.6195	525.2052	263.1062	524.2212	262.6142	4
12	1425.5957	713.3015	1407.5852	704.2962	D	***427.2048***	214.1060	410.1783	205.5928	409.1942	205.1008	3
13	1562.6547	**781.8310**	1544.6441	772.8257	H	***312.1779***	156.5926	295.1513	148.0793			2
14					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of HGYIGEFEYVDDHR

AT1G07770.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.5	1735.7590	0.0048	HGYIGEFEYVDDHR
12.7	1735.7658	-0.0020	FDQVEAPKTMMDHR

AT1G07790.1

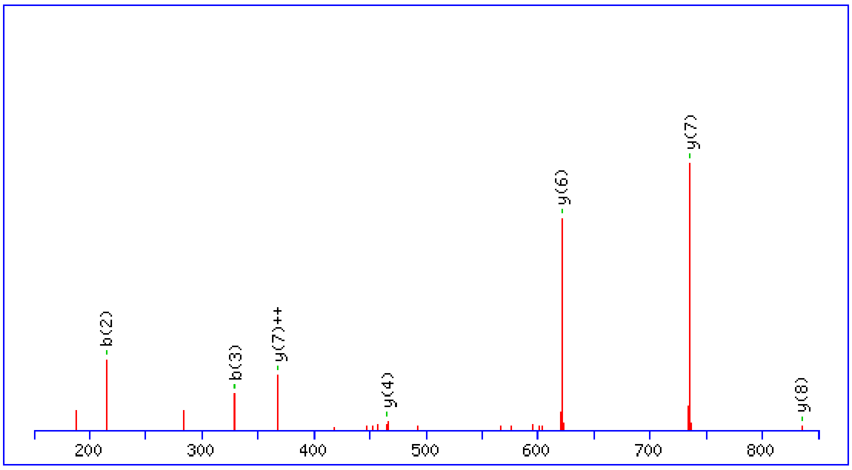
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLPGELAK**
Found in **AT1G07790.1** in **TAIR_Arabidopsis**, Symbols: HTB1 | HTB1; DNA binding | chr1:2413046-2413492 FORWARD

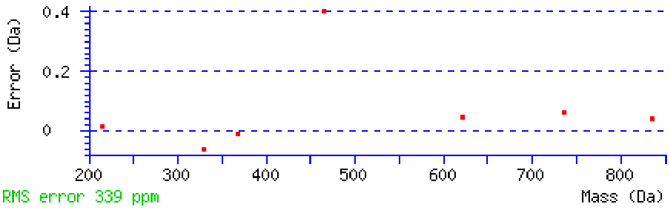
Match to Query 1653: 948.549952 from(475.282252,2+) index(4729)
Title: Elution from: 45.606 to 45.606 scan no 6024 cid35.00 polarity:+
Data file D12h-2_2.mgf

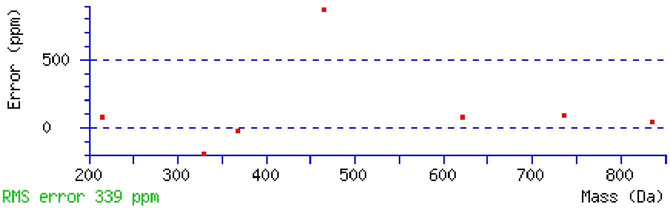
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 948.5504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.0088
Matches : 7/64 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							9
2	**215.1538**	108.0805			V	***835.4766***	418.2419	817.4530	409.2301	817.4660	409.2367	8
3	**329.2349**	165.1211			L	***735.4111***	368.2092	717.3876	359.1974	717.4006	359.2039	7
4	427.2847	214.1460			P	***621.3300***	311.1687	603.3065	302.1569	603.3195	302.1634	6
5	485.3032	243.1552			G	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	5
6	615.3428	308.1751	597.3323	299.1698	E	***465.2617***	233.1345	447.2382	224.1227	447.2512	224.1292	4
7	729.4239	365.2156	711.4134	356.2103	L	335.2221	168.1147	317.1985	159.1029			3
8	801.4581	401.2327	783.4475	392.2274	A	221.1410	111.0741	203.1174	102.0624			2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LVLPGELAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.5	948.5504	-0.0005	LVLPGELAK

AT1G07790.1

1.9	948.5504	-0.0005	INPEILIK

Mascot: http://www.matrixscience.com/

AT1G07890.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRSGFEGAWTSNPLIFDNSYFK**
Found in **AT1G07890.1** in **TAIR_Arabidopsis**, Symbols: MEE6, CS1, APX1 | APX1 (ASCORBATE PEROXIDASE 1); L-ascorbate peroxidase | chr1:2438002-2439432 FORWARD

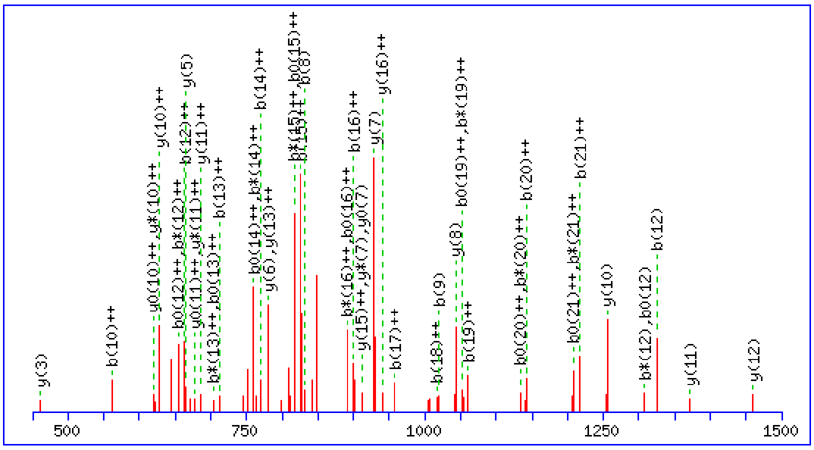
Match to Query 10432: 2579.097873 from(860.706567,3+) index(10215)
Title: Elution from: 96.214 to 96.214 scan no 14462 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

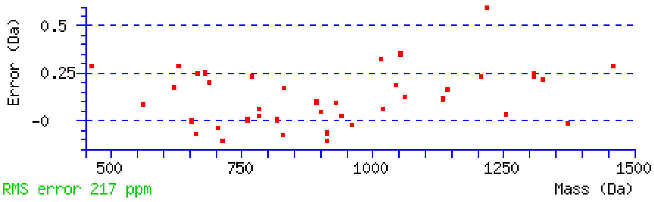
Show Y-axis ☐

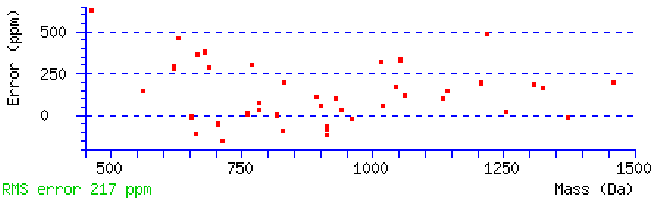


Monoisotopic mass of neutral peptide Mr(calc): 2579.0956
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 4.5e-007
Matches : 51/244 fragment ions using 60 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0313	59.0193			99.0207	50.0140	D							22
2	277.1205	139.0639	259.0969	130.0521	259.1099	130.0586	R	2464.0789	1232.5431	2446.0553	1223.5313	2446.0683	1223.5378	21
3	365.1496	183.0784	347.1260	174.0666	347.1390	174.0731	S	2303.9896	1152.4984	2285.9660	1143.4867	2285.9790	1143.4932	20
4	423.1681	212.0877	405.1445	203.0759	405.1575	203.0824	G	2215.9606	1108.4839	2197.9370	1099.4721	2197.9500	1099.4786	19
5	571.2335	286.1204	553.2099	277.1086	553.2230	277.1151	F	2157.9421	1079.4747	2139.9185	1070.4629	2139.9315	1070.4694	18
6	701.2731	351.1402	683.2496	342.1284	683.2626	342.1349	E	2009.8766	1005.4419	1991.8530	996.4301	1991.8660	996.4367	17
7	759.2916	380.1495	741.2681	371.1377	741.2811	371.1442	G	1879.8370	940.4221	1861.8134	931.4103	1861.8264	931.4168	16
8	**831.3258**	416.1665	813.3022	407.1547	813.3152	407.1613	A	1821.8185	911.4129	1803.7949	902.4011	1803.8079	902.4076	15
9	**1019.3992**	510.2032	1001.3756	501.1914	1001.3886	501.1979	W	1749.7843	875.3958	1731.7607	866.3840	1731.7738	866.3905	14
10	1121.4439	***561.2256***	1103.4203	552.2138	1103.4333	552.2203	T	1561.7109	781.3591	1543.6874	772.3473	1543.7004	772.3538	13
11	1209.4730	605.2401	1191.4494	596.2283	1191.4624	596.2348	S	**1459.6662**	730.3368	1441.6426	721.3250	1441.6557	721.3315	12
12	**1325.5099**	***663.2586***	1307.4864	654.2468	1307.4994	654.2533	N	**1371.6372**	686.3222	1353.6136	677.3104	1353.6266	677.3169	11
13	1423.5597	***712.2835***	1405.5362	703.2717	1405.5492	703.2782	P	**1255.6002**	628.3037	1237.5766	619.2919	1237.5896	619.2984	10
14	1537.6408	***769.3241***	1519.6173	760.3123	1519.6303	760.3188	L	1157.5504	579.2788	1139.5268	570.2670	1139.5398	570.2735	9
15	1651.7219	***826.3646***	1633.6984	817.3528	1633.7114	817.3593	I	**1043.4693**	522.2383	1025.4457	513.2265	1025.4587	513.2330	8
16	1799.7874	***900.3973***	1781.7638	891.3855	1781.7768	891.3921	F	**929.3882**	465.1977	911.3646	456.1859	911.3776	456.1924	7
17	1915.8114	***958.4093***	1897.7878	949.3975	1897.8008	949.4040	D	**781.3227**	391.1650	763.2991	382.1532	763.3122	382.1597	6
18	2031.8484	***1016.4278***	2013.8248	1007.4160	2013.8378	1007.4225	N	**665.2987**	333.1530	647.2752	324.1412	647.2882	324.1477	5
19	2119.8774	***1060.4424***	2101.8538	1051.4306	2101.8669	1051.4371	S	549.2618	275.1345	531.2382	266.1227	531.2512	266.1292	4
20	2283.9378	***1142.4725***	2265.9142	1133.4607	2265.9272	1133.4673	Y	**461.2327**	231.1200	443.2091	222.1082			3
21	2432.0032	***1216.5053***	2413.9797	1207.4935	2413.9927	1207.5000	F	297.1723	149.0898	279.1487	140.0780			2
22							K	149.1069	75.0571	131.0833	66.0453			1

AT1G07890.1





NCBI **BLAST** search of DRSGFEGAWTSNPLIFDNSYFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.7	2579.0956	0.0023	DRSGFEGAWTSNPLIFDNSYFK

Mascot: http://www.matrixscience.com/

AT1G07920.1

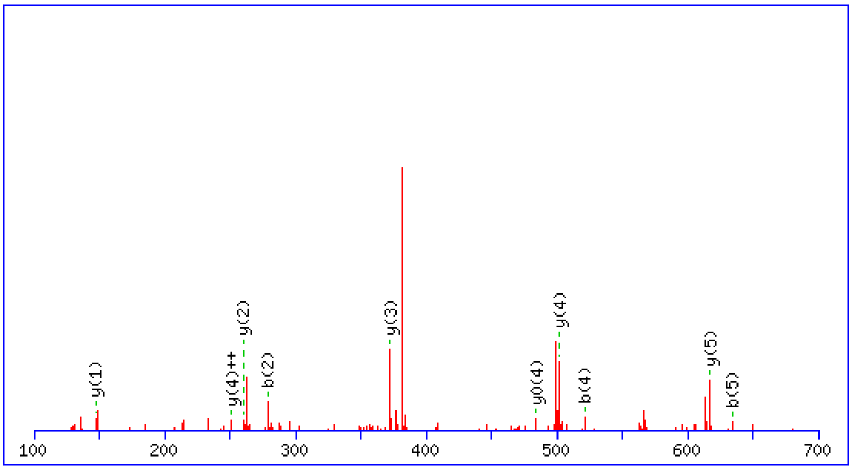
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDEIIK**
Found in **AT1G07920.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1-alpha / EF-1-alpha | chr1:2455556-2456998 FORWARD

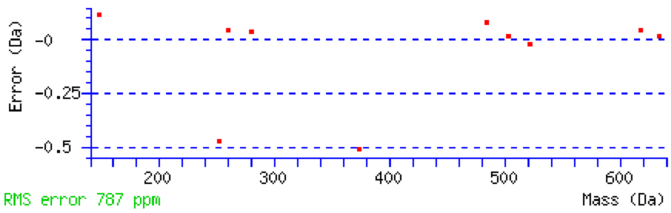
Match to Query 876: 779.407940 from(390.711246,2+) index(1736)
Title: Elution from: 21.868 to 21.868 scan no 2283 cid35.00 polarity:+
Data file D6h-1_3.mgf

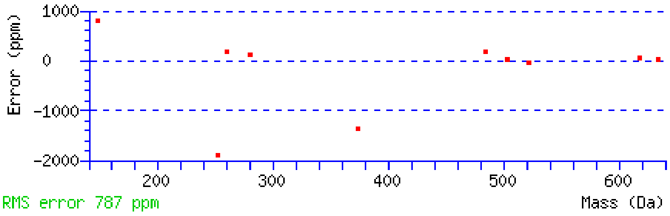
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 779.4065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.019
Matches : 10/42 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							6
2	**279.0975**	140.0524	261.0870	131.0471	D	***617.3505***	309.1789	600.3239	300.6656	599.3399	300.1736	5
3	408.1401	204.5737	390.1296	195.5684	E	***502.3235***	251.6654	485.2970	243.1521	484.3130	242.6601	4
4	**521.2242**	261.1157	503.2136	252.1105	I	***373.2809***	187.1441	356.2544	178.6308			3
5	**634.3083**	317.6578	616.2977	308.6525	I	***260.1969***	130.6021	243.1703	122.0888			2
6					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YDEIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.7	779.4065	0.0014	YDEIIK
5.9	779.4065	0.0014	YLLEDK
5.3	779.4065	0.0014	VYEELK
0.5	779.4065	0.0014	LYDEIK

AT1G07920.1

0.4	779.4065	0.0014	YEVIEK
0.4	779.4065	0.0014	YEVLEK
0.1	779.4065	0.0014	EIEVYK
0.1	779.4065	0.0014	ELEVYK

AT1G08200.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLALDVYNDK**
Found in **AT1G08200.1** in **TAIR_Arabidopsis**, Symbols: AXS2 | AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2) | chr1:2574256-2576606 REVERSE

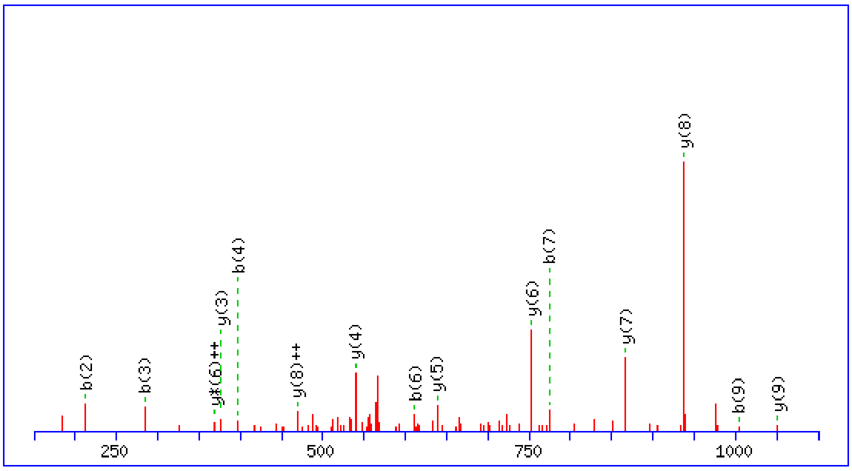
Match to Query 4092: 1148.604698 from(575.309625,2+) index(5618)
Title: Elution from: 49.577 to 49.577 scan no 6985 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1100 Da Full range

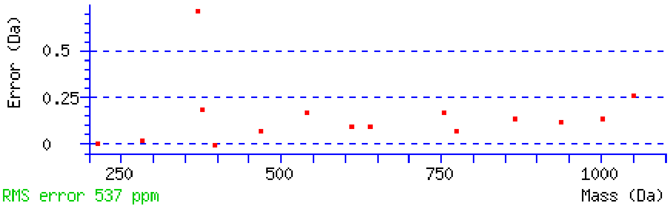
Label all possible matches ○ Label matches used for scoring ●

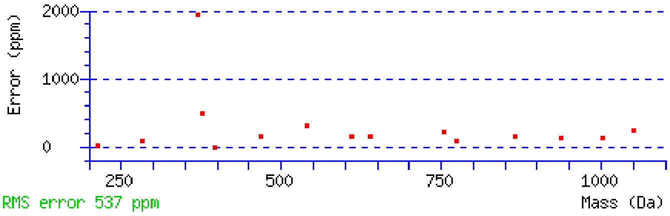
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1148.6077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 1.2e-006
Matches : 15/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							10
2	***213.1598***	107.0835					L	***1050.5466***	525.7769	1033.5201	517.2637	1032.5360	516.7717	9
3	***284.1969***	142.6021					A	***937.4625***	469.2349	920.4360	460.7216	919.4520	460.2296	8
4	***397.2809***	199.1441					L	***866.4254***	433.7164	849.3989	425.2031	848.4149	424.7111	7
5	512.3079	256.6576			494.2973	247.6523	D	***753.3414***	377.1743	736.3148	368.6610	735.3308	368.1690	6
6	***611.3763***	306.1918			593.3657	297.1865	V	***638.3144***	319.6608	621.2879	311.1476	620.3039	310.6556	5
7	***774.4396***	387.7234			756.4291	378.7182	Y	***539.2460***	270.1266	522.2195	261.6134	521.2354	261.1214	4
8	888.4825	444.7449	871.4560	436.2316	870.4720	435.7396	N	***376.1827***	188.5950	359.1561	180.0817	358.1721	179.5897	3
9	***1003.5095***	502.2584	986.4829	493.7451	985.4989	493.2531	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VLALDVYNDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G08200.1

Score	Mr(calc)	Delta	Sequence
65.7	1148.6077	-0.0030	VLALDVYNDK
6.8	1148.6077	-0.0030	VLVQDGIYDK
1.9	1148.6050	-0.0003	AIGRNGSGYVR
0.8	1148.6077	-0.0030	VIDNYVGEIK

AT1G08360.1

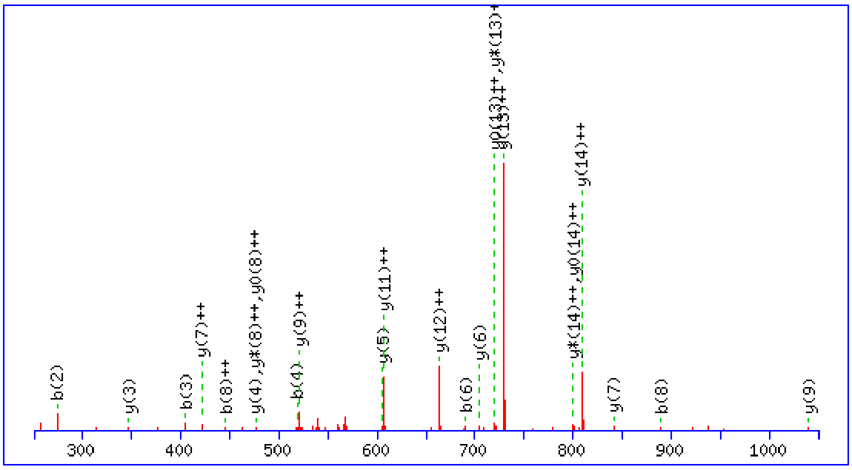
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ICMLGDAQHVEEAEK**
Found in **AT1G08360.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L10A (RPL10aA) | chr1:2636228-2637691 FORWARD

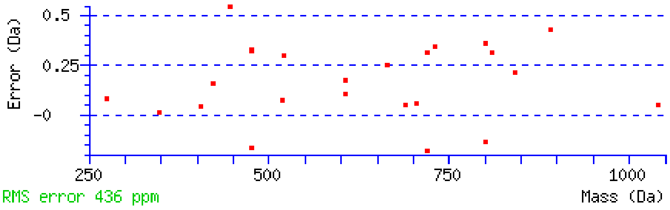
Match to Query 8372: 1728.780624 from(577.267484,3+) index(3863)
Title: Elution from: 36.752 to 36.752 scan no 4842 cid35.00 polarity:+
Data file D6h-3_1.mgf

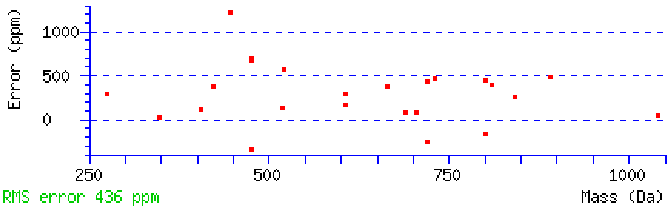
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1728.7811
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00048
Matches : 24/142 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							15
2	**274.1220**	137.5646					C	1616.7043	**808.8558**	1599.6778	**800.3425**	1598.6938	**799.8505**	14
3	**405.1625**	203.0849					M	1456.6737	**728.8405**	1439.6471	**720.3272**	1438.6631	**719.8352**	13
4	**518.2465**	259.6269					L	1325.6332	**663.3202**	1308.6066	654.8070	1307.6226	654.3149	12
5	575.2680	288.1376					G	1212.5491	**606.7782**	1195.5226	598.2649	1194.5386	597.7729	11
6	**690.2949**	345.6511			672.2844	336.6458	D	1155.5277	578.2675	1138.5011	569.7542	1137.5171	569.2622	10
7	761.3321	381.1697			743.3215	372.1644	A	***1040.5007***	**520.7540**	1023.4742	512.2407	1022.4902	511.7487	9
8	**889.3906**	**445.1990**	872.3641	436.6857	871.3801	436.1937	Q	969.4636	485.2354	952.4371	**476.7222**	951.4530	**476.2302**	8
9	1026.4495	513.7284	1009.4230	505.2151	1008.4390	504.7231	H	***841.4050***	**421.2061**	824.3785	412.6929	823.3945	412.2009	7
10	1125.5180	563.2626	1108.4914	554.7493	1107.5074	554.2573	V	***704.3461***	352.6767	687.3196	344.1634	686.3355	343.6714	6
11	1254.5606	627.7839	1237.5340	619.2706	1236.5500	618.7786	E	***605.2777***	303.1425	588.2511	294.6292	587.2671	294.1372	5
12	1383.6031	692.3052	1366.5766	683.7919	1365.5926	683.2999	E	***476.2351***	238.6212	459.2086	230.1079	458.2245	229.6159	4
13	1454.6403	727.8238	1437.6137	719.3105	1436.6297	718.8185	A	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
14	1583.6829	792.3451	1566.6563	783.8318	1565.6723	783.3398	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ICMLGDAQHVEEAEK

AT1G08360.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.6	1728.7811	-0.0005	ICMLGDAQHVEEAEK
5.2	1728.7771	0.0035	DRKSMGVMVDSSSGNK
3.5	1728.7844	-0.0038	KGSAGLMEEMTRMEK
2.7	1728.7844	-0.0038	KGSAGLMEEMTRMEK
2.7	1728.7844	-0.0038	KGSAGLMEEMTRMEK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QMSINSVPKK**
Found in **AT1G08420.1** in **TAIR_Arabidopsis**, Symbols: | kelch repeat-containing protein / serine/threonine phosphoesterase family protein | chr1:2649956-2656561 FORWARD

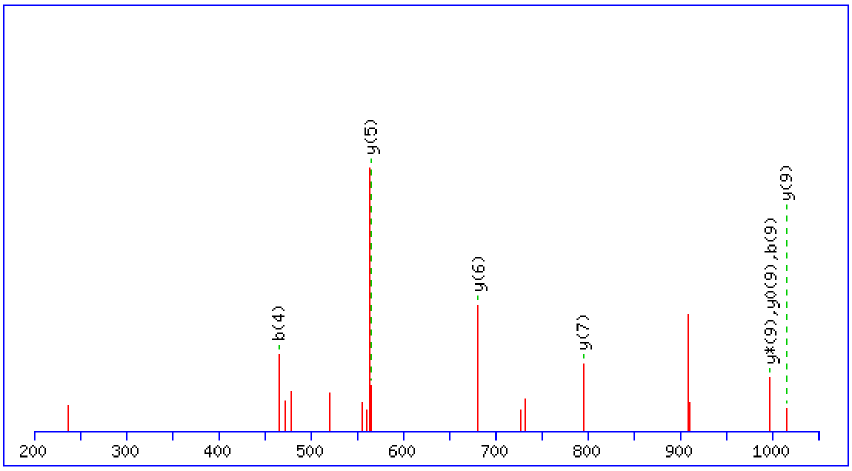
Match to Query 3927: 1144.571264 from(573.292908,2+) index(1356)
Title: Elution from: 19.798 to 19.798 scan no 1871 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

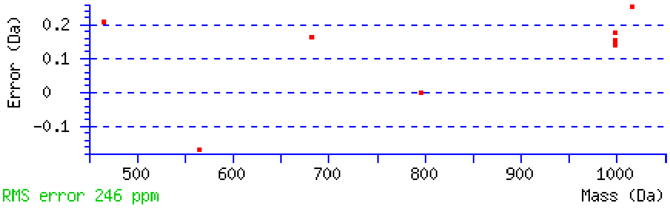
Label all possible matches ○ Label matches used for scoring ●

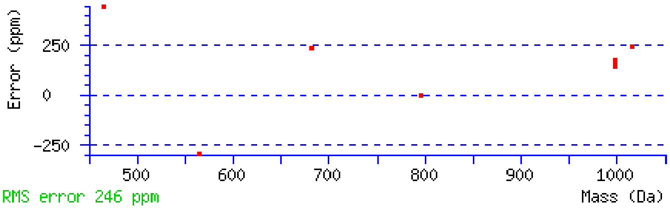
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.5703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.037
Matches : 8/96 fragment ions using 13 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0599	66.0336	113.0363	57.0218			Q							10
2	263.0974	132.0524	245.0739	123.0406			M	***1015.5249***	508.2661	997.5013	499.2543	997.5143	499.2608	9
3	351.1265	176.0669	333.1029	167.0551	333.1159	167.0616	S	883.4874	442.2473	865.4638	433.2355	865.4768	433.2420	8
4	**465.2076**	233.1074	447.1840	224.0956	447.1970	224.1022	I	***795.4583***	398.2328	777.4347	389.2210	777.4477	389.2275	7
5	581.2446	291.1259	563.2210	282.1141	563.2340	282.1207	N	***681.3772***	341.1922	663.3536	332.1805	663.3667	332.1870	6
6	669.2737	335.1405	651.2501	326.1287	651.2631	326.1352	S	***565.3402***	283.1737	547.3166	274.1620	547.3297	274.1685	5
7	769.3391	385.1732	751.3155	376.1614	751.3285	376.1679	V	477.3112	239.1592	459.2876	230.1474			4
8	867.3889	434.1981	849.3653	425.1863	849.3783	425.1928	P	377.2457	189.1265	359.2221	180.1147			3
9	**997.4779**	499.2426	979.4544	490.2308	979.4674	490.2373	K	279.1959	140.1016	261.1723	131.0898			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QMSINSVPKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G08420.1

Score	Mr(calc)	Delta	Sequence
21.8	1144.5703	0.0010	QMSINSVPKK
16.1	1144.5730	-0.0017	MSLSHLLRR
9.1	1144.5703	0.0010	RPSMVEVVSK
8.7	1144.5703	0.0010	KMGEVEIAVR
8.3	1144.5703	0.0010	EANVMLVLAR
6.5	1144.5695	0.0017	IWDVRLNGR
3.5	1144.5703	0.0010	LAKMPENKGK
3.0	1144.5703	0.0010	LMISEARPSK
3.0	1144.5703	0.0010	VLRMAPDVSK
2.9	1144.5703	0.0010	MVTVDGRPIK

AT1G08520.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPFIQIPLGVTEDR**
Found in **AT1G08520.1** in **TAIR_Arabidopsis**, Symbols: PDE166, CHLD | CHLD/PDE166 (PIGMENT DEFECTIVE 166); magnesium chelatase/ nucleoside-triphosphatase/ nucleotide binding | chr1:2696541-2700822 FORWARD

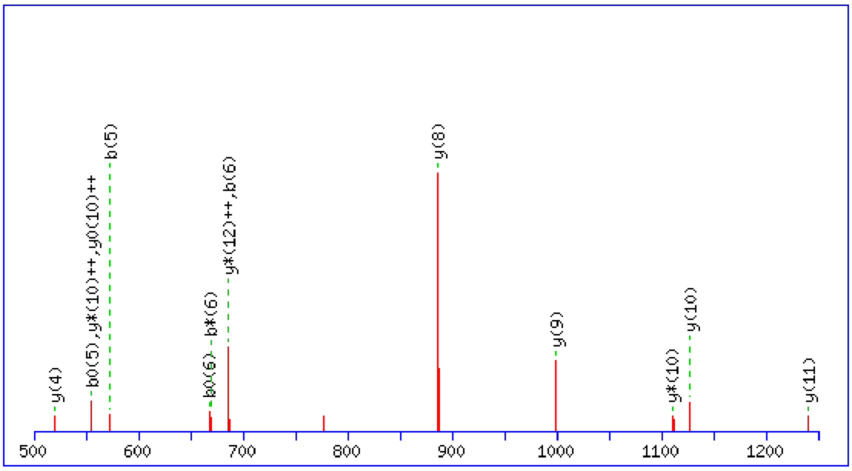
Match to Query 6805: 1570.835074 from(786.424813,2+) index(8633)
Title: Elution from: 77.419 to 77.419 scan no 11607 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1250 Da Full range

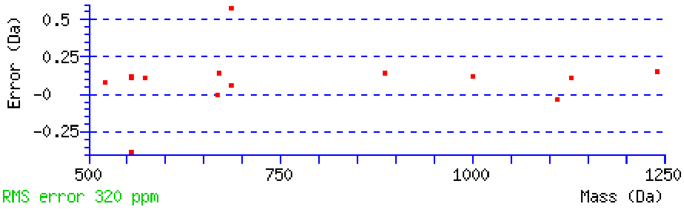
Label all possible matches ○ Label matches used for scoring ●

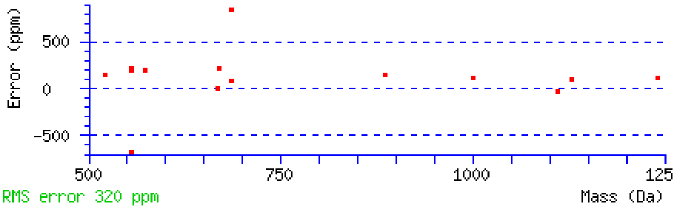
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1570.8355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00055
Matches : 14/146 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**14**
2	185.0921	93.0497			167.0815	84.0444	**P**	1484.8108	742.9090	1467.7842	734.3957	1466.8002	733.9037	**13**
3	332.1605	166.5839			314.1499	157.5786	**F**	1387.7580	694.3826	1370.7314	685.8694	1369.7474	685.3774	**12**
4	445.2445	223.1259			427.2340	214.1206	**I**	***1240.6896***	620.8484	1223.6630	612.3352	1222.6790	611.8431	**11**
5	**573.3031**	287.1552	556.2766	278.6419	555.2926	278.1499	**Q**	***1127.6055***	564.3064	1110.5790	555.7931	1109.5950	555.3011	**10**
6	**686.3872**	343.6972	669.3606	335.1840	668.3766	334.6919	**I**	***999.5469***	500.2771	982.5204	491.7638	981.5364	491.2718	**9**
7	783.4400	392.2236	766.4134	383.7103	765.4294	383.2183	**P**	***886.4629***	443.7351	869.4363	435.2218	868.4523	434.7298	**8**
8	896.5240	448.7656	879.4975	440.2524	878.5135	439.7604	**L**	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	**7**
9	953.5455	477.2764	936.5189	468.7631	935.5349	468.2711	**G**	676.3260	338.6667	659.2995	330.1534	658.3155	329.6614	**6**
10	1052.6139	526.8106	1035.5873	518.2973	1034.6033	517.8053	**V**	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	**5**
11	1153.6616	577.3344	1136.6350	568.8212	1135.6510	568.3291	**T**	***520.2362***	260.6217	503.2096	252.1084	502.2256	251.6164	**4**
12	1282.7042	641.8557	1265.6776	633.3424	1264.6936	632.8504	**E**	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	**3**
13	1397.7311	699.3692	1380.7046	690.8559	1379.7205	690.3639	**D**	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SPFIQIPLGVTEDR

AT1G08520.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.5	1570.8355	-0.0004	SPFIQIPLGVTEDR

Mascot: http://www.matrixscience.com/

AT1G08600.1

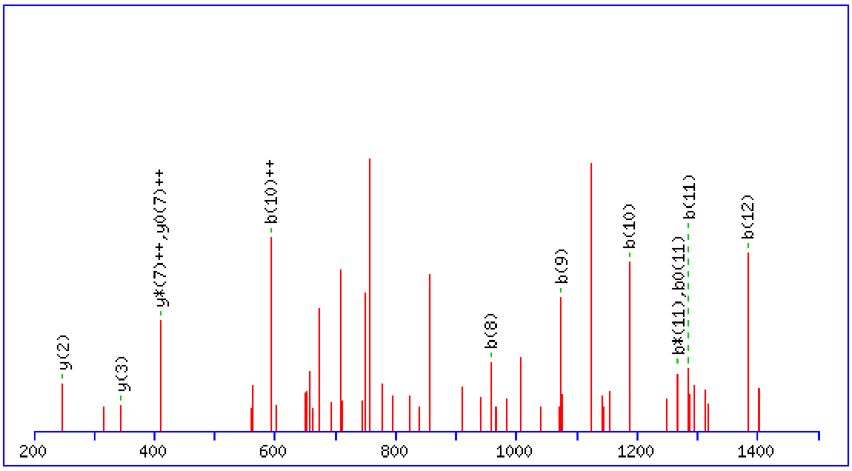
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDMNVVKKDLPPK**
Found in **AT1G08600.1** in **TAIR_Arabidopsis**, Symbols: ATRX, CHR20 | ATRX/CHR20; ATP binding / DNA binding / helicase | chr1:2724565-2733434 FORWARD

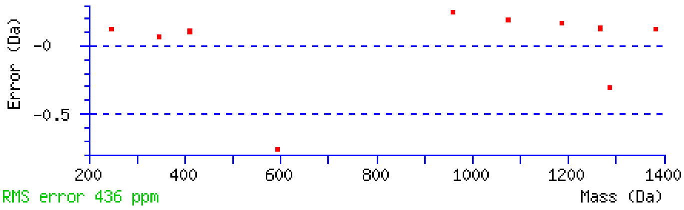
Match to Query 6962: 1530.745332 from(766.379942,2+) index(6954)
Title: Elution from: 60.156 to 60.156 scan no 8868 cid35.00 polarity:+
Data file D1d-3_1.mgf

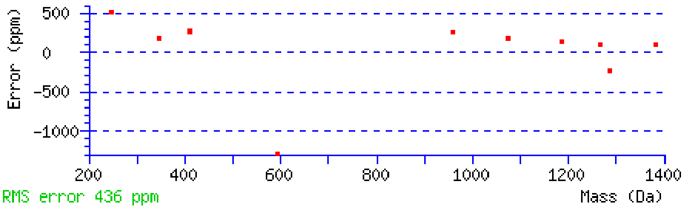
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1530.7493
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.02
Matches : 12/128 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	133.0448	67.0260					**M**							**13**
2	249.0688	125.0380			231.0582	116.0327	**D**	1399.7190	700.3631	1381.6954	691.3513	1381.7084	691.3579	**12**
3	381.1063	191.0568			363.0957	182.0515	**M**	1283.6950	642.3512	1265.6714	633.3394	1265.6845	633.3459	**11**
4	497.1433	249.0753	479.1197	240.0635	479.1327	240.0700	**N**	1151.6575	576.3324	1133.6339	567.3206	1133.6469	567.3271	**10**
5	597.2087	299.1080	579.1852	290.0962	579.1982	290.1027	**V**	1035.6205	518.3139	1017.5969	509.3021	1017.6099	509.3086	**9**
6	697.2742	349.1407	679.2506	340.1289	679.2636	340.1354	**V**	935.5551	468.2812	917.5315	459.2694	917.5445	459.2759	**8**
7	827.3632	414.1852	809.3396	405.1735	809.3527	405.1800	**K**	835.4896	418.2484	817.4660	409.2367	817.4790	409.2432	**7**
8	***957.4523***	479.2298	939.4287	470.2180	939.4417	470.2245	**K**	705.4006	353.2039	687.3770	344.1921	687.3900	344.1986	**6**
9	***1073.4762***	537.2418	1055.4526	528.2300	1055.4657	528.2365	**D**	575.3115	288.1594	557.2880	279.1476	557.3010	279.1541	**5**
10	***1187.5573***	594.2823	1169.5337	585.2705	1169.5468	585.2770	**L**	459.2876	230.1474	441.2640	221.1356			**4**
11	***1285.6071***	643.3072	1267.5835	634.2954	1267.5966	634.3019	**P**	**345.2065**	173.1069	327.1829	164.0951			**3**
12	***1383.6569***	692.3321	1365.6333	683.3203	1365.6464	683.3268	**P**	**247.1567**	124.0820	229.1331	115.0702			**2**
13							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MDMNVVKKDLPPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G08600.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.0	1530.7493	-0.0039	MDMNVVKKDLPPK
7.4	1530.7481	-0.0028	NQIPWLIMFPEK
3.1	1530.7436	0.0017	LMEGDIRNIIDPK
2.9	1530.7410	0.0044	MAEISGLPDDLLVK
2.3	1530.7437	0.0017	MDLEARTLPPNLK
1.4	1530.7436	0.0017	QGLIKENLCVDPK
0.9	1530.7484	-0.0031	LEAEIRELESTPK
0.8	1530.7484	-0.0030	LVVSSATPQEVEQK
0.8	1530.7432	0.0021	MISIISSTYFDLK
0.1	1530.7493	-0.0039	ALEMLEKGVMHLK

AT1G08760.1

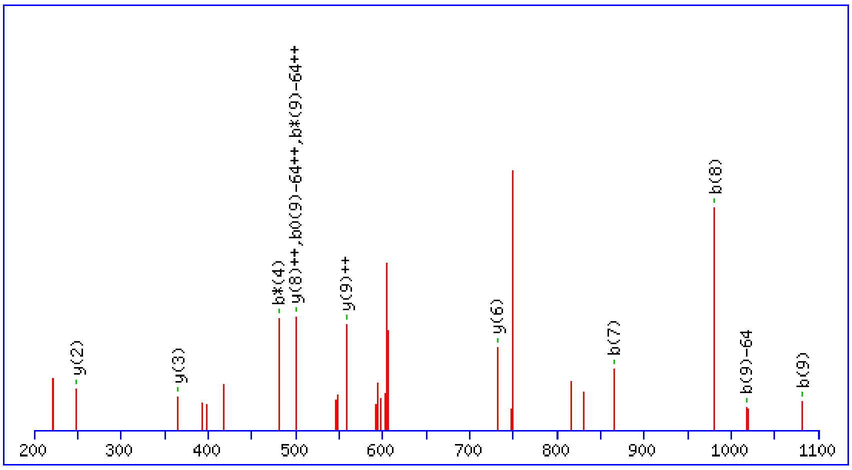
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQHMNTDVK**
Found in **AT1G08760.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13370.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN75715.1); contains InterPro domain Protein of unknown function DUF936, plant (InterPro:IPR010341) | chr1:28054

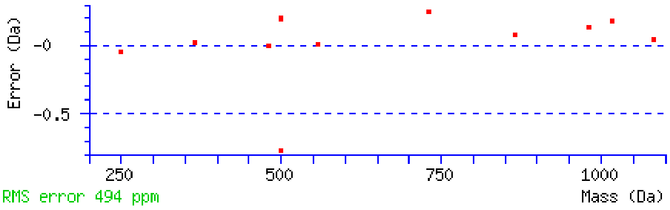
Match to Query 4074: 1228.571012 from(615.292782,2+) index(3169)
Title: Elution from: 30.701 to 30.701 scan no 3927 cid35.00 polarity:+
Data file 0-3_3.mgf

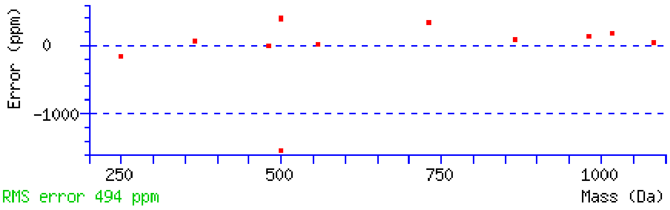
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1228.5680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.021
Matches : 12/138 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							10
2	229.1695	115.0884					L	1115.4942	558.2507	1097.4706	549.2390	1097.4836	549.2455	9
3	359.2221	180.1147	341.1985	171.1029			Q	1001.4131	501.2102	983.3895	492.1984	983.4025	492.2049	8
4	499.2721	250.1397	481.2486	241.1279			H	871.3605	436.1839	853.3369	427.1721	853.3499	427.1786	7
5	647.3046	324.1559	629.2810	315.1441			M	***731.3104***	366.1589	713.2869	357.1471	713.2999	357.1536	6
6	763.3416	382.1744	745.3180	373.1626			N	583.2780	292.1426	565.2544	283.1309	565.2674	283.1374	5
7	***865.3863***	433.1968	847.3627	424.1850	847.3757	424.1915	T	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
8	***981.4103***	491.2088	963.3867	482.1970	963.3997	482.2035	D	***365.1963***	183.1018	347.1727	174.0900	347.1857	174.0965	3
9	***1081.4757***	541.2415	1063.4521	532.2297	1063.4651	532.2362	V	***249.1723***	125.0898	231.1487	116.0780			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LLQHMNTDVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G08760.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	1228.5680	0.0030	LLQHMNTDVK
11.9	1228.5729	-0.0019	FRGLFVGNMR
0.4	1228.5736	-0.0026	MKQYKCLTK
0.1	1228.5728	-0.0017	DPTPQTTALSGK

AT1G08990.1

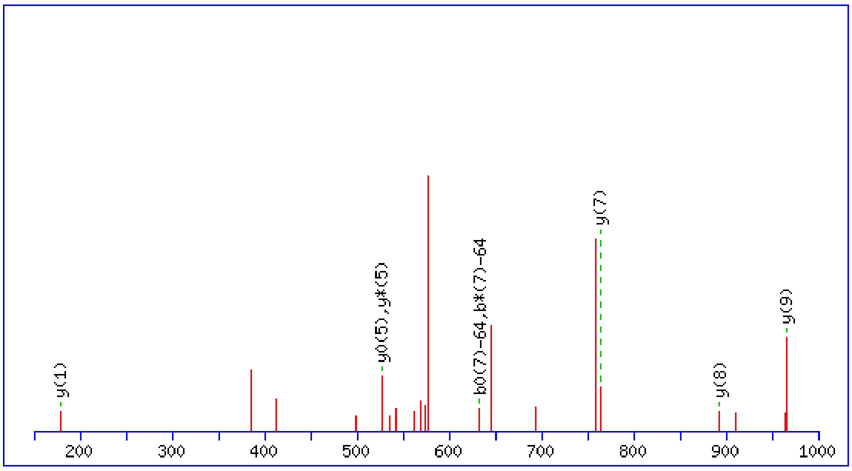
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGAKSKSSSTR**
Found in **AT1G08990.1** in **TAIR_Arabidopsis**, Symbols: PGSIP5 | PGSIP5 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 5); transferase, transferring glycosyl groups | chr1:2888756-2890756 FORWARD

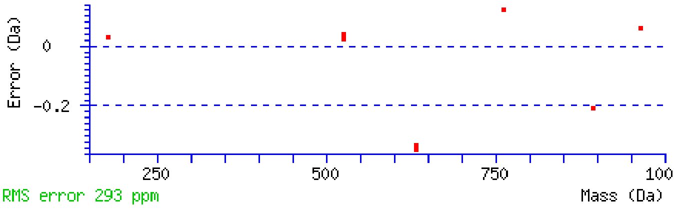
Match to Query 4131: 1170.520882 from(586.267717,2+) index(8414)
Title: Elution from: 73.641 to 73.641 scan no 11139 cid35.00 polarity:+
Data file D1d-3_2.mgf

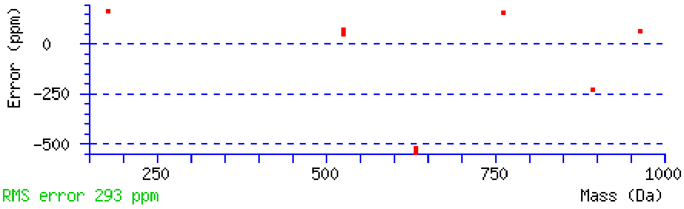
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1170.5239
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.033
Matches : 8/150 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							11
2	207.0582	104.0327					G	1023.4988	512.2530	1005.4752	503.2412	1005.4882	503.2477	10
3	279.0924	140.0498					A	***965.4803***	483.2438	947.4567	474.2320	947.4697	474.2385	9
4	409.1814	205.0943	391.1578	196.0825			K	***893.4461***	447.2267	875.4225	438.2149	875.4356	438.2214	8
5	497.2105	249.1089	479.1869	240.0971	479.1999	240.1036	S	***763.3571***	382.1822	745.3335	373.1704	745.3465	373.1769	7
6	627.2995	314.1534	609.2759	305.1416	609.2889	305.1481	K	675.3280	338.1677	657.3044	329.1559	657.3175	329.1624	6
7	715.3286	358.1679	697.3050	349.1561	697.3180	349.1626	S	545.2390	273.1231	527.2154	264.1113	527.2284	264.1179	5
8	803.3576	402.1824	785.3340	393.1707	785.3470	393.1772	S	457.2099	229.1086	439.1863	220.0968	439.1994	220.1033	4
9	891.3867	446.1970	873.3631	437.1852	873.3761	437.1917	S	369.1809	185.0941	351.1573	176.0823	351.1703	176.0888	3
10	993.4314	497.2193	975.4078	488.2075	975.4208	488.2141	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
11							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MGAKSKSSSTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G08990.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.6	1170.5239	-0.0031	MGAKSKSSSTR
21.3	1170.5223	-0.0014	GFGFITFDEK
9.5	1170.5192	0.0017	NTMMKRSVR
5.7	1170.5201	0.0007	FSSSYSEPKK
2.2	1170.5235	-0.0026	STSEVYAMKK
1.6	1170.5206	0.0003	HGNSELNSIGK
1.5	1170.5228	-0.0019	AGSFFQDKTR
0.1	1170.5188	0.0021	YLQMMNSKK
0.1	1170.5188	0.0021	YLQMMNSKK

AT1G09100.1

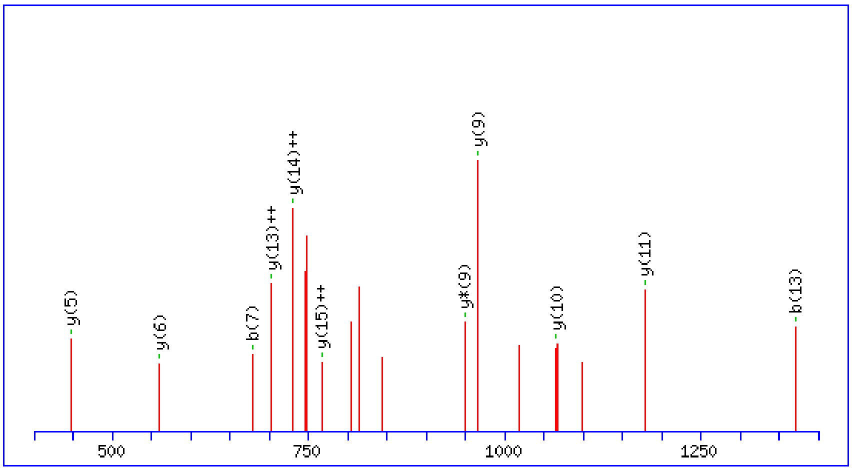
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGPQLVQMFIGDGAK**
Found in **AT1G09100.1** in **TAIR_Arabidopsis**, Symbols: RPT5B | RPT5B (26S PROTEASOME AAA-ATPASE SUBUNIT RPT5B); ATPase/ calmodulin binding | chr1:2936677-2939260 REVERSE

Match to Query 6974: 1643.866430 from(822.940491,2+) index(9580)
Title: Elution from: 91.937 to 91.937 scan no 13655 cid35.00 polarity:+
Data file D1d-1_3.mgf

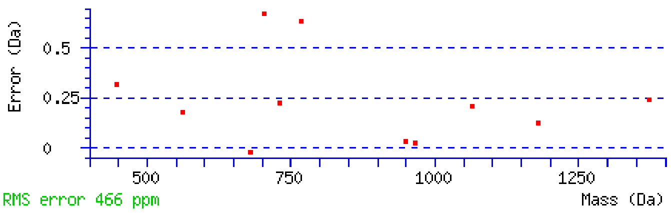
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

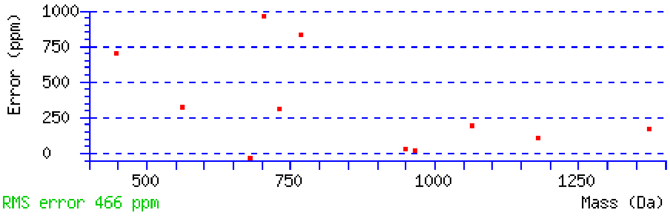


Monoisotopic mass of neutral peptide Mr(calc): 1643.8705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0014
Matches : 11/142 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							16
2	185.1285	93.0679					A	1531.7937	766.4005	1514.7672	757.8872	1513.7832	757.3952	15
3	242.1499	121.5786					G	1460.7566	730.8819	1443.7301	722.3687	1442.7460	721.8767	14
4	339.2027	170.1050					P	1403.7351	702.3712	1386.7086	693.8579	1385.7246	693.3659	13
5	467.2613	234.1343	450.2347	225.6210			Q	1306.6824	653.8448	1289.6558	645.3316	1288.6718	644.8395	12
6	580.3453	290.6763	563.3188	282.1630			L	***1178.6238***	589.8155	1161.5973	581.3023	1160.6132	580.8103	11
7	**679.4137**	340.2105	662.3872	331.6972			V	***1065.5397***	533.2735	1048.5132	524.7602	1047.5292	524.2682	10
8	807.4723	404.2398	790.4458	395.7265			Q	***966.4713***	483.7393	949.4448	475.2260	948.4608	474.7340	9
9	938.5128	469.7600	921.4863	461.2468			M	838.4128	419.7100	821.3862	411.1967	820.4022	410.7047	8
10	1085.5812	543.2942	1068.5547	534.7810			F	707.3723	354.1898	690.3457	345.6765	689.3617	345.1845	7
11	1198.6653	599.8363	1181.6387	591.3230			I	***560.3039***	280.6556	543.2773	272.1423	542.2933	271.6503	6
12	1255.6867	628.3470	1238.6602	619.8337			G	***447.2198***	224.1135	430.1932	215.6003	429.2092	215.1082	5
13	**1370.7137**	685.8605	1353.6871	677.3472	1352.7031	676.8552	D	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	4
14	1427.7351	714.3712	1410.7086	705.8579	1409.7246	705.3659	G	275.1714	138.0893	258.1448	129.5761			3
15	1498.7723	749.8898	1481.7457	741.3765	1480.7617	740.8845	A	218.1499	109.5786	201.1234	101.0653			2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT1G09100.1





NCBI **BLAST** search of LAGPQLVQMFIGDGAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.7	1643.8705	-0.0041	LAGPQLVQMFIGDGAK
7.9	1643.8671	-0.0007	FGLVYVDYKNGLTR
0.9	1643.8631	0.0033	LAGNRLPSFTPEQSK
0.3	1643.8712	-0.0048	RQLLARLDVCMGGR

Mascot: http://www.matrixscience.com/

AT1G09130.1

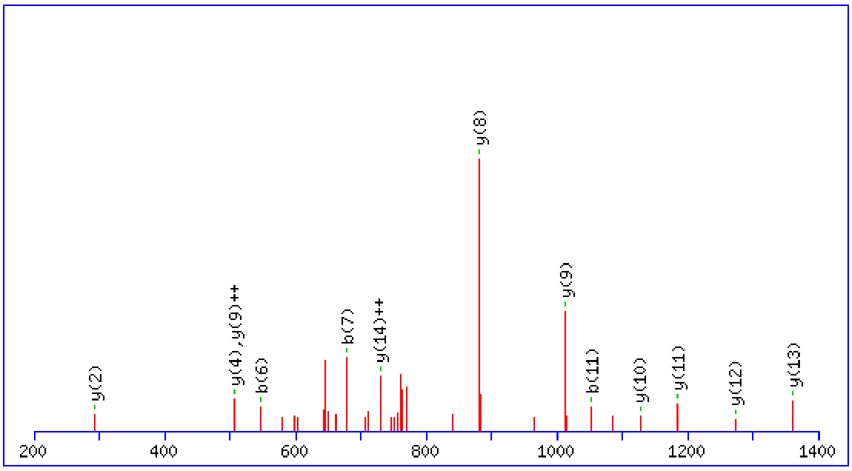
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPSSGLMPASDVLIR**
Found in **AT1G09130.1** in **TAIR_Arabidopsis**, Symbols: | ATP-dependent Clp protease proteolytic subunit, putative | chr1:2940065-2942219 REVERSE

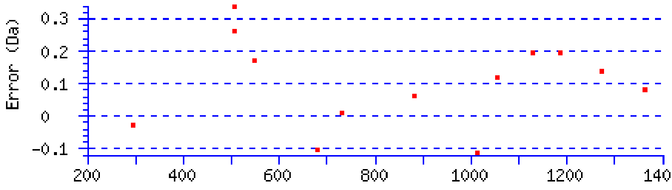
Match to Query 6700: 1558.776590 from(780.395571,2+) index(7051)
Title: Elution from: 62.335 to 62.335 scan no 9167 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

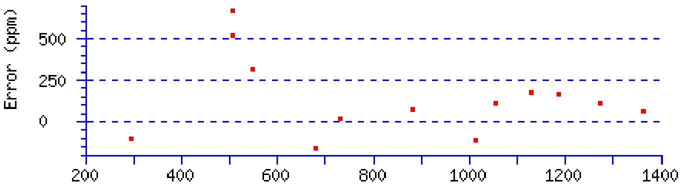


Monoisotopic mass of neutral peptide Mr(calc): 1558.7749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 7.3e-007
Matches : 13/128 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							15
2	199.1225	100.0649			P	1459.7168	730.3620	1441.6932	721.3502	1441.7062	721.3567	14
3	287.1516	144.0794	269.1410	135.0741	S	***1361.6670***	681.3371	1343.6434	672.3253	1343.6564	672.3318	13
4	375.1807	188.0940	357.1701	179.0887	S	***1273.6379***	637.3226	1255.6143	628.3108	1255.6273	628.3173	12
5	433.1991	217.1032	415.1886	208.0979	G	***1185.6088***	593.3081	1167.5853	584.2963	1167.5983	584.3028	11
6	**547.2802**	274.1438	529.2697	265.1385	L	***1127.5903***	564.2988	1109.5668	555.2870	1109.5798	555.2935	10
7	**679.3178**	340.1625	661.3072	331.1572	M	***1013.5092***	507.2583	995.4857	498.2465	995.4987	498.2530	9
8	777.3676	389.1874	759.3570	380.1821	P	***881.4717***	441.2395	863.4481	432.2277	863.4612	432.2342	8
9	849.4017	425.2045	831.3912	416.1992	A	783.4219	392.2146	765.3983	383.2028	765.4114	383.2093	7
10	937.4308	469.2190	919.4202	460.2137	S	711.3878	356.1975	693.3642	347.1857	693.3772	347.1922	6
11	**1053.4548**	527.2310	1035.4442	518.2257	D	623.3587	312.1830	605.3351	303.1712	605.3482	303.1777	5
12	1153.5202	577.2637	1135.5096	568.2585	V	***507.3347***	254.1710	489.3112	245.1592			4
13	1267.6013	634.3043	1249.5907	625.2990	L	407.2693	204.1383	389.2457	195.1265			3
14	1381.6824	691.3448	1363.6718	682.3396	I	***293.1882***	147.0977	275.1646	138.0859			2
15					R	179.1071	90.0572	161.0835	81.0454			1



RMS error 270 ppm



RMS error 270 ppm

AT1G09130.1

NCBI **BLAST** search of VPSSGLMPASDVLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.2	1558.7749	0.0016	VPSSGLMPASDVLIR
7.7	1558.7805	-0.0040	DLIPRMLVVDPMK

Mascot: http://www.matrixscience.com/

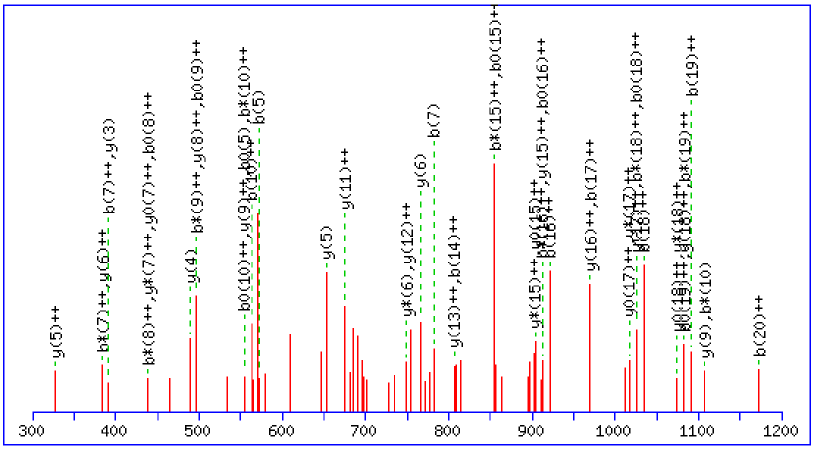
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GKWEAPLIDNPDFKDDPELYVFPK**
Found in **AT1G09210.1** in **TAIR_Arabidopsis**, Symbols: | calreticulin 2 (CRT2) | chr1:2973219-2976657 REVERSE

Match to Query 10983: 2832.404056 from(709.108290,4+) index(9625)
Title: Elution from: 87.368 to 87.368 scan no 13191 cid35.00 polarity:+
Data file D6h-3_1.mgf

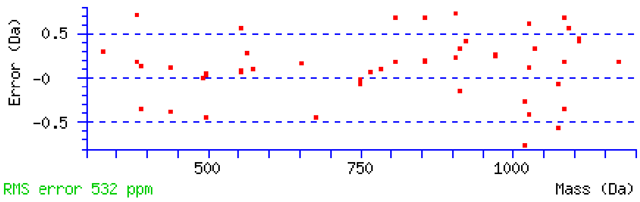
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

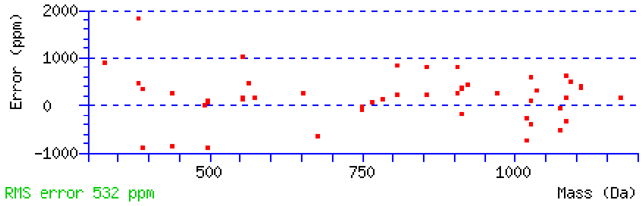


Monoisotopic mass of neutral peptide Mr(calc): 2832.4010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 5.8e-007
Matches : 53/256 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							24
2	186.1237	93.5655	169.0972	85.0522			K	2776.3869	1388.6971	2759.3603	1380.1838	2758.3763	1379.6918	23
3	372.2030	186.6051	355.1765	178.0919			W	2648.2919	1324.6496	2631.2653	1316.1363	2630.2813	1315.6443	22
4	501.2456	251.1264	484.2191	242.6132	483.2350	242.1212	E	2462.2126	1231.6099	2445.1860	1223.0967	2444.2020	1222.6046	21
5	572.2827	286.6450	555.2562	278.1317	554.2722	277.6397	A	2333.1700	1167.0886	2316.1434	1158.5754	2315.1594	1158.0834	20
6	669.3355	335.1714	652.3089	326.6581	651.3249	326.1661	P	2262.1329	1131.5701	2245.1063	1123.0568	2244.1223	1122.5648	19
7	782.4196	**391.7134**	765.3930	383.2001	764.4090	382.7081	L	2165.0801	1083.0437	2148.0536	1074.5304	2147.0695	1074.0384	18
8	895.5036	448.2554	878.4771	439.7422	877.4931	439.2502	I	2051.9960	1026.5017	2034.9695	1017.9884	2033.9855	1017.4964	17
9	1010.5306	505.7689	993.5040	497.2556	992.5200	496.7636	D	1938.9120	969.9596	1921.8854	961.4464	1920.9014	960.9543	16
10	1124.5735	**562.7904**	1107.5469	554.2771	1106.5629	553.7851	N	1823.8850	912.4462	1806.8585	903.9329	1805.8745	903.4409	15
11	1221.6262	611.3168	1204.5997	602.8035	1203.6157	602.3115	P	1709.8421	855.4247	1692.8156	846.9114	1691.8316	846.4194	14
12	1336.6532	668.8302	1319.6266	660.3170	1318.6426	659.8250	D	1612.7894	806.8983	1595.7628	798.3850	1594.7788	797.8930	13
13	1483.7216	742.3644	1466.6951	733.8512	1465.7110	733.3592	F	1497.7624	749.3848	1480.7359	740.8716	1479.7518	740.3796	12
14	1611.8166	**806.4119**	1594.7900	797.8986	1593.8060	797.4066	K	1350.6940	675.8506	1333.6674	667.3374	1332.6834	666.8454	11
15	1726.8435	863.9254	1709.8170	855.4121	1708.8329	854.9201	D	1222.5990	611.8032	1205.5725	603.2899	1204.5885	602.7979	10
16	1841.8705	**921.4389**	1824.8439	912.9256	1823.8599	912.4336	D	**1107.5721**	554.2897	1090.5455	545.7764	1089.5615	545.2844	9
17	1938.9232	**969.9652**	1921.8967	961.4520	1920.9127	960.9600	P	992.5451	496.7762	975.5186	488.2629	974.5346	487.7709	8
18	2067.9658	**1034.4865**	2050.9393	1025.9733	2049.9552	1025.4813	E	895.4924	448.2498	878.4658	439.7366	877.4818	439.2445	7
19	2181.0499	**1091.0286**	2164.0233	1082.5153	2163.0393	1082.0233	L	**766.4498**	383.7285	749.4232	375.2153			6
20	2344.1132	**1172.5602**	2327.0867	1164.0470	2326.1026	1163.5550	Y	**653.3657**	327.1865	636.3392	318.6732			5
21	2443.1816	1222.0944	2426.1551	1213.5812	2425.1711	1213.0892	V	**490.3024**	245.6548	473.2758	237.1416			4
22	2590.2500	1295.6287	2573.2235	1287.1154	2572.2395	1286.6234	F	**391.2340**	196.1206	374.2074	187.6074			3
23	2687.3028	1344.1550	2670.2762	1335.6418	2669.2922	1335.1498	P	244.1656	122.5864	227.1390	114.0731			2
24							K	147.1128	74.0600	130.0863	65.5468			1

AT1G09210.1





NCBI **BLAST** search of GKWEAPLIDNPDFKDDPELYVFPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.4	2832.4010	0.0030	GKWEAPLIDNPDFKDDPELYVFPK

Mascot: http://www.matrixscience.com/

AT1G09270.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSMLRNATWTLSNFCR**
Found in **AT1G09270.1** in **TAIR_Arabidopsis**, Symbols: | importin alpha-1 subunit, putative (IMPA4) | chr1:2994508-2997835 FORWARD

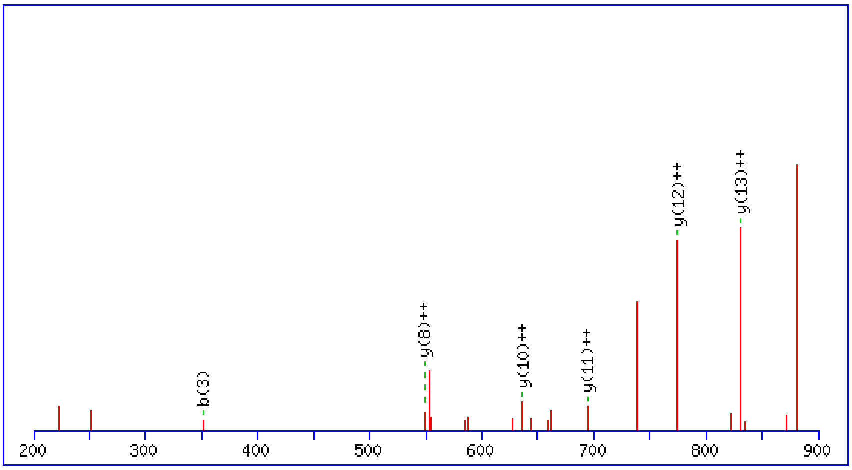
Match to Query 9051: 2010.883521 from(671.301783,3+) index(4383)
Title: Elution from: 40.798 to 40.798 scan no 5505 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

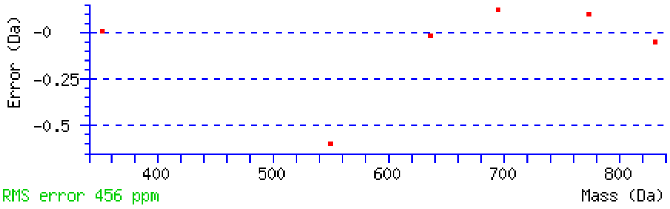
Show Y-axis ☐

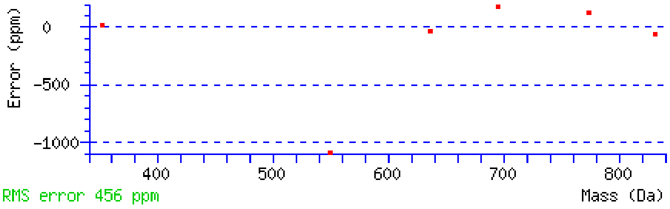


Monoisotopic mass of neutral peptide Mr(calc): 2010.8840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.035
Matches : 6/248 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							16
2	203.1174	102.0624			185.1069	93.0571	S	1897.8102	949.4087	1879.7866	940.3970	1879.7997	940.4035	15
3	351.1499	176.0786			333.1393	167.0733	M	1809.7812	905.3942	1791.7576	896.3824	1791.7706	896.3889	14
4	465.2310	233.1191			447.2204	224.1138	L	1661.7487	831.3780	1643.7251	822.3662	1643.7382	822.3727	13
5	625.3202	313.1637	607.2966	304.1520	607.3097	304.1585	R	1547.6676	774.3374	1529.6440	765.3257	1529.6571	765.3322	12
6	741.3572	371.1822	723.3336	362.1705	723.3467	362.1770	N	1387.5784	694.2928	1369.5548	685.2810	1369.5678	685.2875	11
7	813.3914	407.1993	795.3678	398.1875	795.3808	398.1940	A	1271.5414	636.2743	1253.5178	627.2625	1253.5308	627.2690	10
8	915.4361	458.2217	897.4125	449.2099	897.4255	449.2164	T	1199.5072	600.2573	1181.4836	591.2455	1181.4967	591.2520	9
9	1103.5095	552.2584	1085.4859	543.2466	1085.4989	543.2531	W	1097.4625	549.2349	1079.4389	540.2231	1079.4519	540.2296	8
10	1205.5542	603.2807	1187.5306	594.2689	1187.5436	594.2754	T	909.3891	455.1982	891.3655	446.1864	891.3786	446.1929	7
11	1319.6353	660.3213	1301.6117	651.3095	1301.6247	651.3160	L	807.3444	404.1758	789.3208	395.1641	789.3339	395.1706	6
12	1407.6643	704.3358	1389.6408	695.3240	1389.6538	695.3305	S	693.2633	347.1353	675.2397	338.1235	675.2528	338.1300	5
13	1523.7013	762.3543	1505.6778	753.3425	1505.6908	753.3490	N	605.2343	303.1208	587.2107	294.1090			4
14	1671.7668	836.3870	1653.7432	827.3752	1653.7562	827.3817	F	489.1973	245.1023	471.1737	236.0905			3
15	1833.7915	917.3994	1815.7679	908.3876	1815.7809	908.3941	C	341.1318	171.0695	323.1082	162.0578			2
16							R	179.1071	90.0572	161.0835	81.0454			1

AT1G09270.1





NCBI **BLAST** search of LSMLRNATWTLSNFCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.6	2010.8840	-0.0005	LSMLRNATWTLSNFCR
4.2	2010.8861	-0.0026	RSLMSFDLSSEEFNVTK
2.0	2010.8888	-0.0052	DGSSLVRDMNRLDAFYK
1.3	2010.8840	-0.0005	VRFVNMDPESVRFMAR
0.7	2010.8813	0.0022	VEPTIEHYGCMVDLLGR

Mascot: http://www.matrixscience.com/

AT1G09280.1

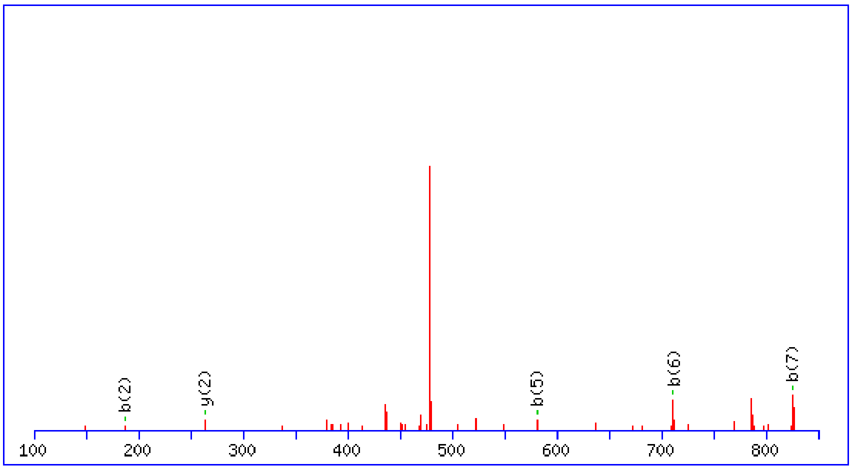
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPYIDEIK**
Found in **AT1G09280.1** in **TAIR_Arabidopsis**, Symbols: | similar to rhodanese-like domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G40760.1); similar to Os12g0563400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001067036.1); similar to hypothetical protein [Vitis vinifera] (GB:CA

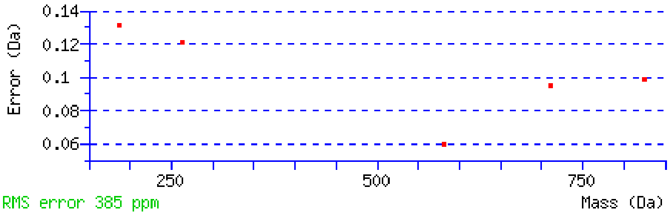
Match to Query 2180: 972.466086 from(487.240319,2+) index(1201)
Title: Elution from: 16.675 to 16.675 scan no 1626 cid35.00 polarity:+
Data file D12h-3_3.mgf

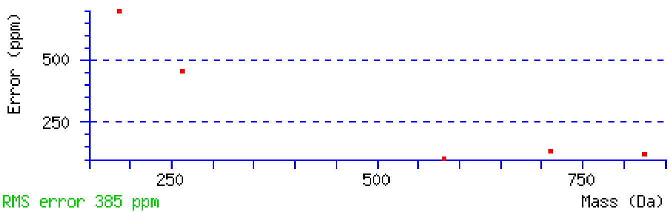
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.026
Matches : 5/66 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							8
2	*187.0861*	94.0467	169.0756	85.0414	P	885.4428	443.2251	867.4193	434.2133	867.4323	434.2198	7
3	351.1465	176.0769	333.1359	167.0716	Y	787.3930	394.2002	769.3695	385.1884	769.3825	385.1949	6
4	465.2276	233.1174	447.2170	224.1122	I	623.3327	312.1700	605.3091	303.1582	605.3221	303.1647	5
5	*581.2516*	291.1294	563.2410	282.1241	D	509.2516	255.1294	491.2280	246.1176	491.2410	246.1241	4
6	*711.2912*	356.1492	693.2806	347.1440	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	*825.3723*	413.1898	807.3617	404.1845	I	263.1880	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SPYIDEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G09280.1

26.6	972.4646	0.0015	SPYIDEIK
17.6	972.4633	0.0028	MVCLPSLK
14.7	972.4651	0.0010	DKNSQGALK
14.3	972.4646	0.0015	EFGEELLK
13.2	972.4646	0.0015	LEFLEGEK
12.1	972.4651	0.0010	AAERGESLK
12.1	972.4673	-0.0012	FINLPDSR
12.1	972.4651	0.0010	QNENKSLK
11.8	972.4633	0.0028	VLSMCPLK
10.4	972.4633	0.0028	MNLTLPMK

AT1G09310.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVSYGTEVTAIVETGK**
Found in **AT1G09310.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G56580.1); similar to unknown [Populus trichocarpa] (GB:ABK94207.1); contains InterPro domain Protein of unknown function DUF538 (InterPro:IPR007493) | chr1:3009111-3009650 FORW

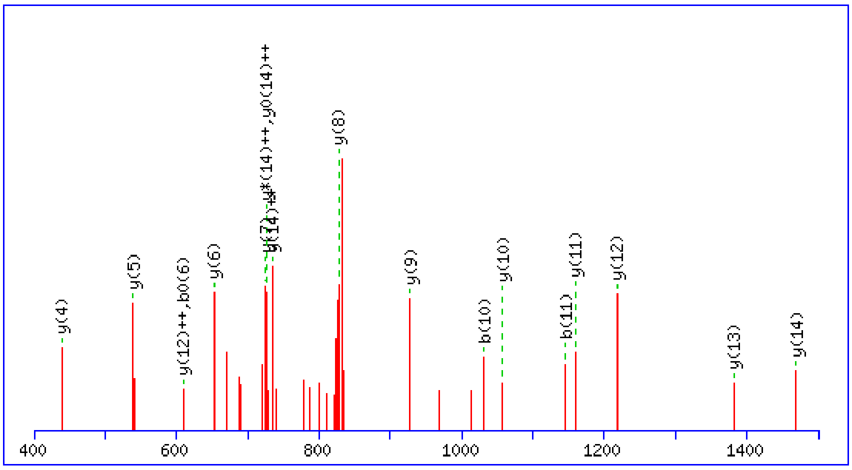
Match to Query 7644: 1682.832628 from(842.423590,2+) index(7116)
Title: Elution from: 62.853 to 62.853 scan no 9342 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

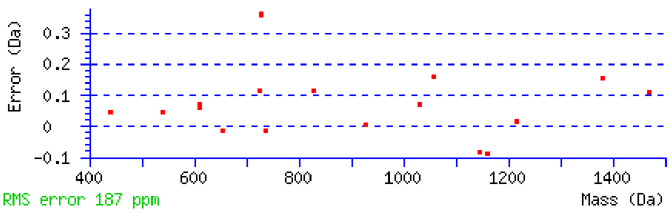
Show Y-axis ☐

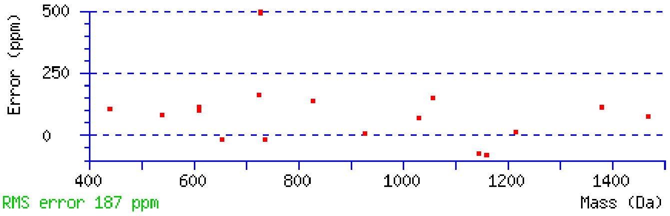


Monoisotopic mass of neutral peptide Mr(calc): 1682.8321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 3.4e-010
Matches : 18/142 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							16
2	215.1538	108.0805			V	1569.7583	785.3828	1551.7347	776.3710	1551.7477	776.3775	15
3	303.1829	152.0951	285.1723	143.0898	S	***1469.6928***	735.3501	1451.6693	726.3383	1451.6823	726.3448	14
4	467.2433	234.1253	449.2327	225.1200	Y	***1381.6638***	691.3355	1363.6402	682.3237	1363.6532	682.3302	13
5	525.2618	263.1345	507.2512	254.1292	G	***1217.6034***	609.3053	1199.5798	600.2936	1199.5928	600.3001	12
6	627.3065	314.1569	609.2959	305.1516	T	***1159.5849***	580.2961	1141.5613	571.2843	1141.5743	571.2908	11
7	757.3461	379.1767	739.3355	370.1714	E	***1057.5402***	529.2737	1039.5166	520.2619	1039.5296	520.2685	10
8	857.4115	429.2094	839.4010	420.2041	V	***927.5006***	464.2539	909.4770	455.2421	909.4900	455.2486	9
9	959.4563	480.2318	941.4457	471.2265	T	***827.4351***	414.2212	809.4115	405.2094	809.4246	405.2159	8
10	**1031.4904**	516.2488	1013.4798	507.2436	A	***725.3904***	363.1988	707.3668	354.1871	707.3798	354.1936	7
11	**1145.5715**	573.2894	1127.5609	564.2841	I	***653.3563***	327.1818	635.3327	318.1700	635.3457	318.1765	6
12	1245.6370	623.3221	1227.6264	614.3168	V	***539.2752***	270.1412	521.2516	261.1294	521.2646	261.1359	5
13	1375.6766	688.3419	1357.6660	679.3366	E	***439.2097***	220.1085	421.1861	211.0967	421.1991	211.1032	4
14	1477.7213	739.3643	1459.7107	730.3590	T	309.1701	155.0887	291.1465	146.0769	291.1595	146.0834	3
15	1535.7398	768.3735	1517.7292	759.3683	G	207.1254	104.0663	189.1018	95.0545			2
16					K	149.1069	75.0571	131.0833	66.0453			1

AT1G09310.1





NCBI **BLAST** search of LVSYGTEVTAIVETGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
102.6	1682.8321	0.0006	LVSYGTEVTAIVETGK
6.4	1682.8300	0.0026	IYRVLQGGTGIPNMK
3.7	1682.8352	-0.0026	SVTSSRARIETSIPR
3.5	1682.8293	0.0033	TLTRFQTVSKHWR
3.1	1682.8278	0.0048	LKLSCNVTDSKLQR
1.8	1682.8357	-0.0030	MRALEKLMASWISK
0.8	1682.8278	0.0048	LDGTMSLIARDRAVK
0.8	1682.8370	-0.0044	LFLETFRLPGESQK
0.4	1682.8348	-0.0022	NPPLVEKAPSQNIEK

Mascot: http://www.matrixscience.com/

AT1G09340.1

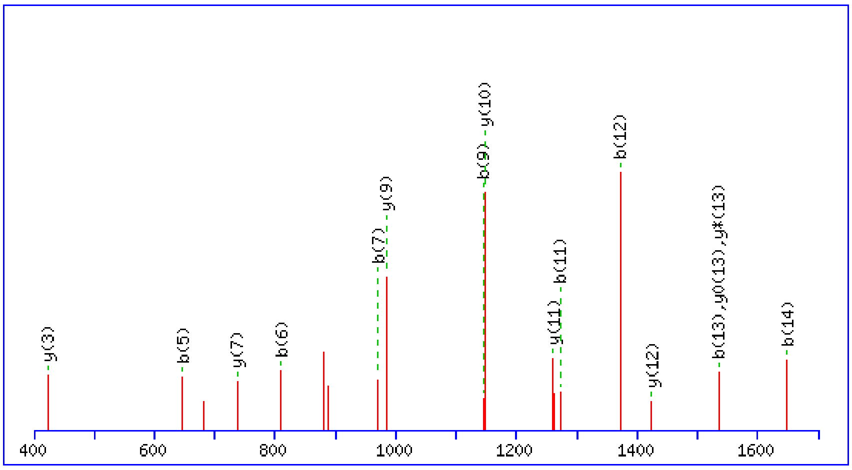
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEQYIYCSSAGVYLK**
Found in **AT1G09340.1** in **TAIR_Arabidopsis**, Symbols: CRB | CRB; binding / catalytic/ coenzyme binding | chr1:3015475-3018037 FORWARD

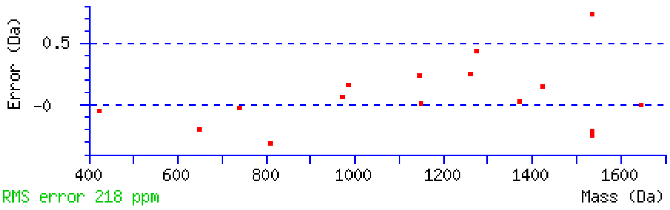
Match to Query 8487: 1792.866192 from(897.440372,2+) index(6731)
Title: Elution from: 60.467 to 60.467 scan no 8654 cid35.00 polarity:+
Data file D6h-2_2.mgf

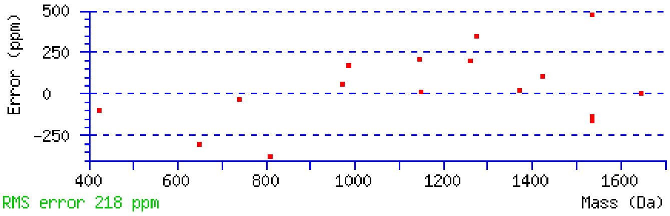
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1792.8705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 8.2e-009
Matches : 16/150 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							15
2	243.1339	122.0706			225.1234	113.0653	E	1680.7938	840.9005	1663.7672	832.3873	1662.7832	831.8952	14
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	Q	1551.7512	776.3792	1534.7246	767.8660	1533.7406	767.3740	13
4	534.2558	267.6316	517.2293	259.1183	516.2453	258.6263	Y	***1423.6926***	712.3499	1406.6661	703.8367	1405.6821	703.3447	12
5	***647.3399***	324.1736	630.3134	315.6603	629.3293	315.1683	I	***1260.6293***	630.8183	1243.6027	622.3050	1242.6187	621.8130	11
6	***810.4032***	405.7053	793.3767	397.1920	792.3927	396.7000	Y	***1147.5452***	574.2762	1130.5187	565.7630	1129.5347	565.2710	10
7	***970.4339***	485.7206	953.4073	477.2073	952.4233	476.7153	C	***984.4819***	492.7446	967.4553	484.2313	966.4713	483.7393	9
8	1057.4659	529.2366	1040.4394	520.7233	1039.4553	520.2313	S	824.4512	412.7293	807.4247	404.2160	806.4407	403.7240	8
9	***1144.4979***	572.7526	1127.4714	564.2393	1126.4874	563.7473	S	***737.4192***	369.2132	720.3927	360.7000	719.4087	360.2080	7
10	1215.5351	608.2712	1198.5085	599.7579	1197.5245	599.2659	A	650.3872	325.6972	633.3606	317.1840			6
11	***1272.5565***	636.7819	1255.5300	628.2686	1254.5460	627.7766	G	579.3501	290.1787	562.3235	281.6654			5
12	***1371.6249***	686.3161	1354.5984	677.8028	1353.6144	677.3108	V	522.3286	261.6679	505.3021	253.1547			4
13	***1534.6883***	767.8478	1517.6617	759.3345	1516.6777	758.8425	Y	***423.2602***	212.1337	406.2336	203.6205			3
14	***1647.7723***	824.3898	1630.7458	815.8765	1629.7618	815.3845	L	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LEQYIYCSSAGVYLK

AT1G09340.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.8	1792.8705	-0.0044	LEQYIYCSSAGVYLK
6.3	1792.8699	-0.0037	MEAMNTINLLQSVGEK
0.8	1792.8625	0.0037	MISDSITNASATSAPTAR
0.5	1792.8699	-0.0037	MEAMNTINLLQSVGEK

AT1G09590.1

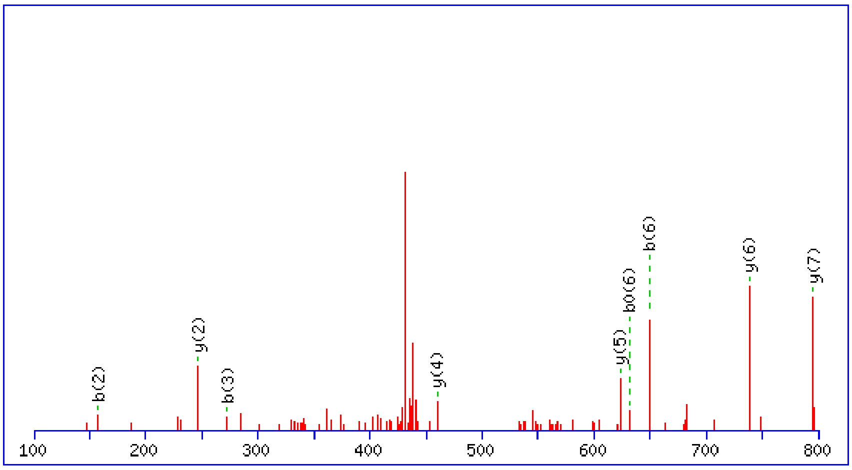
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGDYVDVK**
Found in **AT1G09590.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L21 (RPL21A) | chr1:3106551-3107608 FORWARD

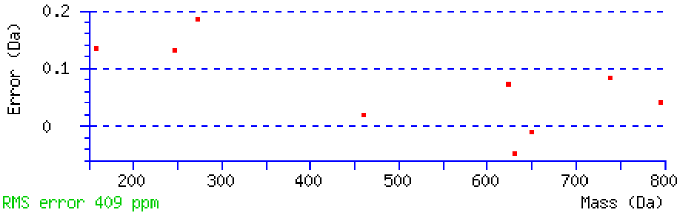
Match to Query 1492: 893.448626 from(447.731589,2+) index(1770)
Title: Elution from: 20.778 to 20.778 scan no 2275 cid35.00 polarity:+
Data file 0-2_3.mgf

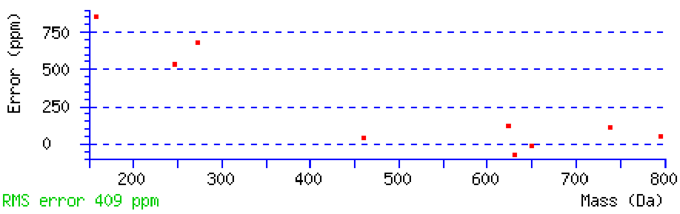
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 893.4495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00052
Matches : 9/62 fragment ions using 14 most intense peaks (help)

#	b	b⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	100.0757	50.5415			V							8
2	**157.0972**	79.0522			G	***795.3883***	398.1978	778.3618	389.6845	777.3777	389.1925	7
3	**272.1241**	136.5657	254.1135	127.5604	D	***738.3668***	369.6871	721.3403	361.1738	720.3563	360.6818	6
4	435.1874	218.0974	417.1769	209.0921	Y	***623.3399***	312.1736	606.3134	303.6603	605.3293	303.1683	5
5	534.2558	267.6316	516.2453	258.6263	V	***460.2766***	230.6419	443.2500	222.1287	442.2660	221.6366	4
6	**649.2828**	325.1450	631.2722	316.1397	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
7	748.3512	374.6792	730.3406	365.6740	V	***246.1812***	123.5942	229.1547	115.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VGDYVDVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	893.4495	-0.0008	VGDYVDVK
21.5	893.4494	-0.0008	VGFEESVK

AT1G09590.1

6.3	893.4494	-0.0008	LNEEYVK
5.3	893.4494	-0.0008	VGESDFLK
3.1	893.4508	-0.0022	RDFPGFR

AT1G09610.1

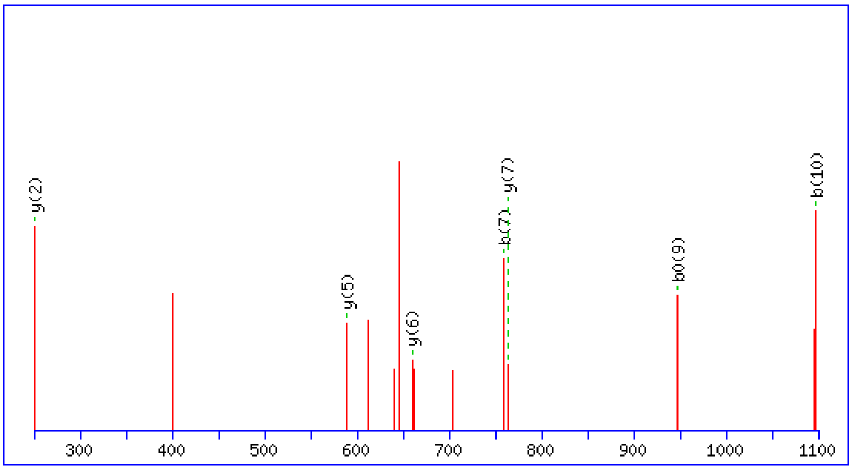
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MTAIYTAGMMAR**
Found in **AT1G09610.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G09990.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN78768.1); contains InterPro domain Protein of unknown function DUF579, plant (InterPro:IPR006514) | chr1:31117

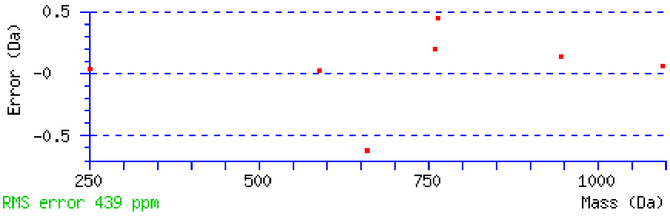
Match to Query 4956: 1346.561892 from(674.288222,2+) index(9726)
Title: Elution from: 90.633 to 90.633 scan no 13630 cid35.00 polarity:+
Data file D6h-1_3.mgf

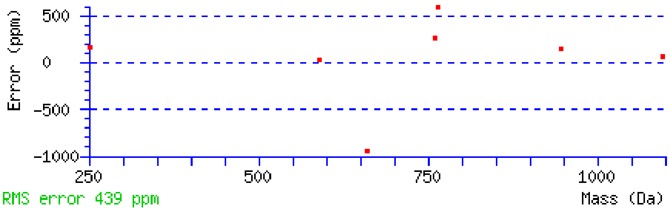
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1346.5591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.022
Matches : 7/150 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260			M							12
2	235.0895	118.0484	217.0789	109.0431	T	1215.5289	608.2681	1197.5053	599.2563	1197.5183	599.2628	11
3	307.1237	154.0655	289.1131	145.0602	A	1113.4842	557.2457	1095.4606	548.2339	1095.4736	548.2404	10
4	421.2048	211.1060	403.1942	202.1007	I	1041.4500	521.2286	1023.4264	512.2169	1023.4395	512.2234	9
5	585.2651	293.1362	567.2546	284.1309	Y	927.3689	464.1881	909.3453	455.1763	909.3584	455.1828	8
6	687.3098	344.1586	669.2993	335.1533	T	***763.3086***	382.1579	745.2850	373.1461	745.2980	373.1526	7
7	**759.3440**	380.1756	741.3334	371.1703	A	***661.2638***	331.1356	643.2403	322.1238			6
8	817.3625	409.1849	799.3519	400.1796	G	***589.2297***	295.1185	571.2061	286.1067			5
9	965.3949	483.2011	947.3844	474.1958	M	531.2112	266.1092	513.1876	257.0974			4
10	**1097.4324**	549.2199	1079.4219	540.2146	M	383.1788	192.0930	365.1552	183.0812			3
11	1169.4666	585.2369	1151.4560	576.2316	A	***251.1412***	126.0743	233.1177	117.0625			2
12					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MTAIYTAGMMAR

AT1G09610.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
22.3	1346.5591	0.0028	MTAIYTAGMMAR	Oxidation M9 56.95%
19.8	1346.5591	0.0028	MTAIYTAGMMAR	Oxidation M10 32.02%
15.2	1346.5591	0.0028	MTAIYTAGMMAR	Oxidation M1 11.03%
3.5	1346.5583	0.0036	SSAASSMISSFNK	
2.9	1346.5618	0.0001	CKFMGCVKGAR	
0.4	1346.5609	0.0010	ERQSEMRSYK	

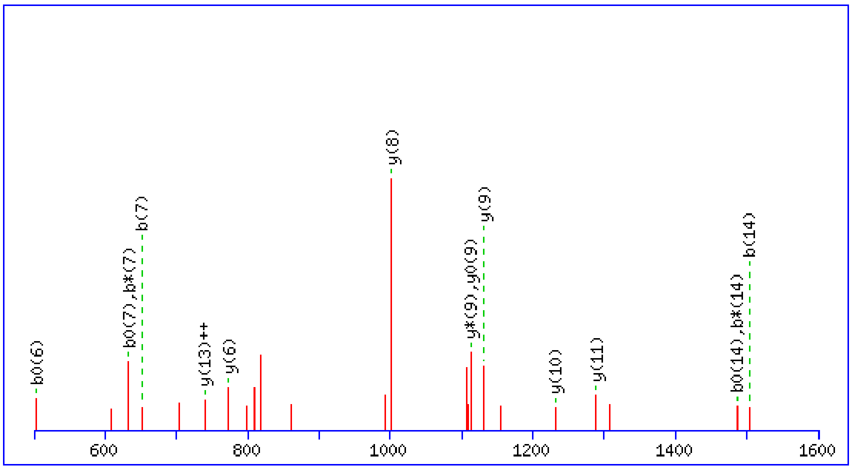
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATGEGVQPQEYTLIK**
Found in **AT1G09620.1** in **TAIR_Arabidopsis**, Symbols: | ATP binding / aminoacyl-tRNA ligase | chr1:3113079-3116457 REVERSE

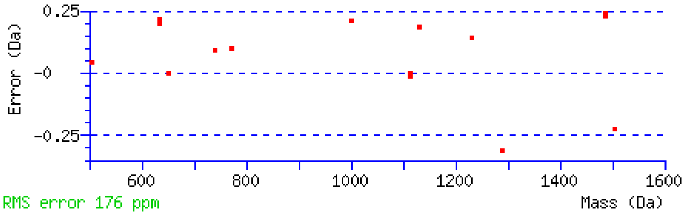
Match to Query 7157: 1650.786016 from(826.400284,2+) index(4477)
Title: Elution from: 42.187 to 42.187 scan no 5733 cid35.00 polarity:+
Data file D1d-2_3.mgf

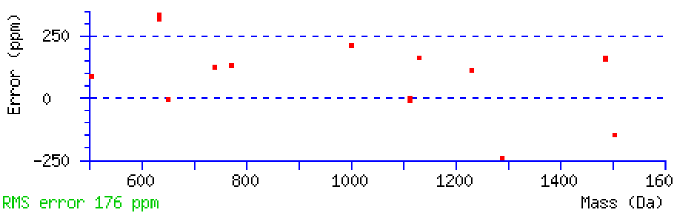
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1650.7825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0013
Matches : 15/148 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							15
2	175.0861	88.0467			157.0756	79.0414	T	1579.7557	790.3815	1561.7321	781.3697	1561.7451	781.3762	14
3	233.1046	117.0560			215.0941	108.0507	G	1477.7109	739.3591	1459.6874	730.3473	1459.7004	730.3538	13
4	363.1443	182.0758			345.1337	173.0705	E	1419.6924	710.3499	1401.6689	701.3381	1401.6819	701.3446	12
5	421.1628	211.0850			403.1522	202.0797	G	***1289.6528***	645.3300	1271.6292	636.3183	1271.6423	636.3248	11
6	521.2282	261.1177			503.2176	252.1125	V	***1231.6343***	616.3208	1213.6107	607.3090	1213.6238	607.3155	10
7	**651.2809**	326.1441	633.2573	317.1323	633.2703	317.1388	Q	***1131.5689***	566.2881	1113.5453	557.2763	1113.5583	557.2828	9
8	749.3307	375.1690	731.3071	366.1572	731.3201	366.1637	P	***1001.5162***	501.2617	983.4926	492.2500	983.5057	492.2565	8
9	879.3833	440.1953	861.3597	431.1835	861.3727	431.1900	Q	903.4664	452.2369	885.4428	443.2251	885.4559	443.2316	7
10	1009.4229	505.2151	991.3994	496.2033	991.4124	496.2098	E	***773.4138***	387.2105	755.3902	378.1987	755.4032	378.2052	6
11	1173.4833	587.2453	1155.4597	578.2335	1155.4727	578.2400	Y	643.3741	322.1907	625.3506	313.1789	625.3636	313.1854	5
12	1275.5280	638.2676	1257.5044	629.2559	1257.5174	629.2624	T	479.3138	240.1605	461.2902	231.1487	461.3032	231.1552	4
13	1389.6091	695.3082	1371.5855	686.2964	1371.5985	686.3029	L	377.2691	189.1382	359.2455	180.1264			3
14	**1503.6902**	752.3487	1485.6666	743.3370	1485.6796	743.3435	I	263.1880	132.0976	245.1644	123.0858			2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ATGEGVQPQEYTLIK

AT1G09620.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.7	1650.7825	0.0035	ATGEGVQPQEYTLIK
11.8	1650.7906	-0.0046	LDTVSKELSSLDEAK
4.0	1650.7908	-0.0048	FVKSLVADMGNHVSK
1.8	1650.7881	-0.0021	ESIEWLVGVMEKSK
1.2	1650.7852	0.0008	TGINKGAIWDEISAR

Mascot: http://www.matrixscience.com/

AT1G09640.1

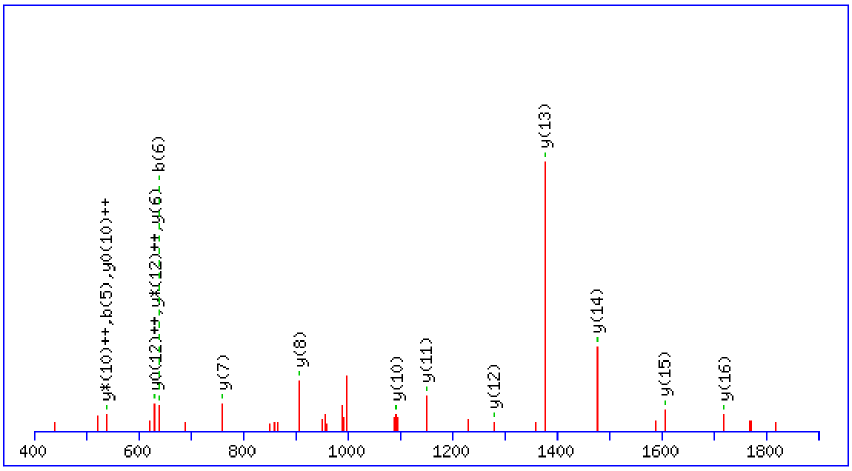
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPVLETPEGSVFESNAIAR**
Found in **AT1G09640.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1B-gamma, putative / eEF-1B gamma, putative | chr1:3120164-3122154 FORWARD

Match to Query 9328: 2014.041088 from(1008.027820,2+) index(7862)
Title: Elution from: 70.045 to 70.045 scan no 10366 cid35.00 polarity:+
Data file D6h-1_2.mgf

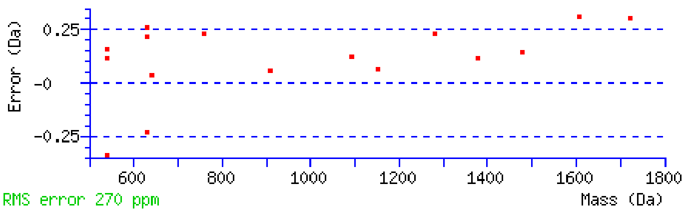
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

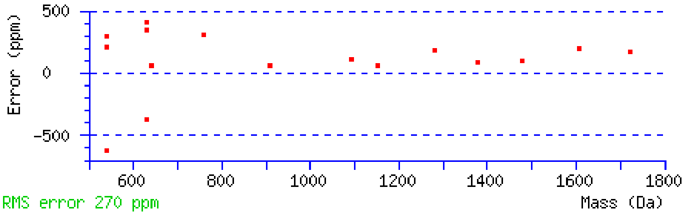


Monoisotopic mass of neutral peptide Mr(calc): 2014.0371
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 96 **Expect:** 8.3e-010
Matches : 16/170 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**19**
2	197.1285	99.0679					**P**	1915.9760	958.4916	1898.9494	949.9784	1897.9654	949.4863	**18**
3	296.1969	148.6021					**V**	1818.9232	909.9652	1801.8967	901.4520	1800.9127	900.9600	**17**
4	409.2809	205.1441					**L**	***1719.8548***	860.4310	1702.8283	851.9178	1701.8442	851.4258	**16**
5	**538.3235**	269.6654			520.3130	260.6601	**E**	***1606.7707***	803.8890	1589.7442	795.3757	1588.7602	794.8837	**15**
6	**639.3712**	320.1892			621.3606	311.1840	**T**	***1477.7281***	739.3677	1460.7016	730.8544	1459.7176	730.3624	**14**
7	736.4240	368.7156			718.4134	359.7103	**P**	***1376.6805***	688.8439	1359.6539	680.3306	1358.6699	679.8386	**13**
8	865.4666	433.2369			847.4560	424.2316	**E**	***1279.6277***	640.3175	1262.6012	631.8042	1261.6171	631.3122	**12**
9	922.4880	461.7477			904.4775	452.7424	**G**	***1150.5851***	575.7962	1133.5586	567.2829	1132.5745	566.7909	**11**
10	1009.5201	505.2637			991.5095	496.2584	**S**	***1093.5636***	547.2855	1076.5371	538.7722	1075.5531	538.2802	**10**
11	1108.5885	554.7979			1090.5779	545.7926	**V**	1006.5316	503.7694	989.5051	495.2562	988.5211	494.7642	**9**
12	1255.6569	628.3321			1237.6463	619.3268	**F**	***907.4632***	454.2352	890.4367	445.7220	889.4526	445.2300	**8**
13	1384.6995	692.8534			1366.6889	683.8481	**E**	***760.3948***	380.7010	743.3682	372.1878	742.3842	371.6958	**7**
14	1471.7315	736.3694			1453.7209	727.3641	**S**	***631.3522***	316.1797	614.3256	307.6665	613.3416	307.1745	**6**
15	1585.7744	793.3909	1568.7479	784.8776	1567.7639	784.3856	**N**	544.3202	272.6637	527.2936	264.1504			**5**
16	1656.8115	828.9094	1639.7850	820.3961	1638.8010	819.9041	**A**	430.2772	215.6423	413.2507	207.1290			**4**
17	1769.8956	885.4514	1752.8691	876.9382	1751.8850	876.4462	**I**	359.2401	180.1237	342.2136	171.6104			**3**
18	1840.9327	920.9700	1823.9062	912.4567	1822.9222	911.9647	**A**	246.1561	123.5817	229.1295	115.0684			**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**

AT1G09640.1





NCBI **BLAST** search of VPVLETPEGSVFESNAIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.7	2014.0371	0.0040	VPVLETPEGSVFESNAIAR

Mascot: http://www.matrixscience.com/

AT1G09750.1

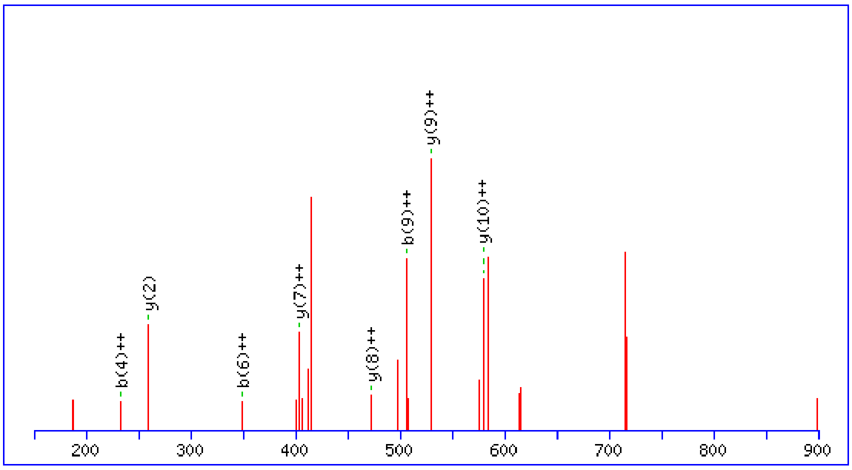
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLHMTSLDLK**
Found in **AT1G09750.1** in **TAIR_Arabidopsis**, Symbols: | chloroplast nucleoid DNA-binding protein-related | chr1:3157543-3158962 FORWARD

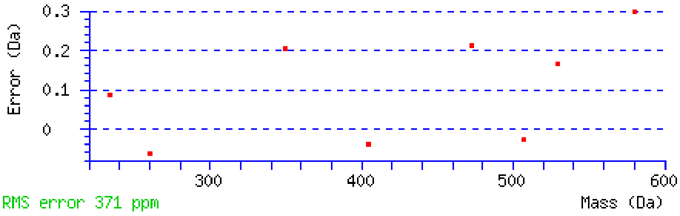
Match to Query 4510: 1270.694895 from(424.572241,3+) index(5796)
Title: Elution from: 51.410 to 51.410 scan no 7367 cid35.00 polarity:+
Data file 0-1_3.mgf

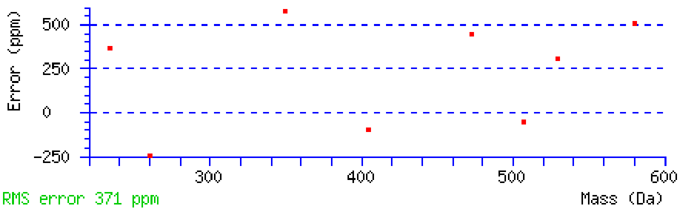
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1270.6955
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.028
Matches : 8/94 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							11
2	215.1390	108.0731	197.1285	99.0679	T	1158.6187	579.8130	1141.5922	571.2997	1140.6082	570.8077	10
3	328.2231	164.6152	310.2125	155.6099	L	1057.5710	529.2892	1040.5445	520.7759	1039.5605	520.2839	9
4	465.2820	***233.1446***	447.2714	224.1394	H	944.4870	472.7471	927.4604	464.2339	926.4764	463.7418	8
5	596.3225	298.6649	578.3119	289.6596	M	807.4281	404.2177	790.4015	395.7044	789.4175	395.2124	7
6	697.3702	***349.1887***	679.3596	340.1834	T	676.3876	338.6974	659.3610	330.1842	658.3770	329.6921	6
7	784.4022	392.7047	766.3916	383.6994	S	575.3399	288.1736	558.3134	279.6603	557.3293	279.1683	5
8	897.4863	449.2468	879.4757	440.2415	L	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
9	1012.5132	***506.7602***	994.5026	497.7550	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
10	1125.5973	563.3023	1107.5867	554.2970	L	260.1969	130.6021	243.1703	122.0888			2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ITLHMTSLDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G09750.1

Score	Mr(calc)	Delta	Sequence
19.1	1270.6955	-0.0006	ITLHMTSLDLK
0.7	1270.6962	-0.0013	VNTFFSLIAFI

AT1G09780.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MIFDAIEQVK**
Found in **AT1G09780.1** in **TAIR_Arabidopsis**, Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative | chr1:3165552-3167814 REVERSE

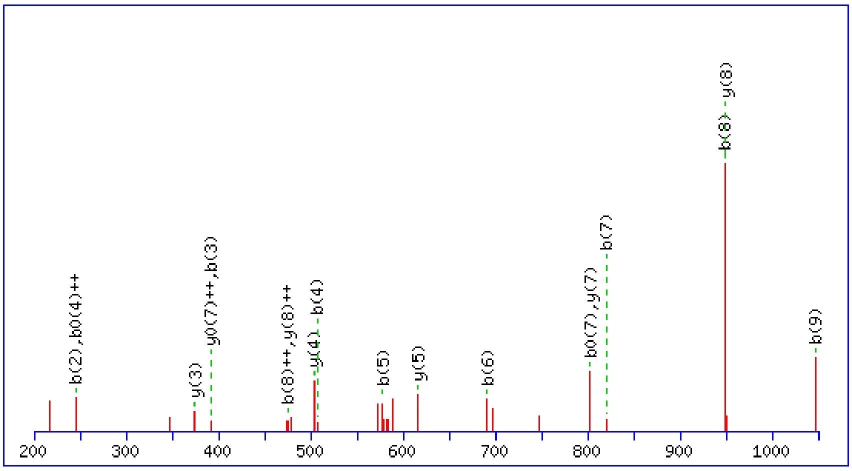
Match to Query 4124: 1192.616488 from(597.315520,2+) index(7725)
Title: Elution from: 69.479 to 69.479 scan no 10134 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

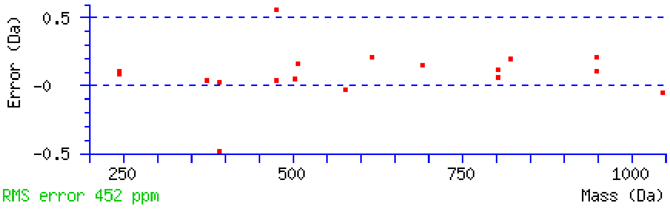
Label all possible matches ○ Label matches used for scoring ●

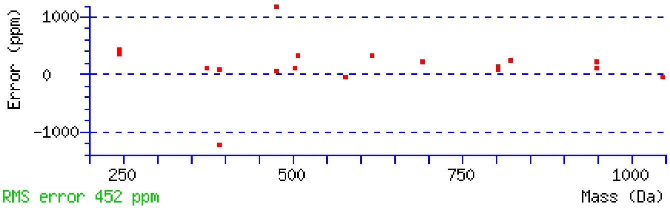
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1192.6162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 3e-006
Matches : 18/82 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							10
2	***245.1318***	123.0696					I	1062.5830	531.7951	1045.5564	523.2819	1044.5724	522.7898	9
3	***392.2002***	196.6038					F	**949.4989**	475.2531	932.4724	466.7398	931.4884	466.2478	8
4	***507.2272***	254.1172			489.2166	245.1119	D	**802.4305**	401.7189	785.4040	393.2056	784.4199	392.7136	7
5	***578.2643***	289.6358			560.2537	280.6305	A	687.4036	344.2054	670.3770	335.6921	669.3930	335.2001	6
6	***691.3484***	346.1778			673.3378	337.1725	I	**616.3665**	308.6869	599.3399	300.1736	598.3559	299.6816	5
7	***820.3910***	410.6991			802.3804	401.6938	E	**503.2824**	252.1448	486.2558	243.6316	485.2718	243.1395	4
8	***948.4495***	474.7284	931.4230	466.2151	930.4390	465.7231	Q	**374.2398**	187.6235	357.2132	179.1103			3
9	***1047.5179***	524.2626	1030.4914	515.7493	1029.5074	515.2573	V	246.1812	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of MIFDAIEQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G09780.1

Score	Mr(calc)	Delta	Sequence
62.2	1192.6162	0.0003	MIFDAIEQVK
14.8	1192.6196	-0.0031	LMLEVLMAGGK
11.1	1192.6200	-0.0035	DEFRETRLK
7.8	1192.6200	-0.0035	ESDRFQGVKK
6.5	1192.6162	0.0003	EPFNIMSIVK
3.7	1192.6160	0.0005	VDTRRSSSASK
3.5	1192.6160	0.0005	GGRKTGASSSASK
2.1	1192.6187	-0.0022	ATTGLSESTTLI

AT1G09870.1

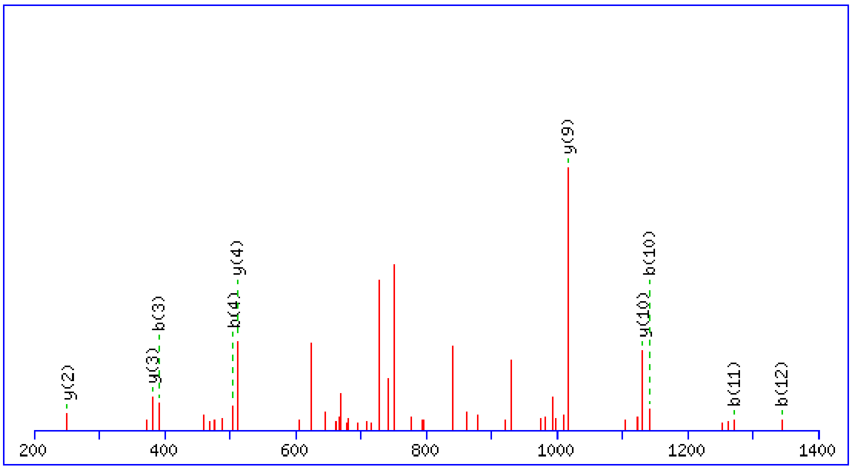
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEKLPPGSYEKAR**
Found in **AT1G09870.1** in **TAIR_Arabidopsis**, Symbols: | histidine acid phosphatase family protein | chr1:3205819-3208446 FORWARD

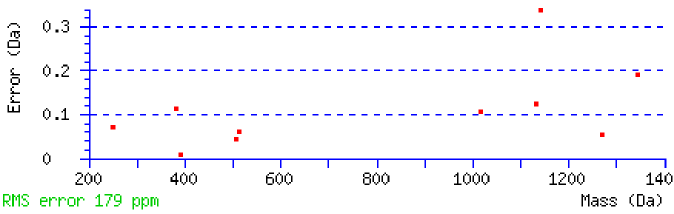
Match to Query 6686: 1520.721488 from(761.368020,2+) index(6132)
Title: Elution from: 54.573 to 54.573 scan no 7774 cid35.00 polarity:+
Data file D12h-3_1.mgf

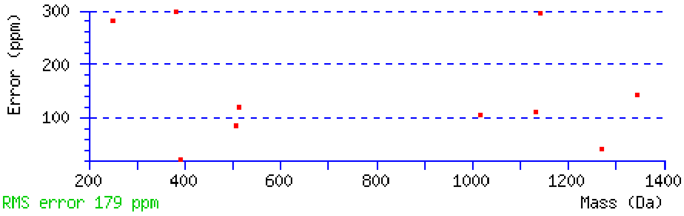
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1520.7195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0036
Matches : 10/134 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							13
2	261.0865	131.0469			243.0760	122.0416	E	1391.6872	696.3472	1373.6636	687.3354	1373.6766	687.3419	12
3	***391.1756***	196.0914	373.1520	187.0796	373.1650	187.0861	K	1261.6476	631.3274	1243.6240	622.3156	1243.6370	622.3221	11
4	***505.2567***	253.1320	487.2331	244.1202	487.2461	244.1267	L	***1131.5585***	566.2829	1113.5349	557.2711	1113.5480	557.2776	10
5	603.3065	302.1569	585.2829	293.1451	585.2959	293.1516	P	***1017.4774***	509.2424	999.4538	500.2306	999.4669	500.2371	9
6	701.3563	351.1818	683.3327	342.1700	683.3457	342.1765	P	919.4276	460.2175	901.4040	451.2057	901.4171	451.2122	8
7	759.3748	380.1910	741.3512	371.1792	741.3642	371.1857	G	821.3778	411.1926	803.3542	402.1808	803.3673	402.1873	7
8	847.4038	424.2056	829.3802	415.1938	829.3933	415.2003	S	763.3593	382.1833	745.3357	373.1715	745.3488	373.1780	6
9	1011.4642	506.2357	993.4406	497.2239	993.4536	497.2304	Y	675.3303	338.1688	657.3067	329.1570	657.3197	329.1635	5
10	***1141.5038***	571.2555	1123.4802	562.2438	1123.4933	562.2503	E	***511.2699***	256.1386	493.2463	247.1268	493.2593	247.1333	4
11	***1271.5928***	636.3001	1253.5693	627.2883	1253.5823	627.2948	K	***381.2303***	191.1188	363.2067	182.1070			3
12	***1343.6270***	672.3171	1325.6034	663.3053	1325.6164	663.3119	A	***251.1412***	126.0743	233.1177	117.0625			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EEKLPPGSYEKAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G09870.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.7	1520.7195	0.0019	EEKLPPGSYEKAR
24.9	1520.7252	-0.0037	EAWLSSINLAICK
18.4	1520.7240	-0.0025	FTHLSPVWYDLK
13.4	1520.7222	-0.0007	DGPTYLSHKKGAAR
8.9	1520.7195	0.0020	RPDLNSTTLFDPK
7.7	1520.7200	0.0015	EGNRIQNAIESLR
7.6	1520.7256	-0.0041	CSIRETHLTKQK
5.8	1520.7229	-0.0014	EKSLPDKLSMEAR
5.5	1520.7249	-0.0034	RGFATHPRSIAER
5.0	1520.7218	-0.0003	YAEAFLPQLSHTK

Mascot: http://www.matrixscience.com/

AT1G10290.1

Mascot Search Results

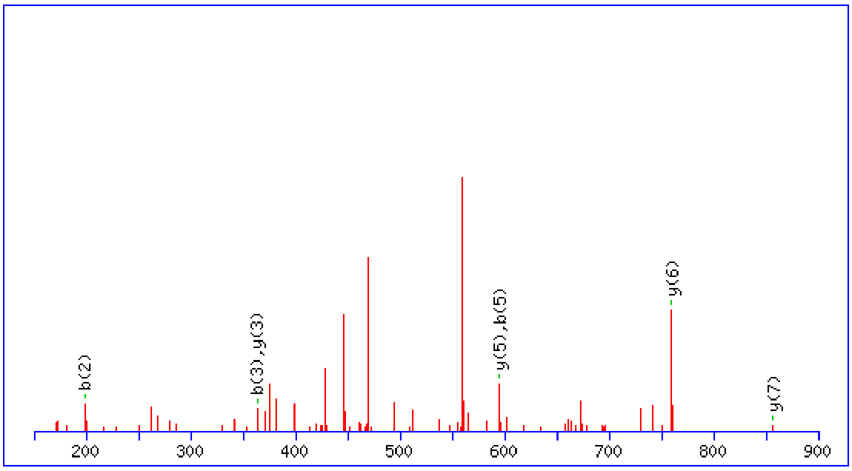
Peptide View

MS/MS Fragmentation of **VPYKTVLK**
Found in **AT1G10290.1** in **TAIR_Arabidopsis**, Symbols: DRP2A, ADL6 | ADL6 (DYNAMIN-LIKE PROTEIN 6) | chr1:3370776-3377122 FORWARD

Match to Query 2240: 956.553294 from(479.283923,2+) index(5285)
Title: Elution from: 47.486 to 47.486 scan no 6616 cid35.00 polarity:+
Data file C7-2_1.mgf

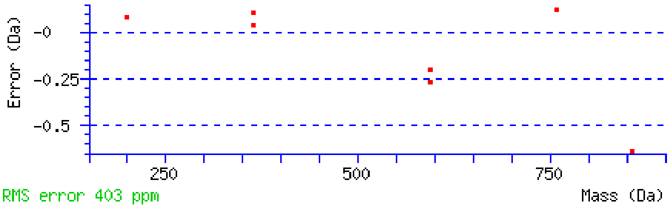
Click mouse within plot area to zoom in by factor of two about that point

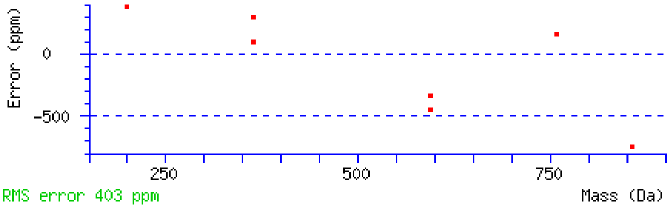
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 956.5555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0036
Matches : 7/64 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400					V							8
2	**199.1225**	100.0649					P	***857.4973***	429.2523	839.4737	420.2405	839.4868	420.2470	7
3	**363.1829**	182.0951					Y	***759.4475***	380.2274	741.4239	371.2156	741.4370	371.2221	6
4	493.2719	247.1396	475.2483	238.1278			K	***595.3872***	298.1972	577.3636	289.1854	577.3766	289.1919	5
5	**595.3166**	298.1620	577.2930	289.1502	577.3061	289.1567	T	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
6	695.3821	348.1947	677.3585	339.1829	677.3715	339.1894	V	***363.2534***	182.1303	345.2298	173.1186			3
7	809.4632	405.2352	791.4396	396.2234	791.4526	396.2299	L	263.1880	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VPYKTVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.9	956.5555	-0.0022	VPYKTVLK

AT1G10290.1

Mascot: http://www.matrixscience.com/

AT1G10320.1

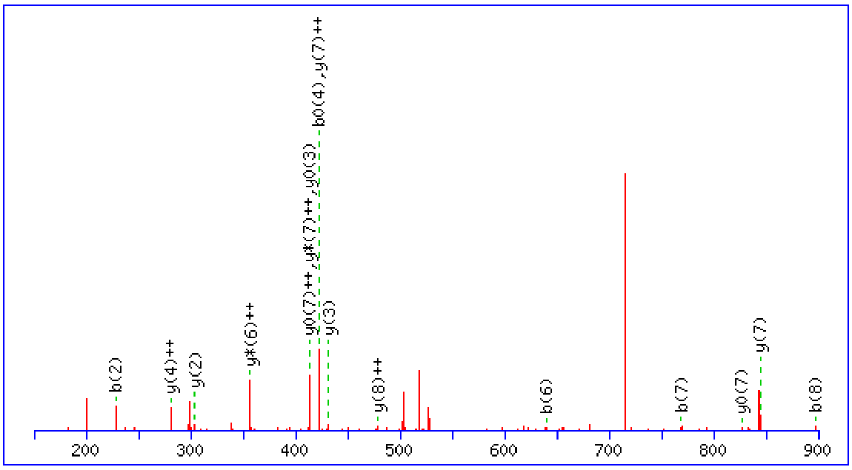
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNDPAEQER**
Found in **AT1G10320.1** in **TAIR_Arabidopsis**, Symbols: | U2 snRNP auxiliary factor-related | chr1:3384166-3388375 REVERSE

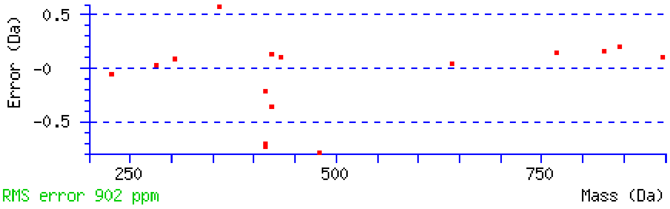
Match to Query 3180: 1070.500914 from(536.257733,2+) index(3214)
Title: Elution from: 32.367 to 32.367 scan no 4008 cid35.00 polarity:+
Data file D12h-3_1.mgf

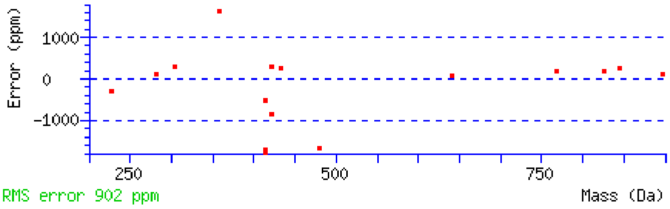
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1070.4992
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.046
Matches : 16/88 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							9
2	***228.1343***	114.5708	211.1077	106.0575			N	958.4225	479.7149	941.3959	471.2016	940.4119	470.7096	8
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	D	**844.3795**	422.6934	827.3530	414.1801	826.3690	413.6881	7
4	440.2140	220.6106	423.1874	212.0974	422.2034	211.6053	P	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	6
5	511.2511	256.1292	494.2245	247.6159	493.2405	247.1239	A	632.2998	316.6536	615.2733	308.1403	614.2893	307.6483	5
6	***640.2937***	320.6505	623.2671	312.1372	622.2831	311.6452	E	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	4
7	***768.3523***	384.6798	751.3257	376.1665	750.3417	375.6745	Q	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	3
8	***897.3949***	449.2011	880.3683	440.6878	879.3843	440.1958	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LNDPAEQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.4	1070.4992	0.0017	LNDPAEQER

AT1G10320.1

3.1	1070.5033	-0.0024	DQIYDVYR

Mascot: http://www.matrixscience.com/

AT1G10370.1

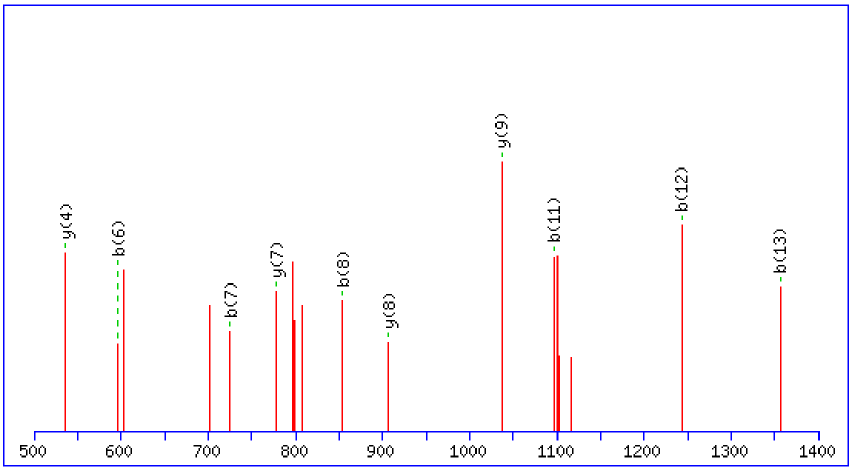
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVIAQLEEGNAFLEK**
Found in **AT1G10370.1** in **TAIR_Arabidopsis**, Symbols: GST30, ATGSTU17, GST30B, ERD9 | ATGSTU17/ERD9/GST30/GST30B (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase | chr1:3397446-3398274 REVERSE

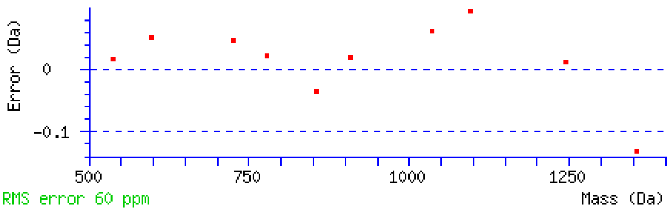
Match to Query 7531: 1630.858772 from(816.436662,2+) index(7703)
Title: Elution from: 66.804 to 66.804 scan no 10028 cid35.00 polarity:+
Data file D1d-3_2.mgf

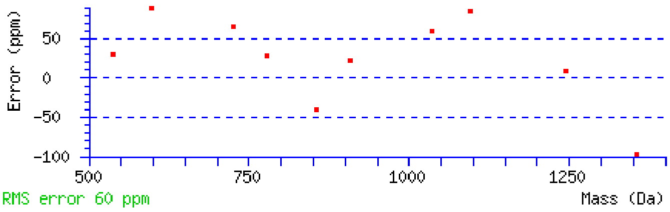
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1630.8566
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 9.2e-005
Matches : 10/146 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							15
2	171.1128	86.0600					V	1560.8268	780.9170	1543.8003	772.4038	1542.8162	771.9118	14
3	284.1969	142.6021					I	1461.7584	731.3828	1444.7318	722.8696	1443.7478	722.3775	13
4	355.2340	178.1206					A	1348.6743	674.8408	1331.6478	666.3275	1330.6638	665.8355	12
5	483.2926	242.1499	466.2660	233.6366			Q	1277.6372	639.3222	1260.6107	630.8090	1259.6266	630.3170	11
6	***596.3766***	298.6920	579.3501	290.1787			L	1149.5786	575.2930	1132.5521	566.7797	1131.5681	566.2877	10
7	***725.4192***	363.2132	708.3927	354.7000	707.4087	354.2080	E	**1036.4946**	518.7509	1019.4680	510.2376	1018.4840	509.7456	9
8	***854.4618***	427.7345	837.4353	419.2213	836.4512	418.7293	E	**907.4520**	454.2296	890.4254	445.7164	889.4414	445.2243	8
9	911.4833	456.2453	894.4567	447.7320	893.4727	447.2400	G	**778.4094**	389.7083	761.3828	381.1951	760.3988	380.7030	7
10	1025.5262	513.2667	1008.4997	504.7535	1007.5156	504.2615	N	721.3879	361.1976	704.3614	352.6843	703.3774	352.1923	6
11	***1096.5633***	548.7853	1079.5368	540.2720	1078.5528	539.7800	A	607.3450	304.1761	590.3184	295.6629	589.3344	295.1709	5
12	***1243.6317***	622.3195	1226.6052	613.8062	1225.6212	613.3142	F	**536.3079**	268.6576	519.2813	260.1443	518.2973	259.6523	4
13	***1356.7158***	678.8615	1339.6892	670.3483	1338.7052	669.8563	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
14	1485.7584	743.3828	1468.7318	734.8696	1467.7478	734.3775	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15							K	147.1128	74.0600	130.0863	65.5468			1





AT1G10370.1

NCBI **BLAST** search of AVIAQLEEGNAFLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.2	1630.8566	0.0022	AVIAQLEEGNAFLEK
12.0	1630.8600	-0.0012	QLQEKINMLELEK

AT1G10630.1

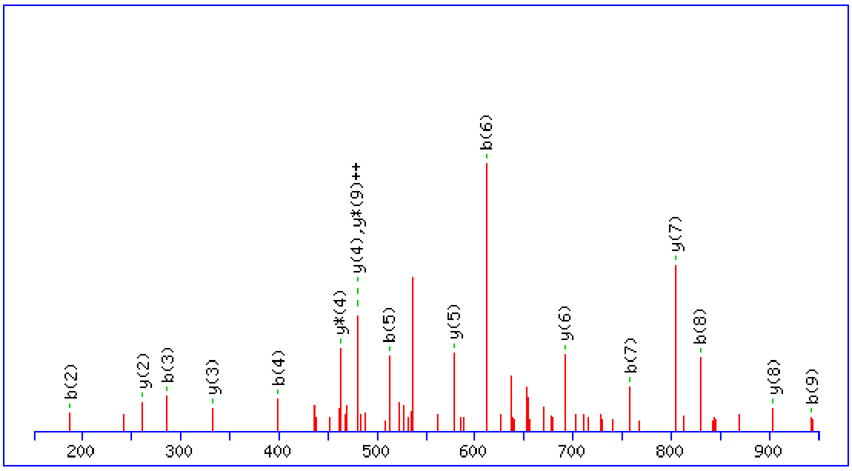
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAVLLVFANK**
Found in **AT1G10630.1** in **TAIR_Arabidopsis**, Symbols: ATARFA1F | ATARFA1F; GTP binding / phospholipase activator/ protein binding | chr1:3513190-3514231 REVERSE

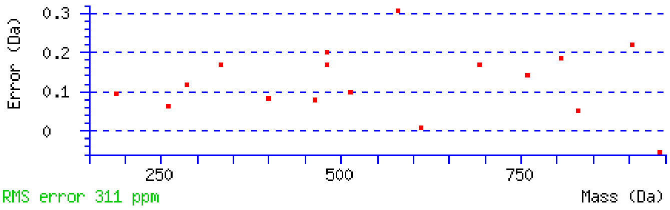
Match to Query 3491: 1088.625486 from(545.320019,2+) index(8277)
Title: Elution from: 72.113 to 72.113 scan no 10817 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

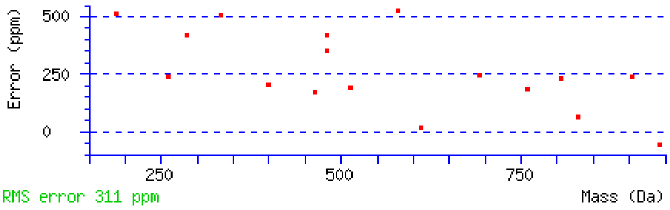


Monoisotopic mass of neutral peptide Mr(calc): 1088.6230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 1.6e-007
Matches : 17/74 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	116.0342	58.5207			98.0237	49.5155	D					10
2	***187.0713***	94.0393			169.0608	85.0340	A	974.6033	487.8053	957.5768	479.2920	9
3	***286.1397***	143.5735			268.1292	134.5682	V	**903.5662**	452.2867	886.5397	443.7735	8
4	***399.2238***	200.1155			381.2132	191.1103	L	**804.4978**	402.7525	787.4713	394.2393	7
5	***512.3079***	256.6576			494.2973	247.6523	L	**691.4137**	346.2105	674.3872	337.6972	6
6	***611.3763***	306.1918			593.3657	297.1865	V	**578.3297**	289.6685	561.3031	281.1552	5
7	***758.4447***	379.7260			740.4341	370.7207	F	**479.2613**	240.1343	462.2347	231.6210	4
8	***829.4818***	415.2445			811.4713	406.2393	A	**332.1928**	166.6001	315.1663	158.0868	3
9	***943.5247***	472.2660	926.4982	463.7527	925.5142	463.2607	N	**261.1557**	131.0815	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468	1



RMS error 311 ppm



RMS error 311 ppm

NCBI **BLAST** search of DAVLLVFANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G10630.1

Score	Mr(calc)	Delta	Sequence
73.3	1088.6230	0.0025	DAVLLVFANK

Mascot: http://www.matrixscience.com/

AT1G10670.1

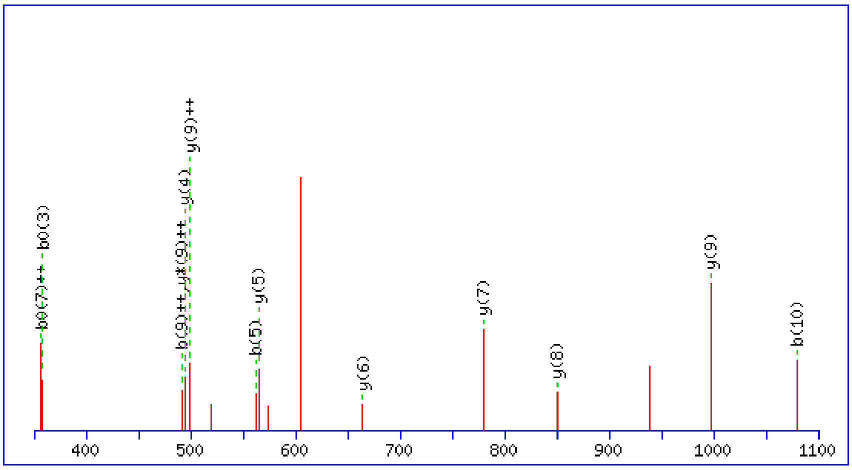
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDFADVATFVK**
Found in **AT1G10670.1** in **TAIR_Arabidopsis**, Symbols: ACLA-1 | ACLA-1 (ATP-citrate lyase A-1) | chr1:3535788-3538099 FORWARD

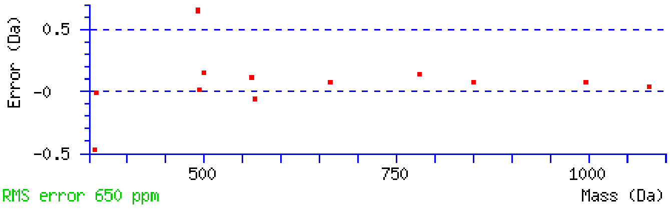
Match to Query 4042: 1224.640120 from(613.327336,2+) index(9153)
Title: Elution from: 84.030 to 84.030 scan no 12666 cid35.00 polarity:+
Data file D6h-2_3.mgf

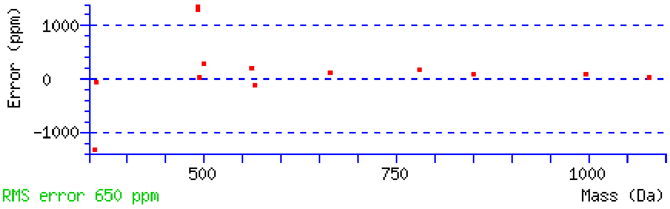
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1224.6391
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 2.4e-005
Matches : 13/92 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							11
2	229.1183	115.0628	211.1077	106.0575	D	1112.5623	556.7848	1095.5357	548.2715	1094.5517	547.7795	10
3	376.1867	188.5970	358.1761	179.5917	F	***997.5353***	499.2713	980.5088	490.7580	979.5247	490.2660	9
4	447.2238	224.1155	429.2132	215.1103	A	***850.4669***	425.7371	833.4403	417.2238	832.4563	416.7318	8
5	**562.2508**	281.6290	544.2402	272.6237	D	***779.4298***	390.2185	762.4032	381.7053	761.4192	381.2132	7
6	661.3192	331.1632	643.3086	322.1579	V	***664.4028***	332.7051	647.3763	324.1918	646.3923	323.6998	6
7	732.3563	366.6818	714.3457	357.6765	A	***565.3344***	283.1709	548.3079	274.6576	547.3239	274.1656	5
8	833.4040	417.2056	815.3934	408.2003	T	***494.2973***	247.6523	477.2708	239.1390	476.2867	238.6470	4
9	980.4724	490.7398	962.4618	481.7345	F	393.2496	197.1285	376.2231	188.6152			3
10	**1079.5408**	540.2740	1061.5302	531.2687	V	246.1812	123.5942	229.1547	115.0810			2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LDFADVATFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G10670.1

Score	Mr(calc)	Delta	Sequence
50.2	1224.6391	0.0011	LDFADVATFVK
10.4	1224.6390	0.0011	LDQVFESLFK
7.0	1224.6424	-0.0023	IDMTTTVLGFK
2.4	1224.6424	-0.0023	EVILYNVTMK
1.4	1224.6397	0.0004	VSRRVFCSSK

AT1G10760.1

Mascot Search Results

Peptide View

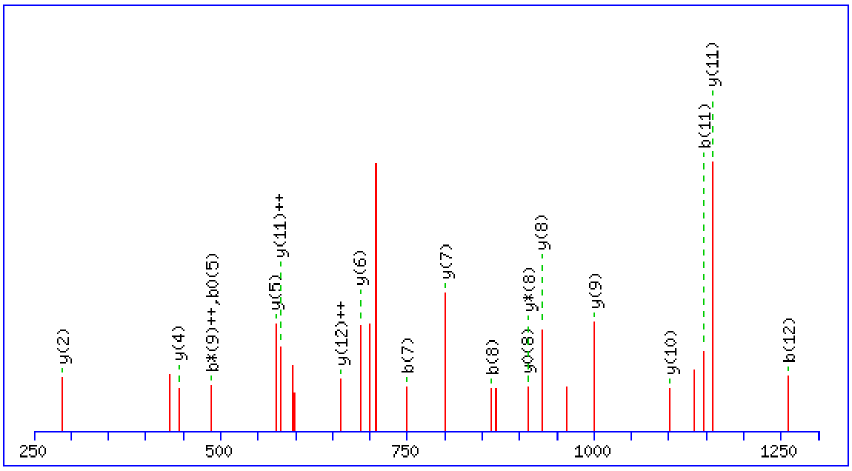
MS/MS Fragmentation of **LYGTAQDIEGVIR**
Found in **AT1G10760.1** in **TAIR_Arabidopsis**, Symbols: SOP1, SOP, GWD1, GWD, SEX1 | SEX1 (STARCH EXCESS 1) | chr1:3581211-3590044 REVERSE

Match to Query 5818: 1433.750598 from(717.882575,2+) index(6444)
Title: Elution from: 55.857 to 55.857 scan no 8228 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

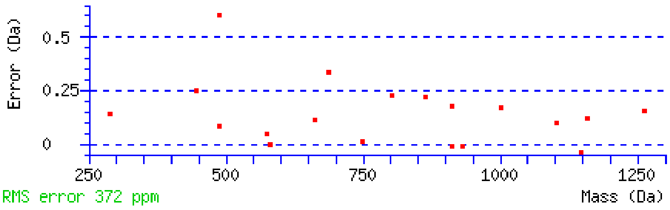
Or, Plot from 250 to 1300 Da Full range

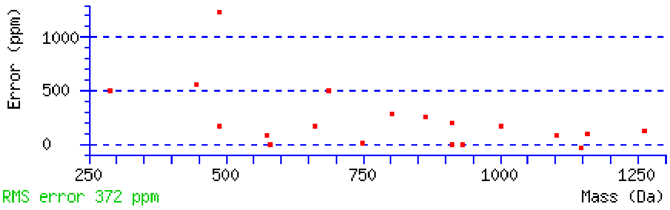
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1433.7514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.3e-007
Matches : 19/120 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							13
2	277.1547	139.0810					Y	1321.6747	661.3410	1304.6481	652.8277	1303.6641	652.3357	12
3	334.1761	167.5917					G	***1158.6113***	579.8093	1141.5848	571.2960	1140.6008	570.8040	11
4	435.2238	218.1155			417.2132	209.1103	T	***1101.5899***	551.2986	1084.5633	542.7853	1083.5793	542.2933	10
5	506.2609	253.6341			488.2504	244.6288	A	***1000.5422***	500.7747	983.5156	492.2615	982.5316	491.7694	9
6	634.3195	317.6634	617.2930	309.1501	616.3089	308.6581	Q	***929.5051***	465.2562	912.4785	456.7429	911.4945	456.2509	8
7	**749.3464**	375.1769	732.3199	366.6636	731.3359	366.1716	D	***801.4465***	401.2269	784.4199	392.7136	783.4359	392.2216	7
8	**862.4305**	431.7189	845.4040	423.2056	844.4199	422.7136	I	***686.4196***	343.7134	669.3930	335.2001	668.4090	334.7081	6
9	991.4731	496.2402	974.4466	487.7269	973.4625	487.2349	E	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	5
10	1048.4946	524.7509	1031.4680	516.2376	1030.4840	515.7456	G	***444.2929***	222.6501	427.2663	214.1368			4
11	**1147.5630**	574.2851	1130.5364	565.7719	1129.5524	565.2798	V	387.2714	194.1394	370.2449	185.6261			3
12	**1260.6470**	630.8272	1243.6205	622.3139	1242.6365	621.8219	I	***288.2030***	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LYGTAQDIEGVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G10760.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.2	1433.7514	-0.0008	LYGTAQDIEGVIR
6.9	1433.7487	0.0019	HDENGNPVKRLR
0.3	1433.7514	-0.0008	IYVGQGENGIASVK

AT1G10780.1

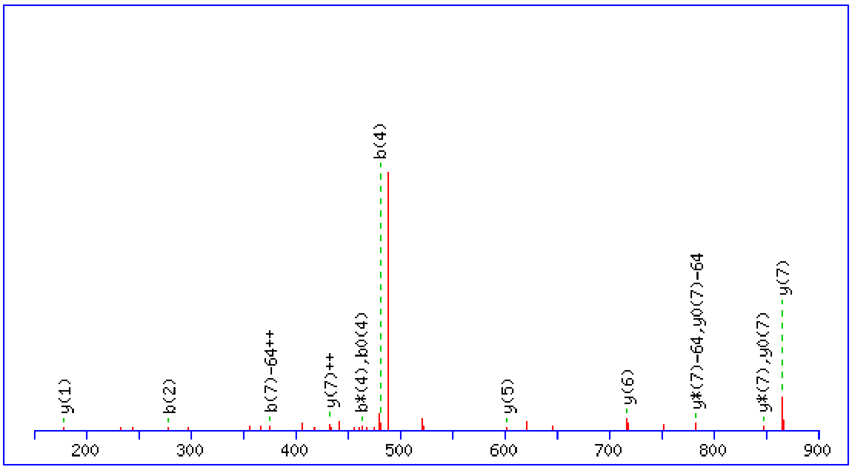
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KMISSSRR**
Found in **AT1G10780.1** in **TAIR_Arabidopsis**, Symbols: | F-box family protein | chr1:3592876-3594311 REVERSE

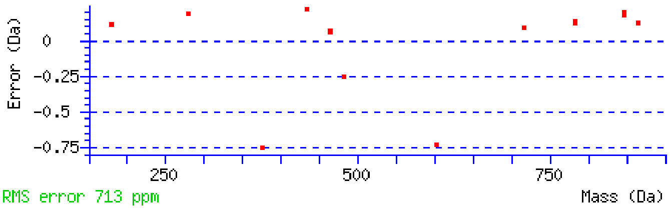
Match to Query 2389: 994.481460 from(498.248006,2+) index(1112)
Title: Elution from: 17.424 to 17.424 scan no 1572 cid35.00 polarity:+
Data file D6h-1_3.mgf

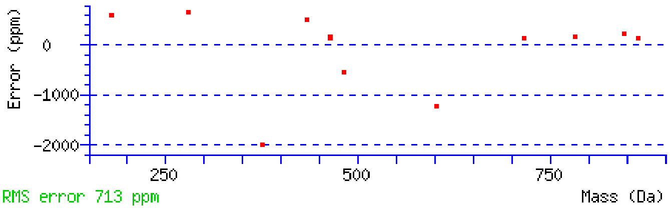
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.4788
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 17 **Expect:** 0.036
Matches : 14/112 fragment ions using 26 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0963	66.0518	113.0727	57.0400			K							8
2	**279.1287**	140.0680	261.1052	131.0562			M	***865.3971***	433.2022	847.3735	424.1904	847.3865	424.1969	7
3	393.2098	197.1086	375.1863	188.0968			I	***717.3646***	359.1860	699.3410	350.1742	699.3541	350.1807	6
4	**481.2389**	241.1231	463.2153	232.1113	463.2283	232.1178	S	***603.2835***	302.1454	585.2599	293.1336	585.2730	293.1401	5
5	569.2680	285.1376	551.2444	276.1258	551.2574	276.1323	S	515.2545	258.1309	497.2309	249.1191	497.2439	249.1256	4
6	657.2970	329.1522	639.2734	320.1404	639.2865	320.1469	S	427.2254	214.1163	409.2018	205.1045	409.2148	205.1111	3
7	817.3863	409.1968	799.3627	400.1850	799.3757	400.1915	R	339.1963	170.1018	321.1728	161.0900			2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KMISSSRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.4	994.4788	0.0026	KMISSSRR

AT1G10780.1

8.3	994.4810	0.0004	VMRYREK
4.5	994.4810	0.0004	LMRDFKR
3.4	994.4806	0.0009	GMFDFLKK
2.7	994.4833	-0.0018	KWMAFKR
2.7	994.4788	0.0026	MTKRSVSR
2.5	994.4810	0.0004	RMYQKQK

AT1G10840.1

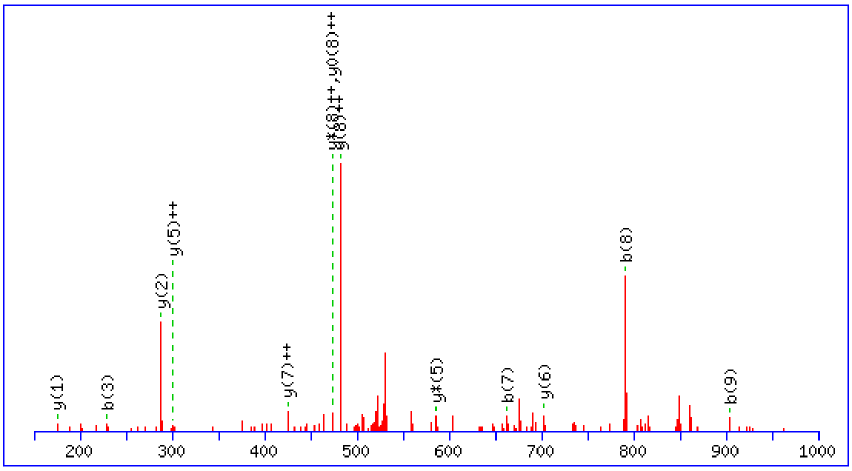
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGNFTGEKLR**
Found in **AT1G10840.1** in **TAIR_Arabidopsis**, Symbols: TIF3H1 | TIF3H1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT H1); translation initiation factor | chr1:3607886-3610300 REVERSE

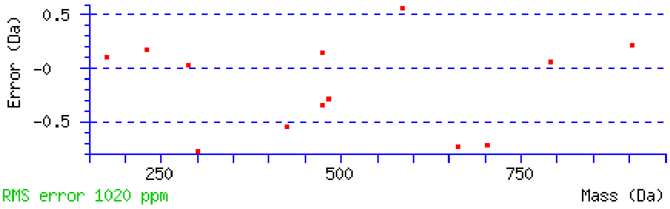
Match to Query 3147: 1077.557434 from(539.785993,2+) index(2604)
Title: Elution from: 27.590 to 27.590 scan no 3270 cid35.00 polarity:+
Data file D6h-3_1.mgf

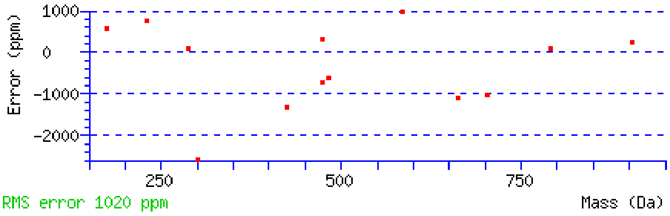
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1077.5567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.015
Matches : 13/90 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	115.0502	58.0287					G	1021.5425	511.2749	1004.5160	502.7616	1003.5320	502.2696	9
3	***229.0931***	115.0502	212.0666	106.5369			N	964.5211	482.7642	947.4945	474.2509	946.5105	473.7589	8
4	376.1615	188.5844	359.1350	180.0711			F	850.4781	425.7427	833.4516	417.2294	832.4676	416.7374	7
5	477.2092	239.1083	460.1827	230.5950	459.1987	230.1030	T	***703.4097***	352.2085	686.3832	343.6952	685.3992	343.2032	6
6	534.2307	267.6190	517.2041	259.1057	516.2201	258.6137	G	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	5
7	***663.2733***	332.1403	646.2467	323.6270	645.2627	323.1350	E	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	4
8	***791.3682***	396.1878	774.3417	387.6745	773.3577	387.1825	K	416.2980	208.6526	399.2714	200.1394			3
9	***904.4523***	452.7298	887.4258	444.2165	886.4417	443.7245	L	***288.2030***	144.6051	271.1765	136.0919			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GGNFTGEKLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G10840.1

Score	Mr(calc)	Delta	Sequence
25.0	1077.5567	0.0007	GGNFTGEKLR
13.1	1077.5567	0.0008	DRNLYELR
9.1	1077.5567	0.0008	EVNYERLR
8.0	1077.5601	-0.0026	TKGAQALSMR
7.5	1077.5567	0.0007	LGYTNQLNR
5.8	1077.5600	-0.0026	SNNKSMLLR
0.8	1077.5576	-0.0001	VMCLPFRR
0.8	1077.5567	0.0007	GERDSVFLR
0.8	1077.5601	-0.0026	MERVSTLSR
0.2	1077.5567	0.0008	AREASEFLR

Mascot: http://www.matrixscience.com/

AT1G11070.1

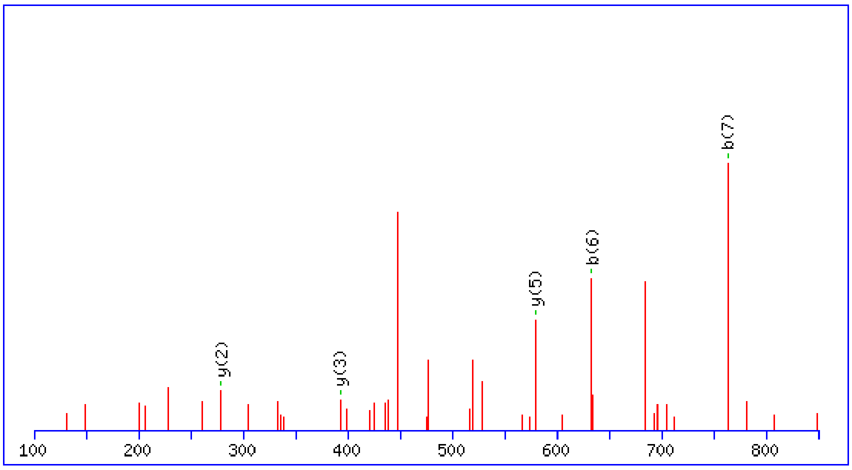
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKEAILEK**
Found in **AT1G11070.1** in **TAIR_Arabidopsis**, Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:3690406-3692826 REVERSE

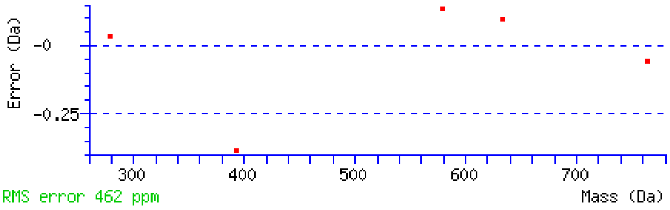
Match to Query 1658: 910.496940 from(456.255746,2+) index(1563)
Title: Elution from: 20.272 to 20.272 scan no 2073 cid35.00 polarity:+
Data file D6h-3_2.mgf

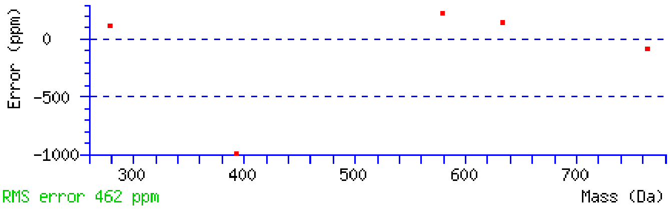
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 910.4984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.045
Matches : 5/76 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							8
2	203.1305	102.0689	185.1069	93.0571			K	839.4715	420.2394	821.4479	411.2276	821.4609	411.2341	7
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	E	709.3825	355.1949	691.3589	346.1831	691.3719	346.1896	6
4	405.2042	203.1058	387.1807	194.0940	387.1937	194.1005	A	***579.3428***	290.1751	561.3193	281.1633	561.3323	281.1698	5
5	519.2853	260.1463	501.2618	251.1345	501.2748	251.1410	I	507.3087	254.1580	489.2851	245.1462	489.2981	245.1527	4
6	***633.3664***	317.1869	615.3428	308.1751	615.3559	308.1816	L	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	***763.4061***	382.2067	745.3825	373.1949	745.3955	373.2014	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AKEAILEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.9	910.4984	-0.0014	AKEAILEK
16.9	910.4984	-0.0014	KVGEVIEK

AT1G11070.1

13.6	910.4984	-0.0014	GAVLATELK
12.0	910.4984	-0.0014	EKAELALK
12.0	910.4984	-0.0014	KEAAEIIK
11.6	910.4984	-0.0014	AGLLSLAEK
11.5	910.4984	-0.0014	AALEELKK
11.5	910.4984	-0.0014	IGIDDIKK
11.5	910.4984	-0.0014	LDGIDLKK
11.5	910.4984	-0.0014	LSAELIQK

AT1G11545.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGWFSMKLK**
Found in **AT1G11545.1** in **TAIR_Arabidopsis**, Symbols: | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr1:3878689-3880286 REVERSE

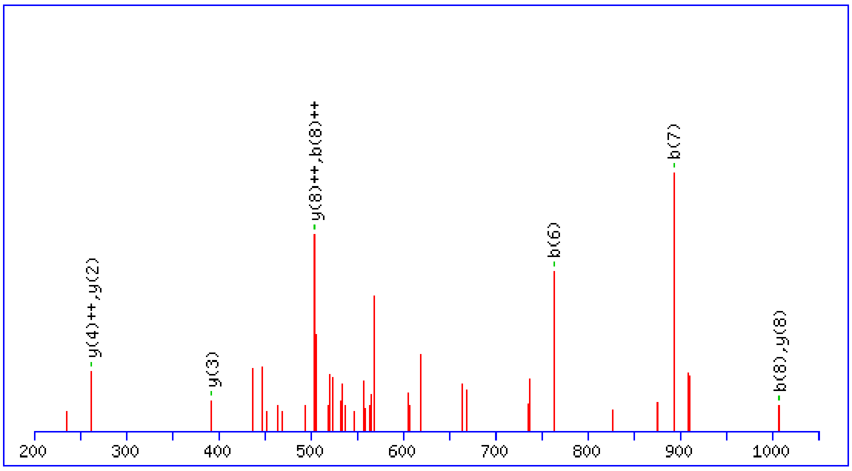
Match to Query 3844: 1154.559008 from(578.286780,2+) index(7223)
Title: Elution from: 64.831 to 64.831 scan no 9487 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

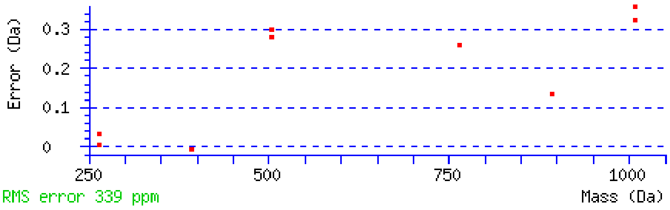
Label all possible matches ○ Label matches used for scoring ●

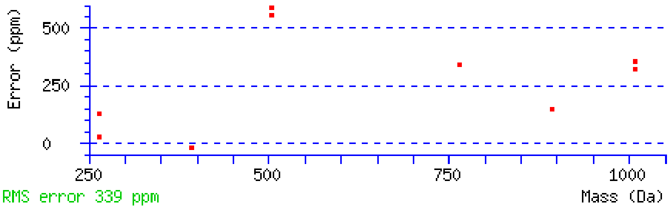
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.5591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0072
Matches : 9/68 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							9
2	207.0912	104.0492					G	***1007.5009***	504.2541	989.4773	495.2423	989.4904	495.2488	8
3	395.1646	198.0859					W	949.4824	475.2448	931.4588	466.2331	931.4719	466.2396	7
4	543.2301	272.1187					F	761.4090	381.2082	743.3855	372.1964	743.3985	372.2029	6
5	631.2591	316.1332			613.2486	307.1279	S	613.3436	307.1754	595.3200	298.1636	595.3330	298.1702	5
6	***763.2966***	382.1520			745.2861	373.1467	M	525.3145	263.1609	507.2909	254.1491			4
7	***893.3857***	447.1965	875.3621	438.1847	875.3751	438.1912	K	***393.2770***	197.1421	375.2534	188.1303			3
8	***1007.4668***	504.2370	989.4432	495.2252	989.4562	495.2317	L	***263.1880***	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FGWFSMKLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G11545.1

26.9	1154.5591	-0.0001	FGWFSMKLK
20.9	1154.5569	0.0022	ELHMFPQIK
10.8	1154.5620	-0.0030	DSLGDRHVLK
5.0	1154.5616	-0.0026	FATKFSDSIK
3.7	1154.5620	-0.0030	DAHESRAILK
1.6	1154.5620	-0.0030	NTKNPTSHLK
1.5	1154.5593	-0.0003	GGDDSAPAIVLK
1.5	1154.5593	-0.0003	QEQGITEPIK
1.5	1154.5620	-0.0030	TLREHAGDLK
1.1	1154.5593	-0.0003	TDPEAIGALQK

Mascot: http://www.matrixscience.com/

AT1G11655.1

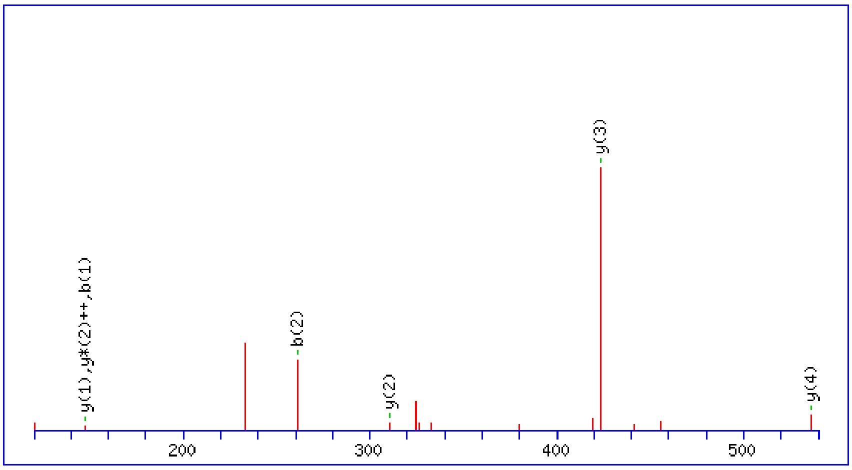
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLIYK**
Found in **AT1G11655.1** in **TAIR_Arabidopsis**

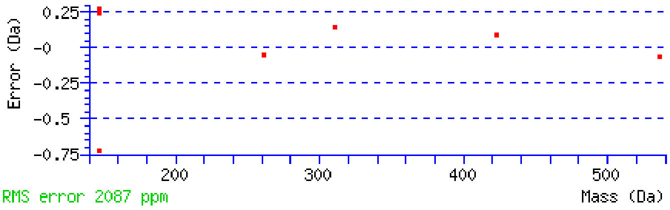
Match to Query 588: 682.404804 from(342.209678,2+) index(3109)
Title: Elution from: 29.936 to 29.936 scan no 3840 cid35.00 polarity:+
Data file D6h-3_3.mgf

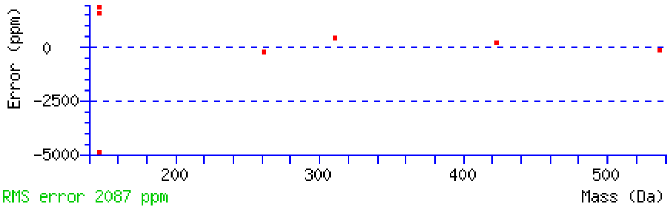
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 540 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 682.4054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0017
Matches : 7/24 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**148.0757**	74.5415	F					5
2	**261.1598**	131.0835	L	*536.3443*	268.6758	519.3177	260.1625	4
3	374.2438	187.6255	I	*423.2602*	212.1337	406.2336	203.6205	3
4	537.3071	269.1572	Y	*310.1761*	155.5917	293.1496	147.0784	2
5			K	*147.1128*	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of FLIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.4	682.4054	-0.0006	FIIYK
28.4	682.4054	-0.0006	FLIYK
28.4	682.4054	-0.0006	FLLYK
19.2	682.4054	-0.0006	FLYLK
13.2	682.4054	-0.0006	IFLYK

AT1G11655.1

8.8	682.4054	-0.0006	IFPPLP

Mascot: http://www.matrixscience.com/

AT1G11750.1

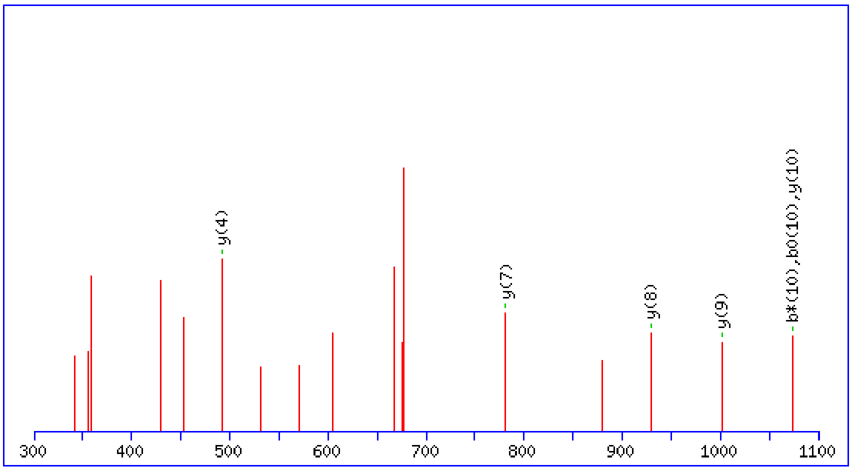
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MYAAFTGQPLEK**
Found in **AT1G11750.1** in **TAIR_Arabidopsis**, Symbols: NCLPP1, NCLPP6, CLPP6 | CLPP6 (Clp protease proteolytic subunit 6); endopeptidase Clp | chr1:3967609-3969535 FORWARD

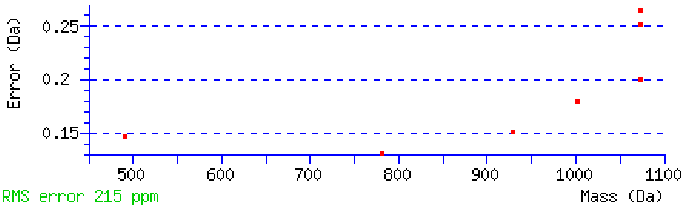
Match to Query 5193: 1368.621148 from(685.317850,2+) index(5125)
Title: Elution from: 46.049 to 46.049 scan no 6456 cid35.00 polarity:+
Data file C7-1_2.mgf

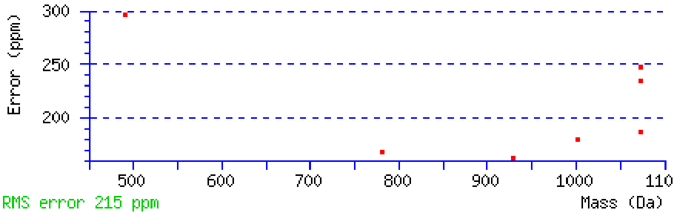
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1368.6176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.002
Matches : 7/106 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							12
2	297.1052	149.0562					Y	1237.5874	619.2973	1219.5638	610.2855	1219.5768	610.2920	11
3	369.1393	185.0733					A	***1073.5270***	537.2671	1055.5034	528.2553	1055.5164	528.2619	10
4	441.1735	221.0904					A	***1001.4929***	501.2501	983.4693	492.2383	983.4823	492.2448	9
5	589.2389	295.1231					F	***929.4587***	465.2330	911.4351	456.2212	911.4481	456.2277	8
6	691.2836	346.1454			673.2731	337.1402	T	***781.3933***	391.2003	763.3697	382.1885	763.3827	382.1950	7
7	749.3021	375.1547			731.2916	366.1494	G	679.3485	340.1779	661.3250	331.1661	661.3380	331.1726	6
8	879.3548	440.1810	861.3312	431.1692	861.3442	431.1757	Q	621.3300	311.1687	603.3065	302.1569	603.3195	302.1634	5
9	977.4046	489.2059	959.3810	480.1941	959.3940	480.2006	P	***491.2774***	246.1423	473.2538	237.1305	473.2668	237.1371	4
10	1091.4857	546.2465	1073.4621	537.2347	1073.4751	537.2412	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
11	1221.5253	611.2663	1203.5017	602.2545	1203.5147	602.2610	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MYAAFTGQPLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G11750.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.4	1368.6176	0.0035	MYAAFTGQPLEK
1.2	1368.6250	-0.0039	AYLSAYNSHSLK
0.9	1368.6237	-0.0025	CGNLKAAMNVFK
0.2	1368.6214	-0.0003	RVLQMMSLDAR

AT1G11770.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDPGLFMRLLLQPVTRNK**
Found in **AT1G11770.1** in **TAIR_Arabidopsis**, Symbols: | electron carrier | chr1:3975678-3977288 FORWARD

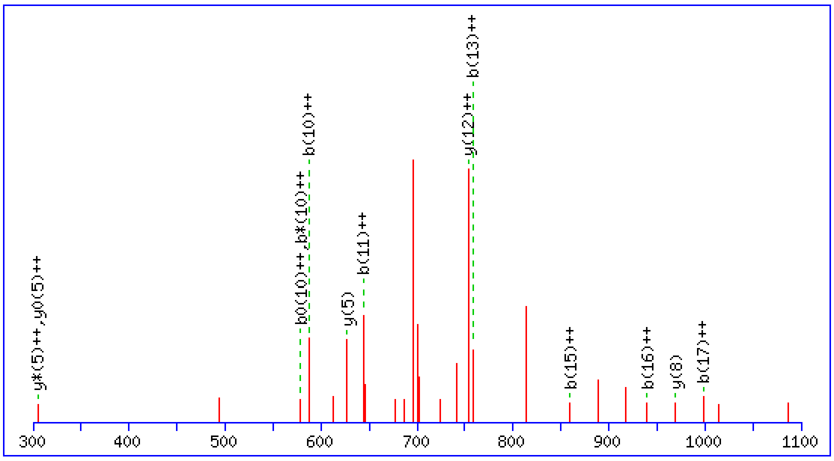
Match to Query 9608: 2141.086356 from(714.702728,3+) index(10237)
Title: Elution from: 96.557 to 96.557 scan no 14290 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●

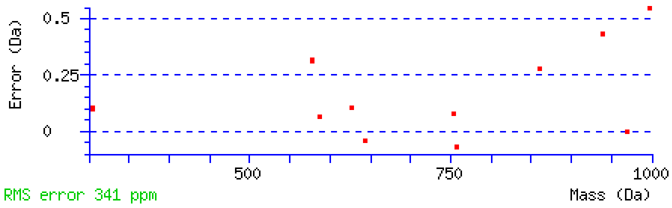
Show Y-axis ☐

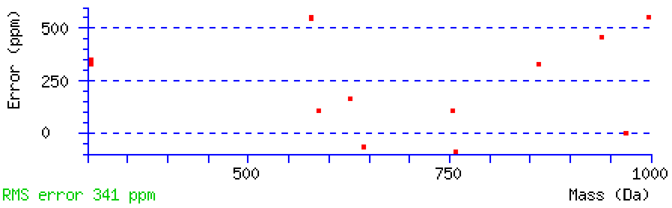


Monoisotopic mass of neutral peptide Mr(calc): 2141.0870
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.031
Matches : 13/284 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							18
2	219.0760	110.0416			201.0654	101.0363	D	2040.0495	1020.5284	2022.0260	1011.5166	2022.0390	1011.5231	17
3	317.1258	159.0665			299.1152	150.0612	P	1924.0256	962.5164	1906.0020	953.5046	1906.0150	953.5111	16
4	375.1443	188.0758			357.1337	179.0705	G	1825.9758	913.4915	1807.9522	904.4797	1807.9652	904.4862	15
5	489.2254	245.1163			471.2148	236.1110	L	1767.9573	884.4823	1749.9337	875.4705	1749.9467	875.4770	14
6	637.2908	319.1490			619.2802	310.1438	F	1653.8762	827.4417	1635.8526	818.4299	1635.8656	818.4364	13
7	785.3232	393.1653			767.3127	384.1600	M	1505.8107	753.4090	1487.7871	744.3972	1487.8001	744.4037	12
8	945.4125	473.2099	927.3889	464.1981	927.4019	464.2046	R	1357.7783	679.3928	1339.7547	670.3810	1339.7677	670.3875	11
9	1059.4936	530.2504	1041.4700	521.2386	1041.4830	521.2452	L	1197.6890	599.3482	1179.6654	590.3364	1179.6785	590.3429	10
10	1173.5747	***587.2910***	1155.5511	578.2792	1155.5641	578.2857	L	1083.6079	542.3076	1065.5843	533.2958	1065.5974	533.3023	9
11	1287.6558	***644.3315***	1269.6322	635.3197	1269.6452	635.3263	L	**969.5268**	485.2671	951.5032	476.2553	951.5163	476.2618	8
12	1417.7084	709.3579	1399.6849	700.3461	1399.6979	700.3526	Q	855.4457	428.2265	837.4221	419.2147	837.4352	419.2212	7
13	1515.7582	***758.3828***	1497.7347	749.3710	1497.7477	749.3775	P	725.3931	363.2002	707.3695	354.1884	707.3825	354.1949	6
14	1615.8237	808.4155	1597.8001	799.4037	1597.8131	799.4102	V	**627.3433**	314.1753	609.3197	305.1635	609.3327	305.1700	5
15	1717.8684	***859.4378***	1699.8448	850.4260	1699.8578	850.4326	T	527.2778	264.1426	509.2543	255.1308	509.2673	255.1373	4
16	1877.9577	***939.4825***	1859.9341	930.4707	1859.9471	930.4772	R	425.2331	213.1202	407.2095	204.1084			3
17	1993.9947	***997.5010***	1975.9711	988.4892	1975.9841	988.4957	N	265.1439	133.0756	247.1203	124.0638			2
18							K	149.1069	75.0571	131.0833	66.0453			1

AT1G11770.1





NCBI **BLAST** search of TDPGLFMRLLLQPVTRNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.8	2141.0870	-0.0006	TDPGLFMRLLLQPVTRNK
17.6	2141.0924	-0.0061	GSLDIKETTSKIIIECLAK
1.9	2141.0890	-0.0027	LLEYLGKNLNVKELDETK
1.1	2141.0892	-0.0028	QGLCVSVLNGLWISKKWK
0.8	2141.0877	-0.0013	TLTDCNTIKKLSILCPLK

Mascot: http://www.matrixscience.com/

AT1G11840.1

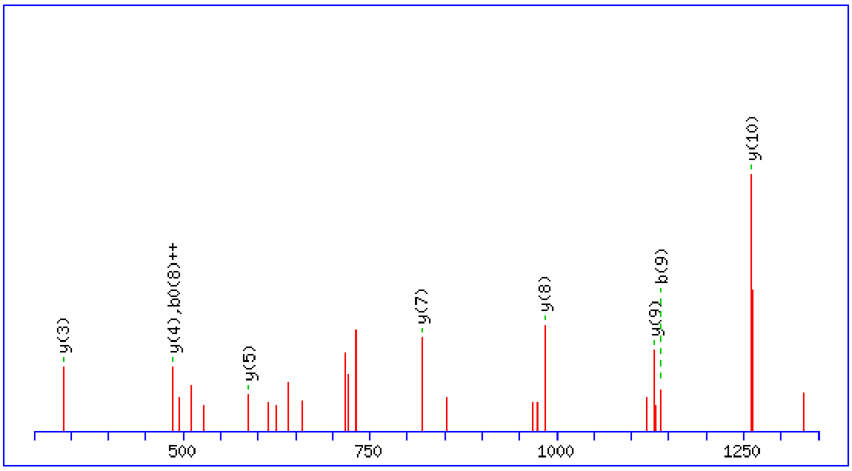
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIEFYTEVFGMK**
Found in **AT1G11840.1** in **TAIR_Arabidopsis**, Symbols: ATGLX1 | ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase | chr1:3996044-3997517 FORWARD

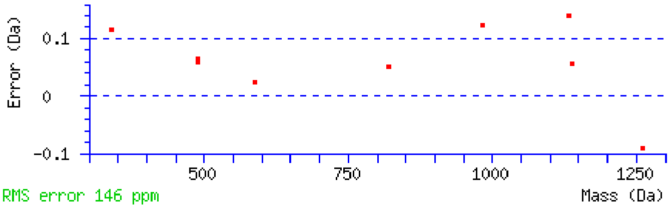
Match to Query 5544: 1476.660532 from(739.337542,2+) index(9011)
Title: Elution from: 84.374 to 84.374 scan no 12505 cid35.00 polarity:+
Data file D1d-1_3.mgf

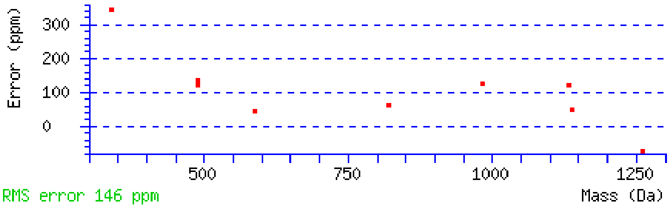
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1476.6621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 8.4e-006
Matches : 9/100 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							12
2	217.1331	109.0702	199.1225	100.0649	I	1375.6247	688.3160	1357.6011	679.3042	1357.6141	679.3107	11
3	347.1727	174.0900	329.1622	165.0847	E	*1261.5436*	631.2754	1243.5200	622.2636	1243.5330	622.2701	10
4	495.2382	248.1227	477.2276	239.1174	F	*1131.5039*	566.2556	1113.4804	557.2438	1113.4934	557.2503	9
5	659.2985	330.1529	641.2880	321.1476	Y	*983.4385*	492.2229	965.4149	483.2111	965.4279	483.2176	8
6	761.3432	381.1753	743.3327	372.1700	T	*819.3781*	410.1927	801.3545	401.1809	801.3676	401.1874	7
7	891.3829	446.1951	873.3723	437.1898	E	717.3334	359.1703	699.3098	350.1586	699.3229	350.1651	6
8	991.4483	496.2278	973.4378	487.2225	V	*587.2938*	294.1505	569.2702	285.1387			5
9	1139.5138	570.2605	1121.5032	561.2552	F	*487.2283*	244.1178	469.2048	235.1060			4
10	1197.5323	599.2698	1179.5217	590.2645	G	*339.1629*	170.0851	321.1393	161.0733			3
11	1329.5698	665.2885	1311.5592	656.2832	M	281.1444	141.0758	263.1208	132.0640			2
12					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TIEFYTEVFGMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G11840.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.1	1476.6621	-0.0015	TIEFYTEVFGMK

Mascot: http://www.matrixscience.com/

AT1G11860.1

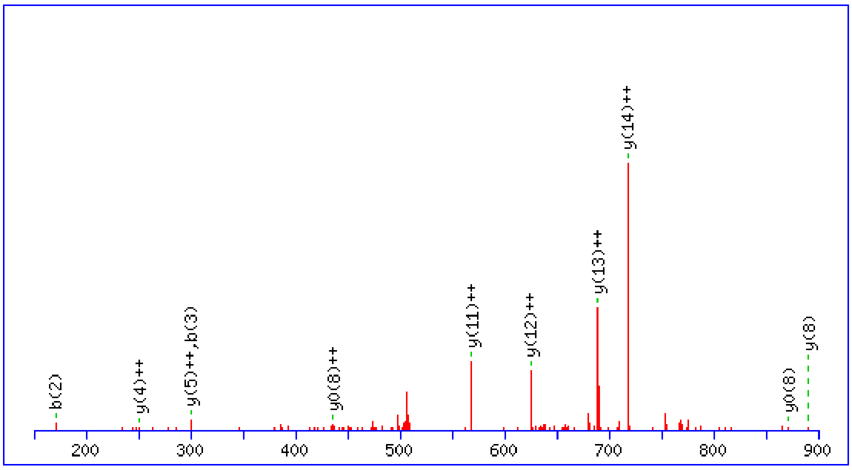
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGEITSGGFSPNLKK**
Found in **AT1G11860.1** in **TAIR_Arabidopsis**, Symbols: | aminomethyltransferase, putative | chr1:4001800-4003244 FORWARD

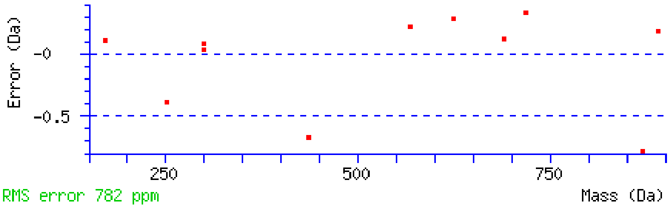
Match to Query 6711: 1546.834650 from(516.618826,3+) index(3965)
Title: Elution from: 37.560 to 37.560 scan no 4990 cid35.00 polarity:+
Data file 0-2_2.mgf

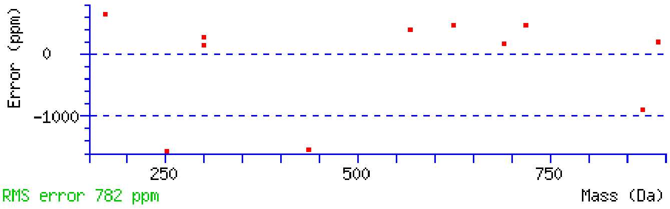
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1546.8355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0039
Matches : 11/132 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							15
2	**171.1128**	86.0600					G	1434.7587	717.8830	1417.7322	709.3697	1416.7482	708.8777	14
3	**300.1554**	150.5813			282.1448	141.5761	E	1377.7373	689.3723	1360.7107	680.8590	1359.7267	680.3670	13
4	413.2395	207.1234			395.2289	198.1181	I	1248.6947	624.8510	1231.6681	616.3377	1230.6841	615.8457	12
5	514.2871	257.6472			496.2766	248.6419	T	1135.6106	568.3089	1118.5840	559.7957	1117.6000	559.3037	11
6	601.3192	301.1632			583.3086	292.1579	S	1034.5629	517.7851	1017.5364	509.2718	1016.5524	508.7798	10
7	658.3406	329.6740			640.3301	320.6687	G	947.5309	474.2691	930.5043	465.7558	929.5203	465.2638	9
8	715.3621	358.1847			697.3515	349.1794	G	890.5094	445.7584	873.4829	437.2451	872.4989	436.7531	8
9	862.4305	431.7189			844.4199	422.7136	F	833.4880	417.2476	816.4614	408.7343	815.4774	408.2423	7
10	949.4625	475.2349			931.4520	466.2296	S	686.4195	343.7134	669.3930	335.2001	668.4090	334.7081	6
11	1046.5153	523.7613			1028.5047	514.7560	P	599.3875	300.1974	582.3610	291.6841			5
12	1160.5582	580.7828	1143.5317	572.2695	1142.5477	571.7775	N	502.3348	251.6710	485.3082	243.1577			4
13	1273.6423	637.3248	1256.6157	628.8115	1255.6317	628.3195	L	388.2918	194.6496	371.2653	186.1363			3
14	1401.7373	701.3723	1384.7107	692.8590	1383.7267	692.3670	K	275.2078	138.1075	258.1812	129.5942			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IGEITSGGFSPNLKK

AT1G11860.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1546.8355	-0.0008	IGEITSGGFSPNLKK
2.1	1546.8355	-0.0008	LENGIGLDLHLSLGP
1.9	1546.8355	-0.0008	IGDLELFRTVQEK
1.4	1546.8389	-0.0042	IVNELSMVLKETR
1.2	1546.8388	-0.0042	LSCVSENLKKLEK

AT1G11910.1

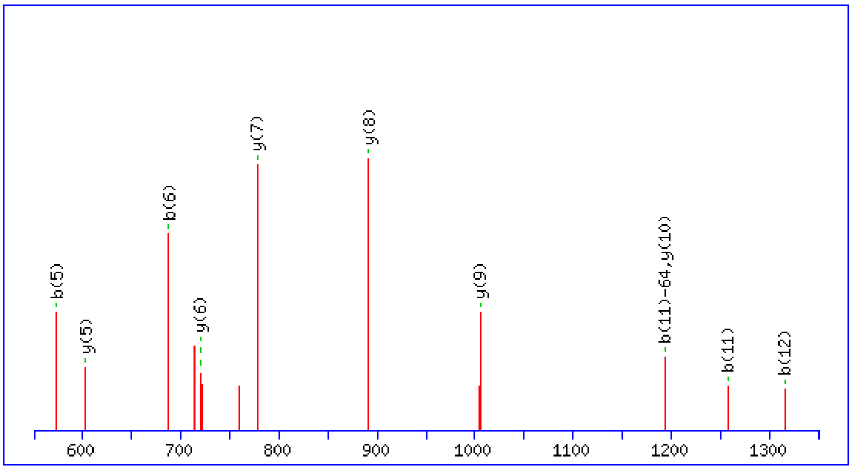
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPLWILGDVFMGK**
Found in **AT1G11910.1** in **TAIR_Arabidopsis**, Symbols: | aspartyl protease family protein | chr1:4017117-4019872 REVERSE

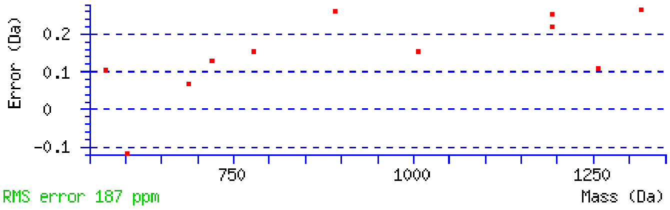
Match to Query 6269: 1462.711860 from(732.363206,2+) index(11215)
Title: Elution from: 109.253 to 109.253 scan no 16058 cid35.00 polarity:+
Data file C7-1_1.mgf

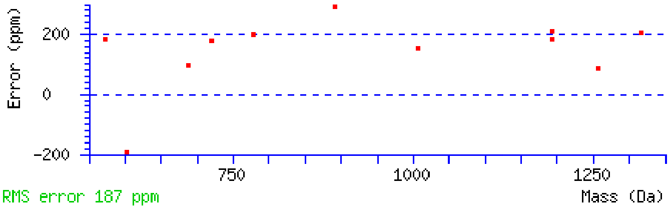
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1462.7089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 60 **Expect:** 9.8e-006
Matches : 11/158 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165			G							13
2	157.0756	79.0414			P	1405.6977	703.3525	1387.6741	694.3407	1387.6871	694.3472	12
3	271.1567	136.0820			L	1307.6479	654.3276	1289.6243	645.3158	1289.6373	645.3223	11
4	459.2301	230.1187			W	*1193.5668*	597.2870	1175.5432	588.2752	1175.5562	588.2817	10
5	*573.3112*	287.1592			I	*1005.4934*	503.2503	987.4698	494.2385	987.4828	494.2450	9
6	*687.3923*	344.1998			L	*891.4123*	446.2098	873.3887	437.1980	873.4017	437.2045	8
7	745.4108	373.2090			G	*777.3312*	389.1692	759.3076	380.1574	759.3206	380.1639	7
8	861.4347	431.2210	843.4242	422.2157	D	*719.3127*	360.1600	701.2891	351.1482	701.3021	351.1547	6
9	961.5002	481.2537	943.4896	472.2484	V	*603.2887*	302.1480	585.2651	293.1362			5
10	1109.5656	555.2865	1091.5551	546.2812	F	503.2233	252.1153	485.1997	243.1035			4
11	*1257.5981*	629.3027	1239.5875	620.2974	M	355.1578	178.0825	337.1342	169.0708			3
12	*1315.6166*	658.3119	1297.6060	649.3066	G	207.1254	104.0663	189.1018	95.0545			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GPLWILGDVFMGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G11910.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.5	1462.7089	0.0030	GPLWILGDVFMGK
3.1	1462.7140	-0.0022	GQEEQVPRVYIK
2.2	1462.7093	0.0025	LLLNLCAHSFTR
2.2	1462.7118	0.0001	EGVELELERRSK
1.0	1462.7089	0.0030	CSFVSGLFPPLPK

AT1G12000.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVEGPASSAAGNPDEIAK**
Found in **AT1G12000.1** in **TAIR_Arabidopsis**, Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:4050157-4053725 REVERSE

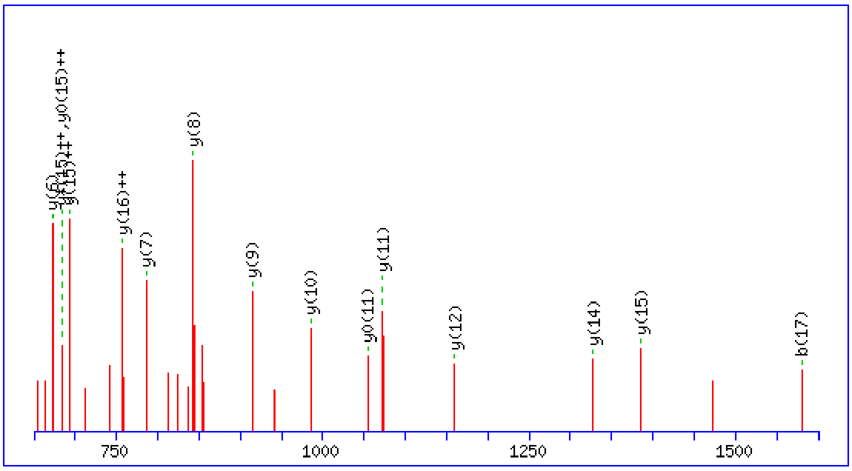
Match to Query 7762: 1724.855596 from(863.435074,2+) index(2465)
Title: Elution from: 29.275 to 29.275 scan no 3232 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 650 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

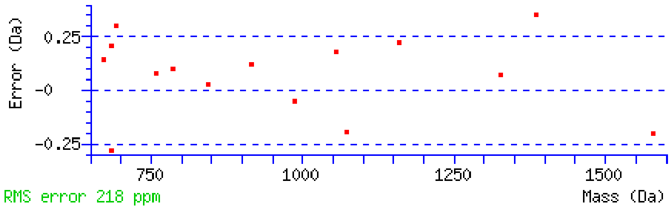
Show Y-axis ☐

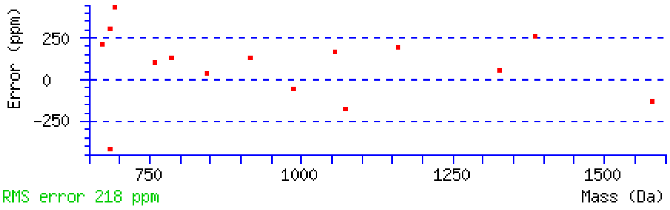


Monoisotopic mass of neutral peptide Mr(calc): 1724.8581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 2e-007
Matches : 16/172 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.0913	57.5493					I							18
2	213.1598	107.0835					V	1612.7813	806.8943	1595.7548	798.3810	1594.7707	797.8890	17
3	342.2023	171.6048			324.1918	162.5995	E	1513.7129	757.3601	1496.6863	748.8468	1495.7023	748.3548	16
4	399.2238	200.1155			381.2132	191.1103	G	***1384.6703***	692.8388	1367.6437	684.3255	1366.6597	683.8335	15
5	496.2766	248.6419			478.2660	239.6366	P	***1327.6488***	664.3281	1310.6223	655.8148	1309.6383	655.3228	14
6	567.3137	284.1605			549.3031	275.1552	A	1230.5961	615.8017	1213.5695	607.2884	1212.5855	606.7964	13
7	654.3457	327.6765			636.3352	318.6712	S	***1159.5590***	580.2831	1142.5324	571.7698	1141.5484	571.2778	12
8	741.3777	371.1925			723.3672	362.1872	S	***1072.5269***	536.7671	1055.5004	528.2538	1054.5164	527.7618	11
9	812.4149	406.7111			794.4043	397.7058	A	***985.4949***	493.2511	968.4684	484.7378	967.4843	484.2458	10
10	883.4520	442.2296			865.4414	433.2243	A	***914.4578***	457.7325	897.4312	449.2193	896.4472	448.7272	9
11	940.4734	470.7404			922.4629	461.7351	G	***843.4207***	422.2140	826.3941	413.7007	825.4101	413.2087	8
12	**1054.5164**	527.7618	1037.4898	519.2485	1036.5058	518.7565	N	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	7
13	1151.5691	576.2882	1134.5426	567.7749	1133.5586	567.2829	P	***672.3563***	336.6818	655.3297	328.1685	654.3457	327.6765	6
14	1266.5961	633.8017	1249.5695	625.2884	1248.5855	624.7964	D	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
15	1395.6387	698.3230	1378.6121	689.8097	1377.6281	689.3177	E	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
16	1508.7227	754.8650	1491.6962	746.3517	1490.7122	745.8597	I	331.2340	166.1206	314.2074	157.6074			3
17	**1579.7598**	790.3836	1562.7333	781.8703	1561.7493	781.3783	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT1G12000.1





NCBI **BLAST** search of IVEGPASSAAGNPDEIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.1	1724.8581	-0.0025	IVEGPASSAAGNPDEIAK
8.9	1724.8515	0.0041	HGMGGAKENELLSAAPK
1.1	1724.8569	-0.0013	GRQGCGIPFYWTKR
0.9	1724.8549	0.0007	EMVTLMEQRTRTAK

Mascot: http://www.matrixscience.com/

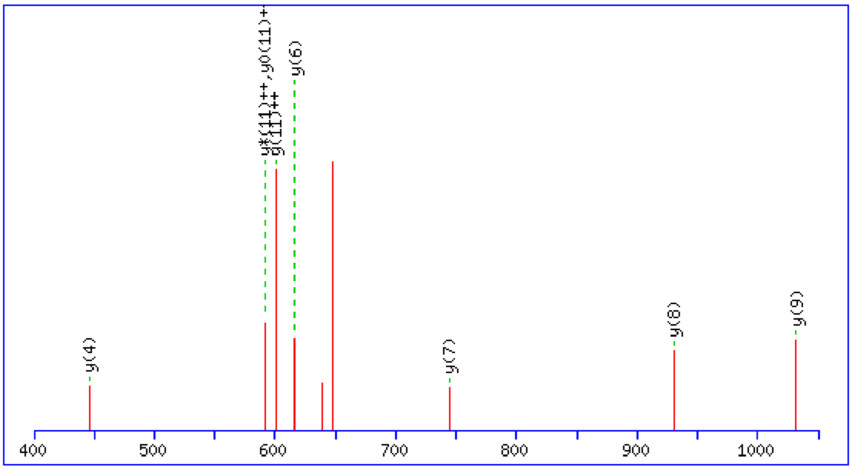
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPATWQGIEAAR**
Found in **AT1G12230.1** in **TAIR_Arabidopsis**, Symbols: | transaldolase, putative | chr1:4148048-4150706 FORWARD

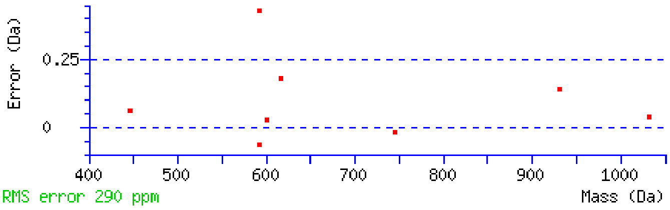
Match to Query 4287: 1311.694048 from(656.854300,2+) index(4927)
Title: Elution from: 46.765 to 46.765 scan no 6348 cid35.00 polarity:+
Data file D1d-1_3.mgf

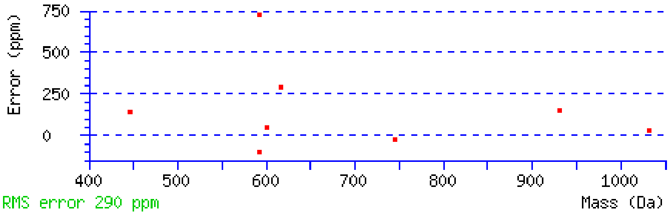
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1311.6935
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 9.9e-005
Matches : 8/110 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							12
2	211.1441	106.0757					P	1199.6167	600.3120	1182.5902	591.7987	1181.6062	591.3067	11
3	282.1812	141.5942					A	1102.5640	551.7856	1085.5374	543.2724	1084.5534	542.7803	10
4	383.2289	192.1181			365.2183	183.1128	T	***1031.5269***	516.2671	1014.5003	507.7538	1013.5163	507.2618	9
5	569.3082	285.1577			551.2976	276.1525	W	***930.4792***	465.7432	913.4526	457.2300	912.4686	456.7380	8
6	697.3668	349.1870	680.3402	340.6738	679.3562	340.1817	Q	***744.3999***	372.7036	727.3733	364.1903	726.3893	363.6983	7
7	754.3883	377.6978	737.3617	369.1845	736.3777	368.6925	G	***616.3413***	308.6743	599.3148	300.1610	598.3307	299.6690	6
8	867.4723	434.2398	850.4458	425.7265	849.4618	425.2345	I	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
9	996.5149	498.7611	979.4884	490.2478	978.5043	489.7558	E	***446.2358***	223.6215	429.2092	215.1082	428.2252	214.6162	4
10	1067.5520	534.2796	1050.5255	525.7664	1049.5415	525.2744	A	317.1932	159.1002	300.1666	150.5870			3
11	1138.5891	569.7982	1121.5626	561.2849	1120.5786	560.7929	A	246.1561	123.5817	229.1295	115.0684			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IPATWQGIEAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G12230.1

Score	Mr(calc)	Delta	Sequence
45.4	1311.6935	0.0005	IPATWQGIEAAR

AT1G12310.1

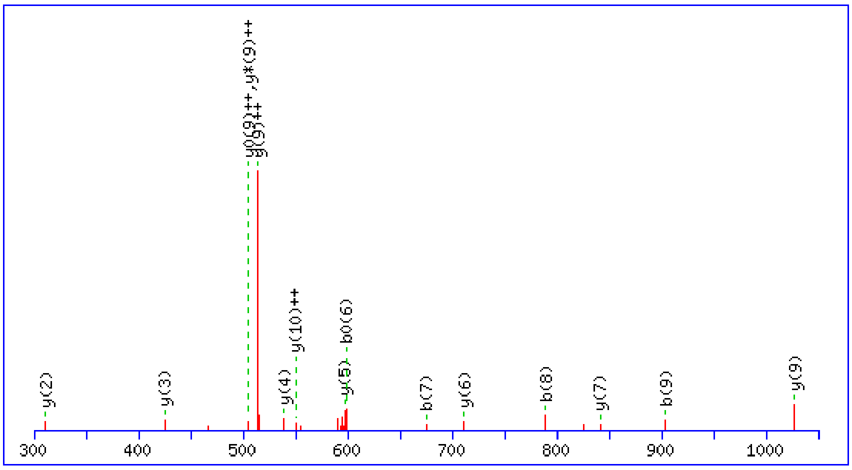
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAPSELGILMR**
Found in **AT1G12310.1** in **TAIR_Arabidopsis**, Symbols: | calmodulin, putative | chr1:4187498-4187944 REVERSE

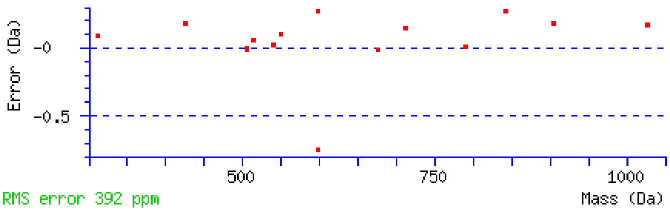
Match to Query 3912: 1212.630858 from(607.322705,2+) index(7651)
Title: Elution from: 69.638 to 69.638 scan no 10088 cid35.00 polarity:+
Data file D1d-2_1.mgf

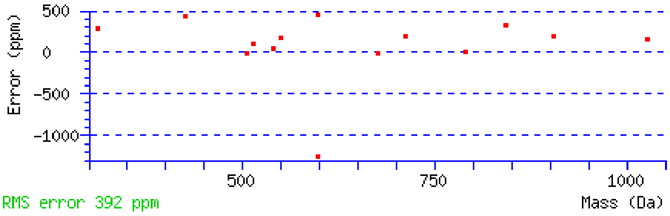
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1212.6329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 4.1e-006
Matches : 15/82 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							11
2	187.1225	94.0649			A	1099.5590	550.2832	1081.5355	541.2714	1081.5485	541.2779	10
3	285.1723	143.0898			P	***1027.5249***	514.2661	1009.5013	505.2543	1009.5143	505.2608	9
4	373.2014	187.1043	355.1908	178.0990	S	929.4751	465.2412	911.4515	456.2294	911.4645	456.2359	8
5	503.2410	252.1241	485.2304	243.1189	E	***841.4460***	421.2267	823.4225	412.2149	823.4355	412.2214	7
6	617.3221	309.1647	599.3115	300.1594	L	***711.4064***	356.2068	693.3828	347.1950			6
7	**675.3406**	338.1739	657.3300	329.1687	G	***597.3253***	299.1663	579.3017	290.1545			5
8	**789.4217**	395.2145	771.4111	386.2092	I	***539.3068***	270.1570	521.2832	261.1453			4
9	**903.5028**	452.2550	885.4922	443.2498	L	***425.2257***	213.1165	407.2021	204.1047			3
10	1035.5403	518.2738	1017.5298	509.2685	M	***311.1446***	156.0759	293.1210	147.0642			2
11					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IAPSELGILMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G12310.1

Score	Mr(calc)	Delta	Sequence
61.7	1212.6329	-0.0020	IAPSELGILMR
13.1	1212.6273	0.0036	IASIDIGSPAVR
4.5	1212.6272	0.0036	TSVPVLALAGDR
2.4	1212.6273	0.0036	IALVPQQSQSK
0.9	1212.6329	-0.0020	ILSEALGPIMR

AT1G12350.1

MATRIX SCIENCE

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIATILK**
Found in **AT1G12350.1** in **TAIR_Arabidopsis**, Symbols: ATCOAB | ATCOAB (4-PHOSPHO-PANTO-THENOYLCYSTEINE SYNTHETASE); catalytic/ phosphopantothenate--cysteine ligase | chr1:4198868-4200631 FORWARD

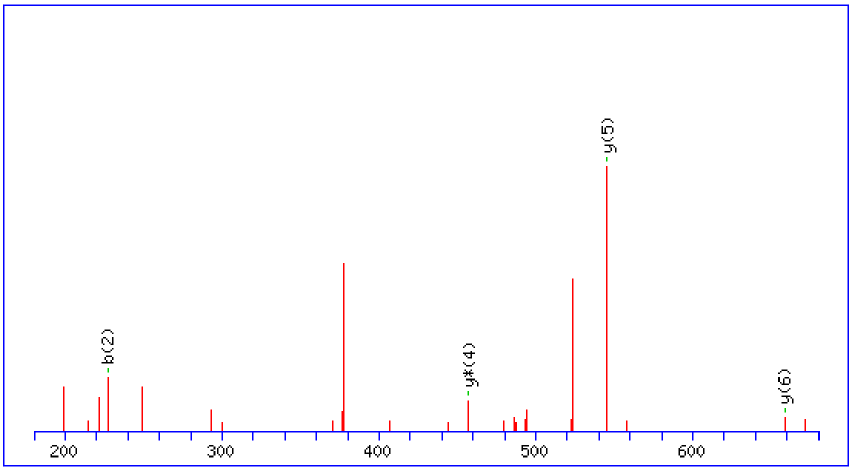
Match to Query 840: 770.526414 from(386.270483,2+) index(4736)
Title: Elution from: 43.873 to 43.873 scan no 6001 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 180 to 680 Da Full range

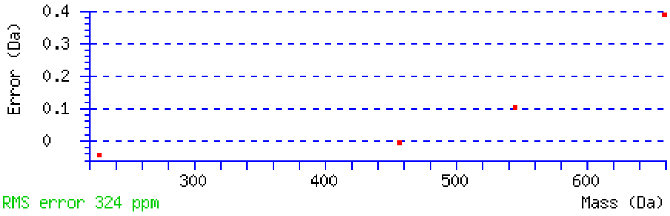
Label all possible matches ○ Label matches used for scoring ●

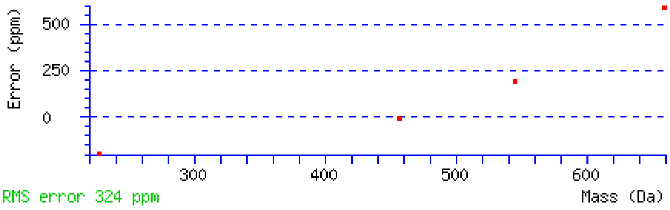
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.5266
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.041
Matches : 4/48 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							7
2	227.1754	114.0913			I	***658.4498***	329.7285	641.4232	321.2153	640.4392	320.7233	6
3	298.2125	149.6099			A	***545.3657***	273.1865	528.3392	264.6732	527.3552	264.1812	5
4	399.2602	200.1337	381.2496	191.1285	T	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
5	512.3443	256.6758	494.3337	247.6705	I	373.2809	187.1441	356.2544	178.6308			3
6	625.4283	313.2178	607.4178	304.2125	L	260.1969	130.6021	243.1703	122.0888			2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LIATILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.8	770.5266	-0.0001	LIATILK
11.2	770.5266	-0.0002	IIVVTVK

AT1G12350.1

11.2	770.5266	-0.0002	LISVVIK
11.2	770.5266	-0.0001	LITIAIK
11.2	770.5266	-0.0002	LIVTVVK

AT1G12410.1

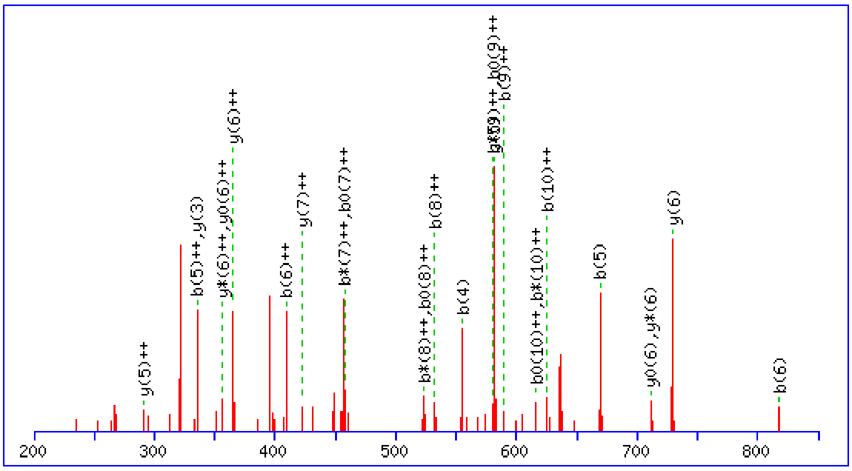
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IRDYLFNELAK**
Found in **AT1G12410.1** in **TAIR_Arabidopsis**, Symbols: CLPP2, NCLPP2, CLPR2 | CLPR2 (Clp protease proteolytic subunit 2); endopeptidase Clp | chr1:4223097-4224952 FORWARD

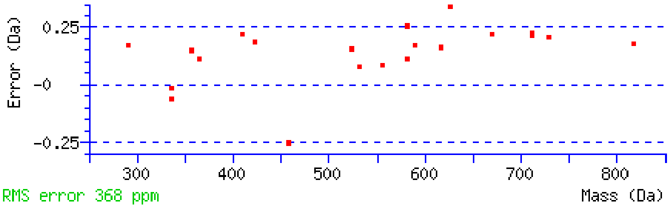
Match to Query 5459: 1396.692528 from(466.571452,3+) index(6166)
Title: Elution from: 54.876 to 54.876 scan no 7904 cid35.00 polarity:+
Data file D6h-3_1.mgf

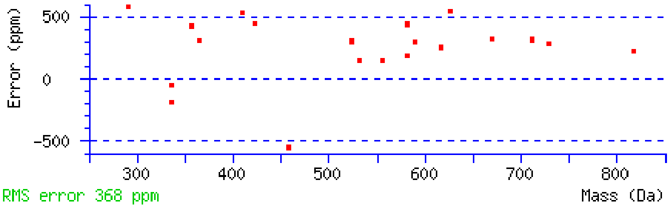
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1396.6927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.035
Matches : 26/108 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							11
2	275.1776	138.0925	257.1540	129.0807			R	1283.6189	642.3131	1265.5953	633.3013	1265.6083	633.3078	10
3	391.2016	196.1044	373.1780	187.0926	373.1910	187.0992	D	1123.5296	562.2685	1105.5061	553.2567	1105.5191	553.2632	9
4	**555.2620**	278.1346	537.2384	269.1228	537.2514	269.1293	Y	1007.5057	504.2565	989.4821	495.2447	989.4951	495.2512	8
5	**669.3431**	***335.1752***	651.3195	326.1634	651.3325	326.1699	L	843.4453	422.2263	825.4217	413.2145	825.4347	413.2210	7
6	**817.4085**	***409.2079***	799.3849	400.1961	799.3980	400.2026	F	**729.3642**	365.1857	711.3406	356.1739	711.3536	356.1805	6
7	933.4455	467.2264	915.4219	458.2146	915.4349	458.2211	N	**581.2987**	291.1530	563.2752	282.1412	563.2882	282.1477	5
8	1063.4851	***532.2462***	1045.4616	523.2344	1045.4746	523.2409	E	465.2617	233.1345	447.2382	224.1227	447.2512	224.1292	4
9	1177.5662	***589.2868***	1159.5427	580.2750	1159.5557	580.2815	L	**335.2221**	168.1147	317.1985	159.1029			3
10	1249.6004	***625.3038***	1231.5768	616.2920	1231.5898	616.2985	A	221.1410	111.0741	203.1174	102.0624			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IRDYLFNELAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G12410.1

Score	Mr(calc)	Delta	Sequence
23.8	1396.6927	-0.0002	IRDYLFNELAK
18.8	1396.6905	0.0021	NLSTRFSVEVTK
13.3	1396.6961	-0.0035	SKVVMTFDLIGR
3.5	1396.6913	0.0012	EGVMRKFICIK
2.2	1396.6931	-0.0006	QRRQEVSSLFK
1.2	1396.6934	-0.0009	MSFTELTISVIK
1.1	1396.6905	0.0021	DLVEFAKTRSSK
0.3	1396.6927	-0.0002	KSFWLETASGKK
0.1	1396.6949	-0.0024	GFISLSVPYFPR

Mascot: http://www.matrixscience.com/

AT1G12450.1

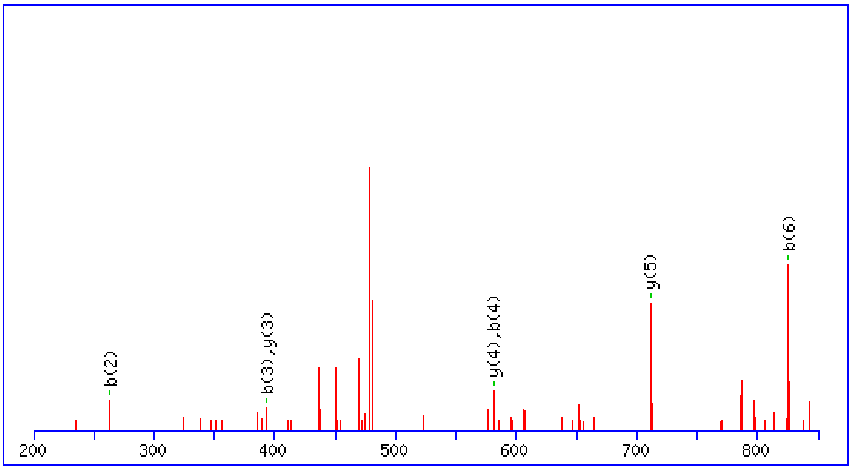
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQEWLKK**
Found in **AT1G12450.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22850.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63604.1); contains InterPro domain SNARE associated Golgi protein (InterPro:IPR015414) | chr1:4244494-42458

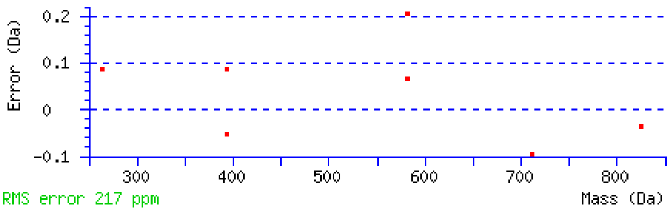
Match to Query 2180: 972.473158 from(487.243855,2+) index(1195)
Title: Elution from: 17.494 to 17.494 scan no 1654 cid35.00 polarity:+
Data file C7-3_3.mgf

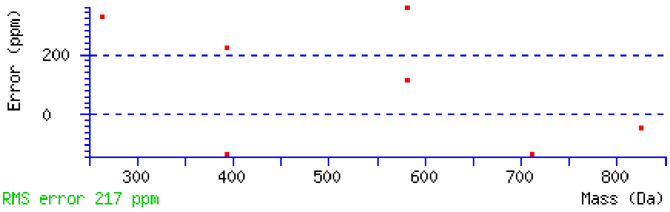
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4729
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0065
Matches : 7/58 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							7
2	***263.0974***	132.0524	245.0739	123.0406			Q	841.4427	421.2250	823.4191	412.2132	823.4321	412.2197	6
3	***393.1371***	197.0722	375.1135	188.0604	375.1265	188.0669	E	**711.3900**	356.1986	693.3664	347.1869	693.3795	347.1934	5
4	***581.2105***	291.1089	563.1869	282.0971	563.1999	282.1036	W	**581.3504**	291.1788	563.3268	282.1670			4
5	695.2916	348.1494	677.2680	339.1376	677.2810	339.1441	L	**393.2770**	197.1421	375.2534	188.1303			3
6	***825.3806***	413.1939	807.3570	404.1821	807.3700	404.1886	K	279.1959	140.1016	261.1723	131.0898			2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MQEWLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.3	972.4729	0.0003	MQEWLKK

AT1G12450.1

21.3	972.4754	-0.0022	DSKDKELK
21.3	972.4707	0.0025	RVMDEALK
19.7	972.4754	-0.0022	EEKSATGLK
15.4	972.4707	0.0025	VCNTNILK
13.5	972.4754	-0.0023	GSSSLSPSLK
13.1	972.4754	-0.0022	ELTNGTSLK
9.6	972.4707	0.0025	MEELGVKR
9.6	972.4707	0.0025	MKESPTLR
9.4	972.4707	0.0025	ELGMQIVR

AT1G12620.1

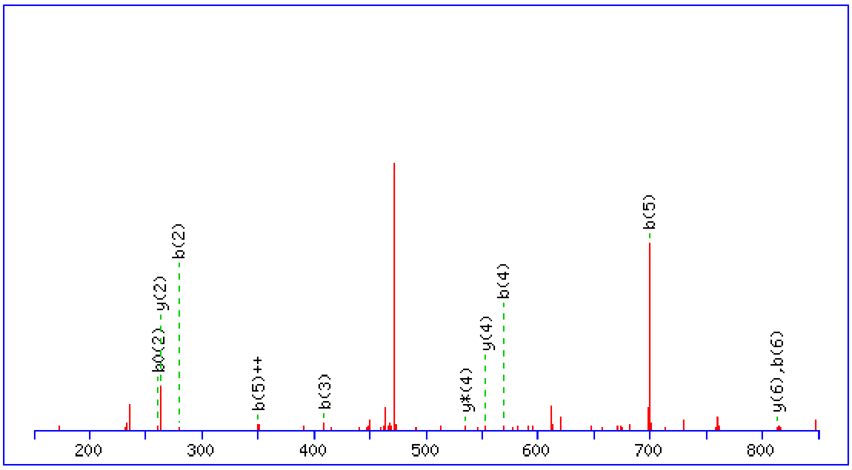
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEERKIK**
Found in **AT1G12620.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:4294881-4296746 REVERSE

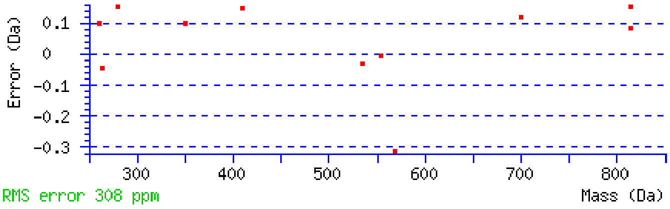
Match to Query 2159: 960.472500 from(481.243526,2+) index(2309)
Title: Elution from: 25.177 to 25.177 scan no 2916 cid35.00 polarity:+
Data file C7-1_1.mgf

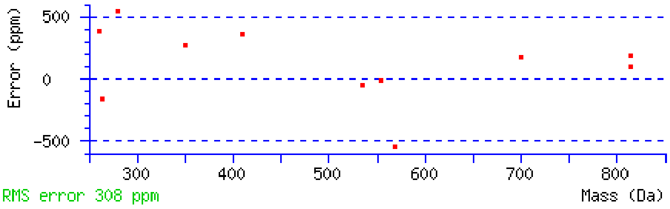
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 960.4707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.034
Matches : 11/84 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							7
2	***279.0793***	140.0433			261.0688	131.0380	E	**813.4455**	407.2264	795.4219	398.2146	795.4349	398.2211	6
3	***409.1190***	205.0631			391.1084	196.0578	E	683.4059	342.2066	665.3823	333.1948	665.3953	333.2013	5
4	***569.2082***	285.1077	551.1846	276.0960	551.1977	276.1025	R	**553.3663**	277.1868	535.3427	268.1750			4
5	***699.2973***	350.1523	681.2737	341.1405	681.2867	341.1470	K	393.2770	197.1421	375.2534	188.1303			3
6	***813.3783***	407.1928	795.3548	398.1810	795.3678	398.1875	I	**263.1880**	132.0976	245.1644	123.0858			2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MEERKIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.2	960.4707	0.0018	MEERKIK
15.5	960.4707	0.0018	AMGKKAAEK

AT1G12620.1

14.2	960.4707	0.0018	MKERLEK
14.2	960.4707	0.0018	KKMAAQEK
14.1	960.4707	0.0018	LEKSMAVR
13.5	960.4707	0.0018	MQSLTLTR
13.5	960.4707	0.0018	MVEARSLK
13.5	960.4707	0.0018	RSEVMSLK
13.5	960.4700	0.0025	TRSQWIR
11.1	960.4733	-0.0008	VRMRQEK

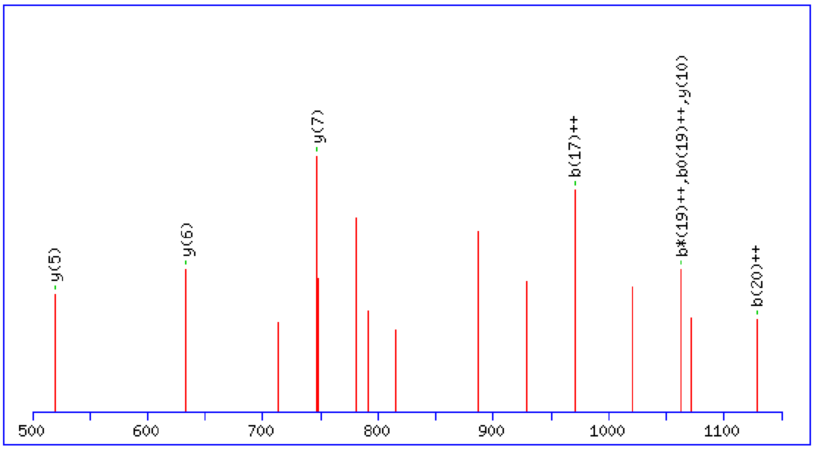
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLSNLVKPEDIVESEHLVTLLAVVPK**
Found in **AT1G12840.1** in **TAIR_Arabidopsis**, Symbols: ATVHA-C, DET3 | DET3 (DE-ETIOLATED 3) | chr1:4375582-4378218 FORWARD

Match to Query 10696: 2887.488176 from(722.879320,4+) index(10883)
Title: Elution from: 115.518 to 115.518 scan no 16118 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

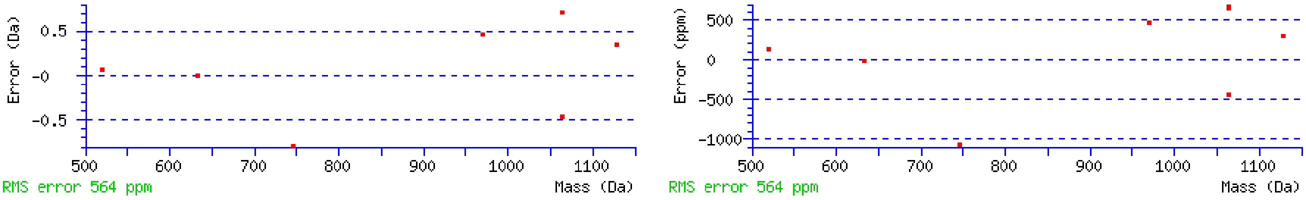


Monoisotopic mass of neutral peptide Mr(calc): 2887.4929
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.0067
Matches : 8/280 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							26
2	231.1124	116.0598			213.1018	107.0545	L	2772.4762	1386.7417	2754.4526	1377.7299	2754.4656	1377.7365	25
3	319.1414	160.0743			301.1309	151.0691	S	2658.3951	1329.7012	2640.3715	1320.6894	2640.3845	1320.6959	24
4	435.1784	218.0928	417.1548	209.0811	417.1678	209.0876	N	2570.3660	1285.6867	2552.3425	1276.6749	2552.3555	1276.6814	23
5	549.2595	275.1334	531.2359	266.1216	531.2489	266.1281	L	2454.3290	1227.6682	2436.3055	1218.6564	2436.3185	1218.6629	22
6	649.3250	325.1661	631.3014	316.1543	631.3144	316.1608	V	2340.2479	1170.6276	2322.2244	1161.6158	2322.2374	1161.6223	21
7	779.4140	390.2106	761.3904	381.1988	761.4034	381.2054	K	2240.1825	1120.5949	2222.1589	1111.5831	2222.1719	1111.5896	20
8	877.4638	439.2355	859.4402	430.2237	859.4532	430.2303	P	2110.0935	1055.5504	2092.0699	1046.5386	2092.0829	1046.5451	19
9	1007.5034	504.2553	989.4798	495.2436	989.4929	495.2501	E	2012.0437	1006.5255	1994.0201	997.5137	1994.0331	997.5202	18
10	1123.5274	562.2673	1105.5038	553.2555	1105.5168	553.2621	D	1882.0040	941.5057	1863.9805	932.4939	1863.9935	932.5004	17
11	1237.6085	619.3079	1219.5849	610.2961	1219.5979	610.3026	I	1765.9801	883.4937	1747.9565	874.4819	1747.9695	874.4884	16
12	1337.6739	669.3406	1319.6504	660.3288	1319.6634	660.3353	V	1651.8990	826.4531	1633.8754	817.4413	1633.8884	817.4478	15
13	1467.7136	734.3604	1449.6900	725.3486	1449.7030	725.3551	E	1551.8335	776.4204	1533.8099	767.4086	1533.8230	767.4151	14
14	1555.7426	778.3750	1537.7191	769.3632	1537.7321	769.3697	S	1421.7939	711.4006	1403.7703	702.3888	1403.7833	702.3953	13
15	1685.7823	843.3948	1667.7587	834.3830	1667.7717	834.3895	E	1333.7648	667.3861	1315.7412	658.3743	1315.7543	658.3808	12
16	1825.8323	913.4198	1807.8087	904.4080	1807.8217	904.4145	H	1203.7252	602.3662	1185.7016	593.3544	1185.7146	593.3610	11
17	1939.9134	**970.4603**	1921.8898	961.4485	1921.9028	961.4550	L	***1063.6752***	532.3412	1045.6516	523.3294	1045.6646	523.3359	10
18	2039.9788	1020.4931	2021.9552	1011.4813	2021.9683	1011.4878	V	949.5941	475.3007	931.5705	466.2889	931.5835	466.2954	9
19	2142.0235	1071.5154	2124.0000	1062.5036	2124.0130	1062.5101	T	849.5286	425.2680	831.5050	416.2562	831.5181	416.2627	8
20	2256.1046	**1128.5560**	2238.0811	1119.5442	2238.0941	1119.5507	L	***747.4839***	374.2456	729.4603	365.2338			7
21	2370.1857	1185.5965	2352.1622	1176.5847	2352.1752	1176.5912	L	***633.4028***	317.2050	615.3792	308.1933			6
22	2442.2199	1221.6136	2424.1963	1212.6018	2424.2093	1212.6083	A	***519.3217***	260.1645	501.2981	251.1527			5
23	2542.2853	1271.6463	2524.2618	1262.6345	2524.2748	1262.6410	V	447.2876	224.1474	429.2640	215.1356			4
24	2642.3508	1321.6790	2624.3272	1312.6672	2624.3402	1312.6737	V	347.2221	174.1147	329.1985	165.1029			3
25	2740.4006	1370.7039	2722.3770	1361.6921	2722.3900	1361.6986	P	247.1567	124.0820	229.1331	115.0702			2

AT1G12840.1

26							**K**	149.1069	75.0571	131.0833	66.0453		**1**



NCBI **BLAST** search of DLSNLVKPEDIVESEHLVTLLAVVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.8	2887.4929	-0.0047	DLSNLVKPEDIVESEHLVTLLAVVPK
2.9	2887.4879	0.0003	VTFQLAAFRLFNLMGIPVLSMFLTK

Mascot: http://www.matrixscience.com/

AT1G12900.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDSTLGIFDADVKPSGDSALSVDGK**
Found in **AT1G12900.1** in **TAIR_Arabidopsis**, Symbols: GAPA-2 | GAPA-2; glyceraldehyde-3-phosphate dehydrogenase | chr1:4392632-4394281 REVERSE

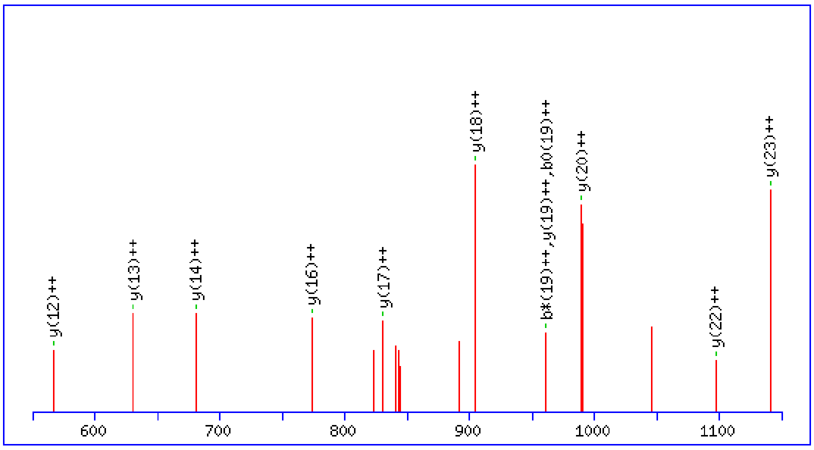
Match to Query 10050: 2556.222624 from(853.081484,3+) index(7761)
Title: Elution from: 70.915 to 70.915 scan no 10345 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1150 Da Full range

Label all possible matches ○ Label matches used for scoring ●

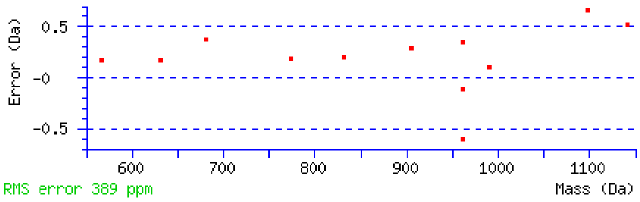
Show Y-axis ☐

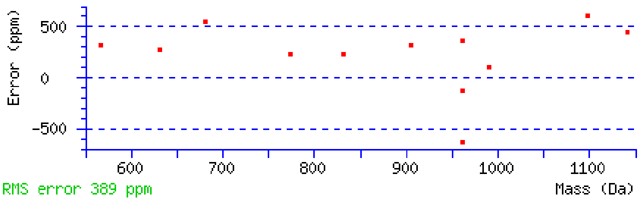


Monoisotopic mass of neutral peptide Mr(calc): 2556.2232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 97 **Expect:** 6.3e-010
Matches : 12/258 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							25
2	279.0975	140.0524			261.0870	131.0471	D	2394.1671	1197.5872	2377.1405	1189.0739	2376.1565	1188.5819	24
3	366.1296	183.5684			348.1190	174.5631	S	2279.1401	1140.0737	2262.1136	1131.5604	2261.1296	1131.0684	23
4	467.1773	234.0923			449.1667	225.0870	T	2192.1081	1096.5577	2175.0816	1088.0444	2174.0976	1087.5524	22
5	580.2613	290.6343			562.2508	281.6290	L	2091.0604	1046.0339	2074.0339	1037.5206	2073.0499	1037.0286	21
6	637.2828	319.1450			619.2722	310.1397	G	1977.9764	989.4918	1960.9498	980.9786	1959.9658	980.4865	20
7	750.3668	375.6871			732.3563	366.6818	I	1920.9549	960.9811	1903.9284	952.4678	1902.9443	951.9758	19
8	897.4353	449.2213			879.4247	440.2160	F	1807.8708	904.4391	1790.8443	895.9258	1789.8603	895.4338	18
9	1012.4622	506.7347			994.4516	497.7295	D	1660.8024	830.9049	1643.7759	822.3916	1642.7919	821.8996	17
10	1083.4993	542.2533			1065.4888	533.2480	A	1545.7755	773.3914	1528.7489	764.8781	1527.7649	764.3861	16
11	1198.5263	599.7668			1180.5157	590.7615	D	1474.7384	737.8728	1457.7118	729.3596	1456.7278	728.8675	15
12	1297.5947	649.3010			1279.5841	640.2957	V	1359.7114	680.3594	1342.6849	671.8461	1341.7009	671.3541	14
13	1425.6896	713.3485	1408.6631	704.8352	1407.6791	704.3432	K	1260.6430	630.8251	1243.6165	622.3119	1242.6325	621.8199	13
14	1522.7424	761.8748	1505.7159	753.3616	1504.7318	752.8696	P	1132.5481	566.7777	1115.5215	558.2644	1114.5375	557.7724	12
15	1609.7744	805.3909	1592.7479	796.8776	1591.7639	796.3856	S	1035.4953	518.2513	1018.4687	509.7380	1017.4847	509.2460	11
16	1666.7959	833.9016	1649.7693	825.3883	1648.7853	824.8963	G	948.4633	474.7353	931.4367	466.2220	930.4527	465.7300	10
17	1781.8228	891.4151	1764.7963	882.9018	1763.8123	882.4098	D	891.4418	446.2245	874.4153	437.7113	873.4312	437.2193	9
18	1868.8549	934.9311	1851.8283	926.4178	1850.8443	925.9258	S	776.4149	388.7111	759.3883	380.1978	758.4043	379.7058	8
19	1939.8920	970.4496	1922.8654	961.9364	1921.8814	961.4443	A	689.3828	345.1951	672.3563	336.6818	671.3723	336.1898	7
20	2052.9760	1026.9917	2035.9495	1018.4784	2034.9655	1017.9864	L	618.3457	309.6765	601.3192	301.1632	600.3352	300.6712	6
21	2140.0081	1070.5077	2122.9815	1061.9944	2121.9975	1061.5024	S	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	5
22	2239.0765	1120.0419	2222.0499	1111.5286	2221.0659	1111.0366	V	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
23	2354.1034	1177.5554	2337.0769	1169.0421	2336.0929	1168.5501	D	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
24	2411.1249	1206.0661	2394.0983	1197.5528	2393.1143	1197.0608	G	204.1343	102.5708	187.1077	94.0575			2

25							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YDSTLGIFDADVKPSGDSALSVDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.5	2556.2232	-0.0005	YDSTLGIFDADVKPSGDSALSVDGK
1.5	2556.2229	-0.0002	VVYCCRNPKDAFVSLWHFMK
0.0	2556.2258	-0.0032	LYHENVIDHFENPRNVGSFNR

AT1G13040.1

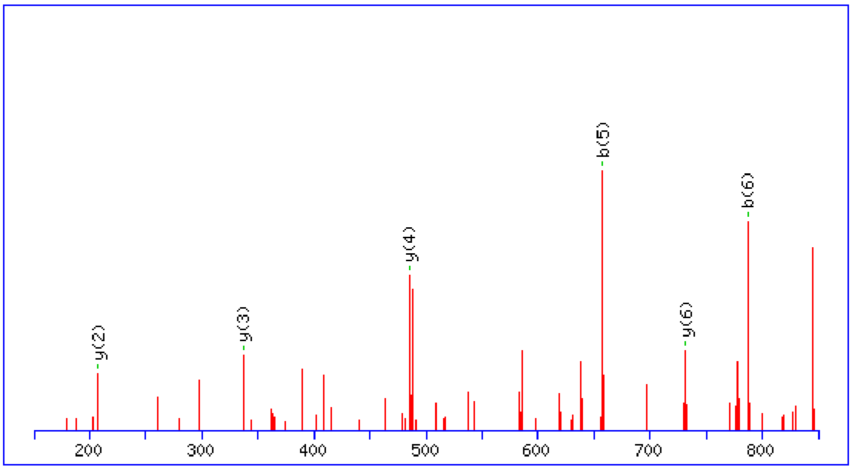
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFEDMKGK**
Found in **AT1G13040.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:4447645-4449198 FORWARD

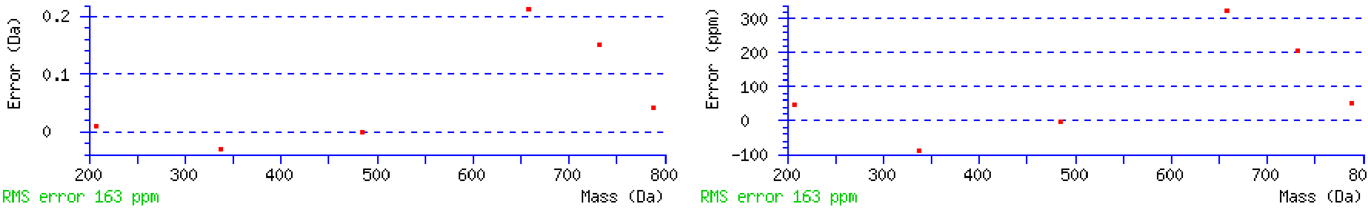
Match to Query 2328: 992.448028 from(497.231290,2+) index(6565)
Title: Elution from: 58.206 to 58.206 scan no 8517 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 992.4497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 32 **Expect:** 0.0052
Matches : 6/100 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							8
2	263.1538	132.0805					F	879.3759	440.1916	861.3523	431.1798	861.3653	431.1863	7
3	393.1935	197.1004			375.1829	188.0951	E	***731.3104***	366.1589	713.2869	357.1471	713.2999	357.1536	6
4	509.2174	255.1124			491.2069	246.1071	D	601.2708	301.1390	583.2472	292.1273	583.2603	292.1338	5
5	**657.2499**	329.1286			639.2393	320.1233	M	***485.2468***	243.1271	467.2233	234.1153			4
6	**787.3389**	394.1731	769.3153	385.1613	769.3283	385.1678	K	***337.2144***	169.1108	319.1908	160.0990			3
7	845.3574	423.1823	827.3338	414.1705	827.3468	414.1771	G	***207.1254***	104.0663	189.1018	95.0545			2
8							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of LFEDMKGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.0	992.4497	-0.0017	LFEDMKGK

AT1G13040.1

19.0	992.4501	-0.0021	KEMTRGGGK
13.2	992.4502	-0.0021	MSREKQGK
9.7	992.4486	-0.0005	FWDIEFK
5.3	992.4463	0.0017	DKYPFDAK
5.3	992.4497	-0.0017	KEMVGSFGL
5.1	992.4497	-0.0017	MYLATQEK
4.9	992.4501	-0.0021	DTKRMGSGK
4.8	992.4463	0.0017	LFDGFQEK
3.8	992.4501	-0.0021	MIARDTTR

AT1G13280.1

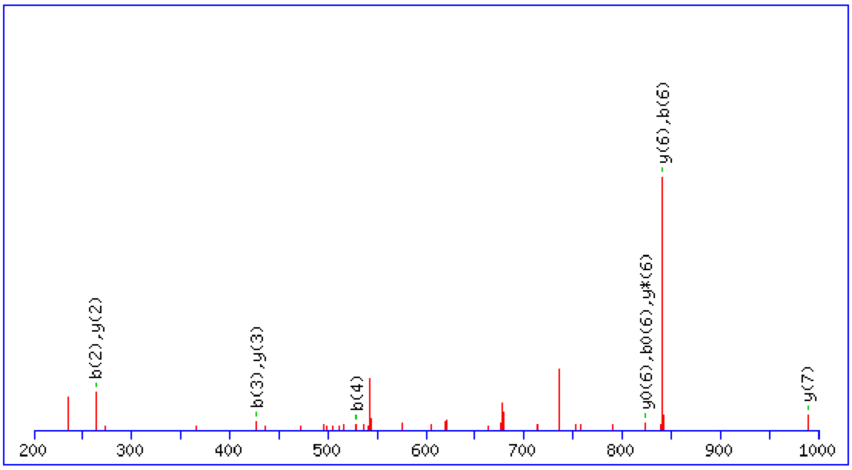
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFYTFYLK**
Found in **AT1G13280.1** in **TAIR_Arabidopsis**, Symbols: AOC4 | AOC4 (ALLENE OXIDE CYCLASE 4) | chr1:4547621-4548549 FORWARD

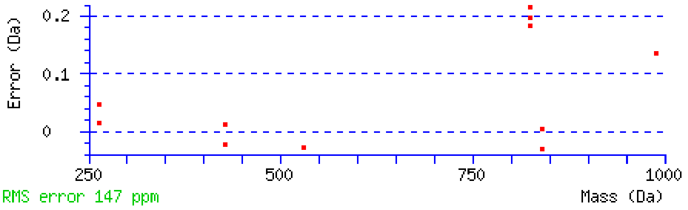
Match to Query 2889: 1102.556244 from(552.285398,2+) index(8020)
Title: Elution from: 71.826 to 71.826 scan no 10630 cid35.00 polarity:+
Data file D12h-2_3.mgf

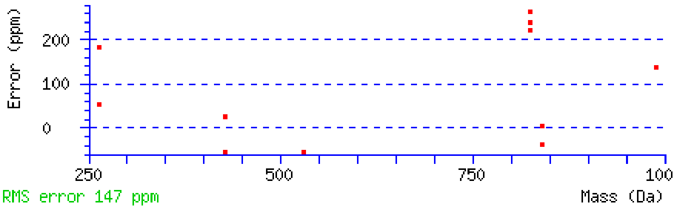
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1102.5581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0012
Matches : 11/56 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	***263.1538***	132.0805			F	***989.4843***	495.2458	971.4607	486.2340	971.4737	486.2405	7
3	***427.2142***	214.1107			Y	***841.4189***	421.2131	823.3953	412.2013	823.4083	412.2078	6
4	***529.2589***	265.1331	511.2483	256.1278	T	677.3585	339.1829	659.3349	330.1711	659.3479	330.1776	5
5	677.3244	339.1658	659.3138	330.1605	F	575.3138	288.1605	557.2902	279.1487			4
6	***841.3847***	421.1960	823.3741	412.1907	Y	***427.2483***	214.1278	409.2248	205.1160			3
7	955.4658	478.2365	937.4552	469.2313	L	***263.1880***	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LFYTFYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.1	1102.5581	-0.0019	LFYTFYLK
17.6	1102.5570	-0.0008	IMDEKSLIK

AT1G13280.1

7.1	1102.5564	-0.0001	LKHSYNSLK
7.1	1102.5559	0.0003	YPFESPLLK
6.3	1102.5537	0.0026	AELLGDAYLK
5.8	1102.5537	0.0026	LQEAYDLIK
4.9	1102.5570	-0.0008	LMATTLPTTK
4.1	1102.5537	0.0026	INEAYEILK
4.1	1102.5593	-0.0030	LVTMYPELK
3.4	1102.5590	-0.0028	QHKRYNLK

AT1G13350.1

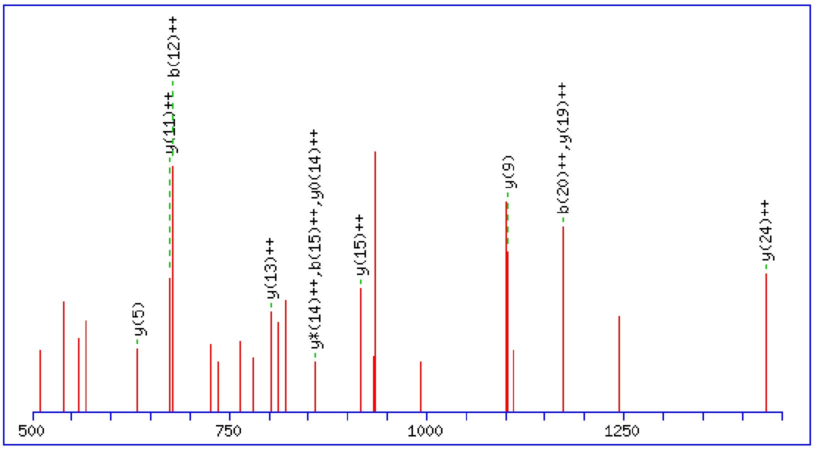
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDNDDKGDVVVWEVEQEDEELNLIEESR**
Found in **AT1G13350.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:4572499-4576544 REVERSE

Match to Query 10975: 3315.522232 from(829.887834,4+) index(10152)
Title: Elution from: 94.189 to 94.189 scan no 14246 cid35.00 polarity:+
Data file C7-1_2.mgf

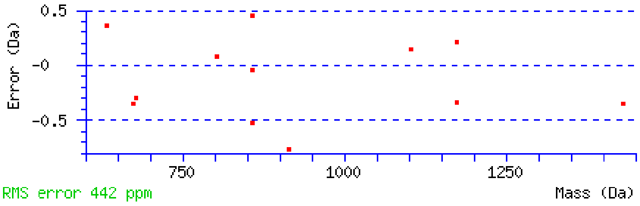
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

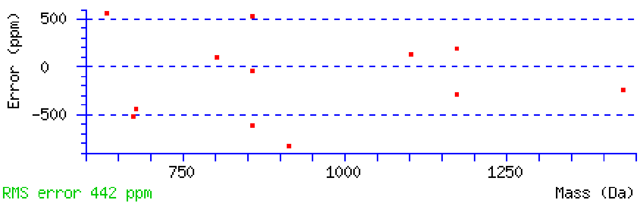


Monoisotopic mass of neutral peptide Mr(calc): 3315.5266
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.026
Matches : 12/316 fragment ions using 23 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							28
2	229.1183	115.0628			211.1077	106.0575	D	3203.4499	1602.2286	3186.4233	1593.7153	3185.4393	1593.2233	27
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	N	3088.4229	1544.7151	3071.3964	1536.2018	3070.4124	1535.7098	26
4	458.1882	229.5977	441.1616	221.0844	440.1776	220.5924	D	2974.3800	1487.6936	2957.3534	1479.1804	2956.3694	1478.6884	25
5	573.2151	287.1112	556.1885	278.5979	555.2045	278.1059	D	2859.3531	1430.1802	2842.3265	1421.6669	2841.3425	1421.1749	24
6	701.3101	351.1587	684.2835	342.6454	683.2995	342.1534	K	2744.3261	1372.6667	2727.2996	1364.1534	2726.3155	1363.6614	23
7	758.3315	379.6694	741.3050	371.1561	740.3210	370.6641	G	2616.2311	1308.6192	2599.2046	1300.1059	2598.2206	1299.6139	22
8	873.3585	437.1829	856.3319	428.6696	855.3479	428.1776	D	2559.2097	1280.1085	2542.1831	1271.5952	2541.1991	1271.1032	21
9	972.4269	486.7171	955.4003	478.2038	954.4163	477.7118	V	2444.1827	1222.5950	2427.1562	1214.0817	2426.1722	1213.5897	20
10	1071.4953	536.2513	1054.4687	527.7380	1053.4847	527.2460	V	2345.1143	1173.0608	2328.0878	1164.5475	2327.1038	1164.0555	19
11	1170.5637	585.7855	1153.5372	577.2722	1152.5531	576.7802	V	2246.0459	1123.5266	2229.0194	1115.0133	2228.0353	1114.5213	18
12	1356.6430	***678.8251***	1339.6165	670.3119	1338.6325	669.8199	W	2146.9775	1073.9924	2129.9509	1065.4791	2128.9669	1064.9871	17
13	1485.6856	743.3464	1468.6591	734.8332	1467.6750	734.3412	E	1960.8982	980.9527	1943.8716	972.4395	1942.8876	971.9474	16
14	1584.7540	792.8807	1567.7275	784.3674	1566.7435	783.8754	V	1831.8556	916.4314	1814.8290	907.9182	1813.8450	907.4262	15
15	1713.7966	***857.4019***	1696.7701	848.8887	1695.7861	848.3967	E	1732.7872	866.8972	1715.7606	858.3840	1714.7766	857.8919	14
16	1841.8552	921.4312	1824.8287	912.9180	1823.8446	912.4260	Q	1603.7446	802.3759	1586.7180	793.8627	1585.7340	793.3706	13
17	1970.8978	985.9525	1953.8712	977.4393	1952.8872	976.9473	E	1475.6860	738.3466	1458.6595	729.8334	1457.6754	729.3414	12
18	2085.9247	1043.4660	2068.8982	1034.9527	2067.9142	1034.4607	D	1346.6434	673.8253	1329.6169	665.3121	1328.6328	664.8201	11
19	2214.9673	1107.9873	2197.9408	1099.4740	2196.9568	1098.9820	E	1231.6165	616.3119	1214.5899	607.7986	1213.6059	607.3066	10
20	2344.0099	***1172.5086***	2326.9834	1163.9953	2325.9994	1163.5033	E	**1102.5739**	551.7906	1085.5473	543.2773	1084.5633	542.7853	9
21	2457.0940	1229.0506	2440.0674	1220.5374	2439.0834	1220.0453	L	973.5313	487.2693	956.5047	478.7560	955.5207	478.2640	8
22	2571.1369	1286.0721	2554.1104	1277.5588	2553.1263	1277.0668	N	860.4472	430.7272	843.4207	422.2140	842.4367	421.7220	7
23	2684.2210	1342.6141	2667.1944	1334.1009	2666.2104	1333.6088	L	746.4043	373.7058	729.3777	365.1925	728.3937	364.7005	6
24	2797.3050	1399.1562	2780.2785	1390.6429	2779.2945	1390.1509	I	**633.3202**	317.1638	616.2937	308.6505	615.3097	308.1585	5
25	2926.3476	1463.6775	2909.3211	1455.1642	2908.3371	1454.6722	E	520.2362	260.6217	503.2096	252.1084	502.2256	251.6164	4

26	3055.3902	1528.1988	3038.3637	1519.6855	3037.3797	1519.1935	**E**	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	**3**
27	3142.4223	1571.7148	3125.3957	1563.2015	3124.4117	1562.7095	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
28							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IDNDDKGDVVVWEVEQEDEELNLIEESR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.0	3315.5266	-0.0044	IDNDDKGDVVVWEVEQEDEELNLIEESR
0.4	3315.5170	0.0053	MRDLVSCFSENSINVTHPLSISSSSSSCSK

Mascot: http://www.matrixscience.com/

AT1G13440.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGIVEGLMTTVHSITATQK**
Found in **AT1G13440.1** in **TAIR_Arabidopsis**, Symbols: GAPC-2 | GAPC-2; glyceraldehyde-3-phosphate dehydrogenase | chr1:4608462-4610491 REVERSE

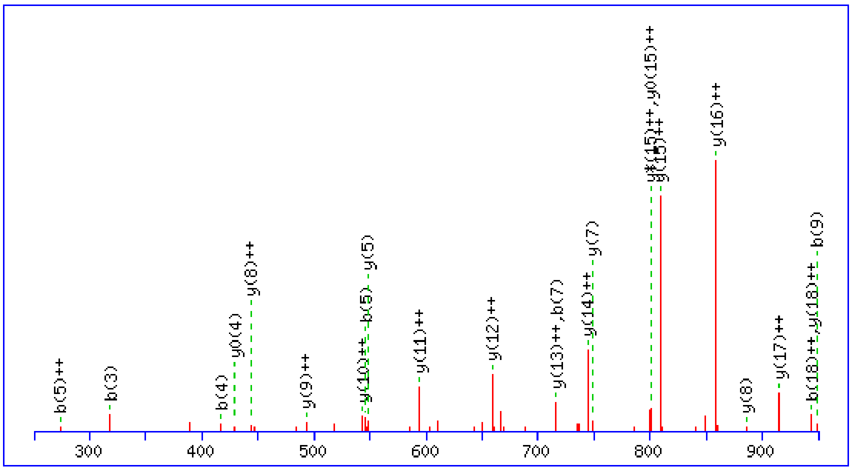
Match to Query 9393: 2032.068546 from(678.363458,3+) index(10505)
Title: Elution from: 100.495 to 100.495 scan no 15012 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 950 Da Full range

Label all possible matches ○ Label matches used for scoring ●

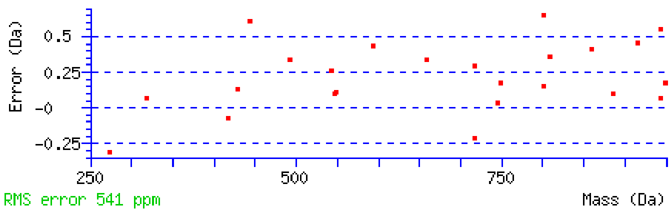
Show Y-axis ☐

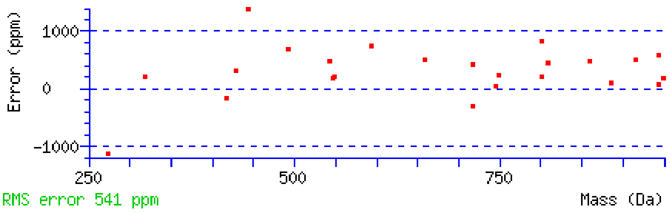


Monoisotopic mass of neutral peptide Mr(calc): 2032.0663
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 102 **Expect:** 2.2e-010
Matches : 24/170 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							19
2	205.0972	103.0522					G	1886.0052	943.5062	1868.9786	934.9930	1867.9946	934.5009	18
3	**318.1812**	159.5942					I	1828.9837	914.9955	1811.9572	906.4822	1810.9731	905.9902	17
4	**417.2496**	209.1285					V	1715.8997	858.4535	1698.8731	849.9402	1697.8891	849.4482	16
5	**546.2922**	**273.6498**			528.2817	264.6445	E	1616.8312	808.9193	1599.8047	800.4060	1598.8207	799.9140	15
6	603.3137	302.1605			585.3031	293.1552	G	1487.7886	744.3980	1470.7621	735.8847	1469.7781	735.3927	14
7	**716.3978**	358.7025			698.3872	349.6972	L	1430.7672	715.8872	1413.7406	707.3740	1412.7566	706.8819	13
8	847.4382	424.2228			829.4277	415.2175	M	1317.6831	659.3452	1300.6566	650.8319	1299.6726	650.3399	12
9	**948.4859**	474.7466			930.4754	465.7413	T	1186.6426	593.8250	1169.6161	585.3117	1168.6321	584.8197	11
10	1049.5336	525.2704			1031.5230	516.2652	T	1085.5950	543.3011	1068.5684	534.7878	1067.5844	534.2958	10
11	1148.6020	574.8046			1130.5914	565.7994	V	984.5473	492.7773	967.5207	484.2640	966.5367	483.7720	9
12	1285.6609	643.3341			1267.6504	634.3288	H	**885.4789**	443.2431	868.4523	434.7298	867.4683	434.2378	8
13	1372.6930	686.8501			1354.6824	677.8448	S	**748.4199**	374.7136	731.3934	366.2003	730.4094	365.7083	7
14	1485.7770	743.3921			1467.7664	734.3869	I	661.3879	331.1976	644.3614	322.6843	643.3774	322.1923	6
15	1586.8247	793.9160			1568.8141	784.9107	T	**548.3039**	274.6556	531.2773	266.1423	530.2933	265.6503	5
16	1657.8618	829.4345			1639.8512	820.4293	A	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
17	1758.9095	879.9584			1740.8989	870.9531	T	376.2191	188.6132	359.1925	180.0999	358.2085	179.6079	3
18	1886.9681	**943.9877**	1869.9415	935.4744	1868.9575	934.9824	Q	275.1714	138.0893	258.1448	129.5761			2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT1G13440.1





NCBI **BLAST** search of FGIVEGLMTTVHSITATQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.9	2032.0663	0.0022	FGIVEGLMTTVHSITATQK
17.4	2032.0663	0.0022	MAVGIFGLIPSSSPDELRK
4.8	2032.0697	-0.0011	MSLSTIASGIGVLELPCLR
2.5	2032.0663	0.0022	ISVGDVLGPLKVMDFSGNGK
2.2	2032.0636	0.0049	MANFGGKLVILGGNQSRDR
2.2	2032.0701	-0.0016	FRLTVVNQLSDELSQQR
1.6	2032.0716	-0.0031	FRISEMLPNAWFHKLK
1.1	2032.0710	-0.0024	HLADHMKPMLINSLKER
0.5	2032.0661	0.0025	KARVSSASASAATGEAAAAVTR
0.4	2032.0728	-0.0043	DVKFILVDVSEEEIELR

Mascot: http://www.matrixscience.com/

AT1G13610.1

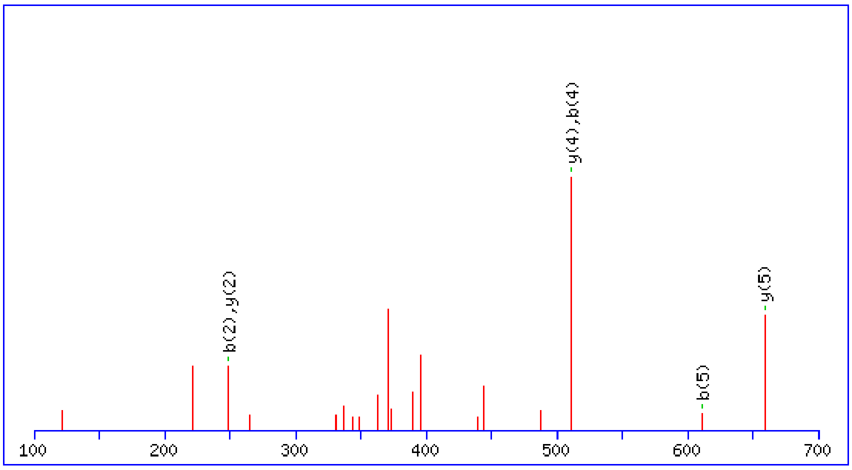
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMYPVK**
Found in **AT1G13610.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G30380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15341.1); contains InterPro domain Alpha/beta hydrolase fold-1 (InterPro:IPR000073) | chr1:4664005-4665972

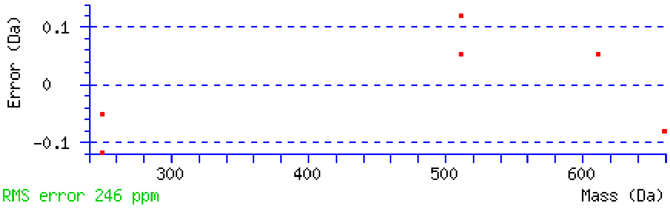
Match to Query 857: 758.372672 from(380.193612,2+) index(4971)
Title: Elution from: 44.887 to 44.887 scan no 6153 cid35.00 polarity:+
Data file 0-1_1.mgf

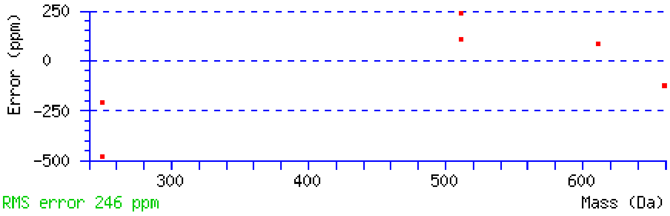
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 758.3731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.0086
Matches : 6/42 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	101.0727	51.0400	V					6
2	***249.1052***	125.0562	M	***659.3149***	330.1611	641.2913	321.1493	5
3	413.1655	207.0864	Y	***511.2825***	256.1449	493.2589	247.1331	4
4	***511.2153***	256.1113	P	347.2221	174.1147	329.1985	165.1029	3
5	***611.2808***	306.1440	V	***249.1723***	125.0898	231.1487	116.0780	2
6			K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of VMYPVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.7	758.3731	-0.0004	VMYPVK

20.8	758.3735	-0.0008	SRMAGVK
20.6	758.3731	-0.0004	VFDMLK
19.0	758.3709	0.0018	VMKETK
18.3	758.3709	0.0018	MSSSIVK
17.3	758.3731	-0.0004	YVPMVK
12.5	758.3709	0.0018	MVEKTK
12.5	758.3709	0.0018	MVTEKK
11.8	758.3731	-0.0004	DFLMVK
9.7	758.3735	-0.0009	NMSLRK

Mascot: http://www.matrixscience.com/

AT1G13650.1

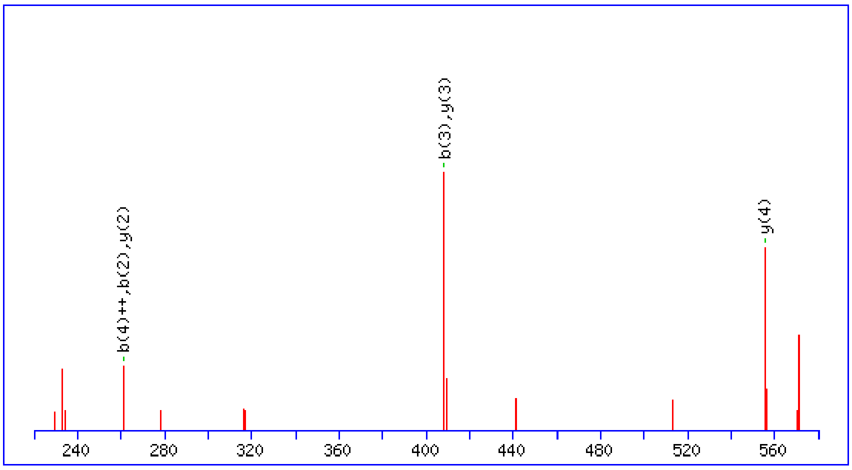
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFFNK**
Found in **AT1G13650.1** in **TAIR_Arabidopsis**

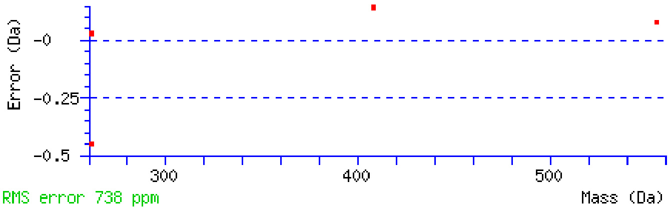
Match to Query 534: 667.369172 from(334.691862,2+) index(4147)
Title: Elution from: 39.804 to 39.804 scan no 5249 cid35.00 polarity:+
Data file 0-3_1.mgf

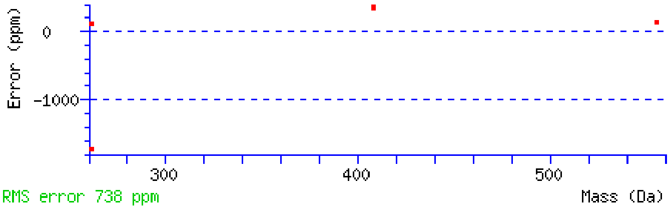
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 667.3693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.007
Matches : 6/26 fragment ions using 4 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			L					5
2	**261.1598**	131.0835			F	***555.2926***	278.1499	538.2660	269.6366	4
3	**408.2282**	204.6177			F	***408.2241***	204.6157	391.1976	196.1024	3
4	522.2711	261.6392	505.2445	253.1259	N	***261.1557***	131.0815	244.1292	122.5682	2
5					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of LFFNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.0	667.3693	-0.0002	LFFNK
13.1	667.3694	-0.0002	LFGFGK
10.9	667.3693	-0.0002	IFNFK
10.9	667.3693	-0.0002	LFNFK
10.6	667.3693	-0.0002	FLFNK

AT1G13650.1

Mascot: http://www.matrixscience.com/

AT1G13930.1

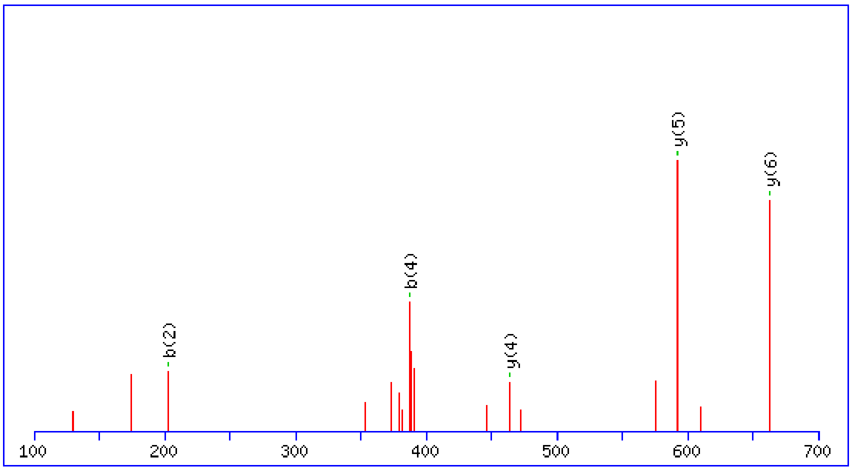
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAQGFLK**
Found in **AT1G13930.1** in **TAIR_Arabidopsis**, Symbols: | similar to nodulin-related [Arabidopsis thaliana] (TAIR:AT2G03440.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63832.1) | chr1:4761088-4761555 FORWARD

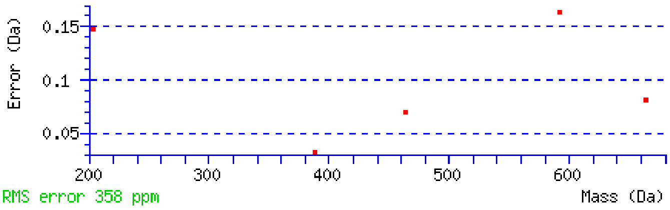
Match to Query 958: 793.414032 from(397.714292,2+) index(2553)
Title: Elution from: 26.898 to 26.898 scan no 3183 cid35.00 polarity:+
Data file 0-3_2.mgf

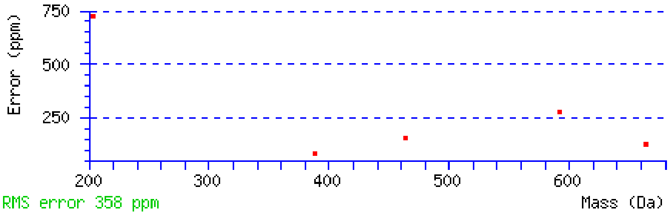
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 793.4156
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.002
Matches : 5/44 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	132.0478	66.5275			M					7
2	***203.0849***	102.0461			A	***663.3824***	332.1949	646.3559	323.6816	6
3	331.1435	166.0754	314.1169	157.5621	Q	***592.3453***	296.6763	575.3188	288.1630	5
4	***388.1649***	194.5861	371.1384	186.0728	G	***464.2867***	232.6470	447.2602	224.1337	4
5	535.2333	268.1203	518.2068	259.6070	F	407.2653	204.1363	390.2387	195.6230	3
6	648.3174	324.6623	631.2908	316.1491	L	260.1969	130.6021	243.1703	122.0888	2
7					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of MAQGFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.5	793.4156	-0.0016	MAQGFLK

AT1G14185.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLGGSSAINGGFYSR**
Found in **AT1G14185.1** in **TAIR_Arabidopsis**, Symbols: | glucose-methanol-choline (GMC) oxidoreductase family protein | chr1:4850279-4851880 FORWARD

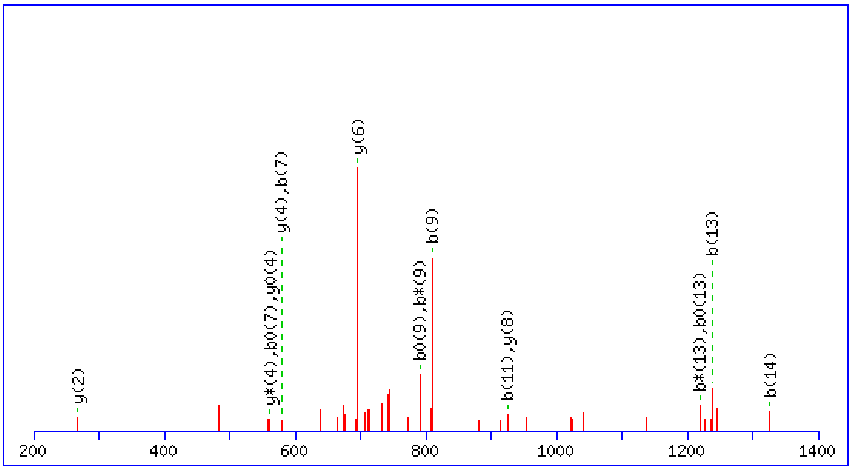
Match to Query 6789: 1502.688338 from(752.351445,2+) index(6371)
Title: Elution from: 55.515 to 55.515 scan no 8072 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

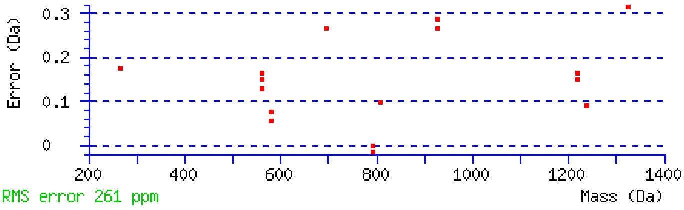
Label all possible matches ○ Label matches used for scoring ●

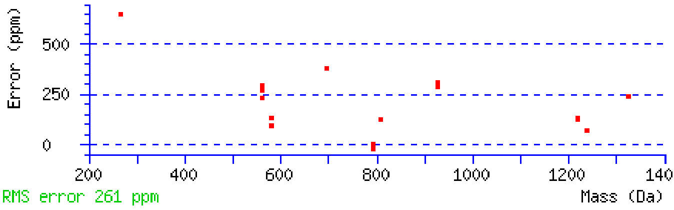
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1502.6856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.043
Matches : 16/142 fragment ion using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							15
2	215.1538	108.0805					L	1403.6274	702.3174	1385.6039	693.3056	1385.6169	693.3121	14
3	273.1723	137.0898					G	1289.5463	645.2768	1271.5228	636.2650	1271.5358	636.2715	13
4	331.1908	166.0990					G	1231.5278	616.2676	1213.5043	607.2558	1213.5173	607.2623	12
5	419.2199	210.1136			401.2093	201.1083	S	1173.5093	587.2583	1155.4858	578.2465	1155.4988	578.2530	11
6	507.2489	254.1281			489.2384	245.1228	S	1085.4803	543.2438	1067.4567	534.2320	1067.4697	534.2385	10
7	***579.2831***	290.1452			561.2725	281.1399	A	997.4512	499.2292	979.4276	490.2175	979.4406	490.2240	9
8	693.3642	347.1857			675.3536	338.1805	I	**925.4171**	463.2122	907.3935	454.2004	907.4065	454.2069	8
9	***809.4012***	405.2042	791.3776	396.1924	791.3906	396.1990	N	811.3360	406.1716	793.3124	397.1598	793.3254	397.1663	7
10	867.4197	434.2135	849.3961	425.2017	849.4091	425.2082	G	**695.2990**	348.1531	677.2754	339.1413	677.2884	339.1478	6
11	***925.4382***	463.2227	907.4146	454.2109	907.4276	454.2175	G	637.2805	319.1439	619.2569	310.1321	619.2699	310.1386	5
12	1073.5036	537.2555	1055.4801	528.2437	1055.4931	528.2502	F	**579.2620**	290.1346	561.2384	281.1228	561.2514	281.1293	4
13	***1237.5640***	619.2856	1219.5404	610.2738	1219.5534	610.2804	Y	431.1965	216.1019	413.1729	207.0901	413.1860	207.0966	3
14	***1325.5931***	663.3002	1307.5695	654.2884	1307.5825	654.2949	S	**267.1362**	134.0717	249.1126	125.0599	249.1256	125.0664	2
15							R	179.1071	90.0572	161.0835	81.0454			1





AT1G14185.1

NCBI **BLAST** search of VLGGSSAINGGFYSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1502.6856	0.0027	VLGGSSAINGGFYSR
7.1	1502.6860	0.0023	LKAGSGSGSGRGFGSR
6.1	1502.6879	0.0005	YYESKLNLNWR
0.3	1502.6852	0.0032	ILAGEELFYDYR
0.3	1502.6890	-0.0006	LNAGDLHEMILSR
0.1	1502.6883	0.0001	NANQTHLVFANPR

AT1G14320.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLSCHGPLANR**
Found in **AT1G14320.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L10 (RPL10A) / Wilm's tumor suppressor protein-related | chr1:4888265-4889403 FORWARD

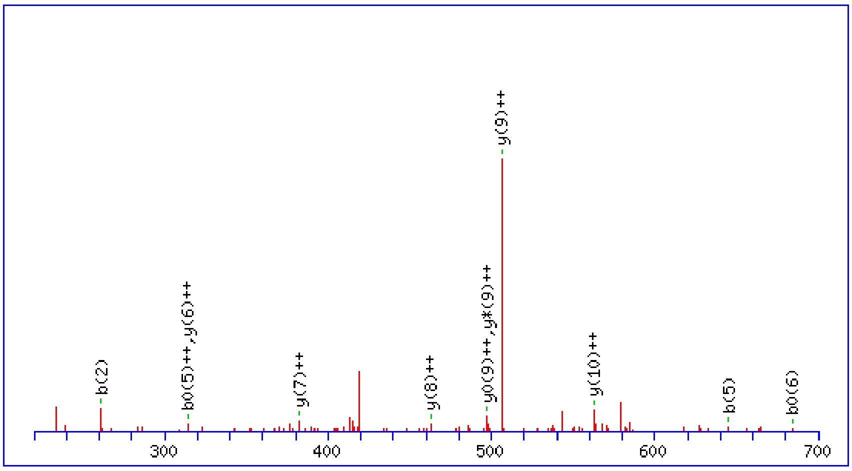
Match to Query 4021: 1270.624656 from(424.548828,3+) index(1818)
Title: Elution from: 25.326 to 25.326 scan no 2464 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 220 to 700 Da Full range

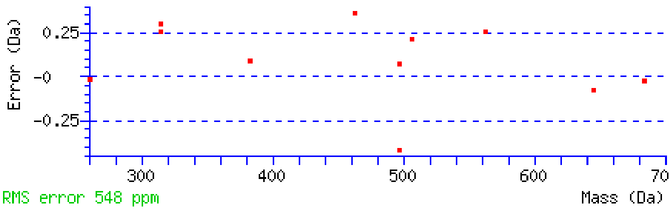
Label all possible matches ○ Label matches used for scoring ●

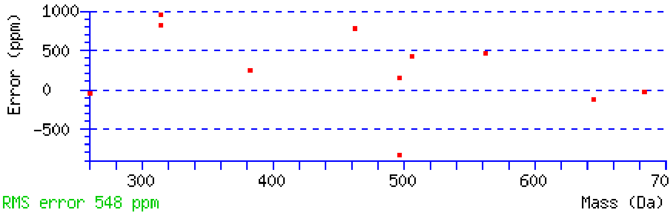
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1270.6241
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.019
Matches : 11/82 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							11
2	**261.1598**	131.0835					L	1124.5629	562.7851	1107.5364	554.2718	1106.5524	553.7798	10
3	348.1918	174.5995			330.1812	165.5942	S	1011.4789	506.2431	994.4523	497.7298	993.4683	497.2378	9
4	508.2224	254.6149			490.2119	245.6096	C	924.4468	462.7271	907.4203	454.2138			8
5	**645.2813**	323.1443			627.2708	314.1390	H	764.4162	382.7117	747.3896	374.1985			7
6	702.3028	351.6550			684.2922	342.6498	G	627.3573	314.1823	610.3307	305.6690			6
7	799.3556	400.1814			781.3450	391.1761	P	570.3358	285.6715	553.3093	277.1583			5
8	912.4396	456.7235			894.4291	447.7182	L	473.2831	237.1452	456.2565	228.6319			4
9	983.4767	492.2420			965.4662	483.2367	A	360.1990	180.6031	343.1724	172.0899			3
10	1097.5197	549.2635	1080.4931	540.7502	1079.5091	540.2582	N	289.1619	145.0846	272.1353	136.5713			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FLSCHGPLANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G14320.1

Score	Mr(calc)	Delta	Sequence
21.6	1270.6241	0.0006	FLSCHGPLANR
4.9	1270.6267	-0.0021	LFEAMSPYVSK
4.9	1270.6241	0.0006	NFSTLAFCRR
4.5	1270.6227	0.0019	DDVVLSLMHDK
3.1	1270.6268	-0.0021	LQIFFDMVDK
2.9	1270.6281	-0.0034	FNFHKYLMR
2.5	1270.6268	-0.0021	IDFYVCLVDK

AT1G14470.1

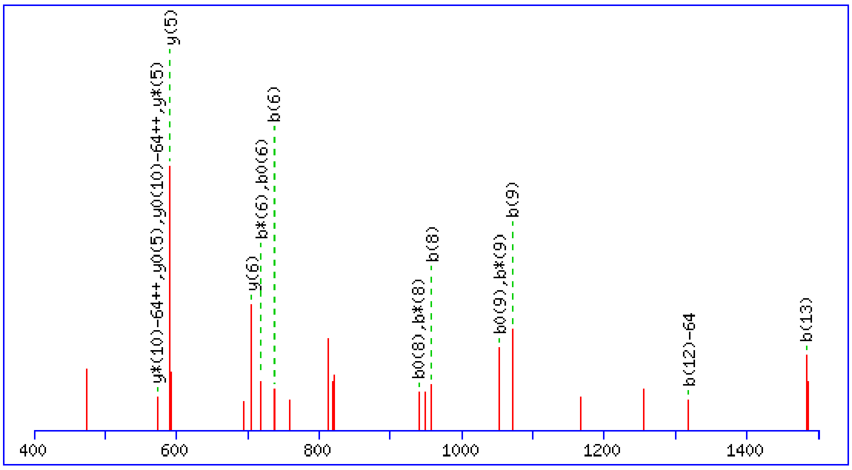
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLVTWNAMISGYTR**
Found in **AT1G14470.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:4954075-4955697 FORWARD

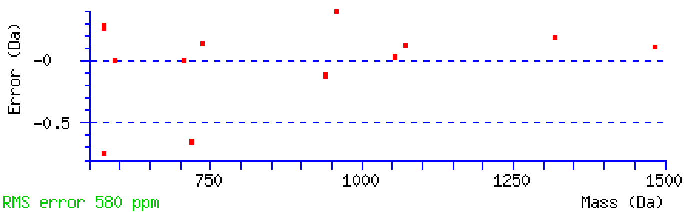
Match to Query 7262: 1660.742286 from(831.378419,2+) index(9863)
Title: Elution from: 97.313 to 97.313 scan no 14232 cid35.00 polarity:+
Data file D1d-1-2.mgf

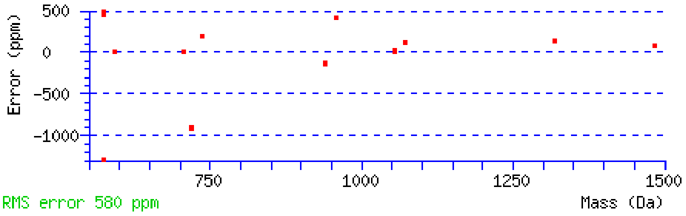
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1660.7388
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.036
Matches : 17/226 fragment ions using 20 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0443	59.0258	99.0207	50.0140			N							14
2	231.1254	116.0663	213.1018	107.0545			L	1545.7091	773.3582	1527.6855	764.3464	1527.6985	764.3529	13
3	331.1908	166.0990	313.1672	157.0873			V	1431.6280	716.3176	1413.6044	707.3058	1413.6174	707.3123	12
4	433.2355	217.1214	415.2120	208.1096	415.2250	208.1161	T	1331.5625	666.2849	1313.5389	657.2731	1313.5519	657.2796	11
5	621.3089	311.1581	603.2853	302.1463	603.2984	302.1528	W	1229.5178	615.2625	1211.4942	606.2507	1211.5072	606.2573	10
6	***737.3459***	369.1766	719.3223	360.1648	719.3353	360.1713	N	1041.4444	521.2258	1023.4208	512.2141	1023.4338	512.2206	9
7	809.3801	405.1937	791.3565	396.1819	791.3695	396.1884	A	925.4074	463.2073	907.3838	454.1956	907.3968	454.2021	8
8	***957.4125***	479.2099	939.3889	470.1981	939.4019	470.2046	M	853.3733	427.1903	835.3497	418.1785	835.3627	418.1850	7
9	***1071.4936***	536.2504	1053.4700	527.2386	1053.4830	527.2452	I	**705.3408**	353.1741	687.3172	344.1623	687.3303	344.1688	6
10	1159.5227	580.2650	1141.4991	571.2532	1141.5121	571.2597	S	**591.2597**	296.1335	573.2361	287.1217	573.2492	287.1282	5
11	1217.5412	609.2742	1199.5176	600.2624	1199.5306	600.2689	G	503.2307	252.1190	485.2071	243.1072	485.2201	243.1137	4
12	1381.6015	691.3044	1363.5779	682.2926	1363.5910	682.2991	Y	445.2122	223.1097	427.1886	214.0979	427.2016	214.1044	3
13	***1483.6462***	742.3268	1465.6227	733.3150	1465.6357	733.3215	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
14							R	179.1071	90.0572	161.0835	81.0454			1





AT1G14470.1

NCBI **BLAST** search of NLVTWNAMISGYTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.2	1660.7388	0.0035	NLVTWNAMISGYTR
8.3	1660.7444	-0.0021	LLENMPMPWEQVR
2.4	1660.7469	-0.0046	TDVTLGTDYLKNMR
0.9	1660.7417	0.0006	STKETAVNGGSSRSTR

AT1G14520.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KMREEYEK**
Found in **AT1G14520.1** in **TAIR_Arabidopsis**, Symbols: MIOX1 | MIOX1 (MYO-INISITOL OXYGENASE); oxidoreductase | chr1:4968371-4969949 REVERSE

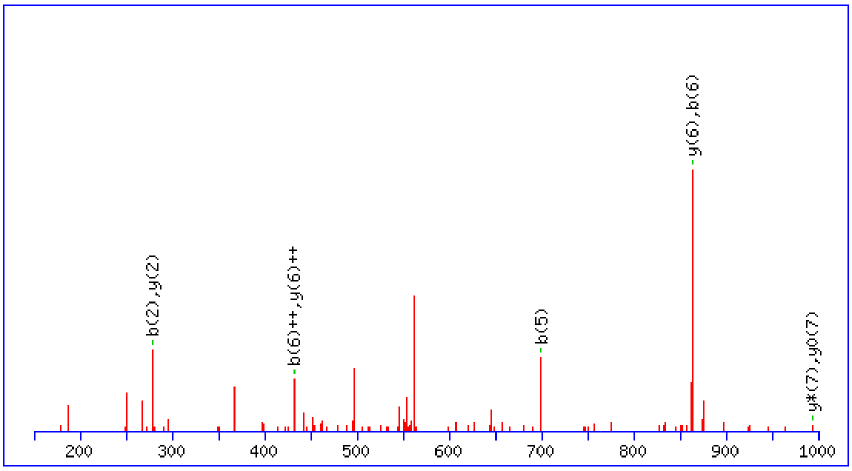
Match to Query 3773: 1140.490460 from(571.252506,2+) index(2635)
Title: Elution from: 25.943 to 25.943 scan no 3220 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

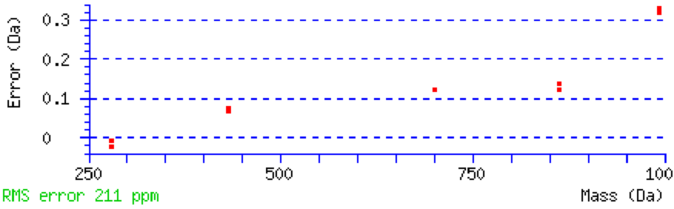
Label all possible matches ○ Label matches used for scoring ●

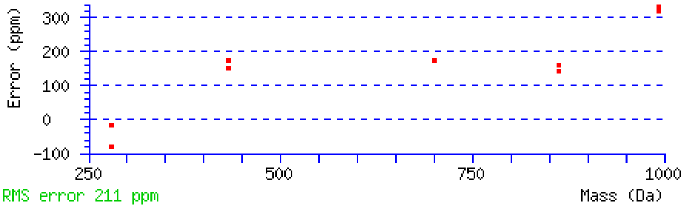
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1140.4896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.021
Matches : 10/114 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							8
2	***279.1287***	140.0680	261.1052	131.0562			M	1011.4078	506.2075	993.3842	497.1957	993.3972	497.2023	7
3	439.2180	220.1126	421.1944	211.1008			R	**863.3754**	432.1913	845.3518	423.1795	845.3648	423.1860	6
4	569.2576	285.1324	551.2340	276.1207	551.2471	276.1272	E	703.2861	352.1467	685.2625	343.1349	685.2756	343.1414	5
5	***699.2973***	350.1523	681.2737	341.1405	681.2867	341.1470	E	573.2465	287.1269	555.2229	278.1151	555.2359	278.1216	4
6	***863.3576***	432.1824	845.3340	423.1707	845.3470	423.1772	Y	443.2069	222.1071	425.1833	213.0953	425.1963	213.1018	3
7	***993.3972***	497.2023	975.3737	488.1905	975.3867	488.1970	E	**279.1465**	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KMREEYEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G14520.1

23.0	1140.4896	0.0009	KMREEYEK
18.4	1140.4922	-0.0018	CNSFLKNSR
18.1	1140.4896	0.0009	NFSMTQKEK
11.0	1140.4895	0.0009	TYVDMEKSR
10.9	1140.4927	-0.0022	MQRSNARSR
10.1	1140.4895	0.0009	DHLEMDIQK
7.7	1140.4896	0.0009	MAKEEYVSR
7.5	1140.4895	0.0009	MTEFNTTLR
7.4	1140.4911	-0.0007	MTIMTMIMK
6.0	1140.4911	-0.0007	MTIMTMIMK

AT1G14810.1

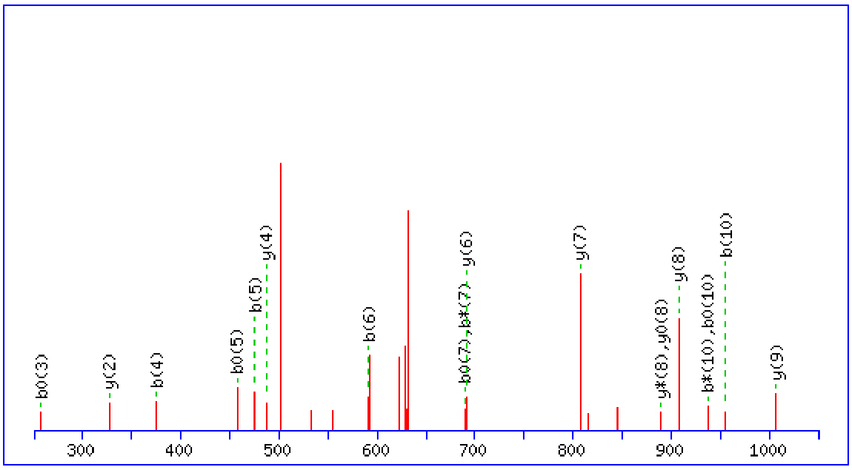
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTIVVDNSSAFR**
Found in **AT1G14810.1** in **TAIR_Arabidopsis**, Symbols: | semialdehyde dehydrogenase family protein | chr1:5102679-5104628 REVERSE

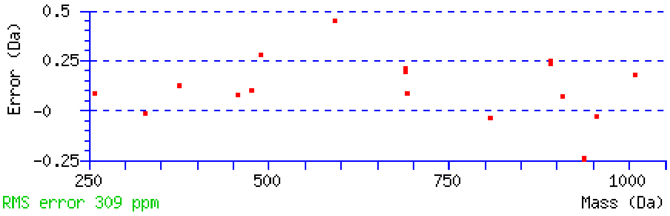
Match to Query 4414: 1280.593212 from(641.303882,2+) index(3542)
Title: Elution from: 33.900 to 33.900 scan no 4423 cid35.00 polarity:+
Data file C7-3_3.mgf

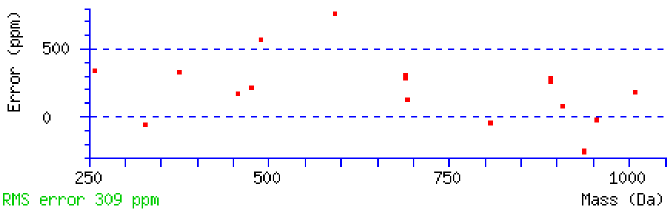
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1280.5937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0005
Matches : 18/112 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							12
2	161.0705	81.0389			143.0599	72.0336	T	1223.5825	612.2949	1205.5589	603.2831	1205.5719	603.2896	11
3	275.1516	138.0794			257.1410	129.0741	I	1121.5378	561.2725	1103.5142	552.2607	1103.5272	552.2672	10
4	**375.2170**	188.1122			357.2065	179.1069	V	***1007.4567***	504.2320	989.4331	495.2202	989.4461	495.2267	9
5	**475.2825**	238.1449			457.2719	229.1396	V	***907.3912***	454.1993	889.3677	445.1875	889.3807	445.1940	8
6	**591.3065**	296.1569			573.2959	287.1516	D	***807.3258***	404.1665	789.3022	395.1547	789.3152	395.1613	7
7	707.3435	354.1754	689.3199	345.1636	689.3329	345.1701	N	***691.3018***	346.1545	673.2782	337.1428	673.2912	337.1493	6
8	795.3725	398.1899	777.3489	389.1781	777.3620	389.1846	S	575.2648	288.1360	557.2412	279.1243	557.2543	279.1308	5
9	883.4016	442.2044	865.3780	433.1926	865.3910	433.1991	S	***487.2358***	244.1215	469.2122	235.1097	469.2252	235.1162	4
10	**955.4357**	478.2215	937.4122	469.2097	937.4252	469.2162	A	399.2067	200.1070	381.1831	191.0952			3
11	1103.5012	552.2542	1085.4776	543.2424	1085.4906	543.2489	F	***327.1725***	164.0899	309.1490	155.0781			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GTIVVDNSSAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G14810.1

Score	Mr(calc)	Delta	Sequence
43.0	1280.5937	-0.0005	GTIVVDNSSAFR
12.8	1280.5946	-0.0014	VLTGWMQKMR
10.8	1280.5897	0.0035	IVGTVGSSMLCK
7.1	1280.5924	0.0009	RLENMNTMKK
6.6	1280.5923	0.0009	MQRIVDSLMR
2.3	1280.5937	-0.0005	TGIEVNRDFSK
2.1	1280.5924	0.0009	SVVPSVRMSMR
1.7	1280.5912	0.0020	MFYSHQLLAR
0.7	1280.5946	-0.0014	VLTGWMQKMR

AT1G14970.1

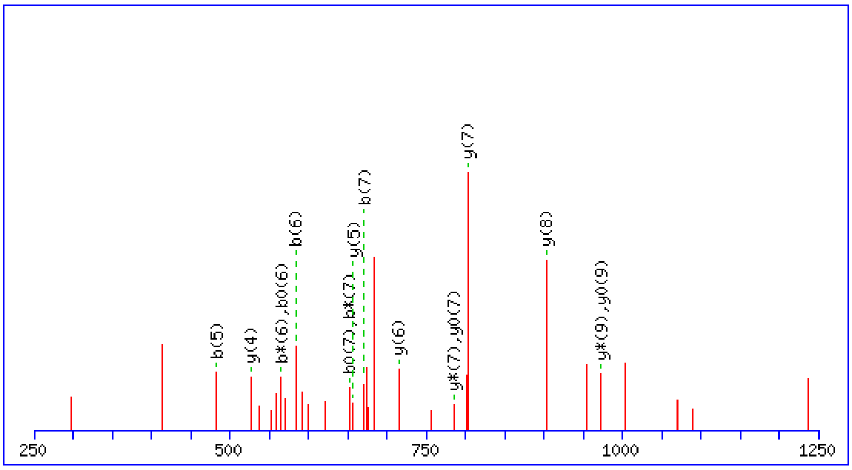
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SKSSSVSGQQQSR**
Found in **AT1G14970.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01480.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN77011.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42288.1); contains InterPro domain Protei

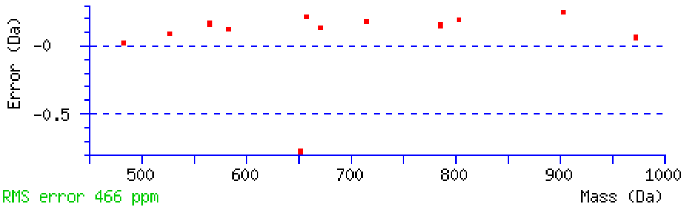
Match to Query 5246: 1384.603134 from(693.308843,2+) index(3253)
Title: Elution from: 32.463 to 32.463 scan no 4063 cid35.00 polarity:+
Data file D6h-1_2.mgf

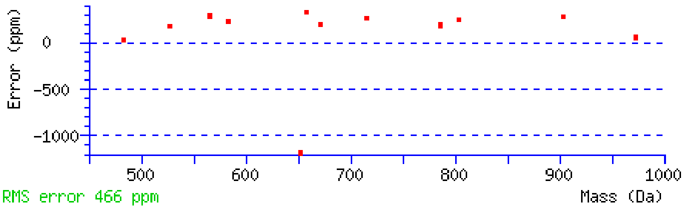
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1384.6051
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.03
Matches : 16/140 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							13
2	219.1254	110.0663	201.1018	101.0545	201.1148	101.0610	K	1297.5833	649.2953	1279.5597	640.2835	1279.5728	640.2900	12
3	307.1544	154.0809	289.1309	145.0691	289.1439	145.0756	S	1167.4943	584.2508	1149.4707	575.2390	1149.4837	575.2455	11
4	395.1835	198.0954	377.1599	189.0836	377.1729	189.0901	S	1079.4652	540.2363	1061.4416	531.2245	1061.4547	531.2310	10
5	**483.2126**	242.1099	465.1890	233.0981	465.2020	233.1046	S	991.4362	496.2217	973.4126	487.2099	973.4256	487.2164	9
6	**583.2780**	292.1426	565.2544	283.1309	565.2674	283.1374	V	***903.4071***	452.2072	885.3835	443.1954	885.3965	443.2019	8
7	**671.3071**	336.1572	653.2835	327.1454	653.2965	327.1519	S	***803.3417***	402.1745	785.3181	393.1627	785.3311	393.1692	7
8	729.3256	365.1664	711.3020	356.1546	711.3150	356.1611	G	***715.3126***	358.1599	697.2890	349.1481	697.3020	349.1547	6
9	859.3782	430.1927	841.3546	421.1810	841.3677	421.1875	Q	***657.2941***	329.1507	639.2705	320.1389	639.2835	320.1454	5
10	989.4309	495.2191	971.4073	486.2073	971.4203	486.2138	Q	***527.2414***	264.1244	509.2179	255.1126	509.2309	255.1191	4
11	1119.4835	560.2454	1101.4599	551.2336	1101.4729	551.2401	Q	397.1888	199.0980	379.1652	190.0862	379.1782	190.0928	3
12	1207.5126	604.2599	1189.4890	595.2481	1189.5020	595.2546	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SKSSSVSGQQQSR

AT1G14970.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.9	1384.6051	-0.0020	SKSSSVSGQQQSR
18.9	1384.6069	-0.0038	DFKSVSSTEGWK
13.6	1384.6033	-0.0002	IGRSSCMTTDLK
12.9	1384.6055	-0.0024	MFLDLCGVKDR
12.5	1384.6029	0.0003	YLEEMLDKGMK
8.0	1384.6029	0.0003	DMESKLDMLFK
5.0	1384.6055	-0.0024	MVDEGMKLFQR
2.7	1384.6055	-0.0024	VMESMAFNITAR
1.0	1384.6060	-0.0028	MAKDGGVSCLRR

AT1G14980.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGENEYHLFRDEDVLGTLHED**
Found in **AT1G14980.1** in **TAIR_Arabidopsis**, Symbols: CPN10 | CPN10 (CHAPERONIN 10) | chr1:5165925-5166649 REVERSE

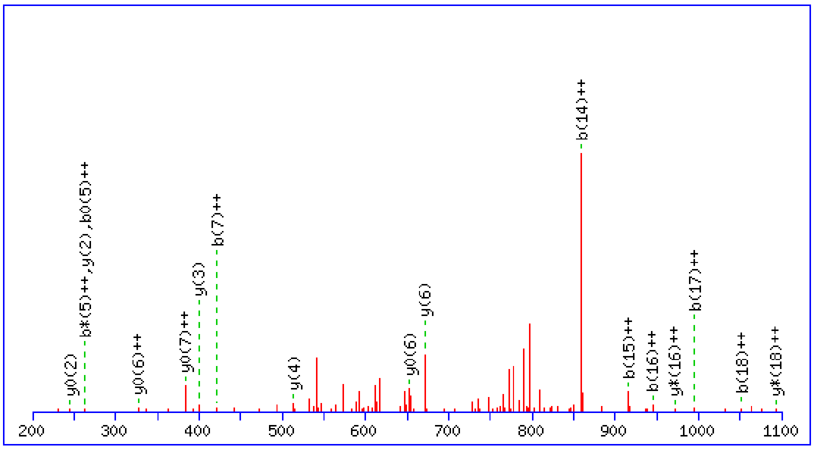
Match to Query 10676: 2500.150544 from(626.044912,4+) index(8262)
Title: Elution from: 74.976 to 74.976 scan no 10957 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●

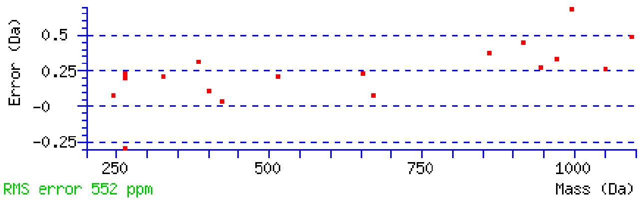
Show Y-axis ☐

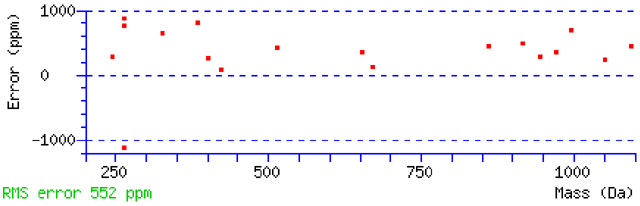


Monoisotopic mass of neutral peptide Mr(calc): 2500.1506
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.0065
Matches : 18/208 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							21
2	171.1128	86.0600					G	2388.0739	1194.5406	2371.0473	1186.0273	2370.0633	1185.5353	20
3	300.1554	150.5813			282.1448	141.5761	E	2331.0524	1166.0298	2314.0258	1157.5166	2313.0418	1157.0246	19
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	N	2202.0098	1101.5085	2184.9833	1092.9953	2183.9992	1092.5033	18
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	E	2087.9669	1044.4871	2070.9403	1035.9738	2069.9563	1035.4818	17
6	706.3042	353.6558	689.2777	345.1425	688.2937	344.6505	Y	1958.9243	979.9658	1941.8977	971.4525	1940.9137	970.9605	16
7	843.3632	***422.1852***	826.3366	413.6719	825.3526	413.1799	H	1795.8610	898.4341	1778.8344	889.9208	1777.8504	889.4288	15
8	956.4472	478.7272	939.4207	470.2140	938.4367	469.7220	L	1658.8020	829.9047	1641.7755	821.3914	1640.7915	820.8994	14
9	1103.5156	552.2615	1086.4891	543.7482	1085.5051	543.2562	F	1545.7180	773.3626	1528.6914	764.8494	1527.7074	764.3573	13
10	1259.6167	630.3120	1242.5902	621.7987	1241.6062	621.3067	R	1398.6496	699.8284	1381.6230	691.3151	1380.6390	690.8231	12
11	1374.6437	687.8255	1357.6171	679.3122	1356.6331	678.8202	D	1242.5485	621.7779			1224.5379	612.7726	11
12	1503.6863	752.3468	1486.6597	743.8335	1485.6757	743.3415	E	1127.5215	564.2644			1109.5109	555.2591	10
13	1618.7132	809.8603	1601.6867	801.3470	1600.7027	800.8550	D	998.4789	499.7431			980.4684	490.7378	9
14	1717.7816	***859.3945***	1700.7551	850.8812	1699.7711	850.3892	V	883.4520	442.2296			865.4414	433.2243	8
15	1830.8657	***915.9365***	1813.8392	907.4232	1812.8551	906.9312	L	784.3836	392.6954			766.3730	383.6901	7
16	1887.8872	***944.4472***	1870.8606	935.9339	1869.8766	935.4419	G	**671.2995**	336.1534			653.2889	327.1481	6
17	1988.9348	***994.9711***	1971.9083	986.4578	1970.9243	985.9658	T	614.2780	307.6427			596.2675	298.6374	5
18	2102.0189	***1051.5131***	2084.9924	1042.9998	2084.0083	1042.5078	L	**513.2304**	257.1188			495.2198	248.1135	4
19	2239.0778	1120.0425	2222.0513	1111.5293	2221.0673	1111.0373	H	**400.1463**	200.5768			382.1357	191.5715	3
20	2368.1204	1184.5638	2351.0939	1176.0506	2350.1099	1175.5586	E	**263.0874**	132.0473			245.0768	123.0420	2
21							D	134.0448	67.5260			116.0342	58.5207	1

AT1G14980.1





NCBI **BLAST** search of LGENEYHLFRDEDVLGTLHED
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.2	2500.1506	-0.0001	LGENEYHLFRDEDVLGTLHED
0.4	2500.1535	-0.0030	AQDLPEVCGEIMLEYSKEVMK

Mascot: http://www.matrixscience.com/

AT1G15140.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAFEFLVK**
Found in **AT1G15140.1** in **TAIR_Arabidopsis**, Symbols: | oxidoreductase NAD-binding domain-containing protein | chr1:5210398-5212132 REVERSE

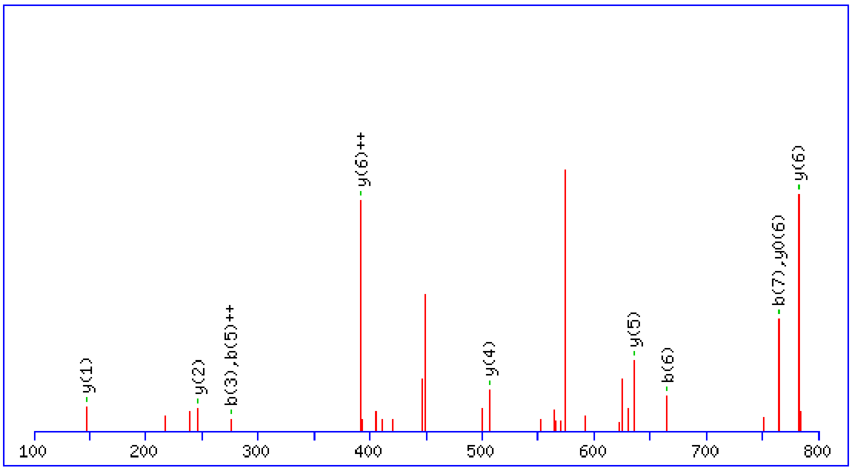
Match to Query 1416: 909.496396 from(455.755474,2+) index(6606)
Title: Elution from: 61.940 to 61.940 scan no 8733 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

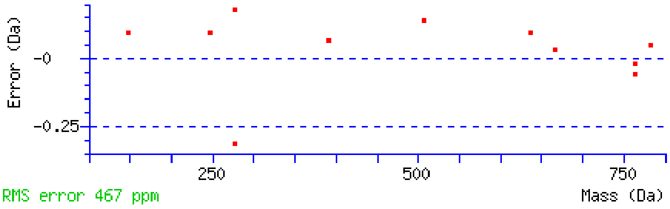
Label all possible matches ○ Label matches used for scoring ●

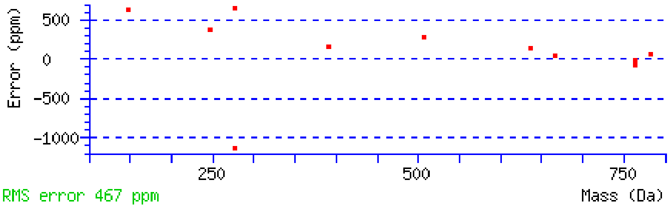
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 909.4960
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00011
Matches : 11/56 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							8
2	129.0659	65.0366			A	853.4818	427.2445	836.4553	418.7313	835.4713	418.2393	7
3	**276.1343**	138.5708			F	***782.4447***	391.7260	765.4182	383.2127	764.4341	382.7207	6
4	405.1769	203.0921	387.1663	194.0868	E	***635.3763***	318.1918	618.3497	309.6785	617.3657	309.1865	5
5	552.2453	276.6263	534.2347	267.6210	F	***506.3337***	253.6705	489.3071	245.1572			4
6	**665.3293**	333.1683	647.3188	324.1630	L	359.2653	180.1363	342.2387	171.6230			3
7	**764.3978**	382.7025	746.3872	373.6972	V	***246.1812***	123.5942	229.1547	115.0810			2
8					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GAFEFLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.1	909.4960	0.0004	GAFEFLVK

AT1G15140.1

12.0	909.4960	0.0004	AFGDFLLK
5.3	909.4960	0.0004	FTAISPFK
0.2	909.4960	0.0004	GFFGLLEK

AT1G15340.1

Mascot Search Results

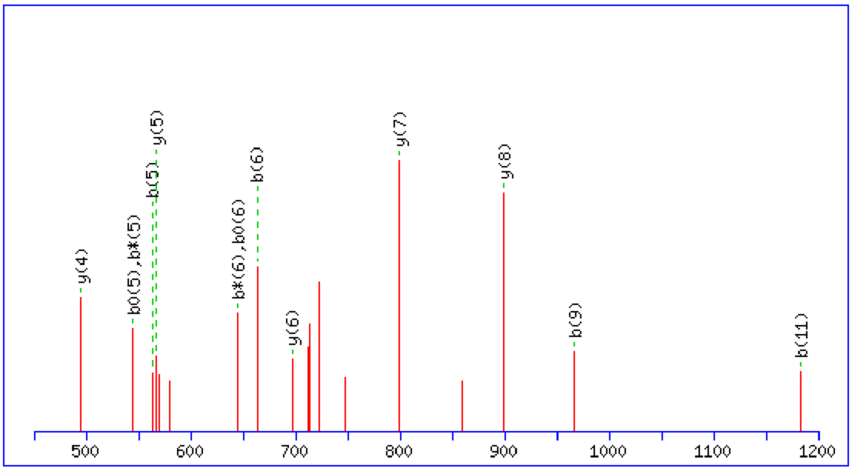
Peptide View

MS/MS Fragmentation of EAQEVVTEADVEK
Found in AT1G15340.1 in TAIR_Arabidopsis, Symbols: MBD10 | MBD10 (methyl-CpG-binding domain 10); DNA binding | chr1:5275890-5277469 REVERSE

Match to Query 6028: 1460.641688 from(731.328120,2+) index(2267)
Title: Elution from: 26.376 to 26.376 scan no 2938 cid35.00 polarity:+
Data file 0-3_1.mgf

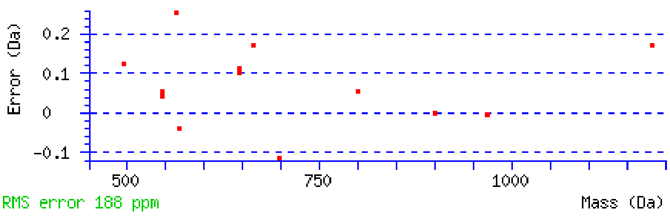
Click mouse within plot area to zoom in by factor of two about that point

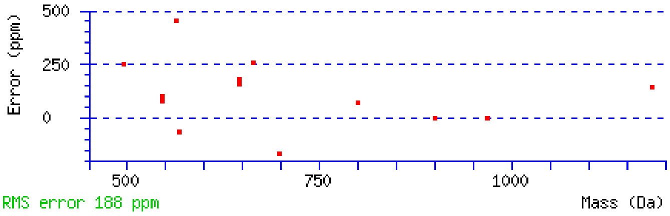
Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1460.6441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 8e-005
Matches : 13/138 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							13
2	203.0811	102.0442			185.0705	93.0389	A	1331.6117	666.3095	1313.5882	657.2977	1313.6012	657.3042	12
3	333.1337	167.0705	315.1101	158.0587	315.1231	158.0652	Q	1259.5776	630.2924	1241.5540	621.2806	1241.5670	621.2872	11
4	463.1733	232.0903	445.1497	223.0785	445.1628	223.0850	E	1129.5249	565.2661	1111.5014	556.2543	1111.5144	556.2608	10
5	***563.2388***	282.1230	545.2152	273.1112	545.2282	273.1177	V	999.4853	500.2463	981.4617	491.2345	981.4748	491.2410	9
6	***663.3042***	332.1558	645.2806	323.1440	645.2937	323.1505	V	***899.4199***	450.2136	881.3963	441.2018	881.4093	441.2083	8
7	765.3489	383.1781	747.3254	374.1663	747.3384	374.1728	T	***799.3544***	400.1808	781.3308	391.1691	781.3439	391.1756	7
8	895.3886	448.1979	877.3650	439.1861	877.3780	439.1926	E	***697.3097***	349.1585	679.2861	340.1467	679.2991	340.1532	6
9	***967.4227***	484.2150	949.3991	475.2032	949.4122	475.2097	A	***567.2701***	284.1387	549.2465	275.1269	549.2595	275.1334	5
10	1083.4467	542.2270	1065.4231	533.2152	1065.4361	533.2217	D	***495.2359***	248.1216	477.2123	239.1098	477.2254	239.1163	4
11	***1183.5121***	592.2597	1165.4886	583.2479	1165.5016	583.2544	V	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	1313.5518	657.2795	1295.5282	648.2677	1295.5412	648.2742	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EAQEVVTEADVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G15340.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.4	1460.6441	-0.0024	EAQEVVTEADVEK
0.2	1460.6382	0.0035	QVYEGFFSGGVEK

AT1G15480.1

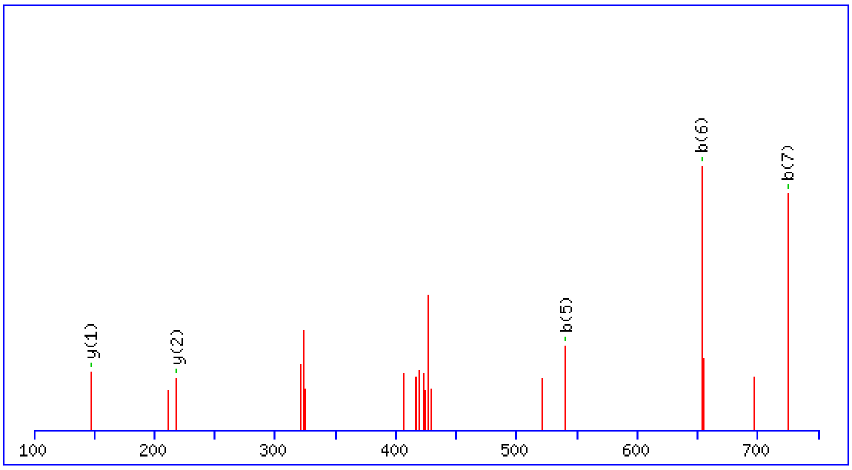
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RLAAQLAK**
Found in **AT1G15480.1** in **TAIR_Arabidopsis**, Symbols: | DNA binding | chr1:5318302-5320417 FORWARD

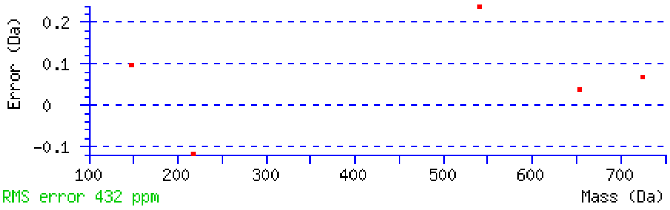
Match to Query 1378: 869.543420 from(435.778986,2+) index(508)
Title: Elution from: 10.804 to 10.804 scan no 780 cid35.00 polarity:+
Data file 0-3_2.mgf

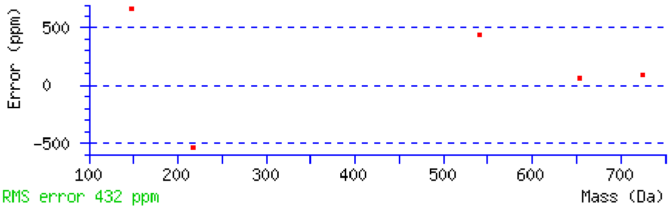
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 869.5446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.049
Matches : 5/56 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	157.1084	79.0578	140.0818	70.5446	R					8
2	270.1925	135.5999	253.1659	127.0866	L	714.4509	357.7291	697.4243	349.2158	7
3	341.2296	171.1184	324.2030	162.6051	A	601.3668	301.1870	584.3402	292.6738	6
4	412.2667	206.6370	395.2401	198.1237	A	530.3297	265.6685	513.3031	257.1552	5
5	***540.3253***	270.6663	523.2987	262.1530	Q	459.2926	230.1499	442.2660	221.6366	4
6	***653.4093***	327.2083	636.3828	318.6950	L	331.2340	166.1206	314.2074	157.6074	3
7	***724.4464***	362.7269	707.4199	354.2136	A	**218.1499**	109.5786	201.1234	101.0653	2
8					K	**147.1128**	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of RLAAQLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.3	869.5446	-0.0012	RAQLALAK
19.3	869.5446	-0.0012	RLAAQLAK

4.8	869.5446	-0.0012	AIEILRR
4.8	869.5447	-0.0013	VVDLIRR

AT1G15690.1

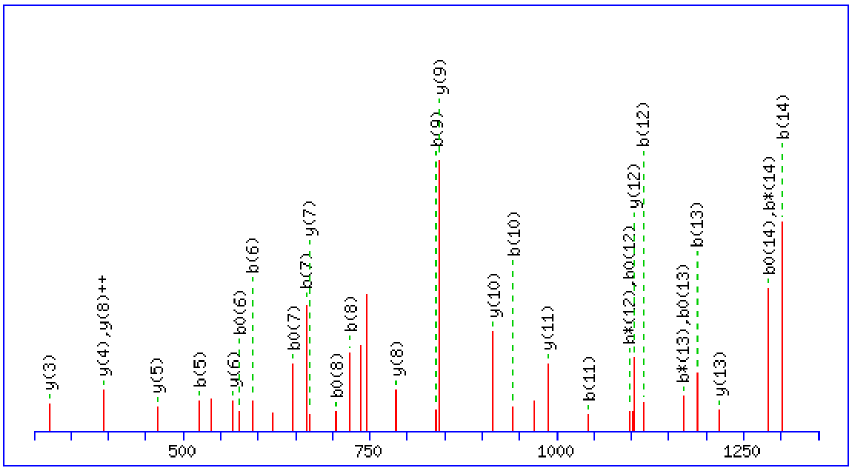
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDALDAAGNTTAAIGK**
Found in **AT1G15690.1** in **TAIR_Arabidopsis**, Symbols: ATAVP3, AVP-3, AVP1 | AVP1 (vacuolar-type H+-pumping pyrophosphatase 1); ATPase | chr1:5399110-5402180 FORWARD

Match to Query 6113: 1506.688536 from(754.351544,2+) index(3814)
Title: Elution from: 36.474 to 36.474 scan no 4763 cid35.00 polarity:+
Data file C7-1_3.mgf

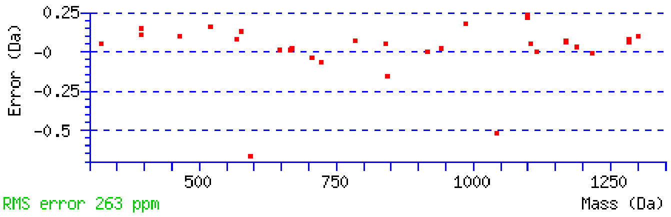
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

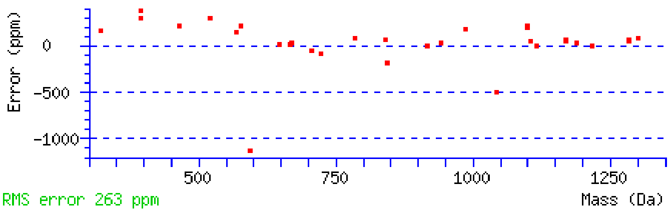


Monoisotopic mass of neutral peptide Mr(calc): 1506.6886
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 9.3e-011
Matches : 31/154 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							16
2	219.0760	110.0416			201.0654	101.0363	D	1405.6512	703.3292	1387.6276	694.3174	1387.6406	694.3240	15
3	291.1101	146.0587			273.0996	137.0534	A	1289.6272	645.3172	1271.6036	636.3055	1271.6167	636.3120	14
4	405.1912	203.0992			387.1807	194.0940	L	***1217.5931***	609.3002	1199.5695	600.2884	1199.5825	600.2949	13
5	***521.2152***	261.1112			503.2046	252.1060	D	***1103.5120***	552.2596	1085.4884	543.2478	1085.5014	543.2543	12
6	***593.2493***	297.1283			575.2388	288.1230	A	***987.4880***	494.2476	969.4644	485.2358	969.4774	485.2424	11
7	***665.2835***	333.1454			647.2729	324.1401	A	***915.4538***	458.2306	897.4303	449.2188	897.4433	449.2253	10
8	***723.3020***	362.1546			705.2914	353.1494	G	***843.4197***	422.2135	825.3961	413.2017	825.4091	413.2082	9
9	***839.3390***	420.1731	821.3154	411.1613	821.3284	411.1678	N	***785.4012***	393.2042	767.3776	384.1924	767.3906	384.1990	8
10	***941.3837***	471.1955	923.3601	462.1837	923.3731	462.1902	T	***669.3642***	335.1857	651.3406	326.1739	651.3536	326.1805	7
11	***1043.4284***	522.2178	1025.4048	513.2061	1025.4178	513.2126	T	***567.3195***	284.1634	549.2959	275.1516	549.3089	275.1581	6
12	***1115.4626***	558.2349	1097.4390	549.2231	1097.4520	549.2296	A	***465.2748***	233.1410	447.2512	224.1292			5
13	***1187.4967***	594.2520	1169.4731	585.2402	1169.4861	585.2467	A	***393.2406***	197.1239	375.2170	188.1122			4
14	***1301.5778***	651.2925	1283.5542	642.2808	1283.5672	642.2873	I	***321.2065***	161.1069	303.1829	152.0951			3
15	1359.5963	680.3018	1341.5727	671.2900	1341.5857	671.2965	G	207.1254	104.0663	189.1018	95.0545			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT1G15690.1





NCBI **BLAST** search of TDALDAAGNTTAAIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.4	1506.6886	-0.0001	TDALDAAGNTTAAIGK
7.9	1506.6895	-0.0010	MEAALAACALPSLR
7.7	1506.6909	-0.0023	TSESNQWLLPSTK
2.2	1506.6854	0.0031	DAGRVFKGWHEGK
0.7	1506.6886	-0.0001	SADDALEKEDKLR
0.6	1506.6886	-0.0000	TQDGGTEVVEAKAGK

Mascot: http://www.matrixscience.com/

AT1G15820.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SWIPAVK**
Found in **AT1G15820.1** in **TAIR_Arabidopsis**, Symbols: CP24, LHCB6 | LHCB6 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding | chr1:5446680-5447671 REVERSE

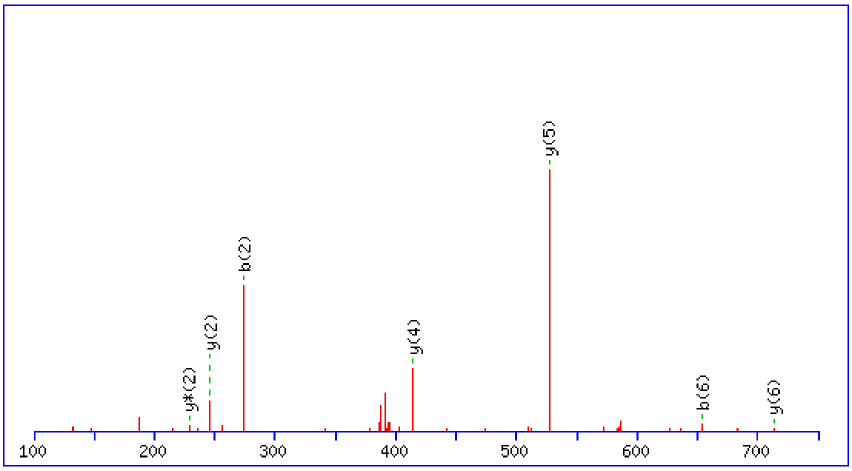
Match to Query 1060: 799.460104 from(400.737328,2+) index(4884)
Title: Elution from: 44.428 to 44.428 scan no 6099 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 750 Da Full range

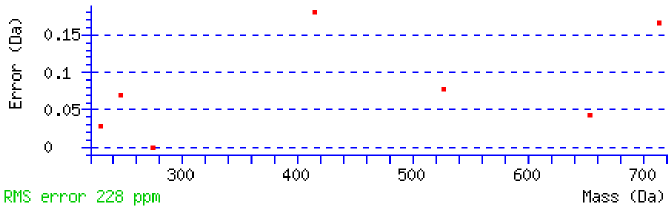
Label all possible matches ○ Label matches used for scoring ●

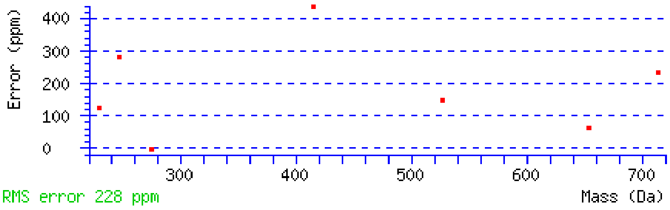
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 799.4592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0011
Matches : 7/48 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.0393	44.5233	70.0287	35.5180	S					7
2	**274.1186**	137.5629	256.1081	128.5577	W	***713.4345***	357.2209	696.4079	348.7076	6
3	387.2027	194.1050	369.1921	185.0997	I	***527.3552***	264.1812	510.3286	255.6679	5
4	484.2554	242.6314	466.2449	233.6261	P	***414.2711***	207.6392	397.2445	199.1259	4
5	555.2926	278.1499	537.2820	269.1446	A	317.2183	159.1128	300.1918	150.5995	3
6	**654.3610**	327.6841	636.3504	318.6788	V	***246.1812***	123.5942	229.1547	115.0810	2
7					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of SWIPAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.6	799.4592	0.0009	SWIPAVK

AT1G15930.1

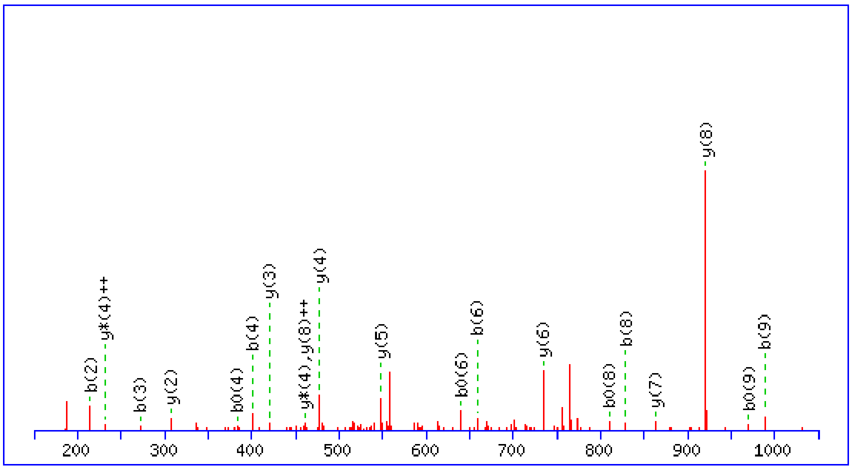
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLGEWAGLCK**
Found in **AT1G15930.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S12 (RPS12A) | chr1:5471696-5472735 FORWARD

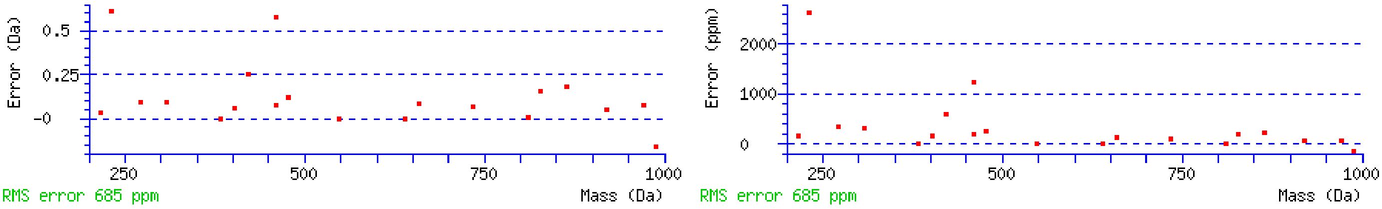
Match to Query 3165: 1133.553534 from(567.784043,2+) index(5409)
Title: Elution from: 49.780 to 49.780 scan no 6981 cid35.00 polarity:+
Data file D12h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1133.5539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 7.7e-005
Matches : 20/78 fragment ions using 34 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	***215.1390***	108.0731	197.1285	99.0679	L	1033.5135	517.2604	1016.4870	508.7471	1015.5030	508.2551	9
3	***272.1605***	136.5839	254.1499	127.5786	G	***920.4295***	460.7184	903.4029	452.2051	902.4189	451.7131	8
4	***401.2031***	201.1052	383.1925	192.0999	E	***863.4080***	432.2076	846.3815	423.6944	845.3974	423.2024	7
5	587.2824	294.1448	569.2718	285.1396	W	***734.3654***	367.6863	717.3389	359.1731			6
6	***658.3195***	329.6634	640.3089	320.6581	A	***548.2861***	274.6467	531.2595	266.1334			5
7	715.3410	358.1741	697.3304	349.1688	G	***477.2490***	239.1281	460.2224	230.6149			4
8	***828.4250***	414.7162	810.4145	405.7109	L	***420.2275***	210.6174	403.2010	202.1041			3
9	***988.4557***	494.7315	970.4451	485.7262	C	***307.1435***	154.0754	290.1169	145.5621			2
10					K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of TLGEWAGLCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G15930.1

46.1	1133.5539	-0.0004	TLGEWAGLCK
13.4	1133.5564	-0.0029	TLADASTAEQK
3.6	1133.5539	-0.0004	LASECLQWK

AT1G15940.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVEPSSSPEVR**
Found in **AT1G15940.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr1:5473666-5478044 FORWARD

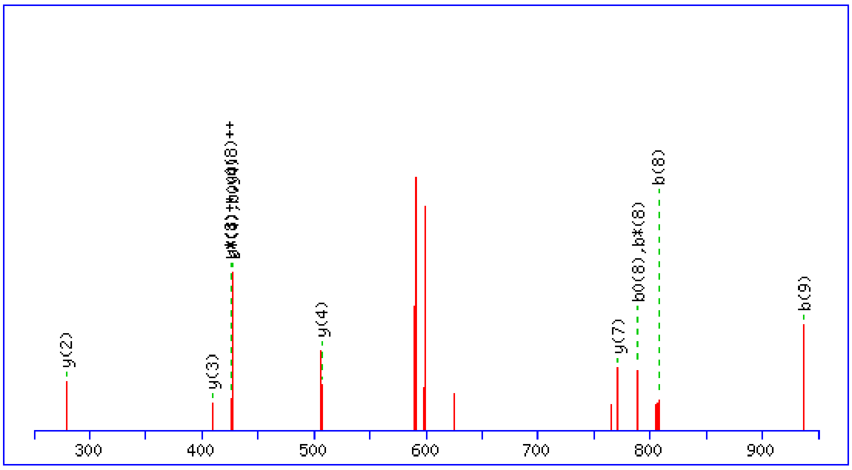
Match to Query 3669: 1214.533484 from(608.274018,2+) index(2846)
Title: Elution from: 30.762 to 30.762 scan no 3626 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 950 Da Full range

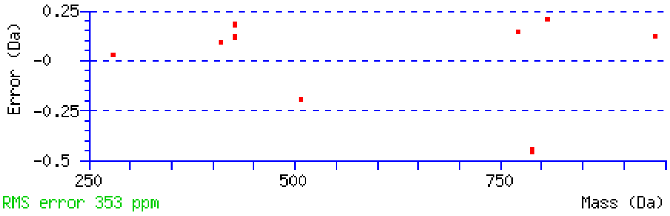
Label all possible matches ○ Label matches used for scoring ●

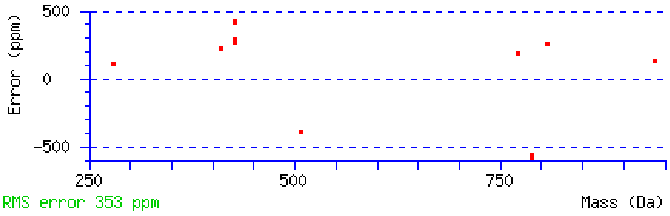
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1214.5338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0066
Matches : 12/112 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							11
2	217.1097	109.0585	199.0861	100.0467			V	1099.5040	550.2557	1081.4804	541.2439	1081.4935	541.2504	10
3	347.1493	174.0783	329.1258	165.0665	329.1388	165.0730	E	999.4386	500.2229	981.4150	491.2111	981.4280	491.2176	9
4	445.1991	223.1032	427.1756	214.0914	427.1886	214.0979	P	869.3990	435.2031	851.3754	426.1913	851.3884	426.1978	8
5	533.2282	267.1177	515.2046	258.1060	515.2176	258.1125	S	***771.3492***	386.1782	753.3256	377.1664	753.3386	377.1729	7
6	621.2573	311.1323	603.2337	302.1205	603.2467	302.1270	S	683.3201	342.1637	665.2965	333.1519	665.3095	333.1584	6
7	709.2863	355.1468	691.2628	346.1350	691.2758	346.1415	S	595.2910	298.1492	577.2674	289.1374	577.2805	289.1439	5
8	**807.3361**	404.1717	789.3126	395.1599	789.3256	395.1664	P	***507.2620***	254.1346	489.2384	245.1228	489.2514	245.1293	4
9	**937.3758**	469.1915	919.3522	460.1797	919.3652	460.1862	E	***409.2122***	205.1097	391.1886	196.0979	391.2016	196.1044	3
10	1037.4412	519.2242	1019.4176	510.2125	1019.4306	510.2190	V	***279.1725***	140.0899	261.1490	131.0781			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NVEPSSSPEVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G15940.1

Score	Mr(calc)	Delta	Sequence
28.7	1214.5338	-0.0003	NVEPSSSPEVR
17.5	1214.5360	-0.0025	ENVPPGFGEQK
9.9	1214.5335	0.0000	KFFGWMQNK
4.9	1214.5311	0.0024	LDDELDNIEK
4.4	1214.5364	-0.0029	HERQDQKEK
4.4	1214.5311	0.0024	KDETPEVEEK
2.3	1214.5360	-0.0025	KFDYSDATVR

AT1G16030.1

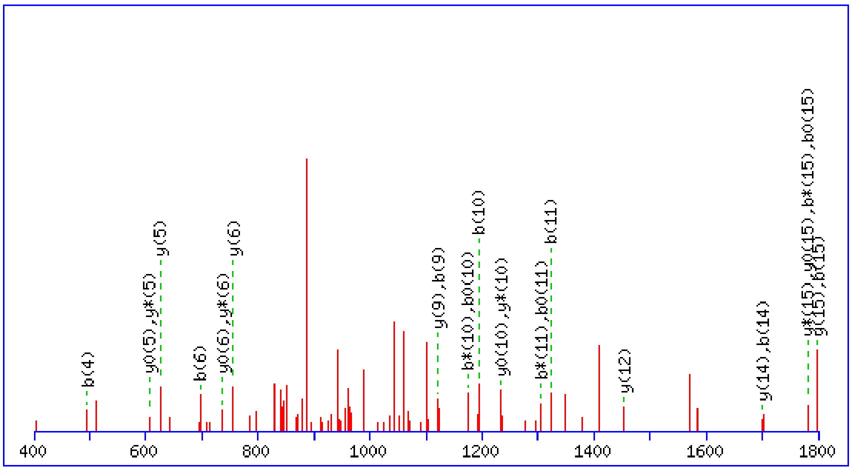
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQDAEKYKAEDEQVK**
Found in **AT1G16030.1** in **TAIR_Arabidopsis**, Symbols: HSP70B | HSP70B (heat shock protein 70B); ATP binding | chr1:5502380-5504320 REVERSE

Match to Query 8810: 1946.838534 from(974.426543,2+) index(7509)
Title: Elution from: 67.180 to 67.180 scan no 9875 cid35.00 polarity:+
Data file D12h-2_3.mgf

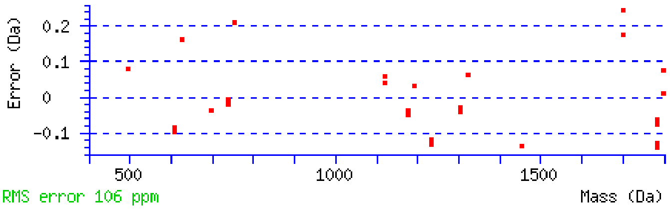
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

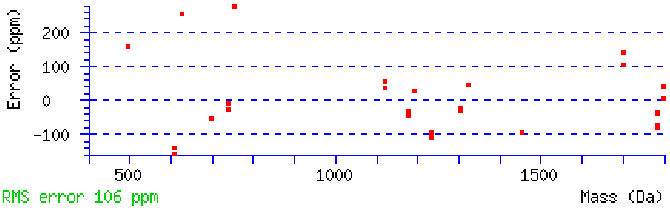


Monoisotopic mass of neutral peptide Mr(calc): 1946.8418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.016
Matches : 27/244 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							16
2	249.1052	125.0562					V	**1799.8166**	900.4120	1781.7930	891.4002	1781.8061	891.4067	15
3	379.1578	190.0825	361.1342	181.0707			Q	**1699.7512**	850.3792	1681.7276	841.3674	1681.7406	841.3739	14
4	***495.1818***	248.0945	477.1582	239.0827	477.1712	239.0892	D	1569.6985	785.3529	1551.6750	776.3411	1551.6880	776.3476	13
5	567.2159	284.1116	549.1924	275.0998	549.2054	275.1063	A	**1453.6746**	727.3409	1435.6510	718.3291	1435.6640	718.3356	12
6	***697.2556***	349.1314	679.2320	340.1196	679.2450	340.1261	E	1381.6404	691.3238	1363.6168	682.3121	1363.6298	682.3186	11
7	827.3446	414.1759	809.3210	405.1641	809.3340	405.1707	K	1251.6008	626.3040	1233.5772	617.2922	1233.5902	617.2987	10
8	991.4050	496.2061	973.3814	487.1943	973.3944	487.2008	Y	**1121.5117**	561.2595	1103.4882	552.2477	1103.5012	552.2542	9
9	***1121.4940***	561.2506	1103.4704	552.2388	1103.4834	552.2454	K	957.4514	479.2293	939.4278	470.2175	939.4408	470.2240	8
10	***1193.5281***	597.2677	1175.5046	588.2559	1175.5176	588.2624	A	827.3624	414.1848	809.3388	405.1730	809.3518	405.1795	7
11	***1323.5678***	662.2875	1305.5442	653.2757	1305.5572	653.2822	E	**755.3282**	378.1677	737.3046	369.1559	737.3176	369.1625	6
12	1439.5917	720.2995	1421.5682	711.2877	1421.5812	711.2942	D	**625.2886**	313.1479	607.2650	304.1361	607.2780	304.1426	5
13	1569.6314	785.3193	1551.6078	776.3075	1551.6208	776.3140	E	509.2646	255.1359	491.2410	246.1241	491.2540	246.1307	4
14	***1699.6840***	850.3456	1681.6604	841.3339	1681.6735	841.3404	Q	379.2250	190.1161	361.2014	181.1043			3
15	***1799.7495***	900.3784	1781.7259	891.3666	1781.7389	891.3731	V	249.1723	125.0898	231.1487	116.0780			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT1G16030.1





NCBI **BLAST** search of MVQDAEKYKAEDEQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	1946.8418	-0.0032	MVQDAEKYKAEDEQVK
6.8	1946.8341	0.0044	QIRCNWATKGATSGEDK
3.2	1946.8404	-0.0019	TMTELDGMICSQLGTLR
2.2	1946.8418	-0.0033	YQNGILSDSAILNMDEK
0.2	1946.8348	0.0037	GVCSKTDEVCIKAESNK

AT1G16080.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALQEMGNGEDLLVK**
Found in **AT1G16080.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown [Populus trichocarpa] (GB:ABK94042.1) | chr1:5514388-5515755 FORWARD

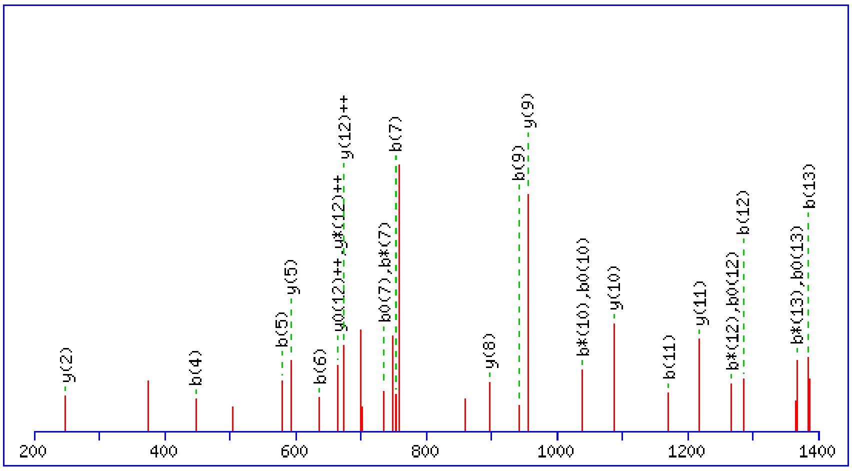
Match to Query 6331: 1532.707580 from(767.361066,2+) index(5462)
Title: Elution from: 48.256 to 48.256 scan no 6962 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

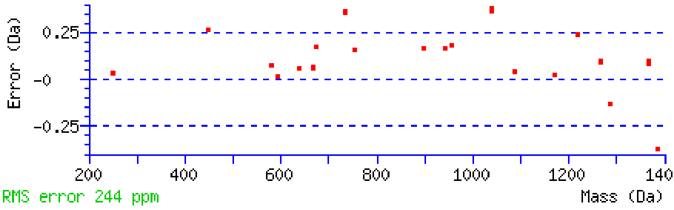
Label all possible matches ○ Label matches used for scoring ●

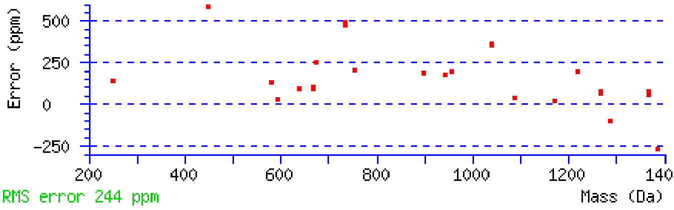
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1532.7099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.3e-006
Matches : 25/138 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					**A**							**14**
2	187.1225	94.0649					**L**	1461.6830	731.3451	1443.6594	722.3334	1443.6725	722.3399	**13**
3	317.1752	159.0912	299.1516	150.0794			**Q**	1347.6019	674.3046	1329.5783	665.2928	1329.5914	665.2993	**12**
4	***447.2148***	224.1110	429.1912	215.0992	429.2042	215.1058	**E**	**1217.5493**	609.2783	1199.5257	600.2665	1199.5387	600.2730	**11**
5	***579.2523***	290.1298	561.2287	281.1180	561.2418	281.1245	**M**	**1087.5096**	544.2585	1069.4861	535.2467	1069.4991	535.2532	**10**
6	***637.2708***	319.1390	619.2472	310.1273	619.2603	310.1338	**G**	**955.4721**	478.2397	937.4485	469.2279	937.4616	469.2344	**9**
7	***753.3078***	377.1575	735.2842	368.1458	735.2973	368.1523	**N**	**897.4536**	449.2304	879.4300	440.2187	879.4431	440.2252	**8**
8	811.3263	406.1668	793.3027	397.1550	793.3157	397.1615	**G**	781.4166	391.2120	763.3930	382.2002	763.4061	382.2067	**7**
9	***941.3659***	471.1866	923.3424	462.1748	923.3554	462.1813	**E**	723.3981	362.2027	705.3745	353.1909	705.3876	353.1974	**6**
10	1057.3899	529.1986	1039.3663	520.1868	1039.3794	520.1933	**D**	**593.3585**	297.1829	575.3349	288.1711	575.3479	288.1776	**5**
11	***1171.4710***	586.2391	1153.4474	577.2274	1153.4605	577.2339	**L**	477.3345	239.1709	459.3109	230.1591			**4**
12	***1285.5521***	643.2797	1267.5285	634.2679	1267.5416	634.2744	**L**	363.2534	182.1303	345.2298	173.1186			**3**
13	***1385.6176***	693.3124	1367.5940	684.3006	1367.6070	684.3071	**V**	**249.1723**	125.0898	231.1487	116.0780			**2**
14							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of ALQEMGNGEDLLVK

AT1G16080.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.4	1532.7099	-0.0023	ALQEMGNGEDLLVK
8.3	1532.7099	-0.0023	QLAEEVDMIPTVR
8.2	1532.7092	-0.0016	RSLYDRYGEAGVK
3.9	1532.7070	0.0006	LLSEVAGSHSRDNK
0.9	1532.7110	-0.0034	KAFSFFGFDPIDK
0.6	1532.7099	-0.0023	IEIEMEKSGHVTK
0.4	1532.7087	-0.0011	AYVTFLAGNGDYVK
0.4	1532.7043	0.0033	DKSTHSATVVDDLK

AT1G16160.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFSSEELK**
Found in **AT1G16160.1** in **TAIR_Arabidopsis**, Symbols: WAKL5 | WAKL5 (WALL ASSOCIATED KINASE-LIKE 5); kinase | chr1:5535967-5538263 FORWARD

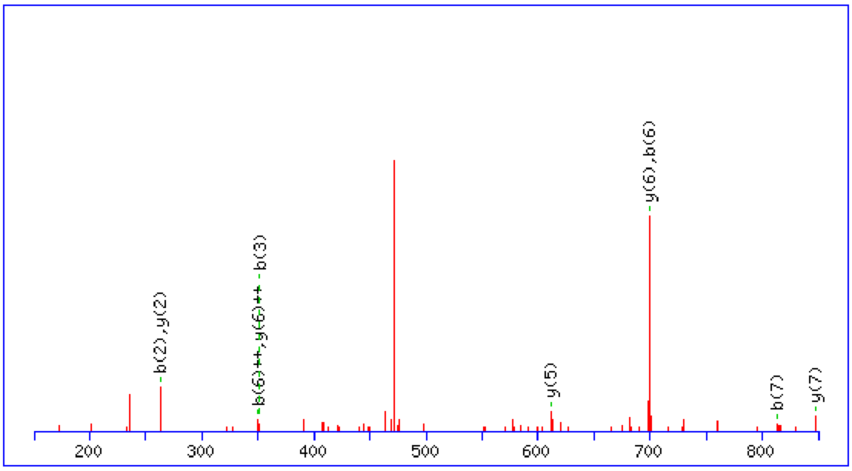
Match to Query 1886: 960.466110 from(481.240331,2+) index(1888)
Title: Elution from: 25.323 to 25.323 scan no 2547 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

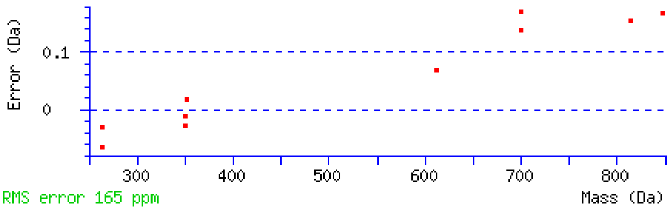
Label all possible matches ○ Label matches used for scoring ●

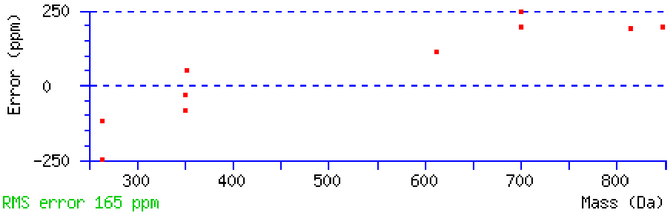
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 960.4646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0095
Matches : 10/62 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	***263.1538***	132.0805			F	***847.3908***	424.1990	829.3672	415.1872	829.3802	415.1938	7
3	***351.1829***	176.0951	333.1723	167.0898	S	***699.3254***	350.1663	681.3018	341.1545	681.3148	341.1610	6
4	439.2120	220.1096	421.2014	211.1043	S	***611.2963***	306.1518	593.2727	297.1400	593.2857	297.1465	5
5	569.2516	285.1294	551.2410	276.1241	E	523.2672	262.1373	505.2436	253.1255	505.2567	253.1320	4
6	***699.2912***	350.1492	681.2806	341.1440	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	***813.3723***	407.1898	795.3617	398.1845	L	***263.1880***	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LFSSEELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.0	960.4646	0.0015	LFSSEELK

AT1G16160.1

25.5	960.4646	0.0015	FITDESLK
15.8	960.4651	0.0010	RSSAAESLK
12.6	960.4673	-0.0012	FLDLQGTR
10.4	960.4673	-0.0012	IFGASNVNK
10.4	960.4673	-0.0012	LFEQREK
10.4	960.4633	0.0028	LMPAMTKK
9.7	960.4633	0.0029	MVCSTIIK
8.5	960.4650	0.0011	TTGSTLVNR
8.2	960.4673	-0.0012	LTGNAFAQK

AT1G16250.1

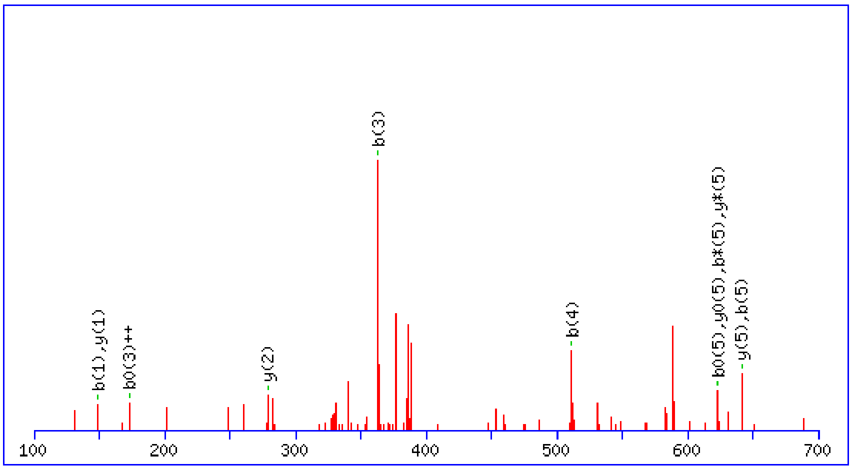
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDPFKK**
Found in **AT1G16250.1** in **TAIR_Arabidopsis**, Symbols: | kelch repeat-containing F-box family protein | chr1:5557208-5558691 FORWARD

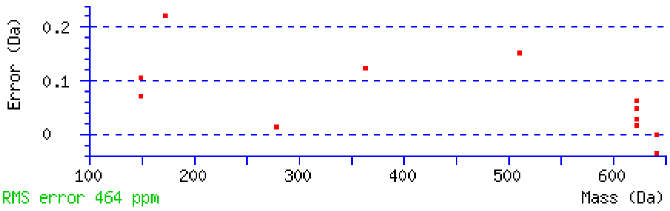
Match to Query 770: 788.395384 from(395.204968,2+) index(1213)
Title: Elution from: 20.793 to 20.793 scan no 1784 cid35.00 polarity:+
Data file D1d-2_2.mgf

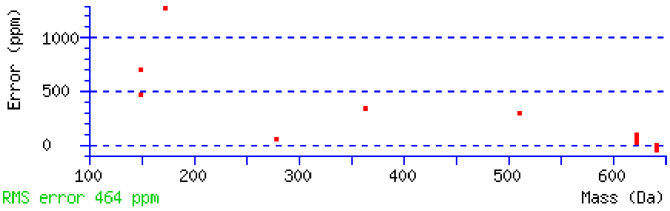
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 788.3933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.025
Matches : 12/42 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***149.0727***	75.0400					F							6
2	265.0967	133.0520			247.0861	124.0467	D	**641.3351**	321.1712	623.3115	312.1594	623.3246	312.1659	5
3	***363.1465***	182.0769			345.1359	173.0716	P	525.3112	263.1592	507.2876	254.1474			4
4	***511.2120***	256.1096			493.2014	247.1043	F	427.2614	214.1343	409.2378	205.1225			3
5	***641.3010***	321.1541	623.2774	312.1423	623.2904	312.1488	K	**279.1959**	140.1016	261.1723	131.0898			2
6							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FDPFKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.6	788.3933	0.0021	FDPFKK
24.2	788.3944	0.0009	MKTEKK
21.0	788.3944	0.0009	KMKTEK
18.7	788.3933	0.0021	VFYPQK

AT1G16250.1

18.0	788.3944	0.0009	ETKMKK
17.9	788.3967	-0.0013	MQIFVK
17.9	788.3944	0.0009	MEKKTK
17.9	788.3971	-0.0017	ARQMKK
17.9	788.3944	0.0009	TEKMKK
16.8	788.3933	0.0021	YLFNPK

AT1G16400.1

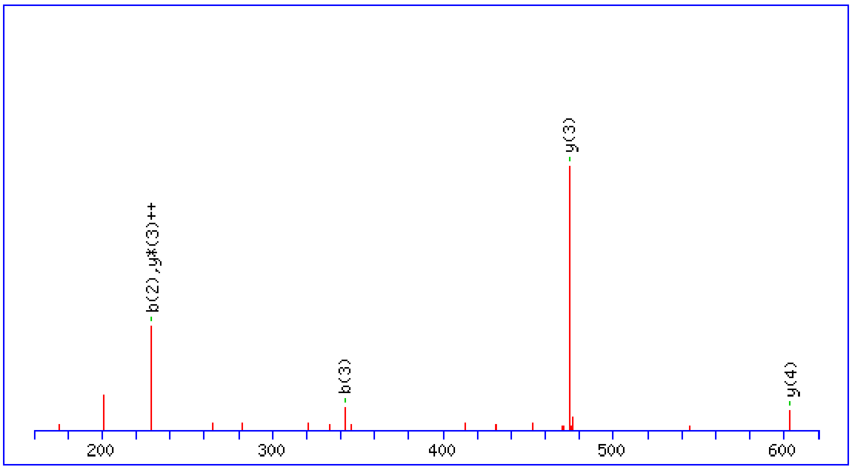
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEIWR**
Found in **AT1G16400.1** in **TAIR_Arabidopsis**

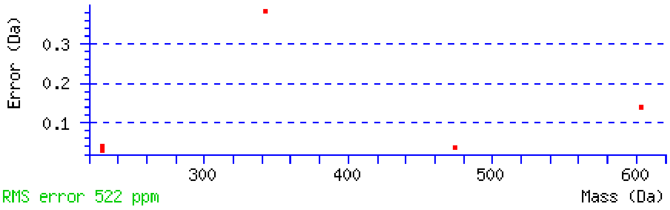
Match to Query 561: 701.388130 from(351.701341,2+) index(2474)
Title: Elution from: 29.334 to 29.334 scan no 3242 cid35.00 polarity:+
Data file D1d-2_2.mgf

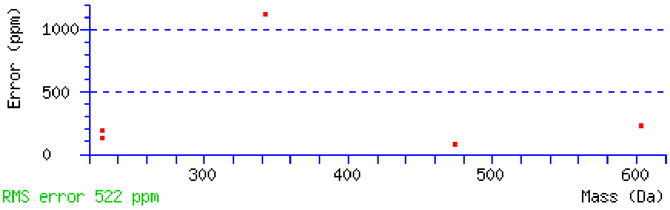
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 620 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 701.3860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.049
Matches : 5/32 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415			**V**							**5**
2	***229.1183***	115.0628	211.1077	106.0575	**E**	***603.3249***	302.1661	586.2984	293.6528	585.3144	293.1608	**4**
3	***342.2023***	171.6048	324.1918	162.5995	**I**	***474.2823***	237.6448	457.2558	229.1315			**3**
4	528.2817	264.6445	510.2711	255.6392	**W**	361.1983	181.1028	344.1717	172.5895			**2**
5					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VEIWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.1	701.3860	0.0021	VEIWR
15.4	701.3860	0.0021	VEWIR
10.6	701.3860	0.0021	EVLWR
10.6	701.3860	0.0021	LDLWR
3.5	701.3860	0.0021	DIWLR

AT1G16400.1

3.5	701.3894	-0.0013	MPVVTR

AT1G16470.1

Mascot Search Results

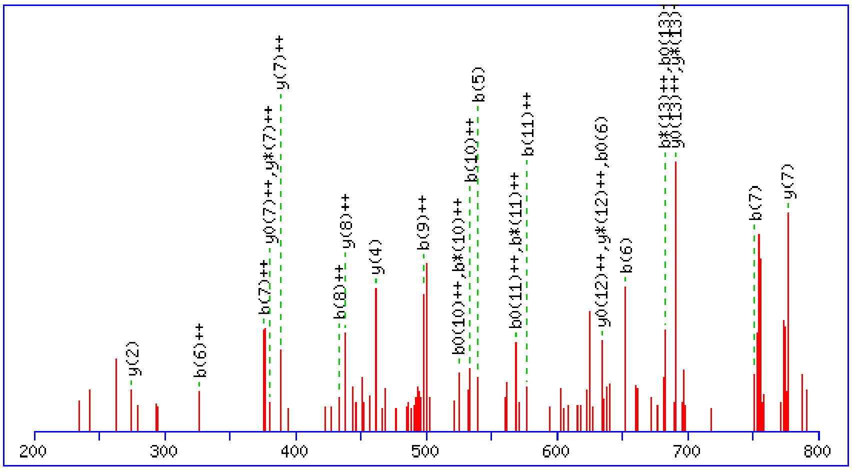
Peptide View

MS/MS Fragmentation of **KLPSILVDEASVQK**
Found in **AT1G16470.1** in **TAIR_Arabidopsis**, Symbols: PAB1 | PAB1 (PROTEASOME SUBUNIT PAB1); peptidase | chr1:5623116-5625433 FORWARD

Match to Query 6733: 1525.870566 from(509.630798,3+) index(5426)
Title: Elution from: 48.801 to 48.801 scan no 6804 cid35.00 polarity:+
Data file D12h-3_1.mgf

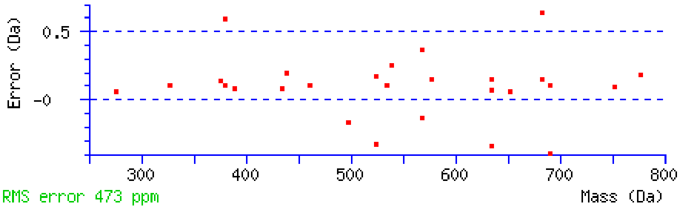
Click mouse within plot area to zoom in by factor of two about that point

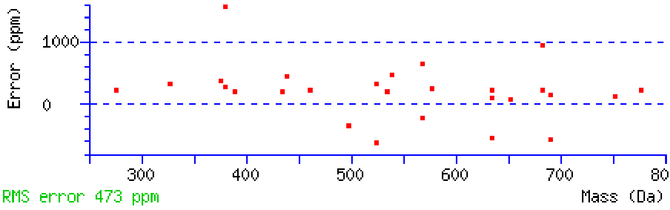
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1525.8715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.00082
Matches : 28/144 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	242.1863	121.5968	225.1598	113.0835			L	1398.7839	699.8956	1381.7573	691.3823	1380.7733	690.8903	13
3	339.2391	170.1232	322.2125	161.6099			P	1285.6998	643.3535	1268.6733	634.8403	1267.6892	634.3483	12
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	S	1188.6470	594.8272	1171.6205	586.3139	1170.6365	585.8219	11
5	**539.3552**	270.1812	522.3286	261.6679	521.3446	261.1759	I	1101.6150	551.3111	1084.5885	542.7979	1083.6045	542.3059	10
6	**652.4392**	***326.7232***	635.4127	318.2100	634.4287	317.7180	L	988.5310	494.7691	971.5044	486.2558	970.5204	485.7638	9
7	**751.5076**	***376.2575***	734.4811	367.7442	733.4971	367.2522	V	875.4469	438.2271	858.4203	429.7138	857.4363	429.2218	8
8	866.5346	***433.7709***	849.5080	425.2577	848.5240	424.7656	D	**776.3785**	388.6929	759.3519	380.1796	758.3679	379.6876	7
9	995.5772	***498.2922***	978.5506	489.7790	977.5666	489.2869	E	661.3515	331.1794	644.3250	322.6661	643.3410	322.1741	6
10	1066.6143	***533.8108***	1049.5877	525.2975	1048.6037	524.8055	A	532.3089	266.6581	515.2824	258.1448	514.2984	257.6528	5
11	1153.6463	***577.3268***	1136.6198	568.8135	1135.6358	568.3215	S	**461.2718**	231.1396	444.2453	222.6263	443.2613	222.1343	4
12	1252.7147	626.8610	1235.6882	618.3477	1234.7042	617.8557	V	374.2398	187.6235	357.2132	179.1103			3
13	1380.7733	***690.8903***	1363.7468	682.3770	1362.7627	681.8850	Q	**275.1714**	138.0893	258.1448	129.5761			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KLPSILVDEASVQK

AT1G16470.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.1	1525.8715	-0.0010	KLPSILVDEASVQK
17.4	1525.8690	0.0015	FLTVIAMAPPKPGGK
5.0	1525.8690	0.0015	SLQSLLMFHILPK
1.4	1525.8729	-0.0023	AAPNGVSRWKSILK
0.3	1525.8689	0.0017	VERRNPLVLSSTR

AT1G16800.1

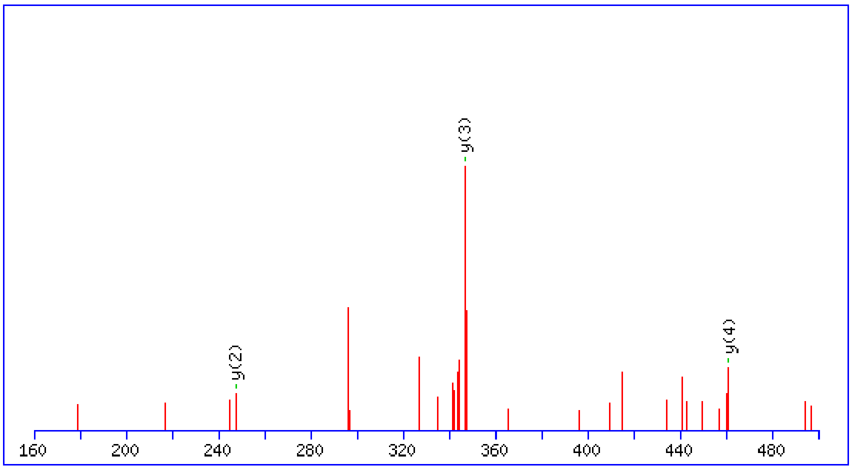
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGPIVPK**
Found in **AT1G16800.1** in **TAIR_Arabidopsis**, Symbols: | tRNA-splicing endonuclease positive effector-related | chr1:5745516-5755256 REVERSE

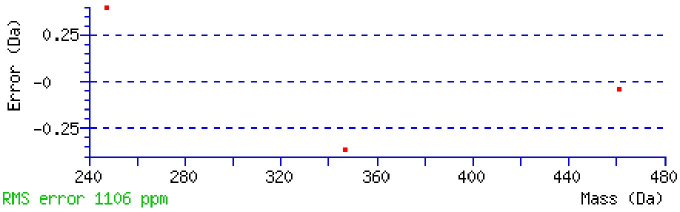
Match to Query 649: 704.392196 from(353.203374,2+) index(1575)
Title: Elution from: 19.440 to 19.440 scan no 2048 cid35.00 polarity:+
Data file C7-2_3.mgf

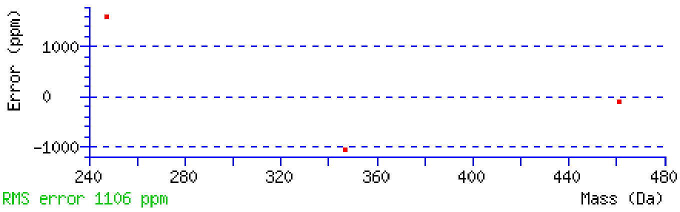
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 704.3933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.0083
Matches : 3/48 fragment ions using 4 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	89.0363	45.0218	71.0258	36.0165	S					7
2	147.0548	74.0311	129.0443	65.0258	G	617.3715	309.1894	599.3479	300.1776	6
3	245.1046	123.0560	227.0941	114.0507	P	559.3530	280.1801	541.3294	271.1684	5
4	359.1857	180.0965	341.1752	171.0912	I	***461.3032***	231.1552	443.2796	222.1435	4
5	459.2512	230.1292	441.2406	221.1239	V	***347.2221***	174.1147	329.1985	165.1029	3
6	557.3010	279.1541	539.2904	270.1488	P	***247.1567***	124.0820	229.1331	115.0702	2
7					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of SGPIVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.8	704.3933	-0.0011	SGPIVPK

Mascot: http://www.matrixscience.com/

AT1G16850.1

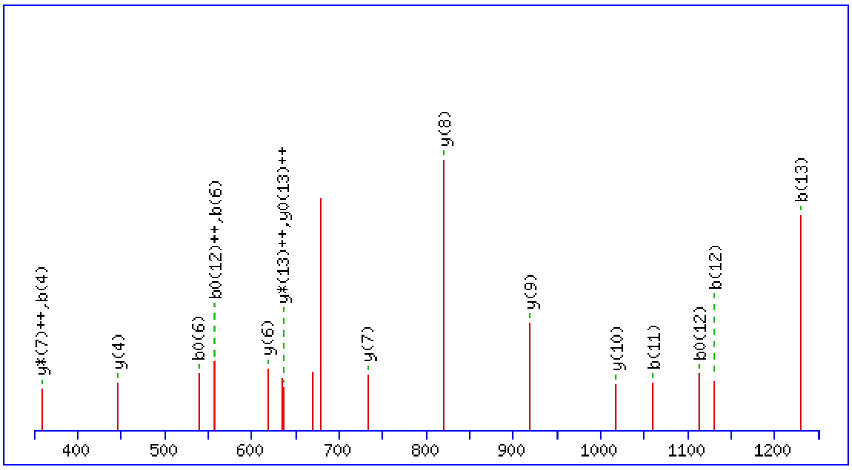
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAAEVVSDTAEAVK**
Found in **AT1G16850.1** in **TAIR_Arabidopsis**, Symbols: | unknown protein | chr1:5765055-5765611 REVERSE

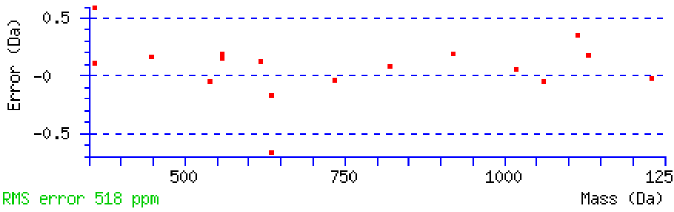
Match to Query 5401: 1375.682442 from(688.848497,2+) index(4119)
Title: Elution from: 37.323 to 37.323 scan no 5100 cid35.00 polarity:+
Data file D1d-3_2.mgf

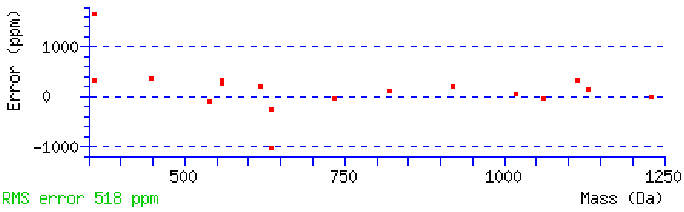
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1375.6831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 3.9e-007
Matches : 17/124 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							14
2	159.0764	80.0418	141.0659	71.0366	A	1289.6583	645.3328	1272.6318	636.8195	1271.6478	636.3275	13
3	230.1135	115.5604	212.1030	106.5551	A	1218.6212	609.8143	1201.5947	601.3010	1200.6107	600.8090	12
4	***359.1561***	180.0817	341.1456	171.0764	E	1147.5841	574.2957	1130.5576	565.7824	1129.5735	565.2904	11
5	458.2245	229.6159	440.2140	220.6106	V	***1018.5415***	509.7744	1001.5150	501.2611	1000.5310	500.7691	10
6	***557.2930***	279.1501	539.2824	270.1448	V	***919.4731***	460.2402	902.4466	451.7269	901.4625	451.2349	9
7	644.3250	322.6661	626.3144	313.6608	S	***820.4047***	410.7060	803.3781	402.1927	802.3941	401.7007	8
8	759.3519	380.1796	741.3414	371.1743	D	***733.3727***	367.1900	716.3461	358.6767	715.3621	358.1847	7
9	860.3996	430.7034	842.3890	421.6982	T	***618.3457***	309.6765	601.3192	301.1632	600.3352	300.6712	6
10	931.4367	466.2220	913.4262	457.2167	A	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	5
11	***1060.4793***	530.7433	1042.4687	521.7380	E	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
12	***1131.5164***	566.2618	1113.5059	557.2566	A	317.2183	159.1128	300.1918	150.5995			3
13	***1230.5848***	615.7961	1212.5743	606.7908	V	246.1812	123.5942	229.1547	115.0810			2
14					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SAAEVVSDTAEAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G16850.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.8	1375.6831	-0.0006	SAAEVVSDTAEAVK
11.8	1375.6844	-0.0020	IDGRDSFINPSR
5.9	1375.6844	-0.0020	DPQESNRKFQK
2.0	1375.6806	0.0019	MDDENLWKVVK
1.7	1375.6819	0.0005	DAMWHKAGHPVK
1.4	1375.6840	-0.0015	EMVGTCLVKDPK
1.0	1375.6831	-0.0006	KGSSSEILSPDEK
1.0	1375.6806	0.0019	EMQQKPLFDPK

AT1G16880.1

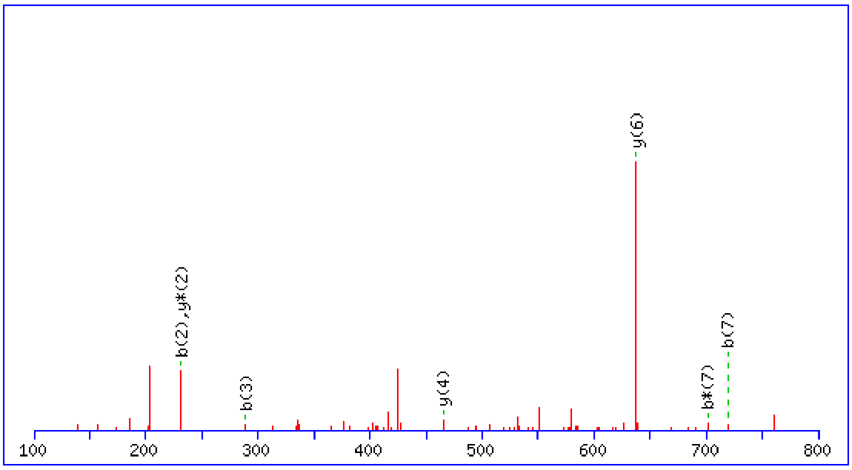
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLGLNVVK**
Found in **AT1G16880.1** in **TAIR_Arabidopsis**, Symbols: | uridylyltransferase-related | chr1:5773789-5776118 FORWARD

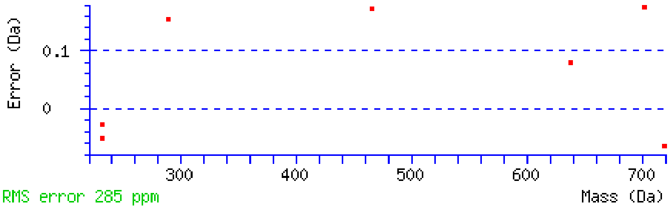
Match to Query 1386: 866.483012 from(434.248782,2+) index(3318)
Title: Elution from: 33.576 to 33.576 scan no 4174 cid35.00 polarity:+
Data file 0-3_1.mgf

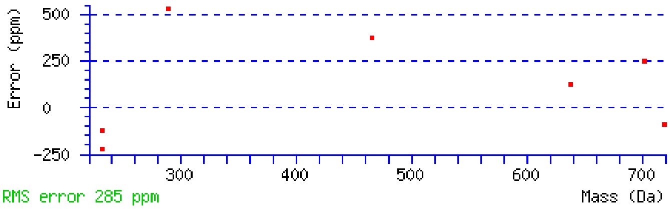
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 866.4852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.048
Matches : 7/56 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	117.0443	59.0258	99.0207	50.0140	N					8
2	***231.1254***	116.0663	213.1018	107.0545	L	751.4555	376.2314	733.4319	367.2196	7
3	***289.1439***	145.0756	271.1203	136.0638	G	***637.3744***	319.1908	619.3508	310.1790	6
4	403.2250	202.1161	385.2014	193.1043	L	579.3559	290.1816	561.3323	281.1698	5
5	519.2620	260.1346	501.2384	251.1228	N	***465.2748***	233.1410	447.2512	224.1292	4
6	619.3274	310.1673	601.3038	301.1556	V	349.2378	175.1225	331.2142	166.1107	3
7	***719.3929***	360.2001	701.3693	351.1883	V	249.1723	125.0898	231.1487	116.0780	2
8					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of NLGLNVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.1	866.4852	-0.0022	NLGLNVVK
12.4	866.4852	-0.0022	NLVKAPSK

6.6	866.4852	-0.0022	NLKPEKK
5.9	866.4852	-0.0022	GNLLLQAK
2.9	866.4852	-0.0022	INPEKKK
2.5	866.4852	-0.0022	AGVAALGLGK
1.3	866.4805	0.0026	LAKKMHK

AT1G16920.1

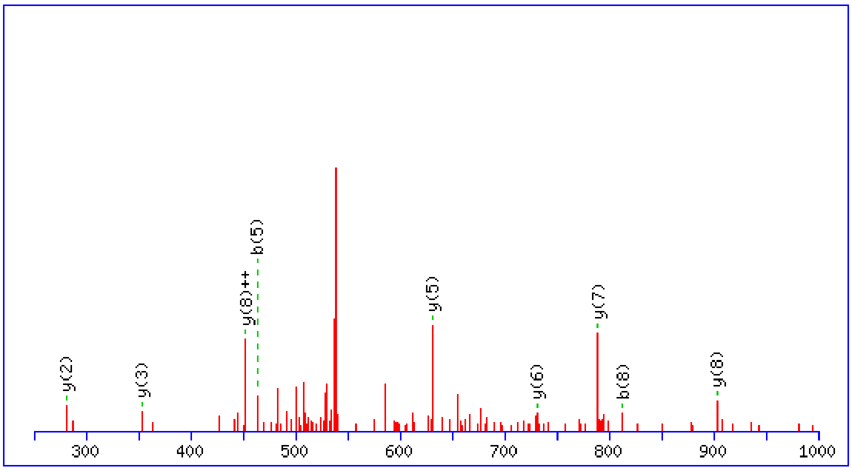
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STIGVEFATR**
Found in **AT1G16920.1** in **TAIR_Arabidopsis**, Symbols: ATRABA4B, ATRABA1B, RAB11 | RAB11 (ARABIDOPSIS RAB GTPASE HOMOLOG A1B); GTP binding | chr1:5787482-5789140 REVERSE

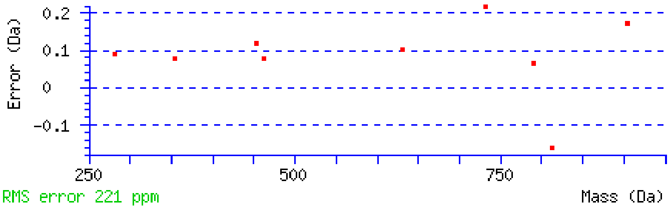
Match to Query 2753: 1092.523498 from(547.269025,2+) index(3594)
Title: Elution from: 36.525 to 36.525 scan no 4611 cid35.00 polarity:+
Data file D1d-1_3.mgf

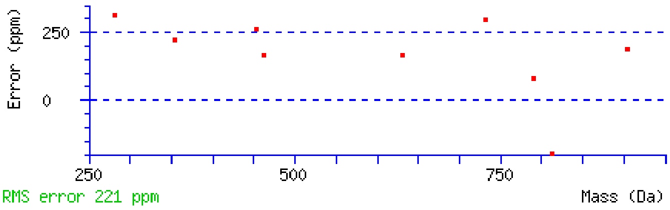
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1092.5226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00032
Matches : 9/88 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							10
2	191.0811	96.0442	173.0705	87.0389	T	1005.5008	503.2540	987.4772	494.2422	987.4902	494.2488	9
3	305.1622	153.0847	287.1516	144.0794	I	***903.4561***	452.2317	885.4325	443.2199	885.4455	443.2264	8
4	363.1807	182.0940	345.1701	173.0887	G	***789.3750***	395.1911	771.3514	386.1793	771.3644	386.1858	7
5	**463.2461**	232.1267	445.2355	223.1214	V	***731.3565***	366.1819	713.3329	357.1701	713.3459	357.1766	6
6	593.2857	297.1465	575.2752	288.1412	E	***631.2910***	316.1492	613.2674	307.1374	613.2805	307.1439	5
7	741.3512	371.1792	723.3406	362.1739	F	501.2514	251.1293	483.2278	242.1175	483.2408	242.1241	4
8	**813.3853**	407.1963	795.3748	398.1910	A	***353.1860***	177.0966	335.1624	168.0848	335.1754	168.0913	3
9	915.4300	458.2187	897.4195	449.2134	T	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	2
10					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of STIGVEFATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G16920.1

Score	Mr(calc)	Delta	Sequence
45.6	1092.5226	0.0009	STIGVEFATR
0.7	1092.5226	0.0009	TKQVNEFSK

AT1G17050.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKAELALK**
Found in **AT1G17050.1** in **TAIR_Arabidopsis**, Symbols: SPS2 | SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2); dimethylallyltranstransferase/ trans-octaprenyltranstransferase | chr1:5829282-5831208 FORWARD

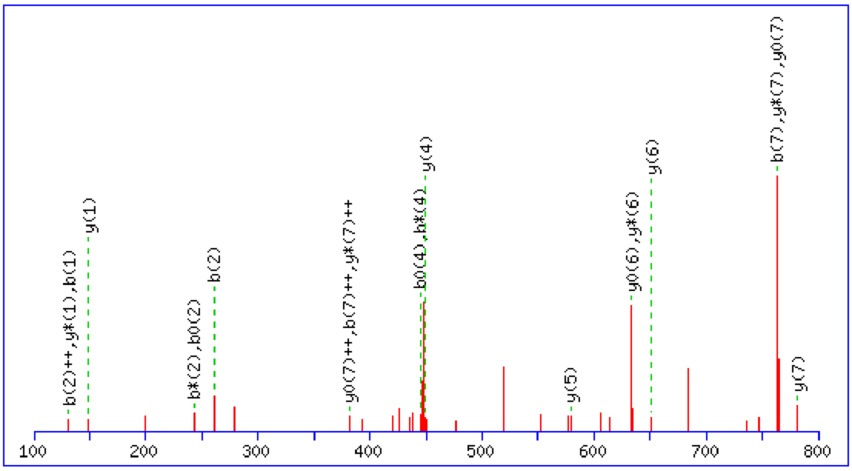
Match to Query 1800: 910.497112 from(456.255832,2+) index(1521)
Title: Elution from: 20.758 to 20.758 scan no 2065 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

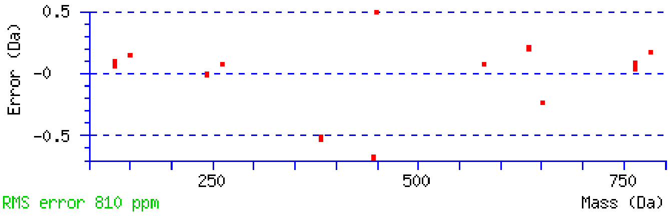
Label all possible matches ○ Label matches used for scoring ●

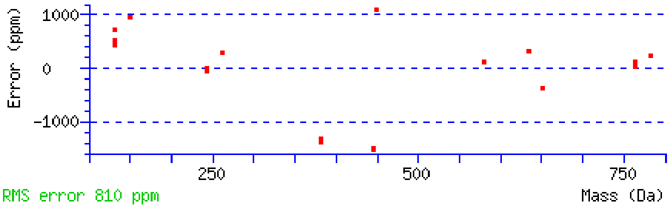
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 910.4984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.016
Matches : 21/74 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	**131.0469**	66.0271			113.0363	57.0218	E							8
2	**261.1359**	131.0716	243.1124	122.0598	243.1254	122.0663	K	***781.4660***	391.2367	763.4424	382.2249	763.4555	382.2314	7
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	A	***651.3770***	326.1921	633.3534	317.1803	633.3664	317.1869	6
4	463.2097	232.1085	445.1861	223.0967	445.1991	223.1032	E	***579.3428***	290.1751	561.3193	281.1633	561.3323	281.1698	5
5	577.2908	289.1490	559.2672	280.1373	559.2802	280.1438	L	***449.3032***	225.1552	431.2796	216.1435			4
6	649.3250	325.1661	631.3014	316.1543	631.3144	316.1608	A	335.2221	168.1147	317.1985	159.1029			3
7	**763.4061**	382.2067	745.3825	373.1949	745.3955	373.2014	L	263.1880	132.0976	245.1644	123.0858			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EKAELALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.5	910.4984	-0.0013	EKAELALK

AT1G17050.1

23.2	910.4984	-0.0013	KVGEVIEK
20.3	910.4984	-0.0013	AGLLSLAEK
18.9	910.4984	-0.0013	EDIVGKIK
18.9	910.4984	-0.0013	AKEAILEK
16.8	910.4984	-0.0013	KEAAEIIK
16.6	910.4984	-0.0013	EKEALALK
14.1	910.4984	-0.0013	VLDEGLKK
13.8	910.4984	-0.0013	EKLVDAVK
12.9	910.4984	-0.0013	LDGIDLKK

AT1G17100.1

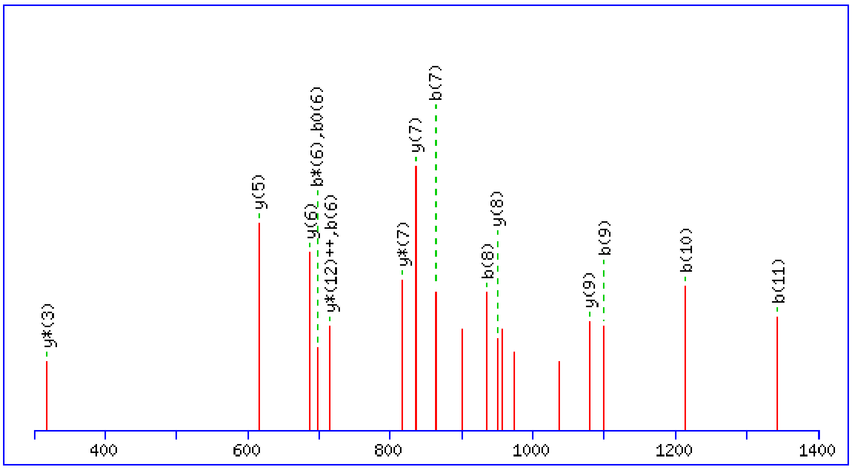
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFFQLFAYIQGK**
Found in **AT1G17100.1** in **TAIR_Arabidopsis**, Symbols: | SOUL heme-binding family protein | chr1:5844759-5845532 FORWARD

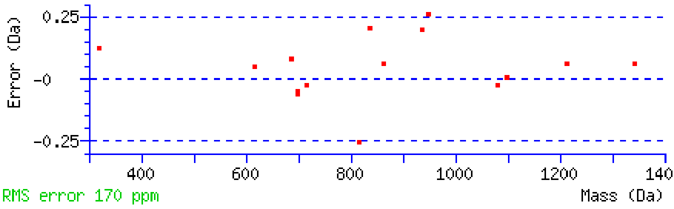
Match to Query 6719: 1548.758798 from(775.386675,2+) index(10983)
Title: Elution from: 111.081 to 111.081 scan no 16078 cid35.00 polarity:+
Data file D12h-2_1.mgf

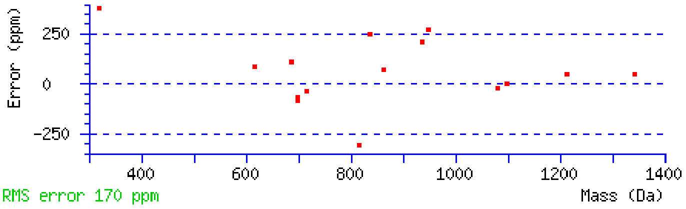
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1548.7553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 2.4e-005
Matches : 16/112 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	103.0520	52.0296			85.0414	43.0244	T					13
2	175.0861	88.0467			157.0756	79.0414	A	1447.7179	724.3626	1429.6943	715.3508	12
3	323.1516	162.0794			305.1410	153.0741	F	1375.6837	688.3455	1357.6601	679.3337	11
4	471.2170	236.1122			453.2065	227.1069	F	1227.6183	614.3128	1209.5947	605.3010	10
5	601.2697	301.1385	583.2461	292.1267	583.2591	292.1332	Q	***1079.5528***	540.2801	1061.5292	531.2683	9
6	***715.3508***	358.1790	697.3272	349.1672	697.3402	349.1737	L	***949.5002***	475.2537	931.4766	466.2419	8
7	***863.4162***	432.2118	845.3926	423.2000	845.4057	423.2065	F	***835.4191***	418.2132	817.3955	409.2014	7
8	***935.4504***	468.2288	917.4268	459.2170	917.4398	459.2235	A	***687.3536***	344.1805	669.3300	335.1687	6
9	***1099.5107***	550.2590	1081.4872	541.2472	1081.5002	541.2537	Y	***615.3195***	308.1634	597.2959	299.1516	5
10	***1213.5918***	607.2996	1195.5683	598.2878	1195.5813	598.2943	I	451.2591	226.1332	433.2355	217.1214	4
11	***1343.6445***	672.3259	1325.6209	663.3141	1325.6339	663.3206	Q	337.1780	169.0926	319.1544	160.0809	3
12	1401.6630	701.3351	1383.6394	692.3233	1383.6524	692.3299	G	207.1254	104.0663	189.1018	95.0545	2
13							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of TAFFQLFAYIQGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G17100.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.5	1548.7553	0.0035	TAFFQLFAYIQGK
2.3	1548.7542	0.0046	MTTPITGKNSPVTGK

Mascot: http://www.matrixscience.com/

AT1G17140.1

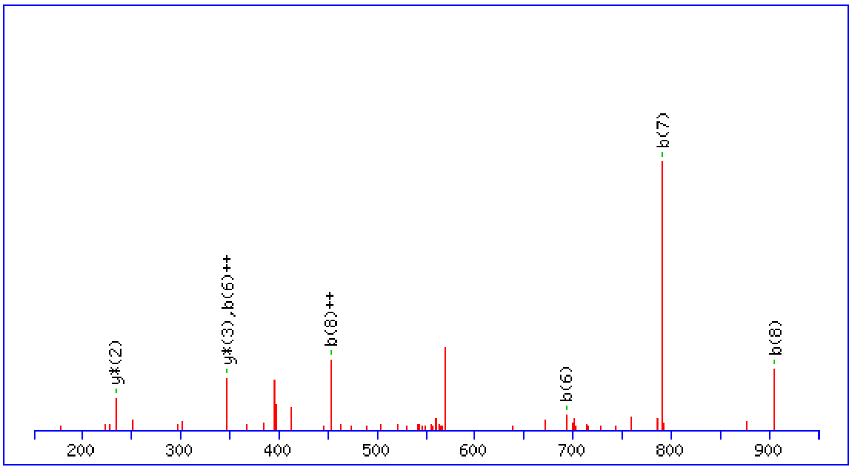
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSKKPNPLAR**
Found in **AT1G17140.1** in **TAIR_Arabidopsis**, Symbols: | tropomyosin-related | chr1:5856733-5857854 REVERSE

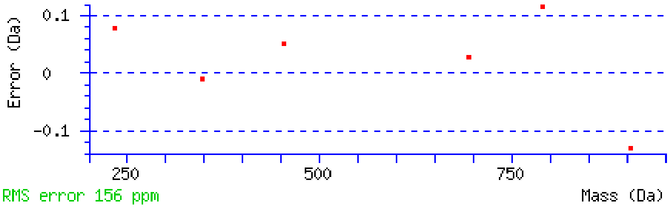
Match to Query 3301: 1154.646796 from(578.330674,2+) index(7027)
Title: Elution from: 64.572 to 64.572 scan no 9310 cid35.00 polarity:+
Data file D1d-1_3.mgf

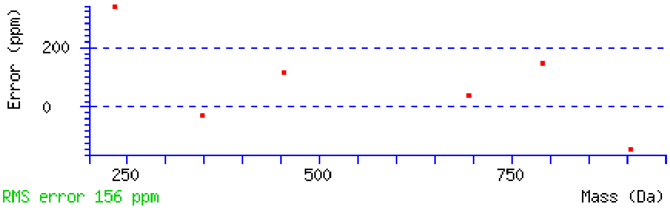
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.6478
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.048
Matches : 7/90 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							10
2	219.1254	110.0663	201.1018	101.0545	201.1148	101.0610	S	1025.5661	513.2867	1007.5425	504.2749	1007.5555	504.2814	9
3	349.2144	175.1108	331.1908	166.0990	331.2038	166.1056	K	937.5370	469.2721	919.5134	460.2603			8
4	479.3034	240.1554	461.2799	231.1436	461.2929	231.1501	K	807.4480	404.2276	789.4244	395.2158			7
5	577.3532	289.1803	559.3297	280.1685	559.3427	280.1750	P	677.3589	339.1831	659.3354	330.1713			6
6	***693.3902***	**347.1988**	675.3667	338.1870	675.3797	338.1935	N	579.3091	290.1582	561.2856	281.1464			5
7	***791.4400***	396.2237	773.4164	387.2119	773.4295	387.2184	P	463.2721	232.1397	445.2486	223.1279			4
8	***905.5211***	**453.2642**	887.4975	444.2524	887.5106	444.2589	L	365.2223	183.1148	347.1988	174.1030			3
9	977.5553	489.2813	959.5317	480.2695	959.5447	480.2760	A	251.1412	126.0743	233.1177	117.0625			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KSKKPNPLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G17140.1

19.8	1154.6478	-0.0010	KSKKPNPLAR
3.5	1154.6451	0.0017	KLADLLELAR
3.5	1154.6452	0.0016	NLLNVNLITK
0.6	1154.6452	0.0016	KPLITLNNTK

AT1G17180.1

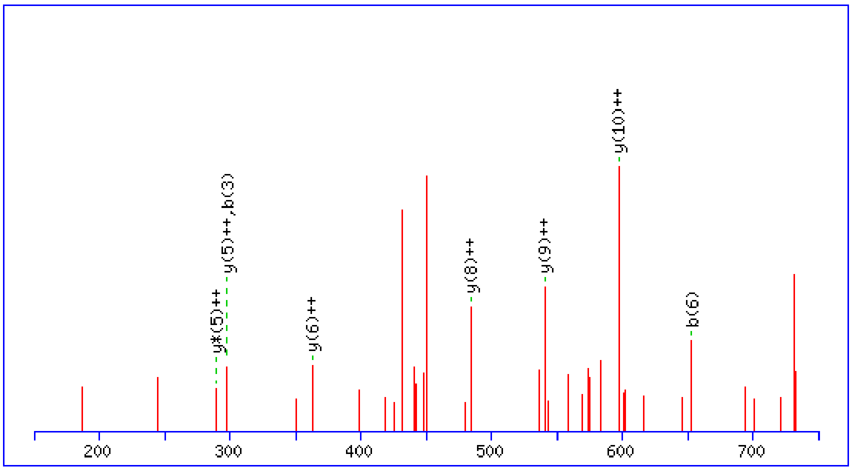
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPILLEMNPVHK**
Found in **AT1G17180.1** in **TAIR_Arabidopsis**, Symbols: ATGSTU25 | ATGSTU25 (Arabidopsis thaliana Glutathione S-transferase (class tau) 25); glutathione transferase | chr1:5872201-5872951 FORWARD

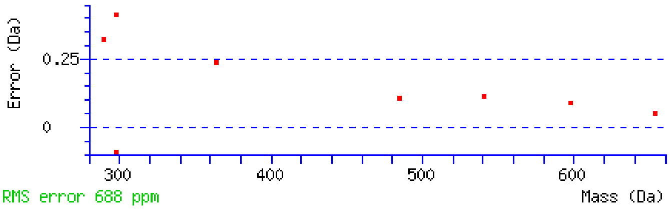
Match to Query 5087: 1376.748060 from(459.923296,3+) index(5511)
Title: Elution from: 48.966 to 48.966 scan no 6986 cid35.00 polarity:+
Data file D12h-1_3.mgf

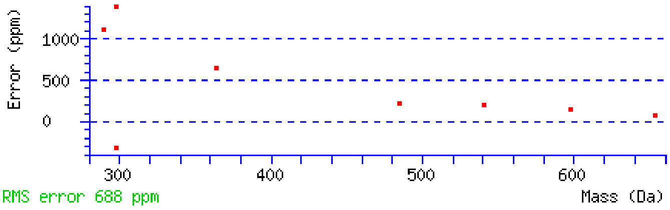
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1376.7486
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.049
Matches : 8/106 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	185.0921	93.0497			167.0815	84.0444	P	1290.7239	645.8656	1273.6973	637.3523	1272.7133	636.8603	11
3	**298.1761**	149.5917			280.1656	140.5864	I	1193.6711	597.3392	1176.6445	588.8259	1175.6605	588.3339	10
4	411.2602	206.1337			393.2496	197.1285	L	1080.5870	540.7972	1063.5605	532.2839	1062.5765	531.7919	9
5	524.3443	262.6758			506.3337	253.6705	L	967.5030	484.2551	950.4764	475.7418	949.4924	475.2498	8
6	**653.3869**	327.1971			635.3763	318.1918	E	854.4189	427.7131	837.3923	419.1998	836.4083	418.7078	7
7	784.4273	392.7173			766.4168	383.7120	M	725.3763	363.1918	708.3498	354.6785			6
8	898.4703	449.7388	881.4437	441.2255	880.4597	440.7335	N	594.3358	297.6715	577.3093	289.1583			5
9	995.5230	498.2652	978.4965	489.7519	977.5125	489.2599	P	480.2929	240.6501	463.2663	232.1368			4
10	1094.5914	547.7994	1077.5649	539.2861	1076.5809	538.7941	V	383.2401	192.1237	366.2136	183.6104			3
11	1231.6504	616.3288	1214.6238	607.8155	1213.6398	607.3235	H	284.1717	142.5895	267.1452	134.0762			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SPILLEMNPVHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G17180.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.8	1376.7486	-0.0005	SPILLEMNPVHK
1.6	1376.7520	-0.0039	KLMGVTMLDVVR
0.0	1376.7459	0.0022	AEPQKPKHMRR

AT1G17220.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTLLDYIR**
Found in **AT1G17220.1** in **TAIR_Arabidopsis**, Symbols: FUG1 | FUG1 (FU-GAERI1); translation initiation factor | chr1:5885376-5890158 FORWARD

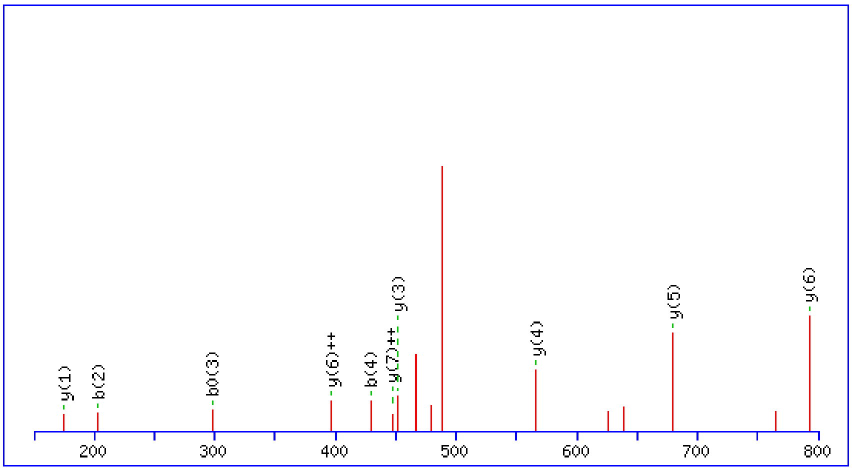
Match to Query 2360: 993.547766 from(497.781159,2+) index(8343)
Title: Elution from: 73.499 to 73.499 scan no 11005 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 800 Da Full range

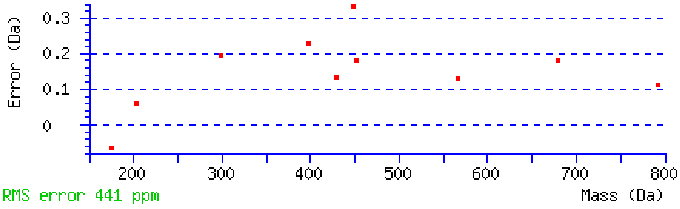
Label all possible matches ○ Label matches used for scoring ●

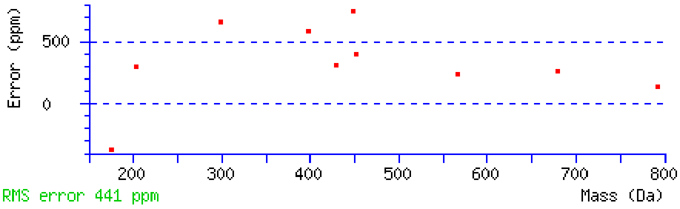
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 993.5495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00034
Matches : 10/64 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							8
2	**203.1026**	102.0550	185.0921	93.0497	T	893.5091	447.2582	876.4825	438.7449	875.4985	438.2529	7
3	316.1867	158.5970	298.1761	149.5917	L	***792.4614***	396.7343	775.4349	388.2211	774.4509	387.7291	6
4	**429.2708**	215.1390	411.2602	206.1337	L	***679.3774***	340.1923	662.3508	331.6790	661.3668	331.1870	5
5	544.2977	272.6525	526.2871	263.6472	D	***566.2933***	283.6503	549.2667	275.1370	548.2827	274.6450	4
6	707.3610	354.1842	689.3505	345.1789	Y	***451.2663***	226.1368	434.2398	217.6235			3
7	820.4451	410.7262	802.4345	401.7209	I	288.2030	144.6051	271.1765	136.0919			2
8					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TTLLDYIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.6	993.5495	-0.0017	TTLLDYIR

AT1G17220.1

7.5	993.5495	-0.0017	TTLSANIFK
0.7	993.5468	0.0010	LVRQHGER
0.3	993.5468	0.0010	ELNGRHIR

AT1G17290.1

Mascot Search Results

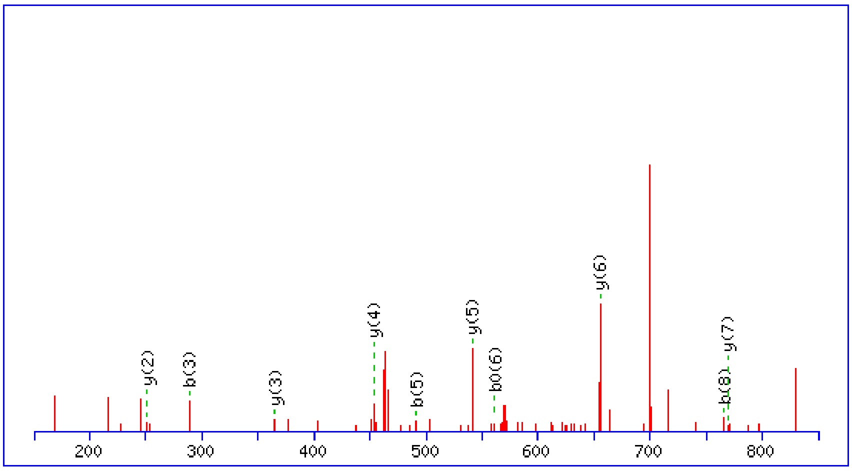
Peptide View

MS/MS Fragmentation of **DGILSSLAR**
Found in **AT1G17290.1** in **TAIR_Arabidopsis**, Symbols: ALAAT1 | ALAAT1 (ALANINE AMINOTRANSFERAS); alanine transaminase | chr1:5922764-5926086 FORWARD

Match to Query 2078: 942.479082 from(472.246817,2+) index(6327)
Title: Elution from: 55.132 to 55.132 scan no 8009 cid35.00 polarity:+
Data file D6h-1_1.mgf

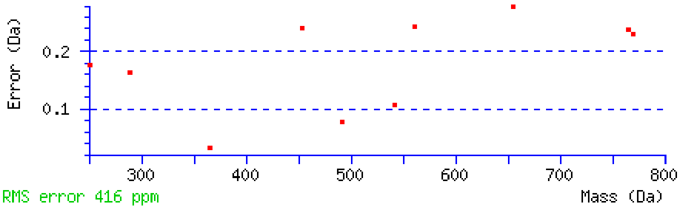
Click mouse within plot area to zoom in by factor of two about that point

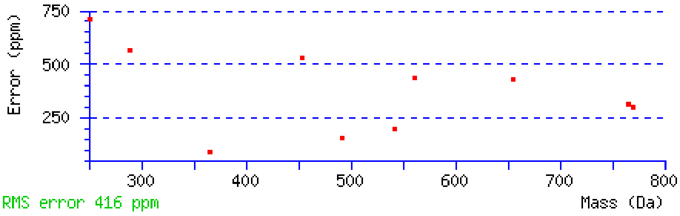
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 942.4779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.016
Matches : 10/74 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							9
2	175.0498	88.0285	157.0392	79.0232	G	827.4612	414.2342	809.4376	405.2224	809.4506	405.2289	8
3	**289.1309**	145.0691	271.1203	136.0638	I	***769.4427***	385.2250	751.4191	376.2132	751.4321	376.2197	7
4	403.2120	202.1096	385.2014	193.1043	L	***655.3616***	328.1844	637.3380	319.1726	637.3510	319.1791	6
5	**491.2410**	246.1241	473.2304	237.1189	S	***541.2805***	271.1439	523.2569	262.1321	523.2699	262.1386	5
6	579.2701	290.1387	561.2595	281.1334	S	***453.2514***	227.1293	435.2278	218.1175	435.2408	218.1241	4
7	693.3512	347.1792	675.3406	338.1739	L	***365.2223***	183.1148	347.1988	174.1030			3
8	**765.3853**	383.1963	747.3748	374.1910	A	***251.1412***	126.0743	233.1177	117.0625			2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DGILSSLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G17290.1

29.9	942.4779	0.0012	DGILSSLAR
15.5	942.4778	0.0012	DAVSLGLTR
11.2	942.4778	0.0012	GLAQSQVTK
7.4	942.4801	-0.0010	SVYSVLHK
6.3	942.4801	-0.0010	LTFDPLAR
5.5	942.4778	0.0012	AVTTSTPVR
5.1	942.4805	-0.0014	QNKLAQAR
0.7	942.4805	-0.0014	IENQRLR
0.7	942.4805	-0.0014	IQNERLR
0.3	942.4778	0.0012	IQKDKDGK

AT1G17370.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGFVSFR**
Found in **AT1G17370.1** in **TAIR_Arabidopsis**, Symbols: UBP1B | UBP1B (OLIGOURIDYLATE BINDING PROTEIN 1B); mRNA 3'-UTR binding | chr1:5951835-5954818 REVERSE

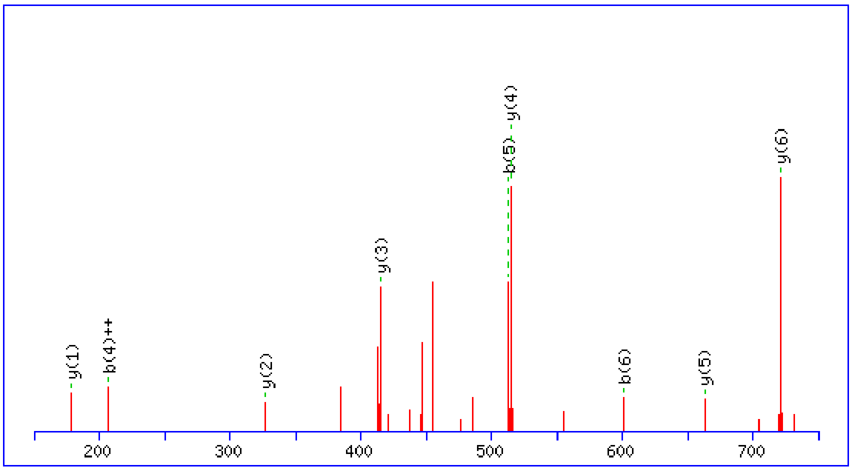
Match to Query 1732: 926.428132 from(464.221342,2+) index(6970)
Title: Elution from: 62.073 to 62.073 scan no 9053 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 750 Da Full range

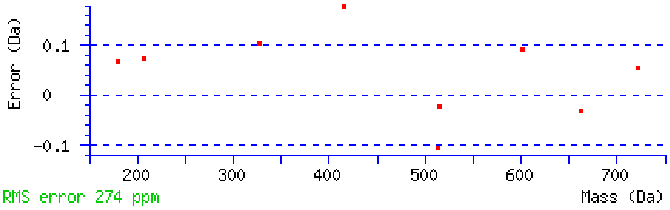
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

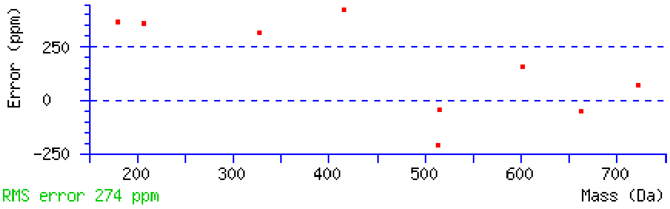


Monoisotopic mass of neutral peptide Mr(calc): 926.4276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 4.1e-006
Matches : 10/56 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165			G							8
2	**207.0912**	104.0492			F	869.4165	435.2119	851.3929	426.2001	851.4059	426.2066	7
3	265.1097	133.0585			G	***721.3510***	361.1791	703.3274	352.1673	703.3404	352.1739	6
4	413.1752	207.0912			F	***663.3325***	332.1699	645.3089	323.1581	645.3219	323.1646	5
5	**513.2406**	257.1239			V	***515.2671***	258.1372	497.2435	249.1254	497.2565	249.1319	4
6	**601.2697**	301.1385	583.2591	292.1332	S	***415.2016***	208.1044	397.1780	199.0926	397.1910	199.0992	3
7	749.3351	375.1712	731.3246	366.1659	F	***327.1725***	164.0899	309.1490	155.0781			2
8					R	***179.1071***	90.0572	161.0835	81.0454			1



RMS error 274 ppm



RMS error 274 ppm

NCBI **BLAST** search of GFGFVSFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.9	926.4276	0.0005	GFGFVSFR

AT1G17370.1

13.5	926.4277	0.0005	GFINYFR
9.6	926.4254	0.0027	QSPPPAYR
3.9	926.4281	0.0000	RYRDFR
0.6	926.4259	0.0023	RIHDSGAR
0.3	926.4259	0.0023	SYRSRSR

AT1G17420.1

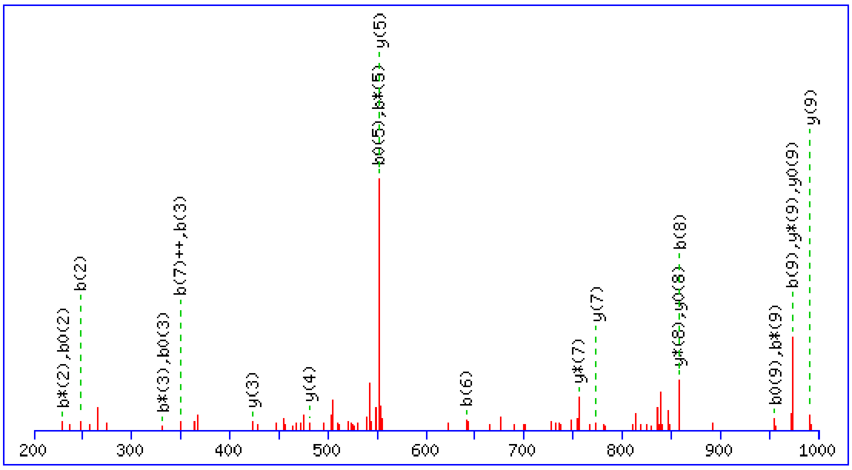
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDTFAAGRLK**
Found in **AT1G17420.1** in **TAIR_Arabidopsis**, Symbols: LOX3 | LOX3 (Lipoxygenase 3); iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | chr1:5977505-5981377 FORWARD

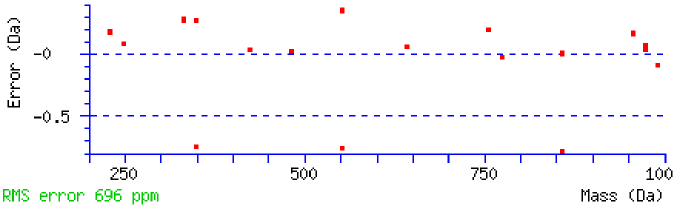
Match to Query 3751: 1120.545448 from(561.280000,2+) index(3353)
Title: Elution from: 33.099 to 33.099 scan no 4161 cid35.00 polarity:+
Data file C7-2_1.mgf

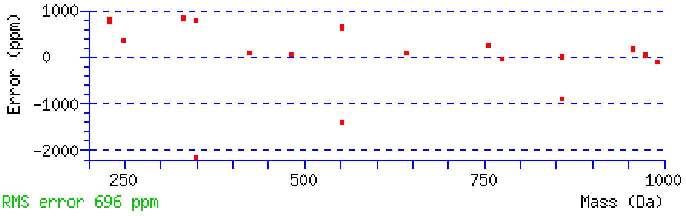
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1120.5435
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.023
Matches : 24/92 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							10
2	***247.0839***	124.0456	229.0603	115.0338	229.0733	115.0403	D	***991.4982***	496.2527	973.4746	487.2409	973.4876	487.2474	9
3	***349.1286***	175.0679	331.1050	166.0562	331.1180	166.0627	T	875.4742	438.2407	857.4506	429.2289	857.4636	429.2354	8
4	497.1941	249.1007	479.1705	240.0889	479.1835	240.0954	F	***773.4295***	387.2184	755.4059	378.2066			7
5	569.2282	285.1177	551.2046	276.1060	551.2176	276.1125	A	625.3640	313.1856	607.3404	304.1739			6
6	***641.2624***	321.1348	623.2388	312.1230	623.2518	312.1295	A	***553.3299***	277.1686	535.3063	268.1568			5
7	699.2809	350.1441	681.2573	341.1323	681.2703	341.1388	G	***481.2957***	241.1515	463.2721	232.1397			4
8	***859.3701***	430.1887	841.3465	421.1769	841.3595	421.1834	R	***423.2772***	212.1423	405.2536	203.1305			3
9	***973.4512***	487.2292	955.4276	478.2175	955.4406	478.2240	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QDTFAAGRLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G17420.1

Score	Mr(calc)	Delta	Sequence
26.2	1120.5435	0.0019	QDTFAAGRLK
19.6	1120.5431	0.0024	FDEFKSLPK
11.7	1120.5435	0.0019	FSGAESRKPK
11.4	1120.5435	0.0019	FIRAAQASDK
10.7	1120.5464	-0.0010	EDTMKFLVK
9.3	1120.5465	-0.0010	MLLISQFDK
8.9	1120.5469	-0.0015	KIKMASGSER
8.6	1120.5469	-0.0015	MSERAKLQK
8.3	1120.5435	0.0019	QFQAIRESK
6.8	1120.5442	0.0012	ELMKTTKDK

Mascot: http://www.matrixscience.com/

AT1G17630.1

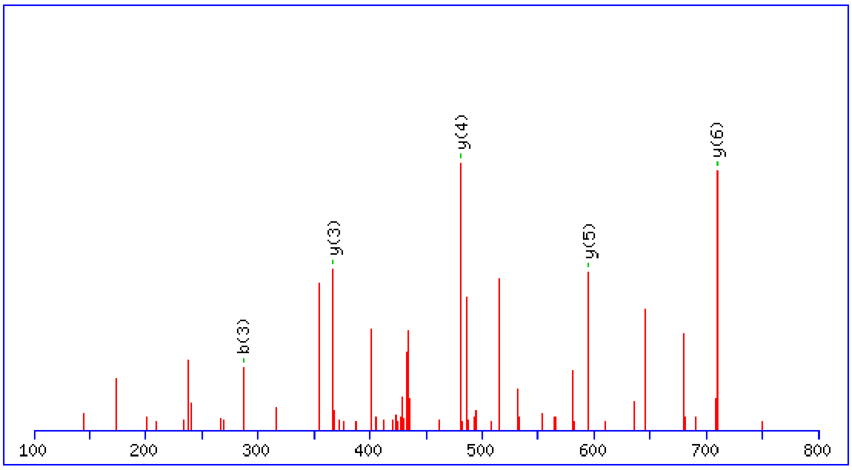
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGLLLDAR**
Found in **AT1G17630.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:6064518-6066713 FORWARD

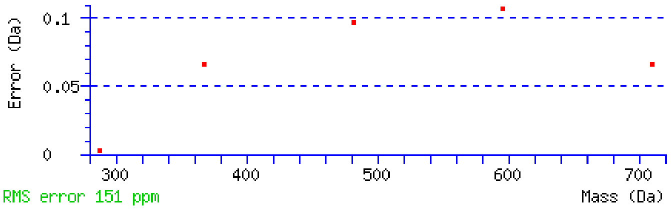
Match to Query 1428: 880.499712 from(441.257132,2+) index(3442)
Title: Elution from: 32.434 to 32.434 scan no 4286 cid35.00 polarity:+
Data file 0-2_3.mgf

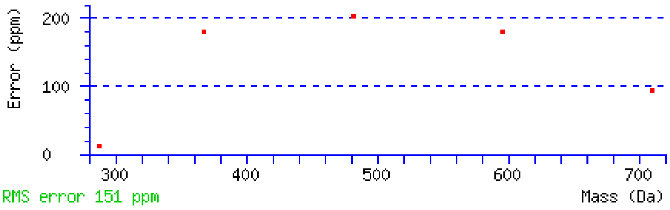
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 880.5008
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.012
Matches : 5/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	173.1069	87.0571			G	767.4270	384.2171	749.4034	375.2054	749.4164	375.2119	7
3	287.1880	144.0976			L	***709.4085***	355.2079	691.3849	346.1961	691.3980	346.2026	6
4	401.2691	201.1382			L	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	5
5	515.3502	258.1787			L	***481.2463***	241.1268	463.2227	232.1150	463.2358	232.1215	4
6	631.3741	316.1907	613.3636	307.1854	D	***367.1652***	184.0862	349.1416	175.0745	349.1547	175.0810	3
7	703.4083	352.2078	685.3977	343.2025	A	251.1412	126.0743	233.1177	117.0625			2
8					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LGLLLDAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.1	880.5008	-0.0011	LGLLLDAR

AT1G17630.1

Mascot: http://www.matrixscience.com/

AT1G17780.2

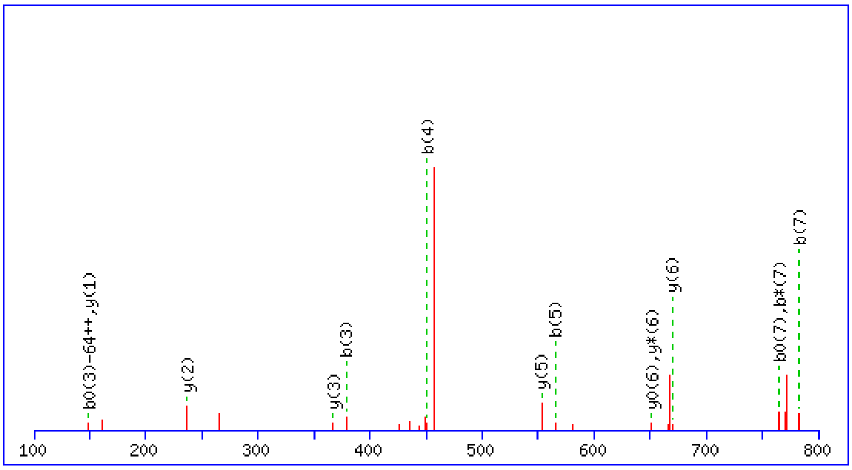
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMDAIKSK**
Found in **AT1G17780.2** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G16575.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN66610.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39378.1) | chr1:6124088-6125159 FORWARD

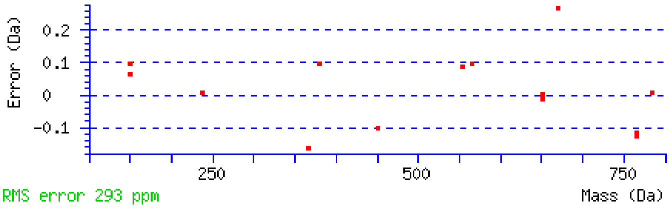
Match to Query 1514: 930.472628 from(466.243590,2+) index(7338)
Title: Elution from: 68.717 to 68.717 scan no 9771 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

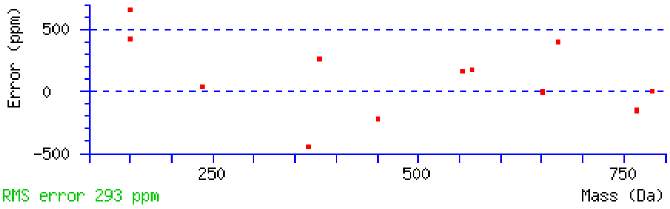


Monoisotopic mass of neutral peptide Mr(calc): 930.4705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0042
Matches : 14/100 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							8
2	263.1208	132.0640					M	817.3966	409.2020	799.3730	400.1902	799.3861	400.1967	7
3	***379.1448***	190.0760			361.1342	181.0707	D	***669.3642***	335.1857	651.3406	326.1739	651.3536	326.1805	6
4	***451.1789***	226.0931			433.1684	217.0878	A	***553.3402***	277.1737	535.3166	268.1620	535.3297	268.1685	5
5	***565.2600***	283.1337			547.2495	274.1284	I	481.3061	241.1567	463.2825	232.1449	463.2955	232.1514	4
6	695.3491	348.1782	677.3255	339.1664	677.3385	339.1729	K	***367.2250***	184.1161	349.2014	175.1043	349.2144	175.1108	3
7	***783.3781***	392.1927	765.3545	383.1809	765.3676	383.1874	S	***237.1359***	119.0716	219.1124	110.0598	219.1254	110.0663	2
8							K	***149.1069***	75.0571	131.0833	66.0453			1



RMS error 293 ppm



RMS error 293 ppm

NCBI **BLAST** search of IMDAIKSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G17780.2

Score	Mr(calc)	Delta	Sequence
34.5	930.4705	0.0022	IMDAIKSK
30.9	930.4705	0.0022	MSEKGLIK
22.9	930.4705	0.0022	MESKIVSK
22.0	930.4705	0.0022	LMGLEKSK
21.5	930.4731	-0.0005	EMRKLNK
19.1	930.4705	0.0022	MLESVKAK
18.7	930.4705	0.0022	MDKASIIK
18.6	930.4704	0.0022	DMKTLVSK
18.3	930.4704	0.0022	MLTGEVKK
17.8	930.4727	-0.0001	MAFLPSLK

Mascot: http://www.matrixscience.com/

AT1G17880.1

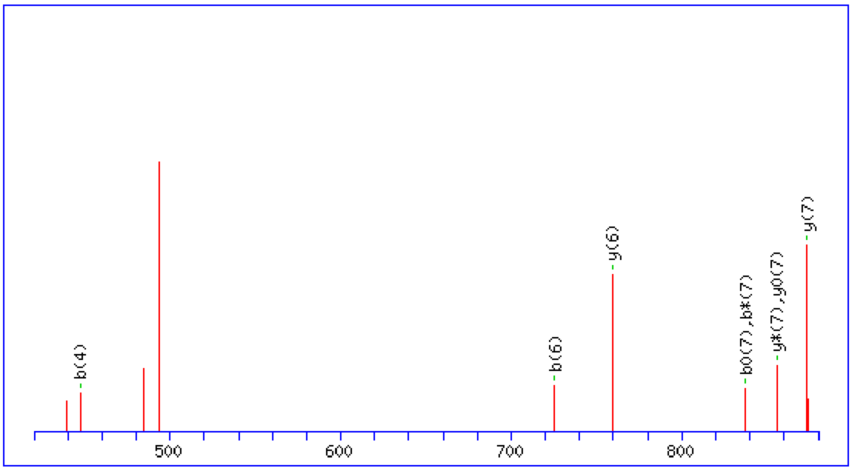
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLAEQFQK**
Found in **AT1G17880.1** in **TAIR_Arabidopsis**, Symbols: | nascent polypeptide-associated complex (NAC) domain-containing protein / BTF3b-like transcription factor, putative | chr1:6152565-6153418 REVERSE

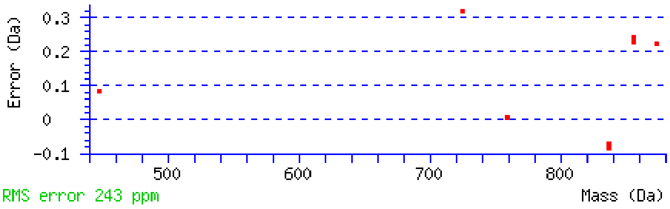
Match to Query 2654: 1002.514156 from(502.264354,2+) index(521)
Title: Elution from: 10.937 to 10.937 scan no 818 cid35.00 polarity:+
Data file C7-2_1.mgf

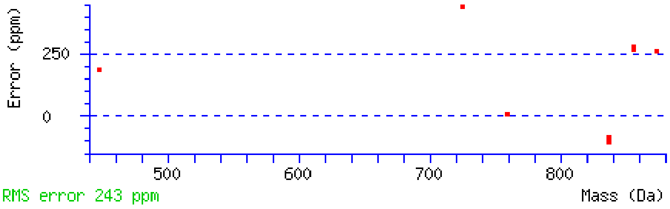
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 420 to 880 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1002.5142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0091
Matches : 9/70 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							8
2	245.1774	123.0923	227.1538	114.0805			L	***873.4325***	437.2199	855.4089	428.2081	855.4219	428.2146	7
3	317.2116	159.1094	299.1880	150.0976			A	***759.3514***	380.1793	741.3278	371.1675	741.3408	371.1741	6
4	***447.2512***	224.1292	429.2276	215.1174	429.2406	215.1239	E	687.3172	344.1623	669.2937	335.1505	669.3067	335.1570	5
5	577.3038	289.1556	559.2802	280.1438	559.2933	280.1503	Q	557.2776	279.1424	539.2540	270.1307			4
6	***725.3693***	363.1883	707.3457	354.1765	707.3587	354.1830	F	427.2250	214.1161	409.2014	205.1043			3
7	***855.4219***	428.2146	837.3983	419.2028	837.4114	419.2093	Q	279.1595	140.0834	261.1359	131.0716			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KLAEQFQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.8	1002.5142	-0.0001	KLAEQFQK

AT1G17880.1

21.6	1002.5142	-0.0001	KAGTFDPKK
20.5	1002.5142	-0.0001	ELQAYLVR
15.1	1002.5142	-0.0001	IAVRFEEK
12.7	1002.5142	-0.0001	EIVKEAFR
12.7	1002.5116	0.0026	EIYVTELK
12.7	1002.5142	-0.0001	ELVLSFAGR
12.7	1002.5120	0.0021	KIVANGSSSK
12.7	1002.5147	-0.0005	KLAQRSER
12.7	1002.5142	-0.0001	KLLFAEDR

Mascot: http://www.matrixscience.com/

AT1G18070.1

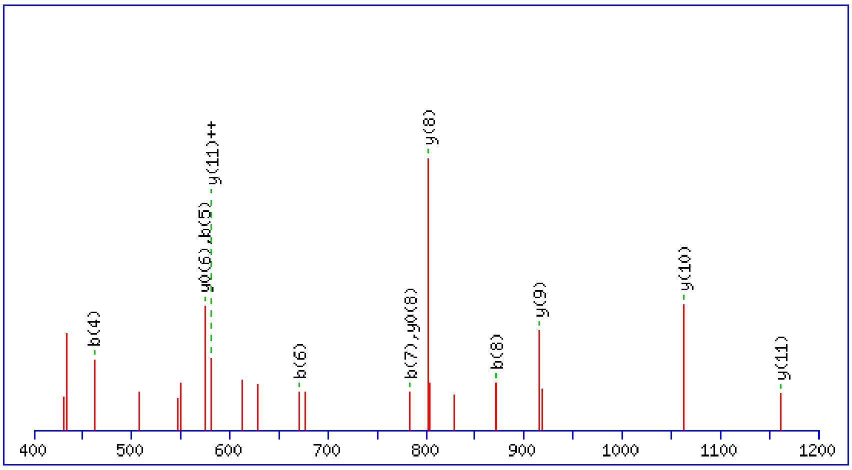
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVVFLPISGLMGK**
Found in **AT1G18070.1** in **TAIR_Arabidopsis**, Symbols: | EF-1-alpha-related GTP-binding protein, putative | chr1:6214229-6218204 REVERSE

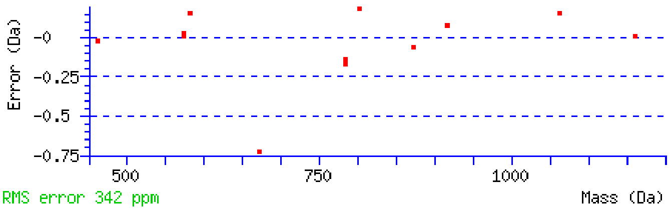
Match to Query 5659: 1374.757452 from(688.386002,2+) index(10927)
Title: Elution from: 103.688 to 103.688 scan no 15422 cid35.00 polarity:+
Data file D12h-1_1.mgf

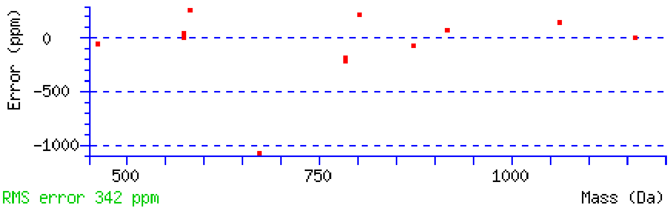
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [400] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1374.7581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.002
Matches : 12/110 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D							13
2	215.1026	108.0550	197.0921	99.0497	V	1260.7384	630.8729	1243.7119	622.3596	1242.7279	621.8676	12
3	314.1710	157.5892	296.1605	148.5839	V	***1161.6700***	581.3387	1144.6435	572.8254	1143.6595	572.3334	11
4	***461.2395***	231.1234	443.2289	222.1181	F	***1062.6016***	531.8044	1045.5751	523.2912	1044.5911	522.7992	10
5	***574.3235***	287.6654	556.3130	278.6601	L	***915.5332***	458.2702	898.5067	449.7570	897.5226	449.2650	9
6	***671.3763***	336.1918	653.3657	327.1865	P	***802.4491***	401.7282	785.4226	393.2149	784.4386	392.7229	8
7	***784.4604***	392.7338	766.4498	383.7285	I	705.3964	353.2018	688.3698	344.6886	687.3858	344.1965	7
8	***871.4924***	436.2498	853.4818	427.2445	S	592.3123	296.6598	575.2858	288.1465	574.3017	287.6545	6
9	928.5138	464.7606	910.5033	455.7553	G	505.2803	253.1438	488.2537	244.6305			5
10	1041.5979	521.3026	1023.5873	512.2973	L	448.2588	224.6330	431.2323	216.1198			4
11	1172.6384	586.8228	1154.6278	577.8176	M	335.1748	168.0910	318.1482	159.5777			3
12	1229.6599	615.3336	1211.6493	606.3283	G	204.1343	102.5708	187.1077	94.0575			2
13					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DVVFLPISGLMGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G18070.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.0	1374.7581	-0.0007	DVVFLPISGLMGK
3.4	1374.7547	0.0027	YLPSLQVIEWK

AT1G18080.1

MATRIX SCIENCE Mascot Search Results

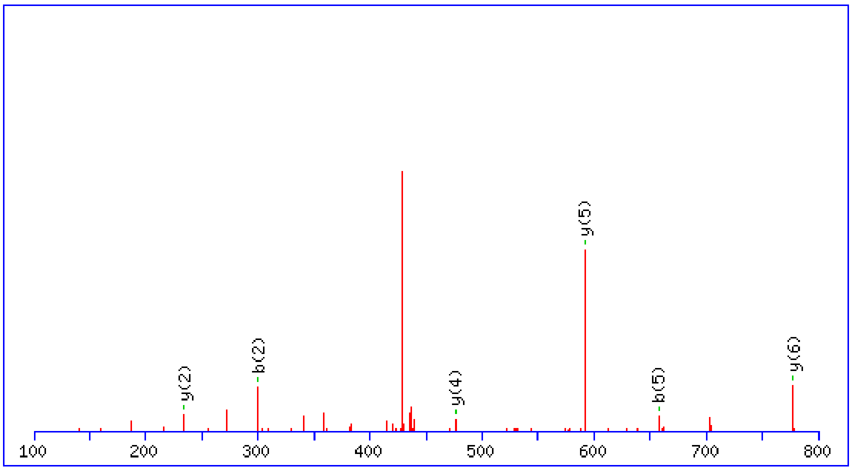
Peptide View

MS/MS Fragmentation of **IWDLESK**
Found in **AT1G18080.1** in **TAIR_Arabidopsis**, Symbols: ATARCA | ATARCA (Arabidopsis thaliana Homolog of the Tobacco ArcA); nucleotide binding | chr1:6222318-6223894 FORWARD

Match to Query 1571: 889.454754 from(445.734653,2+) index(4271)
Title: Elution from: 39.492 to 39.492 scan no 5333 cid35.00 polarity:+
Data file D12h-1_2.mgf

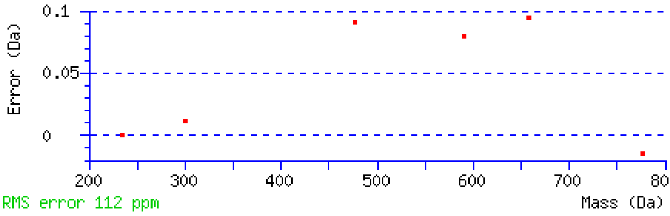
Click mouse within plot area to zoom in by factor of two about that point

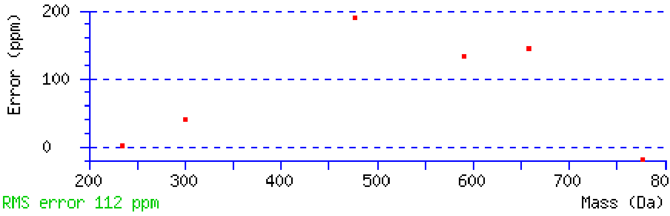
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 889.4545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0013
Matches : 6/54 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			I							7
2	**300.1707**	150.5890			W	*777.3777*	389.1925	760.3512	380.6792	759.3672	380.1872	6
3	415.1976	208.1024	397.1870	199.0972	D	*591.2984*	296.1529	574.2719	287.6396	573.2879	287.1476	5
4	528.2817	264.6445	510.2711	255.6392	L	*476.2715*	238.6394	459.2449	230.1261	458.2609	229.6341	4
5	**657.3243**	329.1658	639.3137	320.1605	E	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
6	744.3563	372.6818	726.3457	363.6765	S	*234.1448*	117.5761	217.1183	109.0628	216.1343	108.5708	2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IWDLESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.7	889.4545	0.0002	IWDLESK
13.9	889.4545	0.0002	LWEVSEK

AT1G18080.1

Mascot: http://www.matrixscience.com/

AT1G18160.1

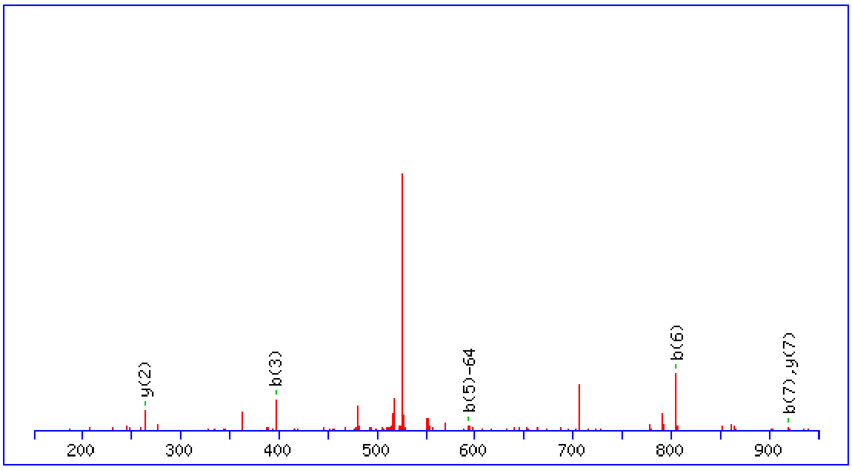
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MNMKKFLK**
Found in **AT1G18160.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:6249119-6253828 FORWARD

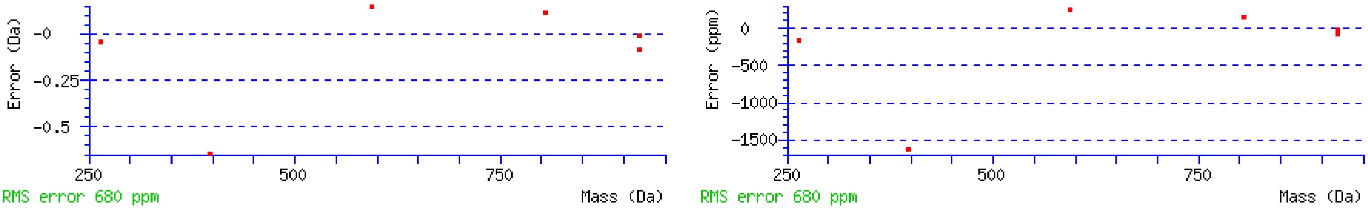
Match to Query 3159: 1066.529342 from(534.271947,2+) index(5904)
Title: Elution from: 51.164 to 51.164 scan no 7511 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1066.5312
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.035
Matches : 6/80 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	149.0397	75.0235			M					8
2	265.0767	133.0420	247.0531	124.0302	N	**919.5060**	460.2566	901.4824	451.2448	7
3	***397.1142***	199.0608	379.0906	190.0490	M	803.4690	402.2381	785.4454	393.2264	6
4	527.2033	264.1053	509.1797	255.0935	K	671.4315	336.2194	653.4079	327.2076	5
5	657.2923	329.1498	639.2687	320.1380	K	541.3425	271.1749	523.3189	262.1631	4
6	***805.3577***	403.1825	787.3342	394.1707	F	411.2534	206.1303	393.2298	197.1186	3
7	***919.4388***	460.2231	901.4153	451.2113	L	**263.1880**	132.0976	245.1644	123.0858	2
8					K	149.1069	75.0571	131.0833	66.0453	1



NCBI **BLAST** search of MNMKKFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
19.7	1066.5312	-0.0018	MNMKKFLK	Oxidation M1 74.03%

AT1G18160.1

15.2	1066.5312	-0.0018	MNMKKFLK	Oxidation M3 25.97%
7.5	1066.5325	-0.0032	VDFGYSKLK	
3.3	1066.5325	-0.0032	GTISSGFLFK	
3.0	1066.5303	-0.0010	ESEIHSLIK	
3.0	1066.5303	-0.0009	LVGANPDEIK	
3.0	1066.5303	-0.0010	NPNEVEILK	
3.0	1066.5325	-0.0032	QSLFGYTLK	
3.0	1066.5303	-0.0009	TDELVHTLK	
2.9	1066.5325	-0.0032	TKKEFFEK	

Mascot: http://www.matrixscience.com/

AT1G18210.1

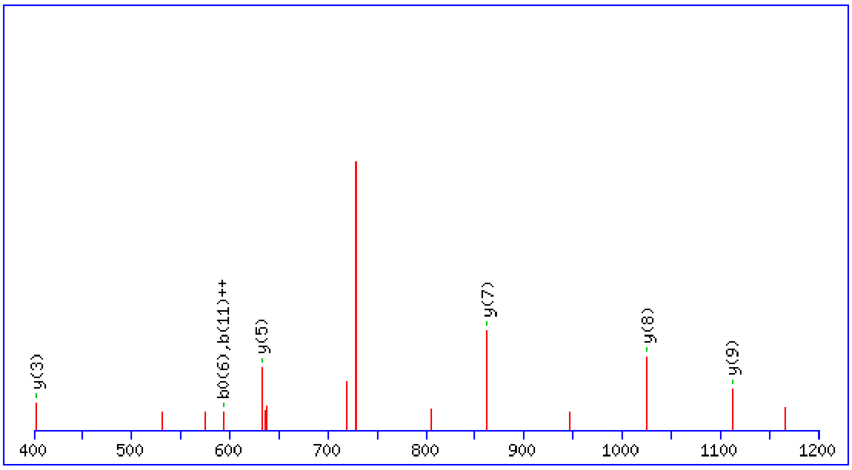
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMGTSYTETELNR**
Found in **AT1G18210.1** in **TAIR_Arabidopsis**, Symbols: | calcium-binding protein, putative | chr1:6268266-6268778 REVERSE

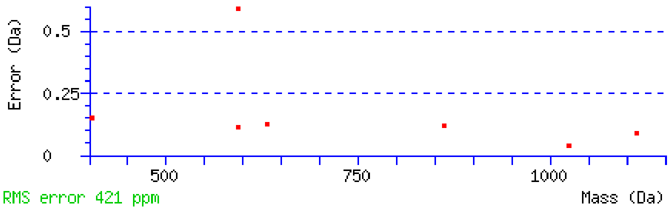
Match to Query 5940: 1471.658536 from(736.836544,2+) index(2936)
Title: Elution from: 29.626 to 29.626 scan no 3658 cid35.00 polarity:+
Data file 0-3_2.mgf

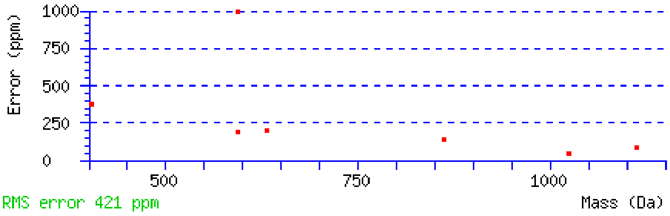
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1471.6613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00023
Matches : 7/110 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							13
2	203.0849	102.0461					M	1401.6315	701.3194	1384.6049	692.8061	1383.6209	692.3141	12
3	260.1063	130.5568					G	1270.5910	635.7991	1253.5644	627.2859	1252.5804	626.7938	11
4	361.1540	181.0806			343.1435	172.0754	T	1213.5695	607.2884	1196.5430	598.7751	1195.5590	598.2831	10
5	448.1860	224.5967			430.1755	215.5914	S	***1112.5218***	556.7646	1095.4953	548.2513	1094.5113	547.7593	9
6	611.2494	306.1283			593.2388	297.1230	Y	***1025.4898***	513.2485	1008.4633	504.7353	1007.4793	504.2433	8
7	712.2971	356.6522			694.2865	347.6469	T	***862.4265***	431.7169	845.3999	423.2036	844.4159	422.7116	7
8	841.3396	421.1735			823.3291	412.1682	E	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	6
9	942.3873	471.6973			924.3768	462.6920	T	***632.3362***	316.6717	615.3097	308.1585	614.3256	307.6665	5
10	1071.4299	536.2186			1053.4194	527.2133	E	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
11	1184.5140	592.7606			1166.5034	583.7553	L	***402.2459***	201.6266	385.2194	193.1133			3
12	1298.5569	649.7821	1281.5304	641.2688	1280.5463	640.7768	N	289.1619	145.0846	272.1353	136.5713			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AMGTSYTETELNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G18210.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.2	1471.6613	-0.0027	AMGTSYTETELNR

Mascot: http://www.matrixscience.com/

AT1G18265.1

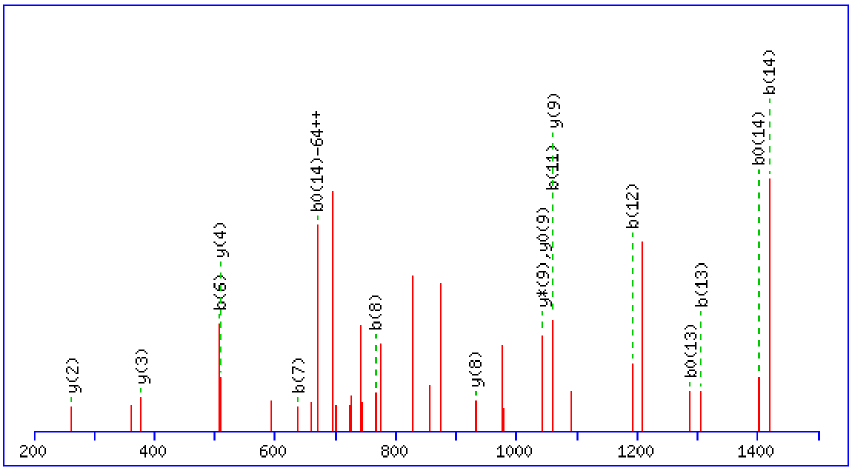
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAESAAEEAMAMLLK**
Found in **AT1G18265.1** in **TAIR_Arabidopsis**, Symbols: | contains InterPro domain Protein of unknown function DUF593 (InterPro:IPR007656) | chr1:6282331-6283173 REVERSE

Match to Query 6883: 1566.687716 from(784.351134,2+) index(8896)
Title: Elution from: 80.415 to 80.415 scan no 12077 cid35.00 polarity:+
Data file 0-2_2.mgf

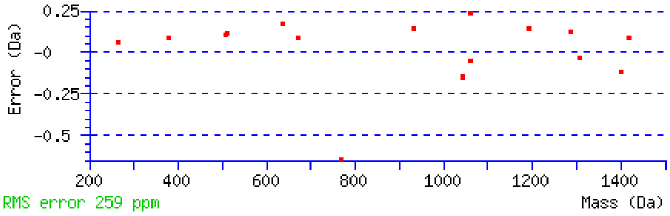
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

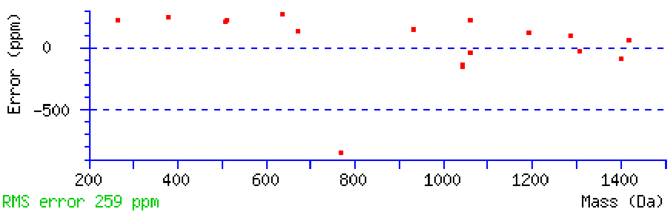


Monoisotopic mass of neutral peptide Mr(calc): 1566.6846
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0023
Matches : 17/192 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244			**A**							**15**
2	145.0756	73.0414			**A**	1495.6577	748.3325	1477.6341	739.3207	1477.6472	739.3272	**14**
3	275.1152	138.0612	257.1046	129.0560	**E**	1423.6236	712.3154	1405.6000	703.3036	1405.6130	703.3101	**13**
4	363.1443	182.0758	345.1337	173.0705	**S**	1293.5839	647.2956	1275.5604	638.2838	1275.5734	638.2903	**12**
5	435.1784	218.0928	417.1678	209.0876	**A**	1205.5549	603.2811	1187.5313	594.2693	1187.5443	594.2758	**11**
6	***507.2126***	254.1099	489.2020	245.1046	**A**	1133.5207	567.2640	1115.4971	558.2522	1115.5102	558.2587	**10**
7	***637.2522***	319.1297	619.2416	310.1245	**E**	**1061.4866**	531.2469	1043.4630	522.2351	1043.4760	522.2416	**9**
8	***767.2918***	384.1495	749.2813	375.1443	**E**	**931.4470**	466.2271	913.4234	457.2153	913.4364	457.2218	**8**
9	839.3260	420.1666	821.3154	411.1613	**A**	801.4073	401.2073	783.3837	392.1955			**7**
10	987.3584	494.1828	969.3478	485.1776	**M**	729.3732	365.1902	711.3496	356.1784			**6**
11	***1059.3926***	530.1999	1041.3820	521.1946	**A**	581.3407	291.1740	563.3172	282.1622			**5**
12	***1191.4301***	596.2187	1173.4195	587.2134	**M**	**509.3066**	255.1569	491.2830	246.1451			**4**
13	***1305.5112***	653.2592	1287.5006	644.2539	**L**	**377.2691**	189.1382	359.2455	180.1264			**3**
14	***1419.5923***	710.2998	1401.5817	701.2945	**L**	**263.1880**	132.0976	245.1644	123.0858			**2**
15					**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT1G18265.1





NCBI **BLAST** search of AAESAAEEAMAMLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.3	1566.6846	0.0031	AAESAAEEAMAMLLK	Oxidation M10 69.17%
31.8	1566.6846	0.0031	AAESAAEEAMAMLLK	Oxidation M12 30.83%
15.6	1566.6920	-0.0043	MLEDARNEIDSLK	
14.4	1566.6855	0.0022	MLKIHMMEDMIK	
12.4	1566.6855	0.0022	MLKIHMMEDMIK	
12.4	1566.6855	0.0022	MLKIHMMEDMIK	
11.7	1566.6846	0.0031	SEGDLAVMKPETMK	
10.4	1566.6866	0.0012	MANLGGGAEAHARFK	
7.9	1566.6920	-0.0043	TSLAKEDSLPMGER	
7.8	1566.6899	-0.0022	MLRDAGAKEVHMR	

Mascot: http://www.matrixscience.com/

AT1G18300.1

Mascot Search Results

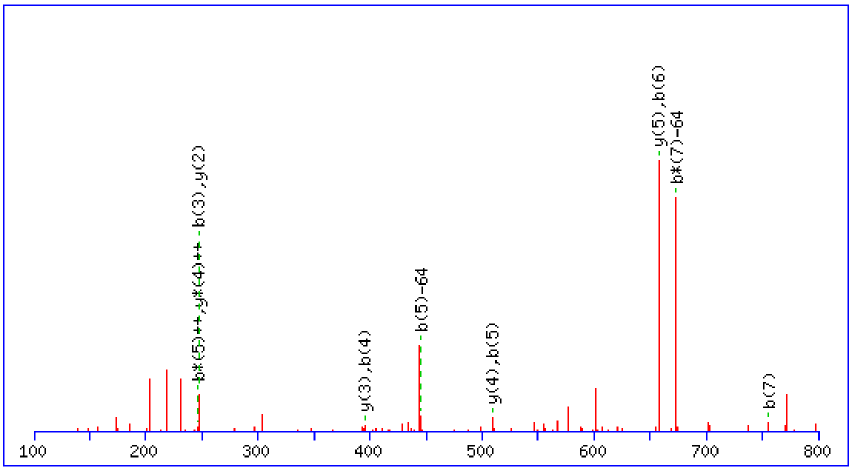
Peptide View

MS/MS Fragmentation of **GKGMLFPK**
Found in **AT1G18300.1** in **TAIR_Arabidopsis**, Symbols: ATNUDT4 | ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase | chr1:6299834-6300792 FORWARD

Match to Query 1525: 902.456776 from(452.235664,2+) index(5393)
Title: Elution from: 47.686 to 47.686 scan no 6866 cid35.00 polarity:+
Data file D6h-3_3.mgf

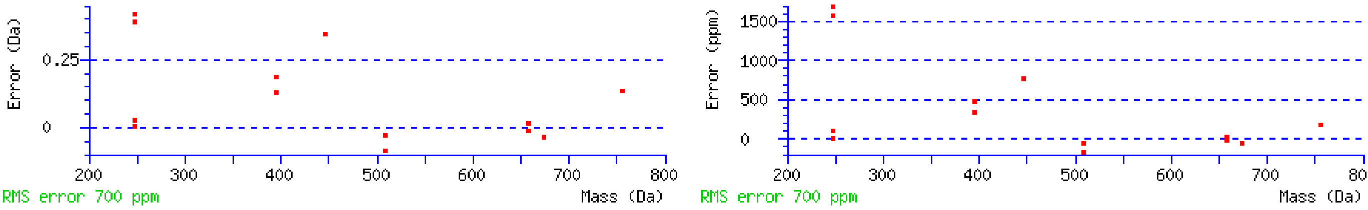
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 902.4544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.035
Matches : 13/82 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	59.0258	30.0165			G					8
2	189.1148	95.0610	171.0912	86.0492	K	845.4432	423.2252	827.4196	414.2134	7
3	***247.1333***	124.0703	229.1097	115.0585	G	715.3542	358.1807	697.3306	349.1689	6
4	***395.1657***	198.0865	377.1422	189.0747	M	**657.3357**	329.1715	639.3121	320.1597	5
5	***509.2468***	255.1271	491.2233	246.1153	L	**509.3032**	255.1552	491.2796	246.1435	4
6	***657.3123***	329.1598	639.2887	320.1480	F	**395.2221**	198.1147	377.1985	189.1029	3
7	***755.3621***	378.1847	737.3385	369.1729	P	**247.1567**	124.0820	229.1331	115.0702	2
8					K	149.1069	75.0571	131.0833	66.0453	1



NCBI **BLAST** search of GKGMLFPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G18300.1

24.0	902.4544	0.0024	GKGMLFPK
17.6	902.4591	-0.0024	IDYLKDK
9.7	902.4591	-0.0024	EATSVLFK
9.1	902.4591	-0.0024	VKYELDK
8.4	902.4548	0.0019	NLARCKK
6.9	902.4591	-0.0024	DALTSFIK
6.4	902.4591	-0.0024	EDYLVKK
6.0	902.4544	0.0024	KYGGLMPK
5.1	902.4569	-0.0001	TVSTKTEK
5.0	902.4548	0.0019	KAVQRCK

AT1G18370.1

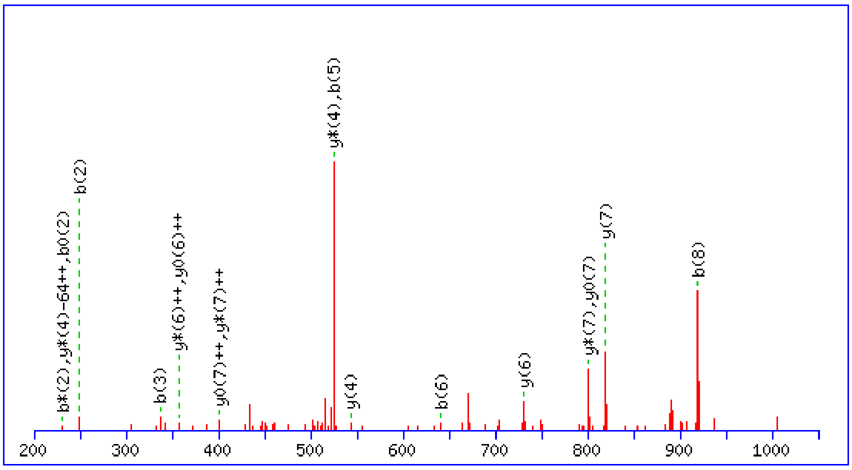
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RSSSVNMKK**
Found in **AT1G18370.1** in **TAIR_Arabidopsis**, Symbols: HIK | HIK (HINKEL); microtubule motor | chr1:6319725-6323813 REVERSE

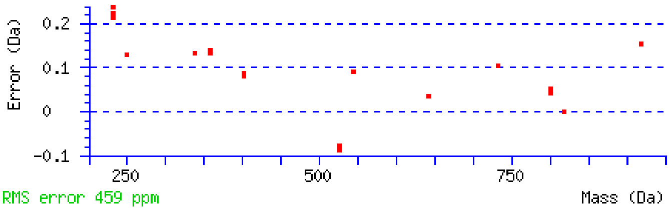
Match to Query 3013: 1066.501554 from(534.258053,2+) index(1580)
Title: Elution from: 20.386 to 20.386 scan no 2092 cid35.00 polarity:+
Data file D6h-3_2.mgf

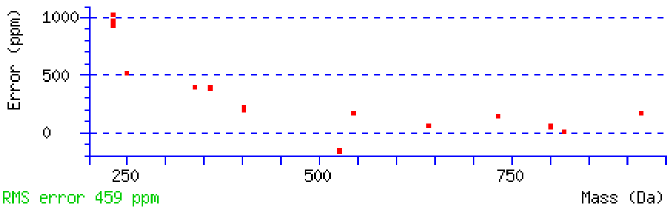
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1066.5000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 29 **Expect:** 0.0073
Matches : 18/126 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							9
2	***249.1256***	125.0664	231.1020	116.0546	231.1150	116.0612	S	907.4180	454.2126	889.3944	445.2008	889.4074	445.2073	8
3	***337.1547***	169.0810	319.1311	160.0692	319.1441	160.0757	S	**819.3889**	410.1981	801.3653	401.1863	801.3783	401.1928	7
4	425.1837	213.0955	407.1601	204.0837	407.1732	204.0902	S	**731.3599**	366.1836	713.3363	357.1718	713.3493	357.1783	6
5	***525.2492***	263.1282	507.2256	254.1164	507.2386	254.1229	V	643.3308	322.1690	625.3072	313.1572			5
6	***641.2862***	321.1467	623.2626	312.1349	623.2756	312.1414	N	**543.2653**	272.1363	525.2418	263.1245			4
7	789.3186	395.1629	771.2950	386.1511	771.3080	386.1577	M	427.2283	214.1178	409.2048	205.1060			3
8	***919.4076***	460.2075	901.3840	451.1957	901.3971	451.2022	K	279.1959	140.1016	261.1723	131.0898			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RSSSVNMKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G18370.1

28.9	1066.5000	0.0016	RSSSVNMKK
23.8	1066.4988	0.0027	RTYNWSVK
12.1	1066.4984	0.0032	TWVDYFVK
11.6	1066.5042	-0.0027	EEDEIVPVK
7.2	1066.5044	-0.0029	MFKGNKWK
6.5	1066.5022	-0.0006	LSCSVRGFK
6.2	1066.5017	-0.0002	GYMFALEVK
2.2	1066.5042	-0.0027	DEEIVEPVK
2.2	1066.5000	0.0016	SRAMTKNTK
2.1	1066.5018	-0.0002	FYNIEMLK

AT1G18410.1

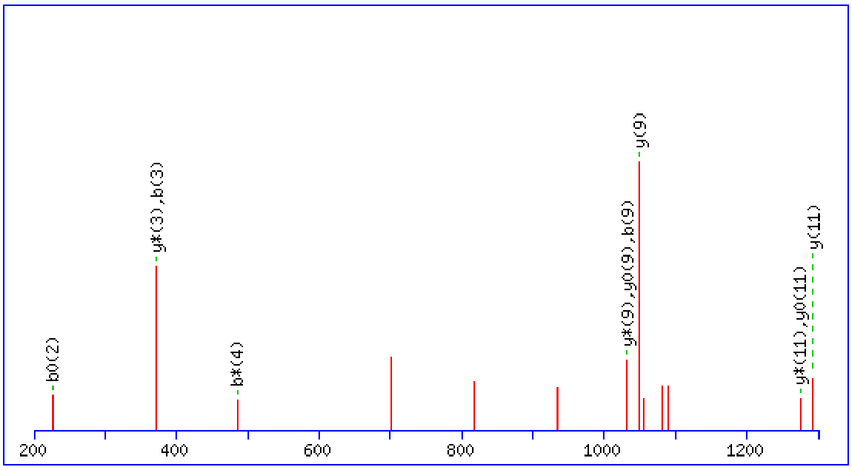
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDKEEDMVGIEK**
Found in **AT1G18410.1** in **TAIR_Arabidopsis**, Symbols: | kinesin motor protein-related | chr1:6336521-6342453 REVERSE

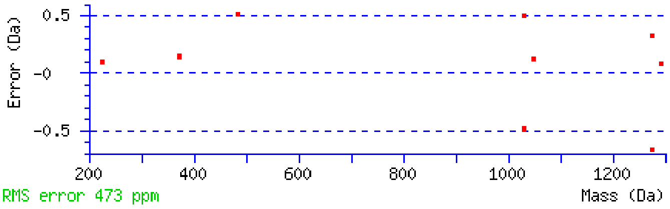
Match to Query 5913: 1419.694618 from(710.854585,2+) index(6255)
Title: Elution from: 54.059 to 54.059 scan no 7856 cid35.00 polarity:+
Data file D1d-3_1.mgf

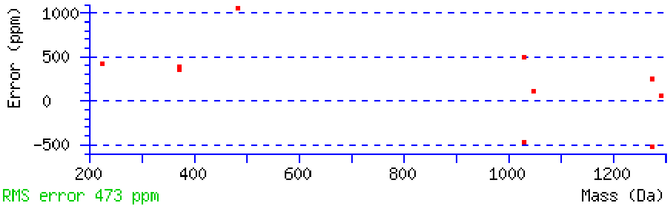
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1419.6915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.018
Matches : 12/128 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							12
2	244.1292	122.5682	227.1026	114.0550	226.1186	113.5629	D	***1292.6039***	646.8056	1275.5773	638.2923	1274.5933	637.8003	11
3	***372.2241***	186.6157	355.1976	178.1024	354.2136	177.6104	K	1177.5769	589.2921	1160.5504	580.7788	1159.5664	580.2868	10
4	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	E	***1049.4820***	525.2446	1032.4554	516.7313	1031.4714	516.2393	9
5	630.3093	315.6583	613.2828	307.1450	612.2988	306.6530	E	920.4394	460.7233	903.4128	452.2100	902.4288	451.7180	8
6	745.3363	373.1718	728.3097	364.6585	727.3257	364.1665	D	791.3968	396.2020	774.3702	387.6887	773.3862	387.1967	7
7	876.3768	438.6920	859.3502	430.1787	858.3662	429.6867	M	676.3698	338.6886	659.3433	330.1753	658.3593	329.6833	6
8	975.4452	488.2262	958.4186	479.7130	957.4346	479.2209	V	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
9	***1032.4666***	516.7370	1015.4401	508.2237	1014.4561	507.7317	G	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
10	1145.5507	573.2790	1128.5242	564.7657	1127.5401	564.2737	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	***1274.5933***	637.8003	1257.5667	629.2870	1256.5827	628.7950	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KDKEEDMVGIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G18410.1

Score	Mr(calc)	Delta	Sequence
22.0	1419.6915	0.0031	KDKEEDMVGIEK
17.8	1419.6915	0.0031	LEELSSDCLVQK
2.9	1419.6954	-0.0007	VNASSQVEERSSK
1.9	1419.6915	0.0031	MLEDLISVQDNK
0.2	1419.6915	0.0031	MAGIEDTANLLEK
0.2	1419.6915	0.0031	MAPGTLTELAGESK

AT1G18540.1

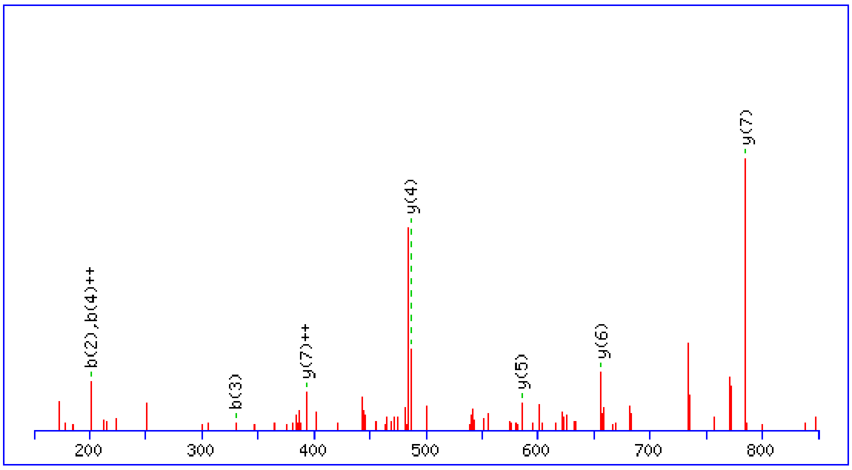
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIEAVPELK**
Found in **AT1G18540.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L6 (RPL6A) | chr1:6377441-6378541 REVERSE

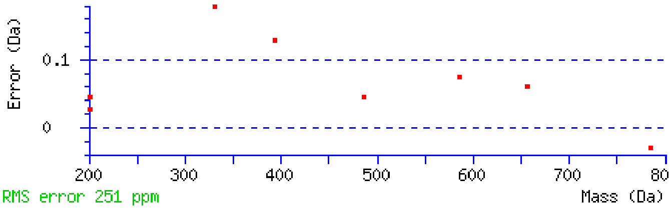
Match to Query 2310: 984.546804 from(493.280678,2+) index(3611)
Title: Elution from: 34.950 to 34.950 scan no 4530 cid35.00 polarity:+
Data file D6h-1_3.mgf

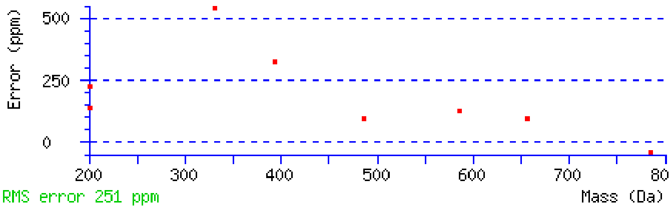
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.5491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.016
Matches : 8/76 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							9
2	**201.1234**	101.0653	183.1128	92.0600	I	898.5244	449.7658	881.4979	441.2526	880.5138	440.7606	8
3	**330.1660**	165.5866	312.1554	156.5813	E	***785.4403***	393.2238	768.4138	384.7105	767.4298	384.2185	7
4	401.2031	201.1052	383.1925	192.0999	A	***656.3978***	328.7025	639.3712	320.1892	638.3872	319.6972	6
5	500.2715	250.6394	482.2609	241.6341	V	***585.3606***	293.1840	568.3341	284.6707	567.3501	284.1787	5
6	597.3243	299.1658	579.3137	290.1605	P	***486.2922***	243.6498	469.2657	235.1365	468.2817	234.6445	4
7	726.3668	363.6871	708.3563	354.6818	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
8	839.4509	420.2291	821.4403	411.2238	L	260.1969	130.6021	243.1703	122.0888			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SIEAVPELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.8	984.5491	-0.0023	SIEAVPELK

AT1G18540.1

0.2	984.5491	-0.0023	SLAEILDPK
0.0	984.5464	0.0004	AERAAAALGR

Mascot: http://www.matrixscience.com/

AT1G18640.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAEWTAR**
Found in **AT1G18640.2** in **TAIR_Arabidopsis**, Symbols: PSP | PSP (3-PHOSPHOSERINE PHOSPHATASE) | chr1:6416516-6418237 REVERSE

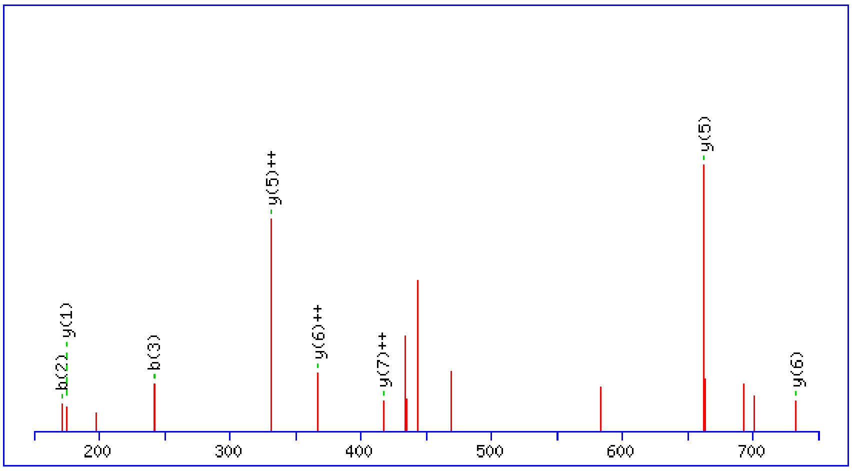
Match to Query 1596: 902.461252 from(452.237902,2+) index(1158)
Title: Elution from: 16.150 to 16.150 scan no 1567 cid35.00 polarity:+
Data file D12h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 750 Da Full range

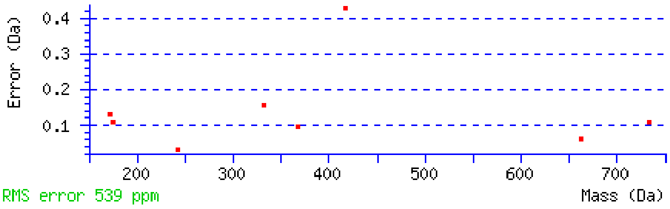
Label all possible matches ○ Label matches used for scoring ●

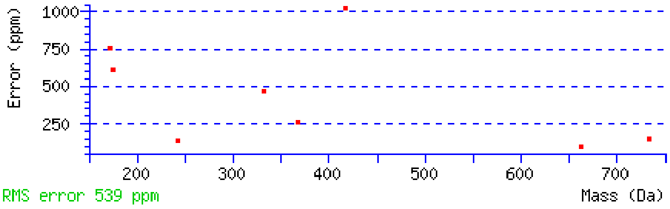
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 902.4610
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.028
Matches : 8/60 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			A							8
2	**171.1128**	86.0600			V	832.4312	416.7192	815.4046	408.2060	814.4206	407.7139	7
3	**242.1499**	121.5786			A	***733.3628***	367.1850	716.3362	358.6717	715.3522	358.1797	6
4	371.1925	186.0999	353.1819	177.0946	E	***662.3257***	331.6665	645.2991	323.1532	644.3151	322.6612	5
5	557.2718	279.1396	539.2613	270.1343	W	533.2831	267.1452	516.2565	258.6319	515.2725	258.1399	4
6	658.3195	329.6634	640.3089	320.6581	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
7	729.3566	365.1819	711.3461	356.1767	A	246.1561	123.5817	229.1295	115.0684			2
8					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AVAEWTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.7	902.4610	0.0003	AVAEWTAR

AT1G18640.2

2.1	902.4610	0.0003	QLTEWAR
0.3	902.4610	0.0002	HPPSSPPGK

Mascot: http://www.matrixscience.com/

AT1G19570.1

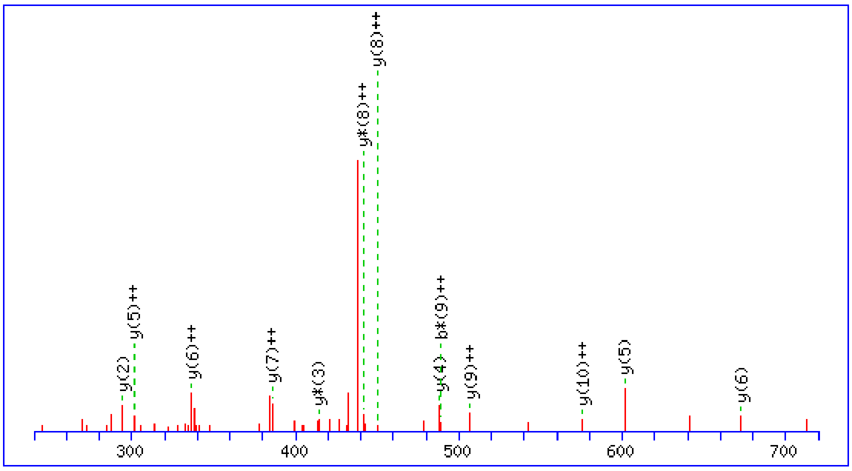
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYHLQVALGHFK**
Found in **AT1G19570.1** in **TAIR_Arabidopsis**, Symbols: DHAR1 | DHAR1 (DEHYDROASCORBATE REDUCTASE); glutathione dehydrogenase (ascorbate) | chr1:6773453-6774404 REVERSE

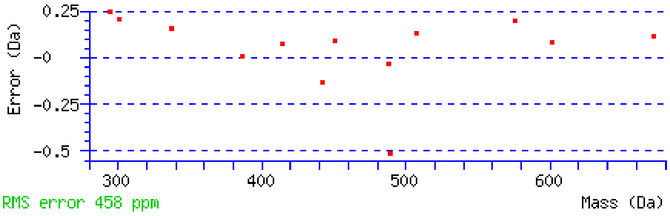
Match to Query 5536: 1424.792316 from(357.205355,4+) index(5189)
Title: Elution from: 45.438 to 45.438 scan no 6501 cid35.00 polarity:+
Data file C7-2_3.mgf

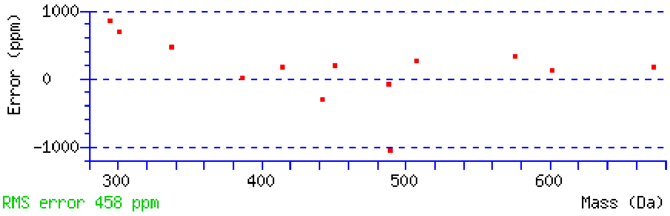
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 240 to 720 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1424.7928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0014
Matches : 14/80 fragment ions using 23 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.0913	57.5493			L					12
2	277.1547	139.0810			Y	1312.7161	656.8617	1295.6895	648.3484	11
3	414.2136	207.6104			H	1149.6527	575.3300	1132.6262	566.8167	10
4	527.2976	264.1525			L	1012.5938	506.8006	995.5673	498.2873	9
5	655.3562	328.1817	638.3297	319.6685	Q	899.5098	450.2585	882.4832	441.7452	8
6	754.4246	377.7160	737.3981	369.2027	V	771.4512	386.2292	754.4246	377.7160	7
7	825.4618	413.2345	808.4352	404.7212	A	***672.3828***	336.6950	655.3562	328.1817	6
8	938.5458	469.7765	921.5193	461.2633	L	***601.3457***	301.1765	584.3191	292.6632	5
9	995.5673	498.2873	978.5407	489.7740	G	***488.2616***	244.6344	471.2350	236.1212	4
10	1132.6262	566.8167	1115.5996	558.3035	H	431.2401	216.1237	414.2136	207.6104	3
11	1279.6946	640.3509	1262.6681	631.8377	F	***294.1812***	147.5942	277.1547	139.0810	2
12					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of LYHLQVALGHFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G19570.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1424.7928	-0.0005	LYHLQVALGHFK

AT1G19910.1

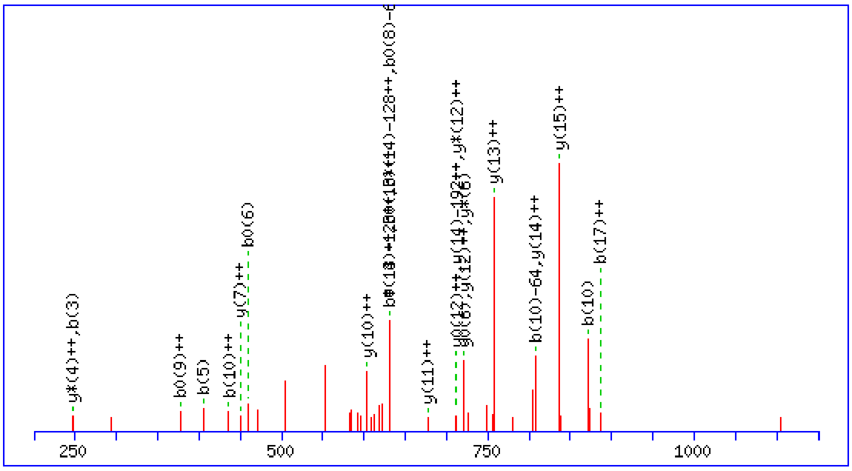
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGVGVASMGVMRPELVMK**
Found in **AT1G19910.1** in **TAIR_Arabidopsis**, Symbols: AVA-2PE, ATVHA-C2, AVA-P2 | AVA-P2 (vacuolar-H+-pumping ATPase 16 kDa proteolipid subunit 2); ATPase | chr1:6913308-6914313 FORWARD

Match to Query 8464: 1916.863668 from(639.961832,3+) index(2807)
Title: Elution from: 28.676 to 28.676 scan no 3523 cid35.00 polarity:+
Data file C7-3_3.mgf

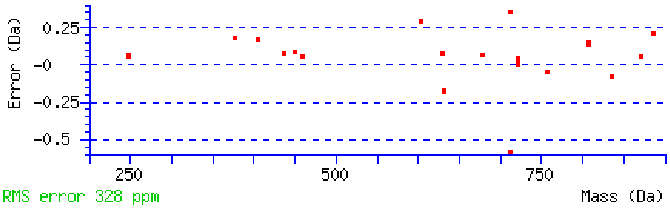
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

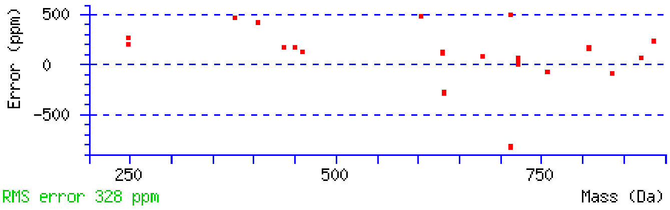


Monoisotopic mass of neutral peptide Mr(calc): 1916.8662
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 **Expect:** 0.00085
Matches : 26/316 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							18
2	147.0548	74.0311			129.0443	65.0258	G	1829.8445	915.4259	1811.8209	906.4141	1811.8339	906.4206	17
3	**247.1203**	124.0638			229.1097	115.0585	V	1771.8260	886.4166	1753.8024	877.4048	1753.8154	877.4113	16
4	305.1388	153.0730			287.1282	144.0677	G	1671.7605	836.3839	1653.7369	827.3721	1653.7499	827.3786	15
5	**405.2042**	203.1058			387.1937	194.1005	V	1613.7420	807.3746	1595.7184	798.3629	1595.7314	798.3694	14
6	477.2384	239.1228			459.2278	230.1175	A	1513.6766	757.3419	1495.6530	748.3301	1495.6660	748.3366	13
7	565.2674	283.1374			547.2569	274.1321	S	1441.6424	721.3248	1423.6188	712.3131	1423.6319	712.3196	12
8	713.2999	357.1536			695.2893	348.1483	M	1353.6134	677.3103	1335.5898	668.2985	1335.6028	668.3050	11
9	771.3184	386.1628			753.3078	377.1575	G	1205.5809	603.2941	1187.5573	594.2823	1187.5704	594.2888	10
10	**871.3838**	**436.1956**			853.3733	427.1903	V	1147.5624	574.2848	1129.5388	565.2731	1129.5519	565.2796	9
11	1019.4163	510.2118			1001.4057	501.2065	M	1047.4970	524.2521	1029.4734	515.2403	1029.4864	515.2468	8
12	1179.5055	590.2564	1161.4819	581.2446	1161.4950	581.2511	R	899.4645	450.2359	881.4410	441.2241	881.4540	441.2306	7
13	1277.5553	639.2813	1259.5317	630.2695	1259.5447	630.2760	P	739.3753	370.1913	721.3517	361.1795	721.3647	361.1860	6
14	1407.5949	704.3011	1389.5714	695.2893	1389.5844	695.2958	E	641.3255	321.1664	623.3019	312.1546	623.3149	312.1611	5
15	1521.6760	761.3417	1503.6525	752.3299	1503.6655	752.3364	L	511.2859	256.1466	493.2623	247.1348			4
16	1621.7415	811.3744	1603.7179	802.3626	1603.7309	802.3691	V	397.2048	199.1060	379.1812	190.0942			3
17	1769.7739	**885.3906**	1751.7503	876.3788	1751.7634	876.3853	M	297.1393	149.0733	279.1157	140.0615			2
18							K	149.1069	75.0571	131.0833	66.0453			1

AT1G19910.1





NCBI **BLAST** search of SGVGVASMGVMRPELVMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.5	1916.8662	-0.0026	SGVGVASMGVMRPELVMK
5.9	1916.8629	0.0008	MIEVAMDALSSSRFGGPK
5.3	1916.8676	-0.0039	TAKQSSTVDFNMPETLK

Mascot: http://www.matrixscience.com/

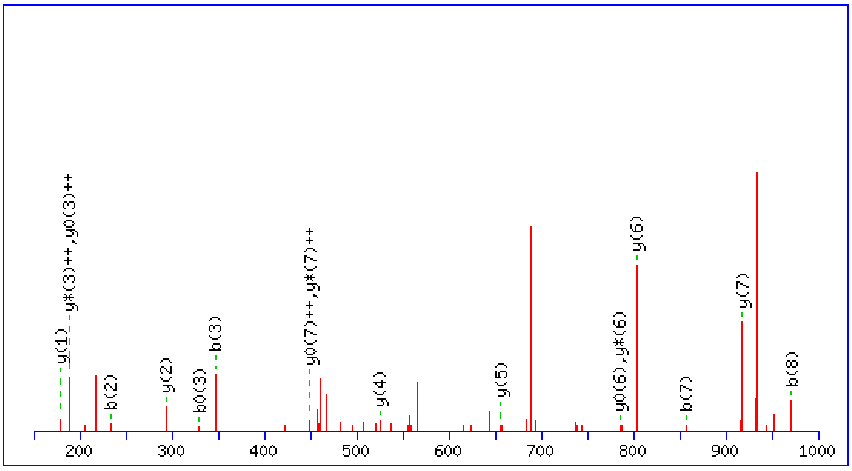
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETIMEETLR**
Found in **AT1G19950.1** in **TAIR_Arabidopsis**, Symbols: HVA22H | HVA22H (HVA22-LIKE PROTEIN H (ATHVA22H)) | chr1:6925034-6926518 FORWARD

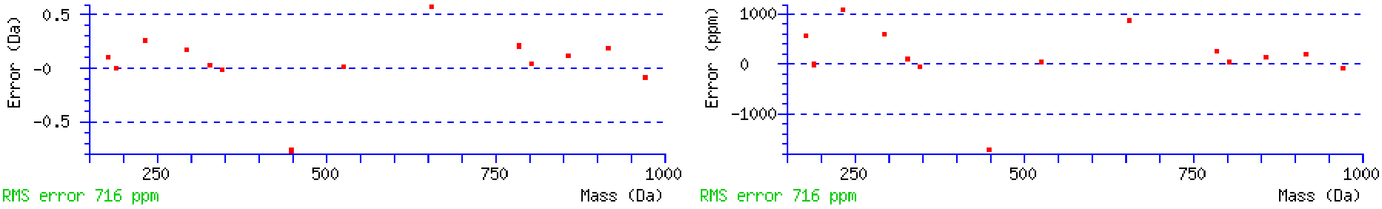
Match to Query 3266: 1148.504920 from(575.259736,2+) index(6420)
Title: Elution from: 60.667 to 60.667 scan no 8440 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1148.5027
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 32 **Expect:** 0.0067
Matches : 17/114 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							9
2	**233.0916**	117.0494	215.0811	108.0442	T	1019.4704	510.2388	1001.4468	501.2270	1001.4598	501.2336	8
3	**347.1727**	174.0900	329.1622	165.0847	I	***917.4257***	459.2165	899.4021	450.2047	899.4151	450.2112	7
4	495.2052	248.1062	477.1946	239.1009	M	***803.3446***	402.1759	785.3210	393.1641	785.3340	393.1707	6
5	625.2448	313.1260	607.2342	304.1207	E	***655.3122***	328.1597	637.2886	319.1479	637.3016	319.1544	5
6	755.2844	378.1458	737.2738	369.1406	E	***525.2725***	263.1399	507.2489	254.1281	507.2620	254.1346	4
7	**857.3291**	429.1682	839.3186	420.1629	T	395.2329	198.1201	377.2093	189.1083	377.2223	189.1148	3
8	**971.4102**	486.2087	953.3997	477.2035	L	***293.1882***	147.0977	275.1646	138.0859			2
9					R	***179.1071***	90.0572	161.0835	81.0454			1



NCBI **BLAST** search of ETIMEETLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G19950.1

Score	Mr(calc)	Delta	Sequence
31.6	1148.5027	0.0022	ETIMEETLR
18.7	1148.5047	0.0002	RAQPNDGFAR
18.3	1148.5054	-0.0005	DDKKMGGIDR
9.0	1148.5050	-0.0001	MPVLYEQDK
6.2	1148.5054	-0.0005	DVACSVQSLR
4.8	1148.5025	0.0025	DVGEDARRGR
4.6	1148.5047	0.0002	WVGDQSRQR
3.8	1148.5054	-0.0005	DAMEGKRPSK
3.5	1148.5054	-0.0005	DMVREEIAR
3.0	1148.5054	-0.0005	QNEMQISLR

AT1G20010.1

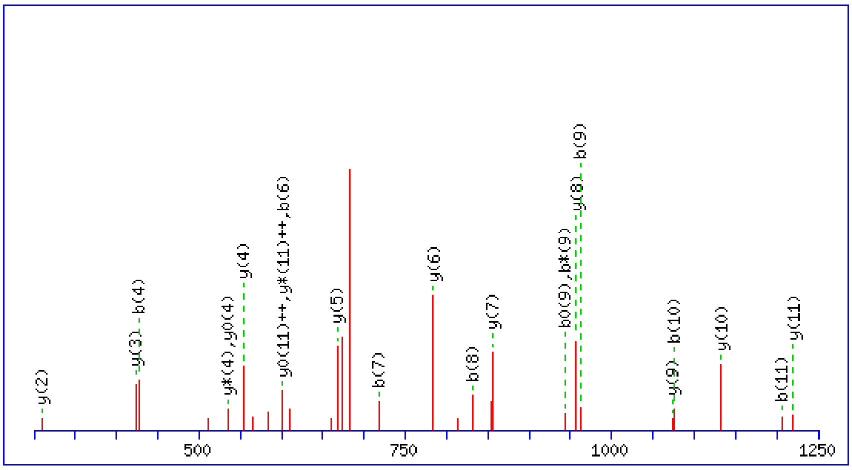
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSGDTADLQLER**
Found in **AT1G20010.1** in **TAIR_Arabidopsis**, Symbols: TUB5 | TUB5 (tubulin beta-5 chain) | chr1:6938024-6940472 REVERSE

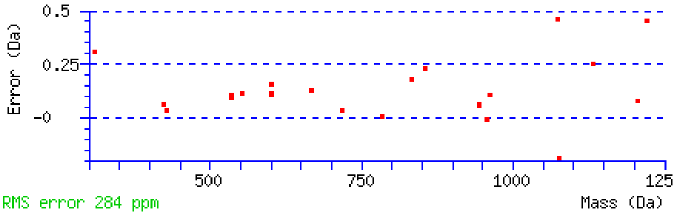
Match to Query 4906: 1382.589112 from(692.301832,2+) index(3154)
Title: Elution from: 32.154 to 32.154 scan no 3981 cid35.00 polarity:+
Data file D12h-2_3.mgf

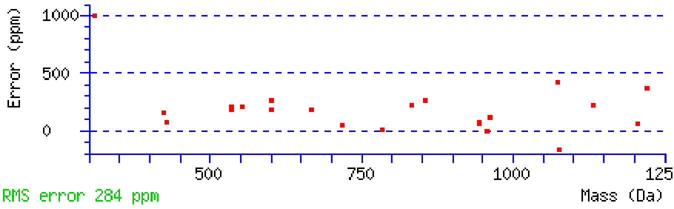
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.5890
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 116 **Expect:** 1.4e-011
Matches : 23/112 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							12
2	253.0967	127.0520			235.0861	118.0467	S	***1219.5359***	610.2716	1201.5124	601.2598	1201.5254	601.2663	11
3	311.1152	156.0612			293.1046	147.0560	G	***1131.5069***	566.2571	1113.4833	557.2453	1113.4963	557.2518	10
4	**427.1392**	214.0732			409.1286	205.0679	D	***1073.4884***	537.2478	1055.4648	528.2360	1055.4778	528.2425	9
5	529.1839	265.0956			511.1733	256.0903	T	***957.4644***	479.2358	939.4408	470.2240	939.4538	470.2306	8
6	**601.2180**	301.1127			583.2075	292.1074	A	***855.4197***	428.2135	837.3961	419.2017	837.4091	419.2082	7
7	**717.2420**	359.1246			699.2315	350.1194	D	***783.3855***	392.1964	765.3620	383.1846	765.3750	383.1911	6
8	**831.3231**	416.1652			813.3126	407.1599	L	***667.3616***	334.1844	649.3380	325.1726	649.3510	325.1791	5
9	**961.3758**	481.1915	943.3522	472.1797	943.3652	472.1862	Q	***553.2805***	277.1439	535.2569	268.1321	535.2699	268.1386	4
10	**1075.4569**	538.2321	1057.4333	529.2203	1057.4463	529.2268	L	***423.2278***	212.1175	405.2042	203.1058	405.2173	203.1123	3
11	**1205.4965**	603.2519	1187.4729	594.2401	1187.4859	594.2466	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of YSGDTADLQLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G20010.1

Score	Mr(calc)	Delta	Sequence
116.1	1382.5890	0.0001	YSGDTADLQLER
26.1	1382.5903	-0.0012	CRDLQEKMQR
12.9	1382.5924	-0.0033	ATASSAVESIMER
2.5	1382.5877	0.0014	MNNSEVLMEKR
1.8	1382.5865	0.0026	NMDGGYIAWVNK
1.2	1382.5865	0.0026	AAMGEDTFWAIR
0.7	1382.5899	-0.0008	CFGEMIGGLVER
0.4	1382.5903	-0.0012	MSNPTRKNMER
0.4	1382.5926	-0.0034	MCGSVHAYVGKR
0.3	1382.5924	-0.0033	KSKNSMGEEDVK

AT1G20020.1

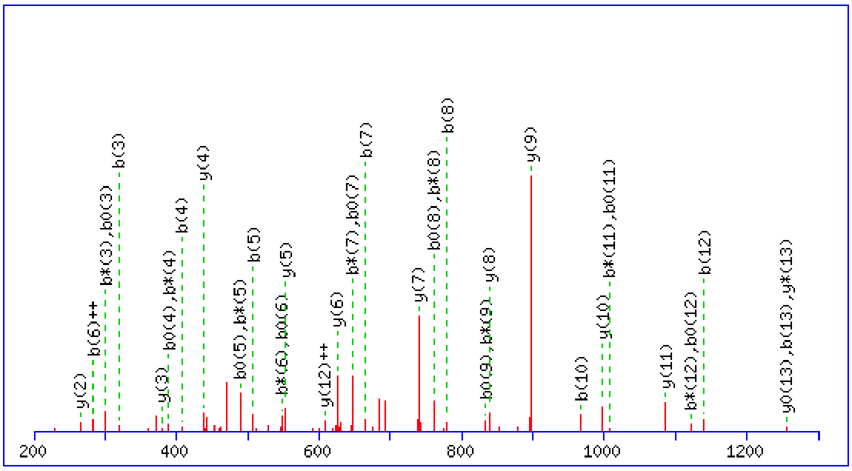
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGQSVGVIADGIDK**
Found in **AT1G20020.1** in **TAIR_Arabidopsis**, Symbols: ATLFNR2 | ATLFNR2 (LEAF FNR 2); NADPH dehydrogenase/ oxidoreductase/ poly(U) binding | chr1:6942842-6944859 FORWARD

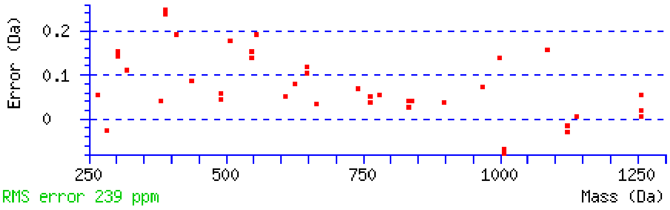
Match to Query 5239: 1402.650502 from(702.332527,2+) index(3940)
Title: Elution from: 36.659 to 36.659 scan no 4903 cid35.00 polarity:+
Data file D12h-1_3.mgf

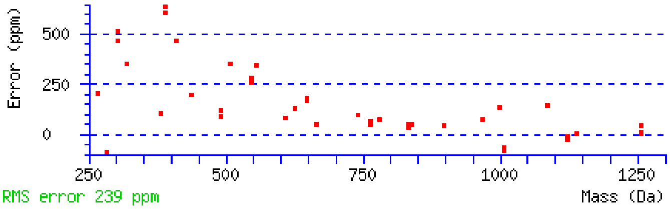
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1402.6516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 93 **Expect:** 2.9e-009
Matches : 40/150 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							14
2	189.0654	95.0363			171.0548	86.0311	G	1273.6193	637.3133	1255.5957	628.3015	1255.6087	628.3080	13
3	**319.1180**	160.0627	301.0945	151.0509	301.1075	151.0574	Q	1215.6008	608.3040	1197.5772	599.2922	1197.5902	599.2987	12
4	**407.1471**	204.0772	389.1235	195.0654	389.1365	195.0719	S	***1085.5481***	543.2777	1067.5246	534.2659	1067.5376	534.2724	11
5	**507.2126**	254.1099	489.1890	245.0981	489.2020	245.1046	V	***997.5191***	499.2632	979.4955	490.2514	979.5085	490.2579	10
6	565.2311	283.1192	547.2075	274.1074	547.2205	274.1139	G	***897.4536***	449.2305	879.4300	440.2187	879.4431	440.2252	9
7	**665.2965**	333.1519	647.2729	324.1401	647.2859	324.1466	V	***839.4351***	420.2212	821.4115	411.2094	821.4246	411.2159	8
8	**779.3776**	390.1924	761.3540	381.1807	761.3670	381.1872	I	***739.3697***	370.1885	721.3461	361.1767	721.3591	361.1832	7
9	851.4118	426.2095	833.3882	417.1977	833.4012	417.2042	A	***625.2886***	313.1479	607.2650	304.1361	607.2780	304.1426	6
10	**967.4357**	484.2215	949.4122	475.2097	949.4252	475.2162	D	***553.2544***	277.1309	535.2308	268.1191	535.2439	268.1256	5
11	1025.4542	513.2308	1007.4307	504.2190	1007.4437	504.2255	G	***437.2304***	219.1189	419.2069	210.1071	419.2199	210.1136	4
12	**1139.5353**	570.2713	1121.5118	561.2595	1121.5248	561.2660	I	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	3
13	**1255.5593**	628.2833	1237.5357	619.2715	1237.5487	619.2780	D	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EGQSVGVIADGIDK

AT1G20020.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.1	1402.6516	-0.0011	EGQSVGVIADGIDK
6.5	1402.6491	0.0014	FKLRASYMEDK
4.9	1402.6539	-0.0034	HYVEELEDKVK
4.5	1402.6516	-0.0011	GEGKGDGELVAIDK
0.1	1402.6516	-0.0011	SLNALVPTNESDK

AT1G20200.1

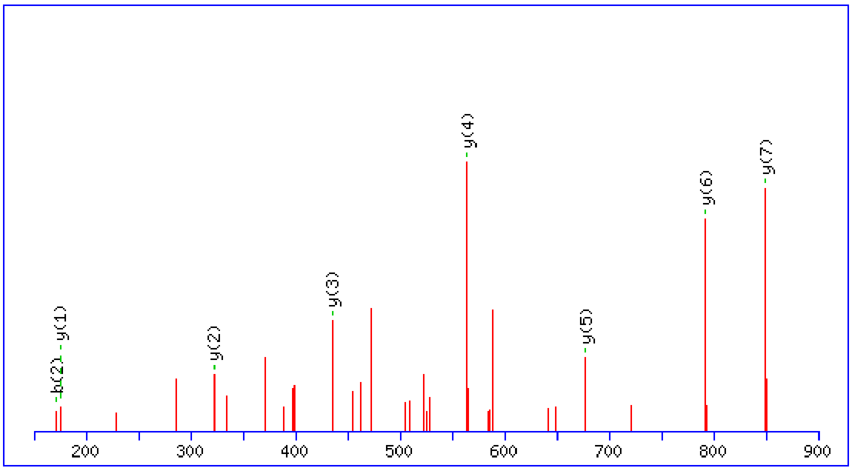
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGDLELFR**
Found in **AT1G20200.1** in **TAIR_Arabidopsis**, Symbols: EMB2719 | EMB2719 (EMBRYO DEFECTIVE 2719) | chr1:7001400-7004145 REVERSE

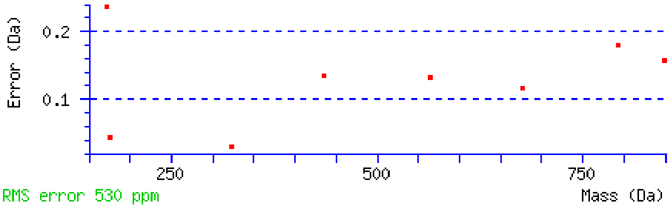
Match to Query 2171: 961.523608 from(481.769080,2+) index(7541)
Title: Elution from: 65.217 to 65.217 scan no 9709 cid35.00 polarity:+
Data file C7-1_1.mgf

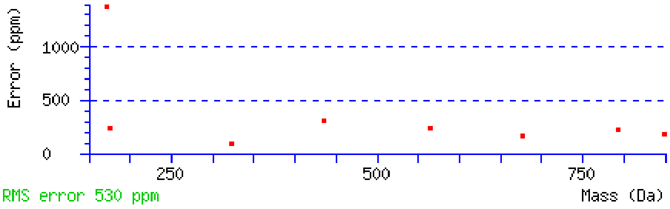
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 961.5233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 8.4e-006
Matches : 8/60 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							8
2	171.1128	86.0600			G	***849.4465***	425.2269	832.4199	416.7136	831.4359	416.2216	7
3	286.1397	143.5735	268.1292	134.5682	D	***792.4250***	396.7162	775.3985	388.2029	774.4145	387.7109	6
4	399.2238	200.1155	381.2132	191.1103	L	***677.3981***	339.2027	660.3715	330.6894	659.3875	330.1974	5
5	528.2664	264.6368	510.2558	255.6316	E	***564.3140***	282.6606	547.2875	274.1474	546.3035	273.6554	4
6	641.3505	321.1789	623.3399	312.1736	L	***435.2714***	218.1394	418.2449	209.6261			3
7	788.4189	394.7131	770.4083	385.7078	F	***322.1874***	161.5973	305.1608	153.0840			2
8					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IGDLELFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.1	961.5233	0.0003	IGDLELFR

AT1G20200.1

13.2	961.5233	0.0003	GEVELIFR
12.0	961.5233	0.0004	IIATPEYR
5.8	961.5246	-0.0010	IARHYFR
4.1	961.5246	-0.0010	AYRHLFR
2.4	961.5233	0.0003	IDPFTLTR

Mascot: http://www.matrixscience.com/

AT1G20260.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYPEEMIQTGISTIDVMNSIAR**
Found in **AT1G20260.2** in **TAIR_Arabidopsis**, Symbols: | (VACUOLAR ATP SYNTHASE SUBUNIT B3); hydrogen ion transmembrane transporter/ hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transporting ATPase, rotational mechanism / hydrogen-exporting ATPase, phosphorylati

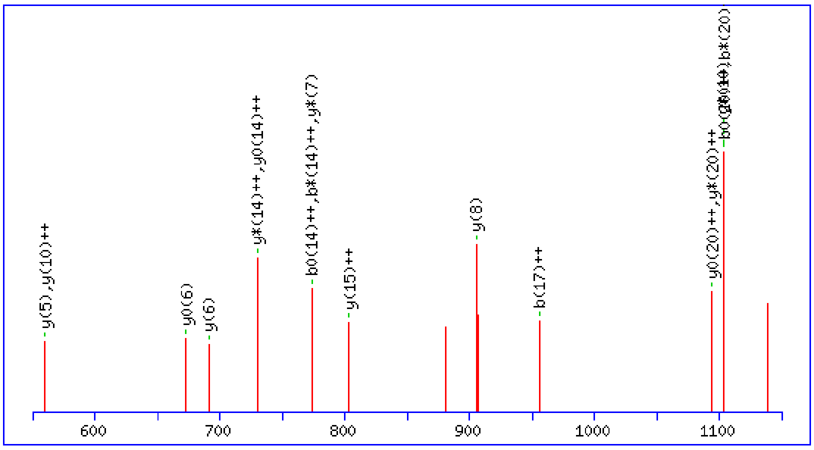
Match to Query 10032: 2468.191833 from(823.737887,3+) index(10519)
Title: Elution from: 111.867 to 111.867 scan no 15701 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1150 Da Full range

Label all possible matches ○ Label matches used for scoring ●

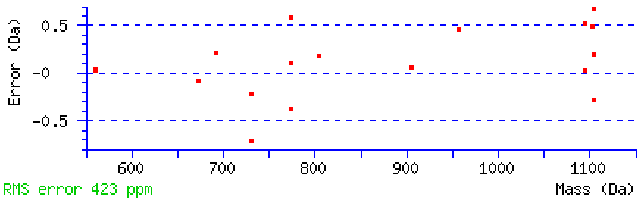
Show Y-axis ☐

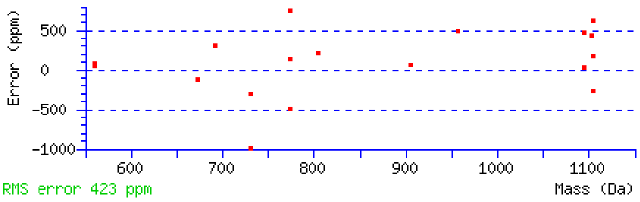


Monoisotopic mass of neutral peptide Mr(calc): 2468.1927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.012
Matches : 18/232 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311			84.0444	42.5258	T							22
2	265.1183	133.0628			247.1077	124.0575	Y	2368.1523	1184.5798	2351.1258	1176.0665	2350.1417	1175.5745	21
3	362.1710	181.5892			344.1605	172.5839	P	2205.0890	1103.0481	2188.0624	1094.5349	2187.0784	1094.0428	20
4	491.2136	246.1105			473.2031	237.1052	E	2108.0362	1054.5217	2091.0097	1046.0085	2090.0257	1045.5165	19
5	620.2562	310.6318			602.2457	301.6265	E	1978.9936	990.0005	1961.9671	981.4872	1960.9831	980.9952	18
6	751.2967	376.1520			733.2862	367.1467	M	1849.9510	925.4792	1832.9245	916.9659	1831.9405	916.4739	17
7	864.3808	432.6940			846.3702	423.6887	I	1718.9105	859.9589	1701.8840	851.4456	1700.9000	850.9536	16
8	992.4394	496.7233	975.4128	488.2100	974.4288	487.7180	Q	1605.8265	803.4169	1588.7999	794.9036	1587.8159	794.4116	15
9	1093.4870	547.2472	1076.4605	538.7339	1075.4765	538.2419	T	1477.7679	739.3876	1460.7414	730.8743	1459.7573	730.3823	14
10	1150.5085	575.7579	1133.4820	567.2446	1132.4979	566.7526	G	1376.7202	688.8638	1359.6937	680.3505	1358.7097	679.8585	13
11	1263.5926	632.2999	1246.5660	623.7866	1245.5820	623.2946	I	1319.6988	660.3530	1302.6722	651.8397	1301.6882	651.3477	12
12	1350.6246	675.8159	1333.5980	667.3027	1332.6140	666.8107	S	1206.6147	603.8110	1189.5881	595.2977	1188.6041	594.8057	11
13	1451.6723	726.3398	1434.6457	717.8265	1433.6617	717.3345	T	1119.5827	560.2950	1102.5561	551.7817	1101.5721	551.2897	10
14	1564.7563	782.8818	1547.7298	774.3685	1546.7458	773.8765	I	1018.5350	509.7711	1001.5084	501.2579	1000.5244	500.7659	9
15	1679.7833	840.3953	1662.7567	831.8820	1661.7727	831.3900	D	***905.4509***	453.2291	888.4244	444.7158	887.4404	444.2238	8
16	1778.8517	889.9295	1761.8251	881.4162	1760.8411	880.9242	V	790.4240	395.7156	773.3974	387.2024	772.4134	386.7103	7
17	1909.8922	955.4497	1892.8656	946.9365	1891.8816	946.4444	M	***691.3556***	346.1814	674.3290	337.6681	673.3450	337.1761	6
18	2023.9351	1012.4712	2006.9086	1003.9579	2005.9245	1003.4659	N	***560.3151***	280.6612	543.2885	272.1479	542.3045	271.6559	5
19	2110.9671	1055.9872	2093.9406	1047.4739	2092.9566	1046.9819	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
20	2224.0512	1112.5292	2207.0247	1104.0160	2206.0406	1103.5240	I	359.2401	180.1237	342.2136	171.6104			3
21	2295.0883	1148.0478	2278.0618	1139.5345	2277.0777	1139.0425	A	246.1561	123.5817	229.1295	115.0684			2
22							R	175.1190	88.0631	158.0924	79.5498			1

AT1G20260.2





NCBI **BLAST** search of TYPEEMIQTGISTIDVMNSIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.2	2468.1927	-0.0009	TYPEEMIQTGISTIDVMNSIAR
3.0	2468.1927	-0.0009	LEGISGDPFTGICISNATISMAAK

Mascot: http://www.matrixscience.com/

AT1G20340.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of NNAGYPHNVVFDEDEIPSGVDVAK
Found in AT1G20340.1 in TAIR_Arabidopsis, Symbols: DRT112 | DRT112 (DNA-damage-repair/toleration protein 112); copper ion binding / electron carrier | chr1:7042760-7043263 REVERSE

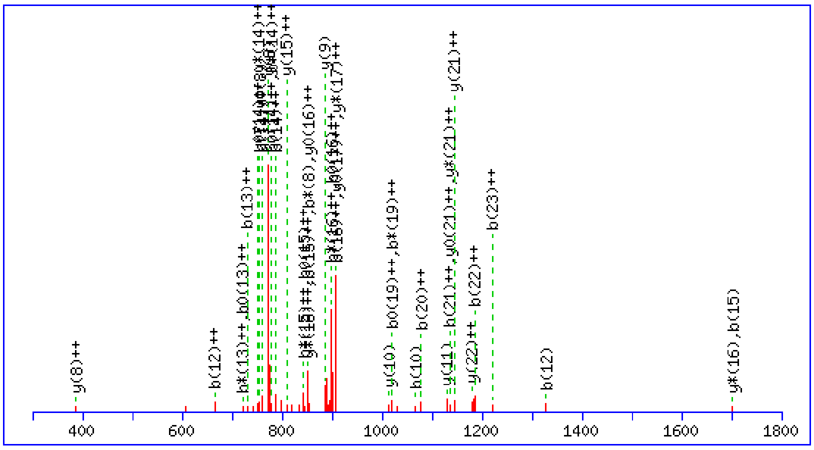
Match to Query 10660: 2585.196753 from(862.739527,3+) index(7190)
Title: Elution from: 63.048 to 63.048 scan no 9216 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

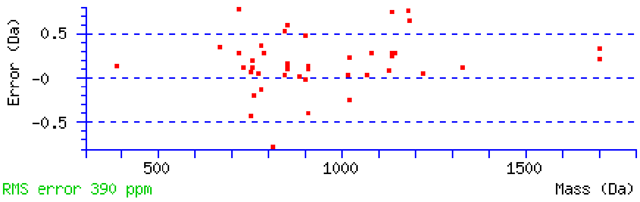
Show Y-axis ☐

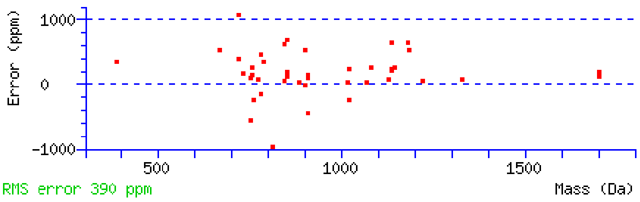


Monoisotopic mass of neutral peptide Mr(calc): 2585.2034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 3.3e-006
Matches : 43/248 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							24
2	229.0931	115.0502	212.0666	106.5369			N	2472.1678	1236.5875	2455.1412	1228.0742	2454.1572	1227.5822	23
3	300.1302	150.5688	283.1037	142.0555			A	2358.1248	1179.5661	2341.0983	1171.0528	2340.1143	1170.5608	22
4	357.1517	179.0795	340.1252	170.5662			G	2287.0877	1144.0475	2270.0612	1135.5342	2269.0772	1135.0422	21
5	520.2150	260.6112	503.1885	252.0979			Y	2230.0663	1115.5368	2213.0397	1107.0235	2212.0557	1106.5315	20
6	617.2678	309.1375	600.2413	300.6243			P	2067.0029	1034.0051	2049.9764	1025.4918	2048.9924	1024.9998	19
7	**754.3267**	377.6670	737.3002	369.1537			H	1969.9502	985.4787	1952.9236	976.9654	1951.9396	976.4734	18
8	868.3696	434.6885	851.3431	426.1752			N	1832.8912	916.9493	1815.8647	908.4360	1814.8807	907.9440	17
9	967.4381	484.2227	950.4115	475.7094			V	1718.8483	859.9278	1701.8218	851.4145	1700.8378	850.9225	16
10	**1066.5065**	533.7569	1049.4799	525.2436			V	1619.7799	810.3936	1602.7534	801.8803	1601.7693	801.3883	15
11	1213.5749	607.2911	1196.5483	598.7778			F	1520.7115	760.8594	1503.6849	752.3461	1502.7009	751.8541	14
12	**1328.6018**	***664.8046***	1311.5753	656.2913	1310.5913	655.7993	D	1373.6431	687.3252	1356.6165	678.8119	1355.6325	678.3199	13
13	1457.6444	***729.3258***	1440.6179	720.8126	1439.6339	720.3206	E	1258.6161	629.8117	1241.5896	621.2984	1240.6056	620.8064	12
14	1572.6714	***786.8393***	1555.6448	778.3260	1554.6608	777.8340	D	**1129.5735**	565.2904	1112.5470	556.7771	1111.5630	556.2851	11
15	**1701.7140**	***851.3606***	1684.6874	842.8473	1683.7034	842.3553	E	**1014.5466**	507.7769	997.5201	499.2637	996.5360	498.7717	10
16	1814.7980	***907.9026***	1797.7715	899.3894	1796.7875	898.8974	I	**885.5040**	443.2556	868.4775	434.7424	867.4934	434.2504	9
17	1911.8508	956.4290	1894.8242	947.9158	1893.8402	947.4237	P	**772.4199**	386.7136	755.3934	378.2003	754.4094	377.7083	8
18	1998.8828	999.9450	1981.8563	991.4318	1980.8722	990.9398	S	675.3672	338.1872	658.3406	329.6740	657.3566	329.1819	7
19	2055.9043	1028.4558	2038.8777	1019.9425	2037.8937	1019.4505	G	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	6
20	2154.9727	***1077.9900***	2137.9461	1069.4767	2136.9621	1068.9847	V	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
21	2269.9996	***1135.5035***	2252.9731	1126.9902	2251.9891	1126.4982	D	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
22	2369.0680	***1185.0377***	2352.0415	1176.5244	2351.0575	1176.0324	V	317.2183	159.1128	300.1918	150.5995			3
23	2440.1052	***1220.5562***	2423.0786	1212.0429	2422.0946	1211.5509	A	218.1499	109.5786	201.1234	101.0653			2
24							K	147.1128	74.0600	130.0863	65.5468			1

AT1G20340.1





NCBI **BLAST** search of NNAGYPHNVVFDEDEIPSGVDVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.7	2585.2034	-0.0067	NNAGYPHNVVFDEDEIPSGVDVAK
9.5	2585.1964	0.0004	MAEMEINFMVFNPIIDGLGEAGR
9.5	2585.1964	0.0004	MAEMEINFMVFNPIIDGLGEAGR
9.3	2585.2011	-0.0043	AFFYGWMLKPLVFGDYPDEMK
6.1	2585.1922	0.0046	DWETVDDGFASSFVEEGKLDALR
4.1	2585.2030	-0.0062	MDLLDCLDTTWSGAVVYVDEGVK
1.5	2585.1930	0.0037	IGMDVAASEFFMKDGRYDLNFK
1.4	2585.1964	0.0004	MAEMEINFMVFNPIIDGLGEAGR
0.7	2585.2027	-0.0060	ANSMANEITEEDDSLGHQIRDLK
0.3	2585.2036	-0.0068	GMREKGIEPDIATFNIMMNSQR

Mascot: http://www.matrixscience.com/

AT1G20440.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNVPEHETPTVATEESPATTTEVTDR**
Found in **AT1G20440.1** in **TAIR_Arabidopsis**, Symbols: RD17, COR47 | COR47 (cold regulated 47) | chr1:7084712-7085654 REVERSE

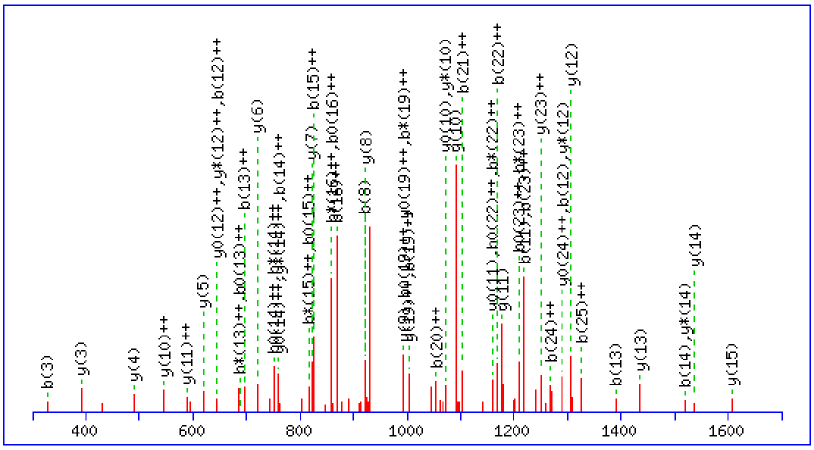
Match to Query 11262: 2824.299591 from(942.440473,3+) index(3512)
Title: Elution from: 33.511 to 33.511 scan no 4327 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

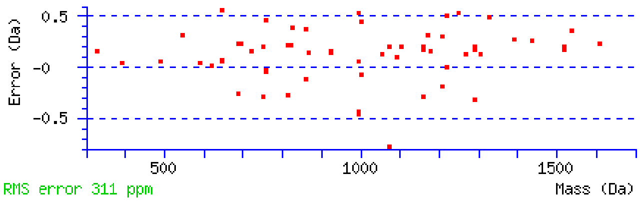
Show Y-axis ☐

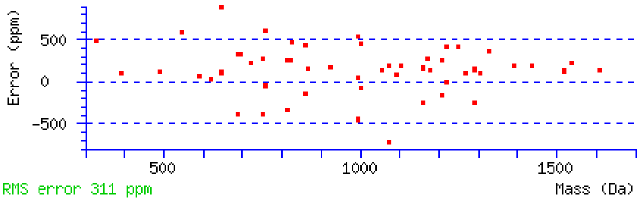


Monoisotopic mass of neutral peptide Mr(calc): 2824.2999
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 125 **Expect:** 5.5e-013
Matches : 60/290 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			**N**							**26**
2	229.0931	115.0502	212.0666	106.5369			**N**	2711.2642	1356.1358	2694.2377	1347.6225	2693.2537	1347.1305	**25**
3	**328.1615**	164.5844	311.1350	156.0711			**V**	2597.2213	1299.1143	2580.1948	1290.6010	2579.2107	1290.1090	**24**
4	425.2143	213.1108	408.1878	204.5975			**P**	2498.1529	1249.5801	2481.1264	1241.0668	2480.1423	1240.5748	**23**
5	554.2569	277.6321	537.2304	269.1188	536.2463	268.6268	**E**	2401.1001	1201.0537	2384.0736	1192.5404	2383.0896	1192.0484	**22**
6	691.3158	346.1615	674.2893	337.6483	673.3052	337.1563	**H**	2272.0575	1136.5324	2255.0310	1128.0191	2254.0470	1127.5271	**21**
7	820.3584	410.6828	803.3319	402.1696	802.3478	401.6776	**E**	2134.9986	1068.0030	2117.9721	1059.4897	2116.9881	1058.9977	**20**
8	**921.4061**	461.2067	904.3795	452.6934	903.3955	452.2014	**T**	2005.9560	1003.4817	1988.9295	994.9684	1987.9455	994.4764	**19**
9	1018.4588	509.7331	1001.4323	501.2198	1000.4483	500.7278	**P**	1904.9084	952.9578	1887.8818	944.4445	1886.8978	943.9525	**18**
10	1119.5065	560.2569	1102.4800	551.7436	1101.4960	551.2516	**T**	1807.8556	904.4314	1790.8290	895.9182	1789.8450	895.4262	**17**
11	**1218.5749**	609.7911	1201.5484	601.2778	1200.5644	600.7858	**V**	1706.8079	853.9076	1689.7814	845.3943	1688.7974	844.9023	**16**
12	**1289.6121**	***645.3097***	1272.5855	636.7964	1271.6015	636.3044	**A**	***1607.7395***	804.3734	1590.7130	795.8601	1589.7289	795.3681	**15**
13	**1390.6597**	***695.8335***	1373.6332	687.3202	1372.6492	686.8282	**T**	***1536.7024***	768.8548	1519.6758	760.3416	1518.6918	759.8495	**14**
14	**1519.7023**	***760.3548***	1502.6758	751.8415	1501.6918	751.3495	**E**	***1435.6547***	718.3310	1418.6282	709.8177	1417.6441	709.3257	**13**
15	1648.7449	***824.8761***	1631.7184	816.3628	1630.7344	815.8708	**E**	***1306.6121***	653.8097	1289.5856	645.2964	1288.6016	644.8044	**12**
16	1735.7769	***868.3921***	1718.7504	859.8788	1717.7664	859.3868	**S**	***1177.5695***	589.2884	1160.5430	580.7751	1159.5590	580.2831	**11**
17	1832.8297	916.9185	1815.8032	908.4052	1814.8191	907.9132	**P**	***1090.5375***	545.7724	1073.5109	537.2591	1072.5269	536.7671	**10**
18	1903.8668	952.4371	1886.8403	943.9238	1885.8563	943.4318	**A**	***993.4847***	497.2460	976.4582	488.7327	975.4742	488.2407	**9**
19	2004.9145	***1002.9609***	1987.8880	994.4476	1986.9039	993.9556	**T**	***922.4476***	461.7274	905.4211	453.2142	904.4371	452.7222	**8**
20	2105.9622	***1053.4847***	2088.9356	1044.9715	2087.9516	1044.4794	**T**	***821.3999***	411.2036	804.3734	402.6903	803.3894	402.1983	**7**
21	2207.0099	***1104.0086***	2189.9833	1095.4953	2188.9993	1095.0033	**T**	***720.3523***	360.6798	703.3257	352.1665	702.3417	351.6745	**6**
22	2336.0525	***1168.5299***	2319.0259	1160.0166	2318.0419	1159.5246	**E**	***619.3046***	310.1559	602.2780	301.6427	601.2940	301.1506	**5**
23	2435.1209	***1218.0641***	2418.0943	1209.5508	2417.1103	1209.0588	**V**	***490.2620***	245.6346	473.2354	237.1214	472.2514	236.6293	**4**
24	2536.1685	***1268.5879***	2519.1420	1260.0746	2518.1580	1259.5826	**T**	***391.1936***	196.1004	374.1670	187.5872	373.1830	187.0951	**3**
25	2651.1955	***1326.1014***	2634.1689	1317.5881	2633.1849	1317.0961	**D**	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	**2**

26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of NNVPEHETPTVATEESPATTTEVTDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
124.5	2824.2999	-0.0003	NNVPEHETPTVATEESPATTTEVTDR

Mascot: http://www.matrixscience.com/

AT1G20450.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **HEEEEENKPSLLDK**
Found in **AT1G20450.1** in **TAIR_Arabidopsis**, Symbols: LTI45, ERD10, LTI29 | ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10) | chr1:7088225-7089097 REVERSE

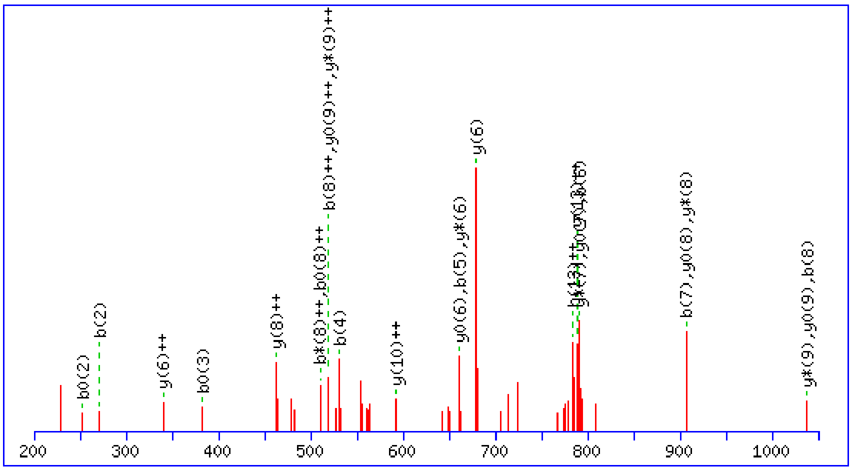
Match to Query 8350: 1714.738314 from(572.586714,3+) index(963)
Title: Elution from: 15.867 to 15.867 scan no 1379 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

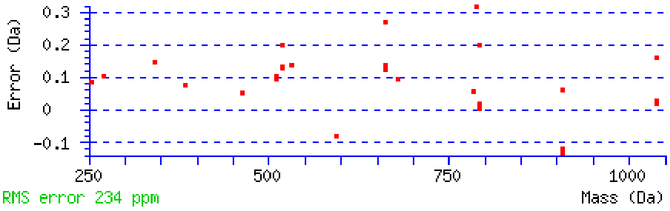
Label all possible matches ○ Label matches used for scoring ●

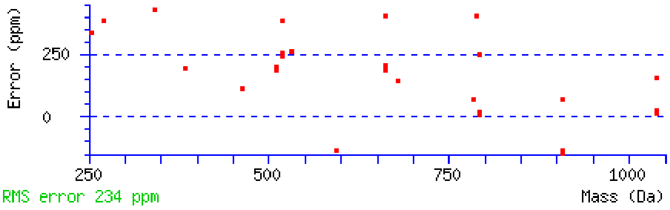
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1714.7388
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00058
Matches : 27/140 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	141.0573	71.0323					H							14
2	***271.0969***	136.0521			253.0864	127.0468	E	1575.6961	788.3517	1557.6725	779.3399	1557.6855	779.3464	13
3	401.1365	201.0719			383.1260	192.0666	E	1445.6565	723.3319	1427.6329	714.3201	1427.6459	714.3266	12
4	***531.1762***	266.0917			513.1656	257.0864	E	1315.6168	658.3121	1297.5932	649.3003	1297.6063	649.3068	11
5	***661.2158***	331.1115			643.2052	322.1063	E	1185.5772	593.2922	1167.5536	584.2804	1167.5666	584.2870	10
6	***791.2554***	396.1314			773.2449	387.1261	E	1055.5376	528.2724	1037.5140	519.2606	1037.5270	519.2671	9
7	***907.2924***	454.1499	889.2688	445.1381	889.2819	445.1446	N	925.4979	463.2526	907.4744	454.2408	907.4874	454.2473	8
8	***1037.3815***	**519.1944**	1019.3579	510.1826	1019.3709	510.1891	K	809.4609	405.2341	791.4374	396.2223	791.4504	396.2288	7
9	1135.4313	568.2193	1117.4077	559.2075	1117.4207	559.2140	P	679.3719	340.1896	661.3483	331.1778	661.3613	331.1843	6
10	1223.4603	612.2338	1205.4367	603.2220	1205.4498	603.2285	S	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	5
11	1337.5414	669.2744	1319.5178	660.2626	1319.5309	660.2691	L	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
12	1451.6225	726.3149	1433.5989	717.3031	1433.6120	717.3096	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
13	1567.6465	**784.3269**	1549.6229	775.3151	1549.6359	775.3216	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of HEEEEENKPSLLDK

AT1G20450.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.0	1714.7388	-0.0005	HEEEEENKPSLLDK
8.3	1714.7385	-0.0002	EGEIPFWMLAFSDR
1.2	1714.7394	-0.0011	ASGSHAPRQKGMQYR
0.7	1714.7356	0.0027	YINNLYQNHPDRF

Mascot: http://www.matrixscience.com/

AT1G20530.1

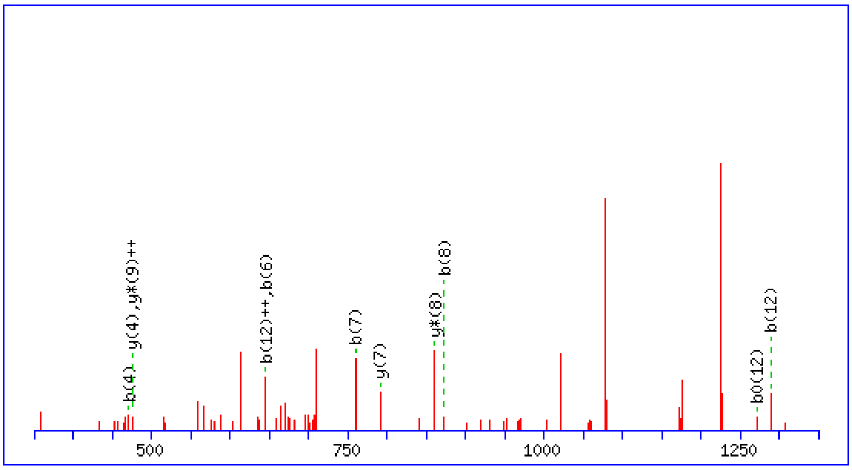
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQKVSSDLSEVTK**
Found in **AT1G20530.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17110.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN74079.1); contains InterPro domain Protein of unknown function DUF632 (InterPro:IPR006867); contains InterPro

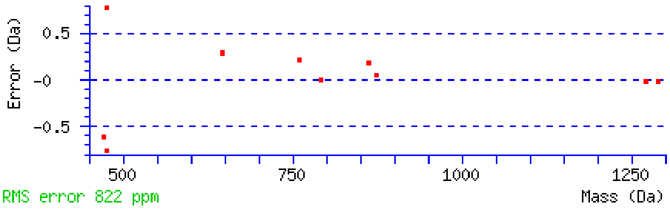
Match to Query 5595: 1434.716686 from(718.365619,2+) index(5696)
Title: Elution from: 52.900 to 52.900 scan no 7320 cid35.00 polarity:+
Data file D1d-2_1.mgf

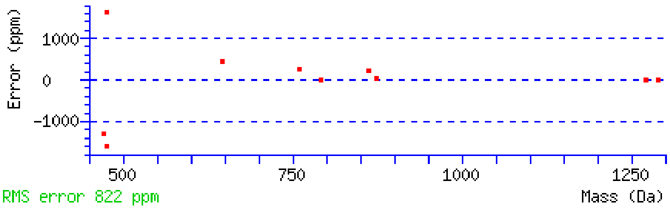
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1434.7202
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.032
Matches : 11/140 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							13
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	1320.7005	660.8539	1303.6740	652.3406	1302.6900	651.8486	12
3	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	K	1192.6420	596.8246	1175.6154	588.3113	1174.6314	587.8193	11
4	***471.2562***	236.1317	454.2296	227.6185	453.2456	227.1264	V	1064.5470	532.7771	1047.5204	524.2639	1046.5364	523.7719	10
5	558.2882	279.6477	541.2617	271.1345	540.2776	270.6425	S	965.4786	483.2429	948.4520	474.7297	947.4680	474.2376	9
6	***645.3202***	323.1638	628.2937	314.6505	627.3097	314.1585	S	878.4466	439.7269	861.4200	431.2136	860.4360	430.7216	8
7	***760.3472***	380.6772	743.3206	372.1640	742.3366	371.6719	D	**791.4145**	396.2109	774.3880	387.6976	773.4040	387.2056	7
8	***873.4312***	437.2193	856.4047	428.7060	855.4207	428.2140	L	676.3876	338.6974	659.3610	330.1842	658.3770	329.6921	6
9	960.4633	480.7353	943.4367	472.2220	942.4527	471.7300	S	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
10	1089.5059	545.2566	1072.4793	536.7433	1071.4953	536.2513	E	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	4
11	1188.5743	594.7908	1171.5477	586.2775	1170.5637	585.7855	V	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	***1289.6220***	645.3146	1272.5954	636.8013	1271.6114	636.3093	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DQKVSSDLSEVTK

AT1G20530.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.4	1434.7202	-0.0035	DQKVSSDLSEVTK
5.7	1434.7136	0.0030	SDRMVENAKLEK
4.6	1434.7177	-0.0010	VEEWMTIQKQK
4.5	1434.7202	-0.0035	KSSDSGVVSIAEEK
1.0	1434.7137	0.0030	SIKSVASSMTGHSK

AT1G20620.1

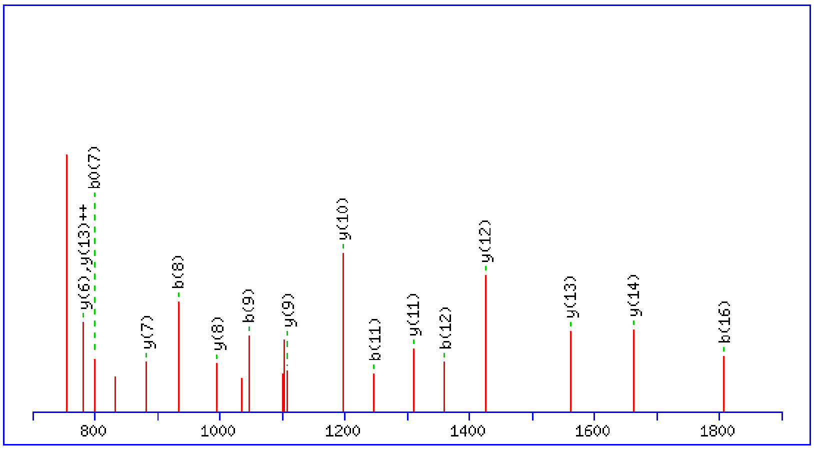
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFFEVTHDISNLTCADFLR**
Found in **AT1G20620.1** in **TAIR_Arabidopsis**, Symbols: SEN2, CAT3 | CAT3 (CATALASE 3); catalase | chr1:7143132-7146183 FORWARD

Match to Query 9661: 2241.050222 from(1121.532387,2+) index(10083)
Title: Elution from: 99.457 to 99.457 scan no 14640 cid35.00 polarity:+
Data file D1d-2_2.mgf

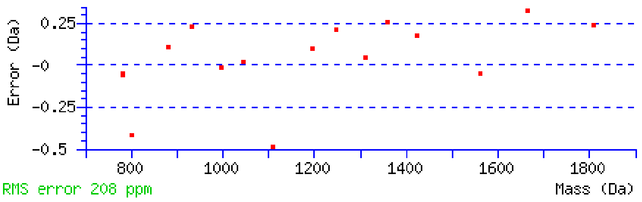
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 700 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

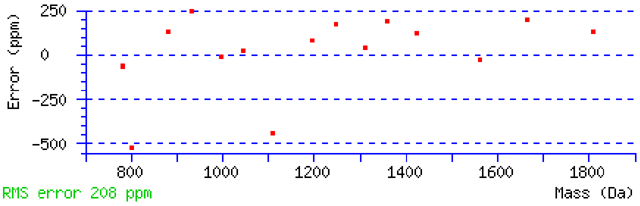


Monoisotopic mass of neutral peptide Mr(calc): 2241.0525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 1.8e-006
Matches : 16/184 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							19
2	205.0972	103.0522					F	2185.0383	1093.0228	2168.0117	1084.5095	2167.0277	1084.0175	18
3	352.1656	176.5864					F	2037.9699	1019.4886	2020.9433	1010.9753	2019.9593	1010.4833	17
4	481.2082	241.1077			463.1976	232.1024	E	1890.9014	945.9544	1873.8749	937.4411	1872.8909	936.9491	16
5	580.2766	290.6419			562.2660	281.6366	V	1761.8588	881.4331	1744.8323	872.9198	1743.8483	872.4278	15
6	681.3243	341.1658			663.3137	332.1605	T	***1662.7904***	831.8989	1645.7639	823.3856	1644.7799	822.8936	14
7	818.3832	409.6952			800.3726	400.6899	H	***1561.7428***	781.3750	1544.7162	772.8617	1543.7322	772.3697	13
8	**933.4101**	467.2087			915.3995	458.2034	D	***1424.6838***	712.8456	1407.6573	704.3323	1406.6733	703.8403	12
9	**1046.4942**	523.7507			1028.4836	514.7454	I	***1309.6569***	655.3321	1292.6303	646.8188	1291.6463	646.3268	11
10	1133.5262	567.2667			1115.5156	558.2615	S	***1196.5728***	598.7901	1179.5463	590.2768	1178.5623	589.7848	10
11	**1247.5691**	624.2882	1230.5426	615.7749	1229.5586	615.2829	N	***1109.5408***	555.2740	1092.5143	546.7608	1091.5302	546.2688	9
12	**1360.6532**	680.8302	1343.6266	672.3170	1342.6426	671.8250	L	***995.4979***	498.2526	978.4713	489.7393	977.4873	489.2473	8
13	1461.7009	731.3541	1444.6743	722.8408	1443.6903	722.3488	T	***882.4138***	441.7105	865.3873	433.1973	864.4033	432.7053	7
14	1621.7315	811.3694	1604.7050	802.8561	1603.7210	802.3641	C	***781.3661***	391.1867	764.3396	382.6734	763.3556	382.1814	6
15	1692.7686	846.8880	1675.7421	838.3747	1674.7581	837.8827	A	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	5
16	**1807.7956**	904.4014	1790.7690	895.8882	1789.7850	895.3961	D	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
17	1954.8640	977.9356	1937.8374	969.4224	1936.8534	968.9304	F	435.2714	218.1394	418.2449	209.6261			3
18	2067.9481	1034.4777	2050.9215	1025.9644	2049.9375	1025.4724	L	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT1G20620.1





NCBI **BLAST** search of GFFEVTHDISNLTCADFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.1	2241.0525	-0.0023	GFFEVTHDISNLTCADFLR

Mascot: http://www.matrixscience.com/

AT1G20696.1

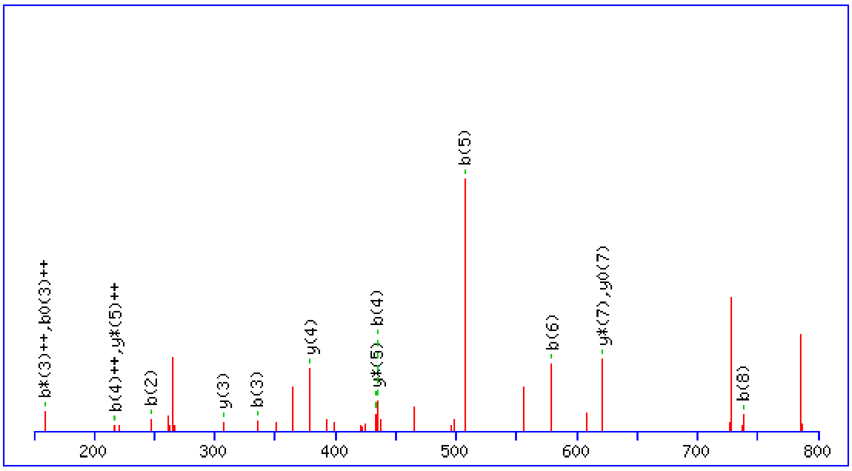
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NKSVAAVGK**
Found in **AT1G20696.1** in **TAIR_Arabidopsis**, Symbols: NFD3, NFD03, HMGB3 | HMGB3 (HIGH MOBILITY GROUP B 3); transcription factor | chr1:7179815-7181164 FORWARD

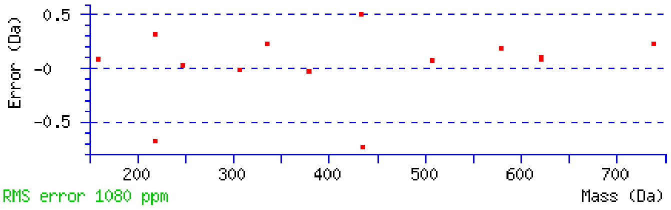
Match to Query 1577: 884.470360 from(443.242456,2+) index(6041)
Title: Elution from: 53.489 to 53.489 scan no 7638 cid35.00 polarity:+
Data file 0-2_1.mgf

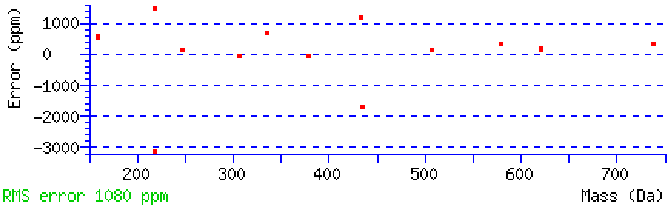
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 884.4724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0057
Matches : 15/80 fragment ions using 26 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	***247.1333***	124.0703	229.1097	115.0585			K	769.4427	385.2250	751.4191	376.2132	751.4321	376.2197	8
3	***335.1624***	168.0848	317.1388	159.0730	317.1518	159.0795	S	639.3536	320.1805	621.3300	311.1687	621.3431	311.1752	7
4	***435.2278***	218.1175	417.2042	209.1058	417.2173	209.1123	V	551.3246	276.1659	533.3010	267.1541			6
5	***507.2620***	254.1346	489.2384	245.1228	489.2514	245.1293	A	451.2591	226.1332	433.2355	217.1214			5
6	***579.2961***	290.1517	561.2725	281.1399	561.2856	281.1464	A	**379.2250**	190.1161	361.2014	181.1043			4
7	679.3616	340.1844	661.3380	331.1726	661.3510	331.1791	V	**307.1908**	154.0990	289.1672	145.0873			3
8	***737.3801***	369.1937	719.3565	360.1819	719.3695	360.1884	G	207.1254	104.0663	189.1018	95.0545			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NKSVAAVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G20696.1

33.7	884.4724	-0.0020	NKSVAAVGK
12.7	884.4724	-0.0020	TREILNK
11.7	884.4719	-0.0016	DFIEILK
11.7	884.4724	-0.0020	SGKNILNK
7.7	884.4724	-0.0020	VKKEGAGGK
6.3	884.4724	-0.0020	RGSELALK
6.1	884.4724	-0.0020	KASSQKPK
5.9	884.4724	-0.0020	NQKKVEK
0.2	884.4724	-0.0020	LTRENIK

AT1G21450.1

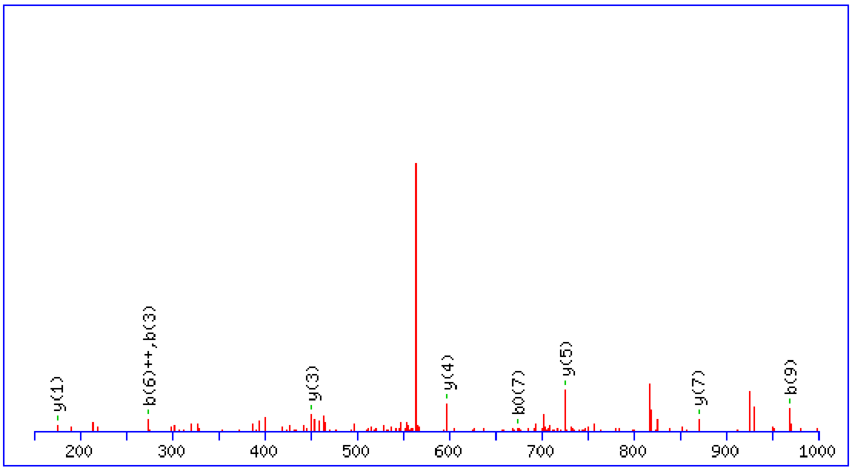
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAASGKFIYR**
Found in **AT1G21450.1** in **TAIR_Arabidopsis**, Symbols: SCL1 | SCL1 (SCARECROW-LIKE 1); transcription factor | chr1:7509710-7511491 FORWARD

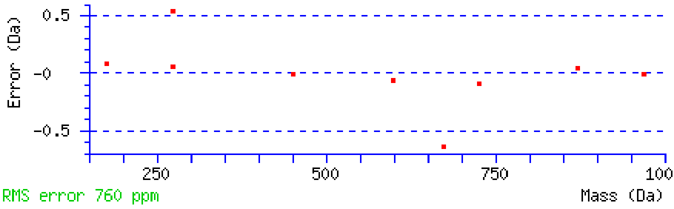
Match to Query 3664: 1142.588074 from(572.301313,2+) index(4523)
Title: Elution from: 41.457 to 41.457 scan no 5712 cid35.00 polarity:+
Data file D6h-3_2.mgf

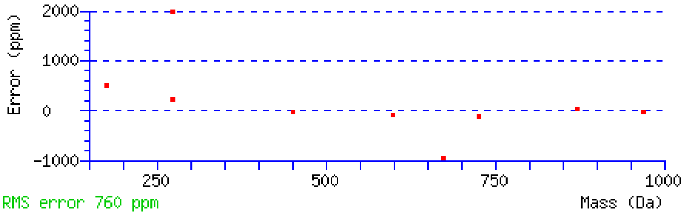
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1142.5906
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.021
Matches : 9/80 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					**M**							**10**
2	203.0849	102.0461					**A**	1012.5574	506.7824	995.5309	498.2691	994.5469	497.7771	**9**
3	**274.1220**	137.5646					**A**	941.5203	471.2638	924.4938	462.7505	923.5098	462.2585	**8**
4	361.1540	181.0806			343.1435	172.0754	**S**	***870.4832***	435.7452	853.4567	427.2320	852.4726	426.7400	**7**
5	418.1755	209.5914			400.1649	200.5861	**G**	783.4512	392.2292	766.4246	383.7160			**6**
6	546.2704	273.6389	529.2439	265.1256	528.2599	264.6336	**K**	***726.4297***	363.7185	709.4032	355.2052			**5**
7	693.3389	347.1731	676.3123	338.6598	675.3283	338.1678	**F**	***598.3348***	299.6710	581.3082	291.1577			**4**
8	806.4229	403.7151	789.3964	395.2018	788.4124	394.7098	**I**	***451.2663***	226.1368	434.2398	217.6235			**3**
9	**969.4863**	485.2468	952.4597	476.7335	951.4757	476.2415	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
10							**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of MAASGKFIYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G21450.1

Score	Mr(calc)	Delta	Sequence
19.6	1142.5906	-0.0025	MAASGKFIYR
5.3	1142.5866	0.0015	VPMAAAGNGLSR
2.1	1142.5904	-0.0024	AASSSHGKRSR
1.8	1142.5906	-0.0026	MPRFPPSAPK
0.4	1142.5866	0.0015	MATHAALAVSR

AT1G21750.1

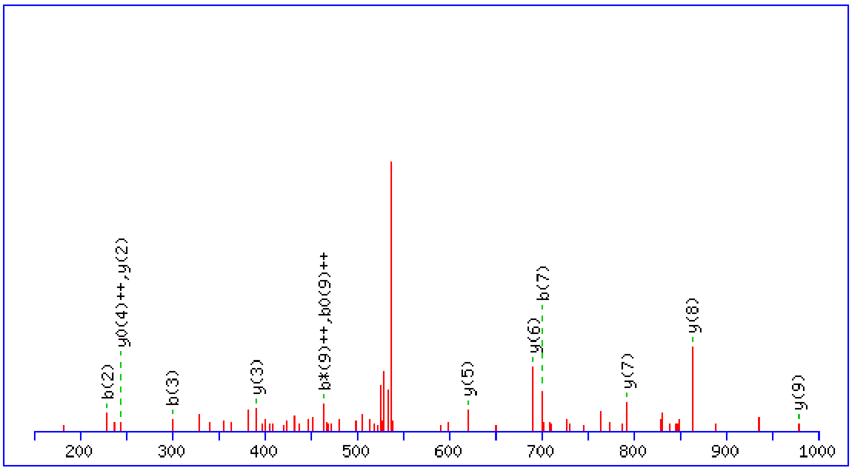
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDATANDFPK**
Found in **AT1G21750.1** in **TAIR_Arabidopsis**, Symbols: ATPDIL1-1 | ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase | chr1:7645756-7648503 FORWARD

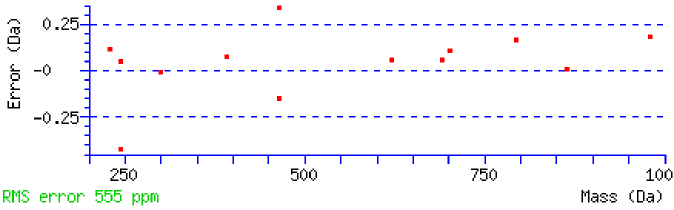
Match to Query 3344: 1090.532504 from(546.273528,2+) index(2822)
Title: Elution from: 28.950 to 28.950 scan no 3528 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

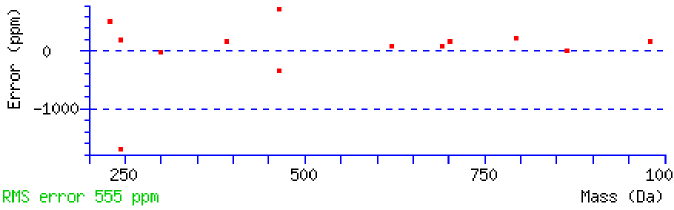


Monoisotopic mass of neutral peptide Mr(calc): 1090.5295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 2.2e-006
Matches : 13/90 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							10
2	**229.1183**	115.0628			211.1077	106.0575	D	***978.4527***	489.7300	961.4262	481.2167	960.4421	480.7247	9
3	**300.1554**	150.5813			282.1448	141.5761	A	***863.4258***	432.2165	846.3992	423.7032	845.4152	423.2112	8
4	401.2031	201.1052			383.1925	192.0999	T	***792.3886***	396.6980	775.3621	388.1847	774.3781	387.6927	7
5	472.2402	236.6237			454.2296	227.6185	A	***691.3410***	346.1741	674.3144	337.6608	673.3304	337.1688	6
6	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	N	***620.3039***	310.6556	603.2773	302.1423	602.2933	301.6503	5
7	**701.3101**	351.1587	684.2835	342.6454	683.2995	342.1534	D	506.2609	253.6341	489.2344	245.1208	488.2504	244.6288	4
8	848.3785	424.6929	831.3519	416.1796	830.3679	415.6876	F	***391.2340***	196.1206	374.2074	187.6074			3
9	945.4312	473.2193	928.4047	464.7060	927.4207	464.2140	P	***244.1656***	122.5864	227.1390	114.0731			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 555 ppm



RMS error 555 ppm

NCBI **BLAST** search of LDATANDFPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G21750.1

Score	Mr(calc)	Delta	Sequence
64.1	1090.5295	0.0030	LDATANDFPK
14.2	1090.5329	-0.0003	LNTIIDCDK
10.2	1090.5295	0.0030	EVAGQAPYEK
1.4	1090.5302	0.0023	GGGTKACRER
0.7	1090.5329	-0.0004	EQTVVVECK
0.3	1090.5295	0.0030	AIDFSNPEAK

Mascot: http://www.matrixscience.com/

AT1G22275.1

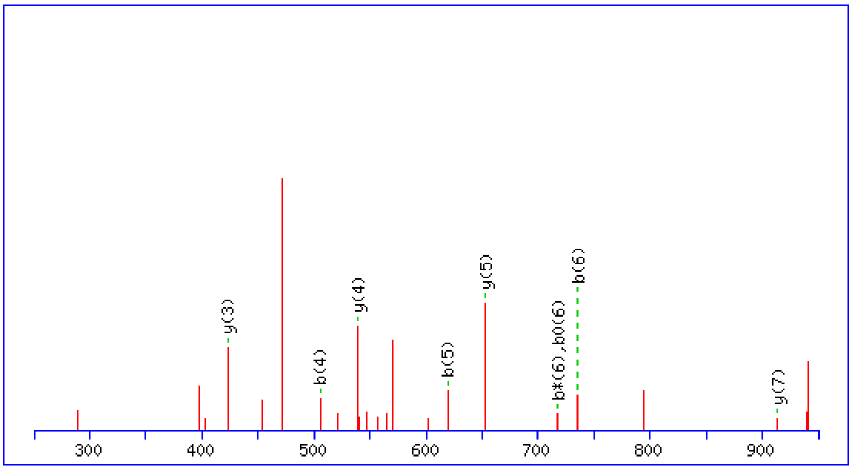
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQEELDLQR**
Found in **AT1G22275.1** in **TAIR_Arabidopsis**, Symbols: ZYP1, ZYP1b | ZYP1b | chr1:7867234-7872055 FORWARD

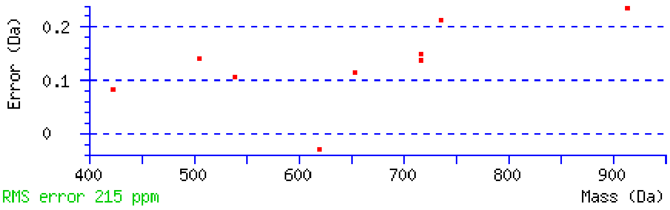
Match to Query 3806: 1156.552394 from(579.283473,2+) index(3095)
Title: Elution from: 32.150 to 32.150 scan no 3882 cid35.00 polarity:+
Data file D6h-2_2.mgf

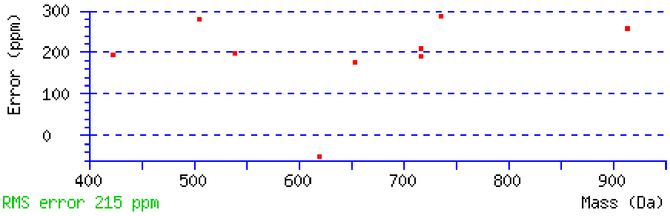
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1156.5516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.039
Matches : 9/84 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							9
2	245.1410	123.0741	227.1174	114.0624			Q	1043.4778	522.2425	1025.4542	513.2308	1025.4673	513.2373	8
3	375.1806	188.0940	357.1571	179.0822	357.1701	179.0887	E	***913.4252***	457.2162	895.4016	448.2044	895.4146	448.2109	7
4	**505.2203**	253.1138	487.1967	244.1020	487.2097	244.1085	E	783.3855	392.1964	765.3620	383.1846	765.3750	383.1911	6
5	**619.3014**	310.1543	601.2778	301.1425	601.2908	301.1490	L	***653.3459***	327.1766	635.3223	318.1648	635.3354	318.1713	5
6	**735.3254**	368.1663	717.3018	359.1545	717.3148	359.1610	D	***539.2648***	270.1360	521.2412	261.1243	521.2543	261.1308	4
7	849.4065	425.2069	831.3829	416.1951	831.3959	416.2016	L	***423.2408***	212.1241	405.2173	203.1123			3
8	979.4591	490.2332	961.4355	481.2214	961.4485	481.2279	Q	309.1597	155.0835	291.1362	146.0717			2
9							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LQEELDLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1156.5516	0.0008	LQEELDLQR

AT1G22275.1

5.2	1156.5543	-0.0019	SLRNDHGTLK
2.0	1156.5516	0.0008	ITTVSSHVDGK
0.9	1156.5491	0.0033	VYRIFCTGK
0.2	1156.5516	0.0008	LSGAGPSNVDVK

Mascot: http://www.matrixscience.com/

AT1G22300.1

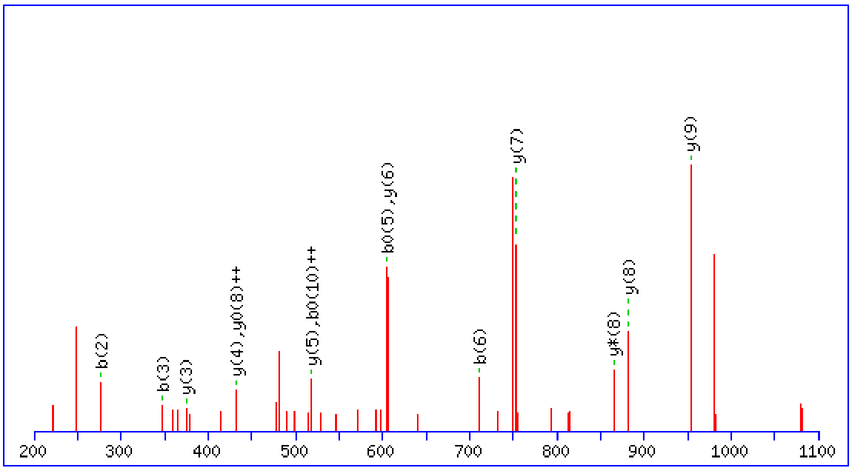
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLAEFSSGAER**
Found in **AT1G22300.1** in **TAIR_Arabidopsis**, Symbols: GF14 EPSILON, GRF10 | GRF10 (GENERAL REGULATORY FACTOR 10); protein phosphorylated amino acid binding | chr1:7879135-7881092 REVERSE

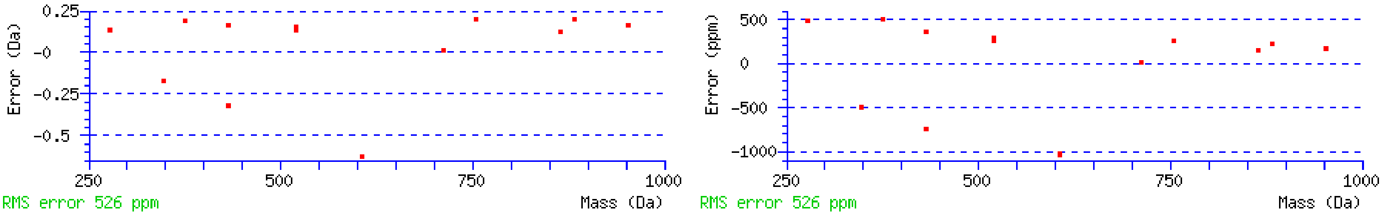
Match to Query 4327: 1228.569936 from(615.292244,2+) index(3333)
Title: Elution from: 34.208 to 34.208 scan no 4208 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1228.5724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 7.7e-005
Matches : 14/92 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							11
2	**277.1547**	139.0810			L	1066.5164	533.7618	1049.4898	525.2485	1048.5058	524.7565	10
3	**348.1918**	174.5995			A	***953.4323***	477.2198	936.4058	468.7065	935.4217	468.2145	9
4	477.2344	239.1208	459.2238	230.1155	E	***882.3952***	441.7012	865.3686	433.1880	864.3846	432.6959	8
5	624.3028	312.6550	606.2922	303.6498	F	***753.3526***	377.1799	736.3260	368.6667	735.3420	368.1747	7
6	**711.3348**	356.1710	693.3243	347.1658	S	***606.2842***	303.6457	589.2576	295.1325	588.2736	294.6404	6
7	798.3668	399.6871	780.3563	390.6818	S	***519.2522***	260.1297	502.2256	251.6164	501.2416	251.1244	5
8	855.3883	428.1978	837.3777	419.1925	G	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	4
9	926.4254	463.7164	908.4149	454.7111	A	***375.1987***	188.1030	358.1721	179.5897	357.1881	179.0977	3
10	1055.4680	528.2376	1037.4575	519.2324	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11					R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of YLAEFSSGAER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G22300.1

Score	Mr(calc)	Delta	Sequence
43.0	1228.5724	-0.0025	YLAEFSSGAER
4.8	1228.5731	-0.0031	MTDEERHRR
2.0	1228.5724	-0.0025	YLTFNNDQSK

AT1G22620.1

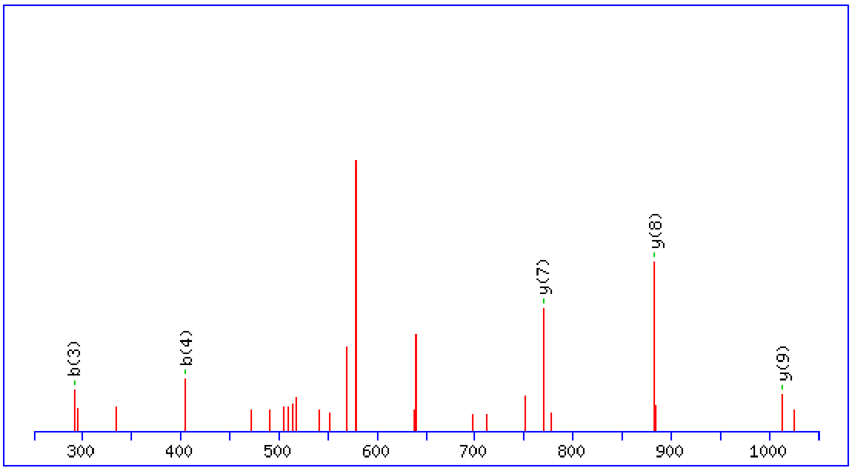
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASQLSHANTAR**
Found in **AT1G22620.1** in **TAIR_Arabidopsis**, Symbols: ATSAC1 | ATSAC1 (SUPPRESSOR OF ACTIN 1); phosphoinositide 5-phosphatase | chr1:7997878-8002776 REVERSE

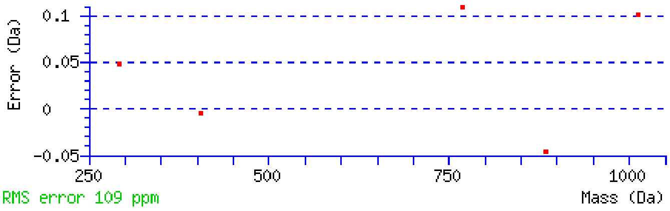
Match to Query 3931: 1172.525788 from(587.270170,2+) index(1469)
Title: Elution from: 18.744 to 18.744 scan no 1931 cid35.00 polarity:+
Data file C7-2_3.mgf

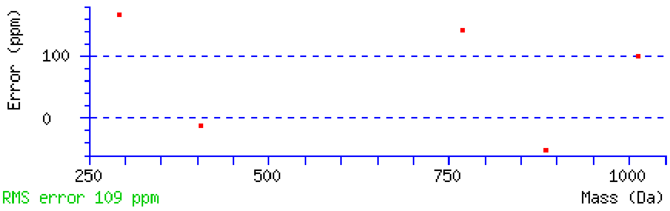
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1172.5259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.034
Matches : 5/110 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							11
2	161.0705	81.0389			143.0599	72.0336	S	1101.4990	551.2531	1083.4754	542.2413	1083.4884	542.2478	10
3	**291.1231**	146.0652	273.0996	137.0534	273.1126	137.0599	Q	***1013.4699***	507.2386	995.4463	498.2268	995.4594	498.2333	9
4	**405.2042**	203.1058	387.1807	194.0940	387.1937	194.1005	L	***883.4173***	442.2123	865.3937	433.2005	865.4067	433.2070	8
5	493.2333	247.1203	475.2097	238.1085	475.2227	238.1150	S	***769.3362***	385.1717	751.3126	376.1599	751.3256	376.1664	7
6	633.2833	317.1453	615.2597	308.1335	615.2727	308.1400	H	681.3071	341.1572	663.2835	332.1454	663.2966	332.1519	6
7	705.3175	353.1624	687.2939	344.1506	687.3069	344.1571	A	541.2571	271.1322	523.2335	262.1204	523.2465	262.1269	5
8	821.3545	411.1809	803.3309	402.1691	803.3439	402.1756	N	469.2230	235.1151	451.1994	226.1033	451.2124	226.1098	4
9	923.3992	462.2032	905.3756	453.1914	905.3886	453.1979	T	353.1860	177.0966	335.1624	168.0848	335.1754	168.0913	3
10	995.4333	498.2203	977.4097	489.2085	977.4228	489.2150	A	251.1412	126.0743	233.1177	117.0625			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ASQLSHANTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G22620.1

Score	Mr(calc)	Delta	Sequence
22.0	1172.5259	-0.0001	ASQLSHANTAR
7.5	1172.5254	0.0004	REWEIDPSK
3.6	1172.5281	-0.0023	REDYLAHPR
2.5	1172.5259	-0.0001	ASNRPSEAPAR
2.5	1172.5254	0.0004	SAGQSPWLGEK
2.3	1172.5281	-0.0023	EWRRGLGPGE
1.5	1172.5232	0.0026	DNGDAQNLLAK
1.4	1172.5288	-0.0030	MGATEPAVVER
0.9	1172.5261	-0.0003	TVEMTPEEVK

Mascot: http://www.matrixscience.com/

AT1G22780.1

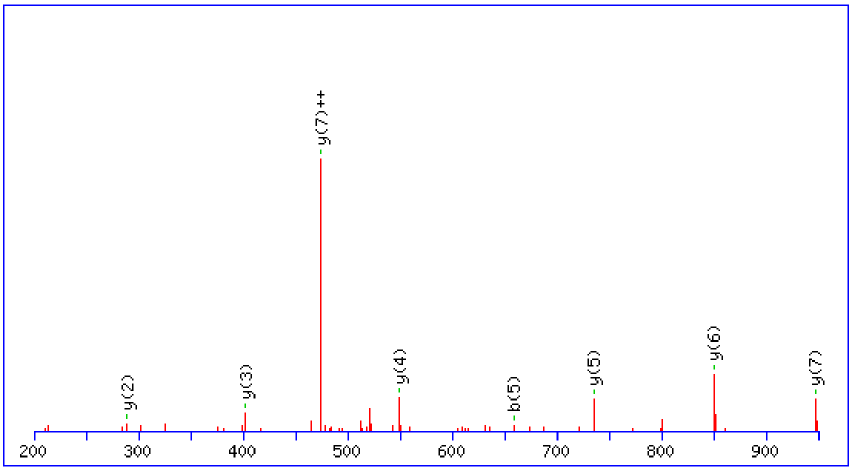
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPDWFLNR**
Found in **AT1G22780.1** in **TAIR_Arabidopsis**, Symbols: RPS18A, PFL1, PFL | PFL (POINTED FIRST LEAVES); structural constituent of ribosome | chr1:8067979-8069152 FORWARD

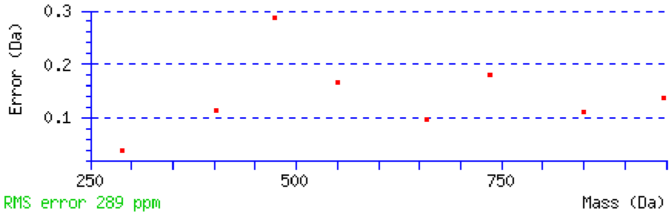
Match to Query 3254: 1059.549678 from(530.782115,2+) index(8165)
Title: Elution from: 71.149 to 71.149 scan no 10663 cid35.00 polarity:+
Data file D1d-3_1.mgf

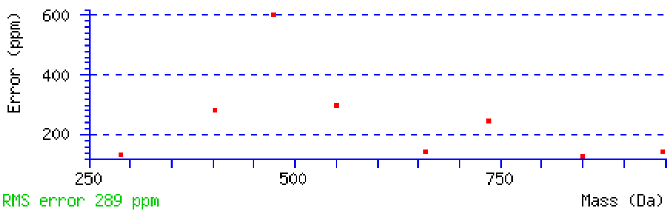
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1059.5502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 1.5e-005
Matches : 8/58 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							8
2	211.1441	106.0757					P	947.4734	474.2403	930.4468	465.7271	929.4628	465.2350	7
3	326.1710	163.5892			308.1605	154.5839	D	850.4206	425.7139	833.3941	417.2007	832.4100	416.7087	6
4	512.2504	256.6288			494.2398	247.6235	W	735.3937	368.2005	718.3671	359.6872			5
5	659.3188	330.1630			641.3082	321.1577	F	549.3144	275.1608	532.2878	266.6475			4
6	772.4028	386.7051			754.3923	377.6998	L	402.2459	201.6266	385.2194	193.1133			3
7	886.4458	443.7265	869.4192	435.2132	868.4352	434.7212	N	289.1619	145.0846	272.1353	136.5713			2
8							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IPDWFLNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.6	1059.5502	-0.0005	IPDWFLNR

AT1G22780.1

5.7	1059.5495	0.0002	IIEEMRNR
2.7	1059.5495	0.0002	ACIEANVKR

Mascot: http://www.matrixscience.com/

AT1G22840.1

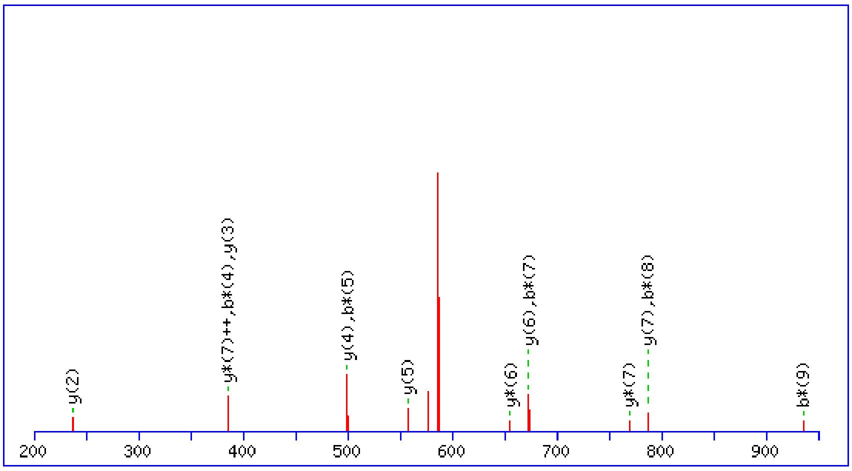
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGPNLNGLFGR**
Found in **AT1G22840.1** in **TAIR_Arabidopsis**, Symbols: CYTC-1, ATCYTC-A | ATCYTC-A/CYTC-1 (CYTOCHROME C-1); electron carrier | chr1:8079373-8080275 FORWARD

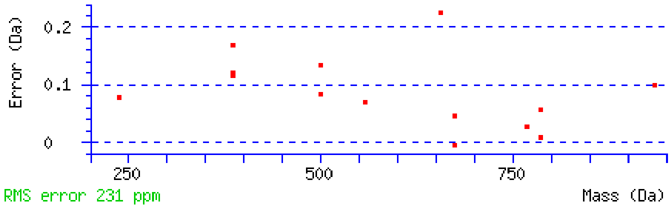
Match to Query 3483: 1188.559094 from(595.286823,2+) index(5945)
Title: Elution from: 55.199 to 55.199 scan no 7759 cid35.00 polarity:+
Data file D1d-1_3.mgf

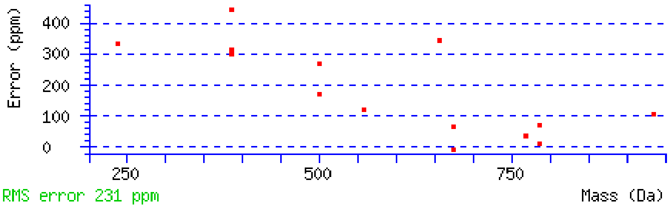
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1188.5594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00025
Matches : 14/80 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	131.0599	66.0336	113.0363	57.0218	**Q**					**11**
2	189.0784	95.0428	171.0548	86.0311	**G**	1059.5140	530.2607	1041.4904	521.2489	**10**
3	287.1282	144.0677	269.1046	135.0560	**P**	1001.4955	501.2514	983.4719	492.2396	**9**
4	403.1652	202.0862	385.1416	193.0745	**N**	903.4457	452.2265	885.4221	443.2147	**8**
5	517.2463	259.1268	499.2227	250.1150	**L**	***787.4087***	394.2080	769.3852	385.1962	**7**
6	633.2833	317.1453	615.2597	308.1335	**N**	***673.3276***	337.1675	655.3041	328.1557	**6**
7	691.3018	346.1545	673.2782	337.1428	**G**	***557.2906***	279.1490	539.2671	270.1372	**5**
8	805.3829	403.1951	787.3593	394.1833	**L**	***499.2721***	250.1397	481.2486	241.1279	**4**
9	953.4484	477.2278	935.4248	468.2160	**F**	***385.1910***	193.0992	367.1675	184.0874	**3**
10	1011.4669	506.2371	993.4433	497.2253	**G**	***237.1256***	119.0664	219.1020	110.0546	**2**
11					**R**	179.1071	90.0572	161.0835	81.0454	**1**





NCBI **BLAST** search of QGPNLNGLFGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G22840.1

Score	Mr(calc)	Delta	Sequence
45.8	1188.5594	-0.0003	QGPNLNGLFGR
19.1	1188.5623	-0.0032	GDILFLHMSK
5.2	1188.5601	-0.0010	DAIVILSCER
3.8	1188.5623	-0.0032	KHLMDYLEK
3.5	1188.5572	0.0019	AAVGPPSSSSRR
3.2	1188.5567	0.0024	AESELNWKAK
2.9	1188.5567	0.0024	IKTWGGSDPSK

Mascot: http://www.matrixscience.com/

AT1G23190.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESQEALSPLVDLALK**
Found in **AT1G23190.1** in **TAIR_Arabidopsis**, Symbols: | phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative | chr1:8219935-8224175 FORWARD

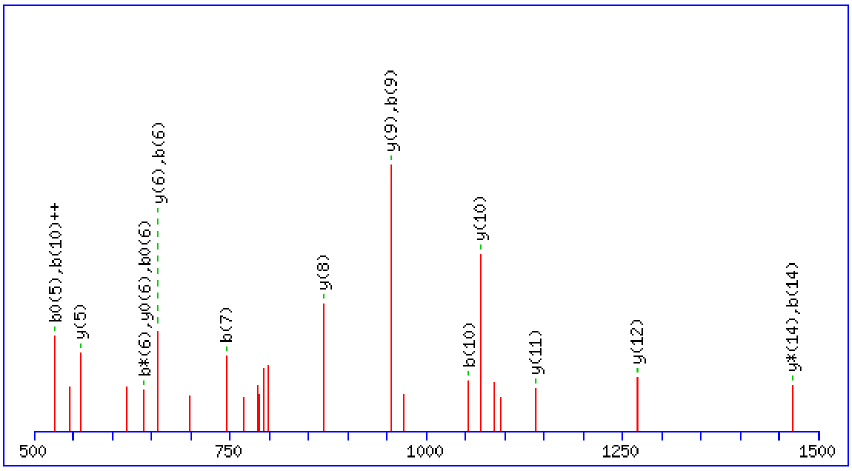
Match to Query 7391: 1611.871616 from(806.943084,2+) index(9570)
Title: Elution from: 86.596 to 86.596 scan no 13071 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1500 Da Full range

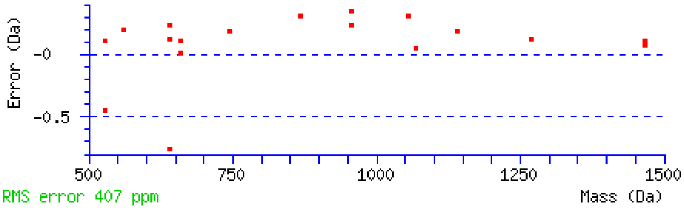
Label all possible matches ○ Label matches used for scoring ●

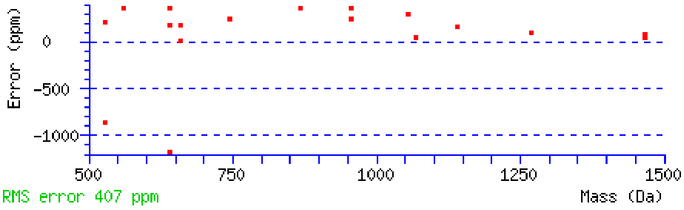
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1611.8719
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 1.5e-007
Matches : 18/156 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	217.0819	109.0446			199.0713	100.0393	S	1483.8366	742.4220	1466.8101	733.9087	1465.8261	733.4167	14
3	345.1405	173.0739	328.1139	164.5606	327.1299	164.0686	Q	1396.8046	698.9059	1379.7781	690.3927	1378.7940	689.9007	13
4	474.1831	237.5952	457.1565	229.0819	456.1725	228.5899	E	***1268.7460***	634.8767	1251.7195	626.3634	1250.7355	625.8714	12
5	545.2202	273.1137	528.1936	264.6005	527.2096	264.1084	A	***1139.7034***	570.3554	1122.6769	561.8421	1121.6929	561.3501	11
6	***658.3042***	329.6558	641.2777	321.1425	640.2937	320.6505	L	***1068.6663***	534.8368	1051.6398	526.3235	1050.6558	525.8315	10
7	***745.3363***	373.1718	728.3097	364.6585	727.3257	364.1665	S	***955.5823***	478.2948	938.5557	469.7815	937.5717	469.2895	9
8	842.3890	421.6982	825.3625	413.1849	824.3785	412.6929	P	***868.5502***	434.7788	851.5237	426.2655	850.5397	425.7735	8
9	***955.4731***	478.2402	938.4466	469.7269	937.4625	469.2349	L	771.4975	386.2524	754.4709	377.7391	753.4869	377.2471	7
10	***1054.5415***	527.7744	1037.5150	519.2611	1036.5310	518.7691	V	***658.4134***	329.7103	641.3869	321.1971	640.4028	320.7051	6
11	1169.5685	585.2879	1152.5419	576.7746	1151.5579	576.2826	D	***559.3450***	280.1761	542.3184	271.6629	541.3344	271.1708	5
12	1282.6525	641.8299	1265.6260	633.3166	1264.6420	632.8246	L	444.3180	222.6627	427.2915	214.1494			4
13	1353.6896	677.3485	1336.6631	668.8352	1335.6791	668.3432	A	331.2340	166.1206	314.2074	157.6074			3
14	***1466.7737***	733.8905	1449.7472	725.3772	1448.7631	724.8852	L	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





AT1G23190.1

NCBI **BLAST** search of ESQEALSPLVDLALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.2	1611.8719	-0.0003	ESQEALSPLVDLALK
12.1	1611.8733	-0.0016	WPNLEVEVSKKQR
1.1	1611.8692	0.0024	TSNRTALQVLPGNNK

Mascot: http://www.matrixscience.com/

AT1G23290.1

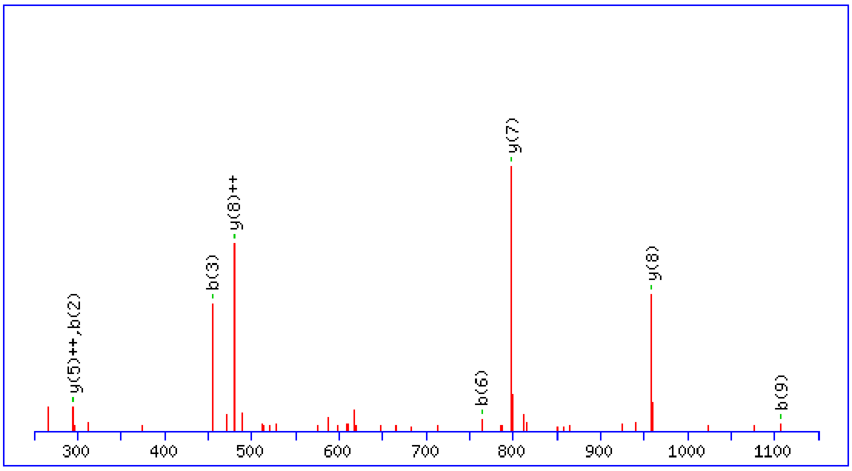
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFCPIVNLDK**
Found in **AT1G23290.1** in **TAIR_Arabidopsis**, Symbols: RPL27AB, RPL27A | RPL27A (RIBOSOMAL PROTEIN L27A); structural constituent of ribosome | chr1:8262996-8263436 FORWARD

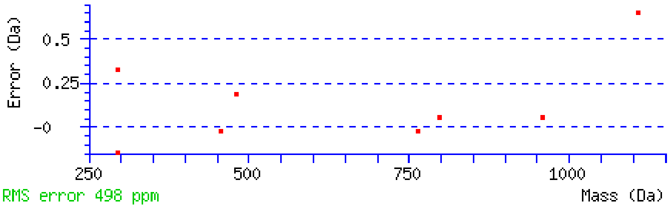
Match to Query 3974: 1251.633414 from(626.823983,2+) index(6998)
Title: Elution from: 63.244 to 63.244 scan no 9237 cid35.00 polarity:+
Data file D1d-2_3.mgf

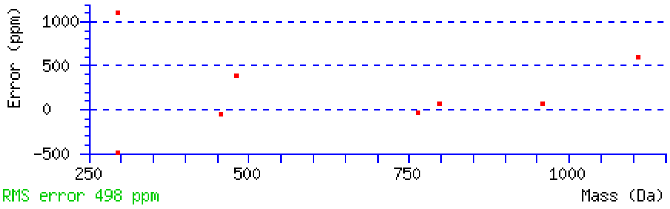
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [250] to [1150] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1251.6322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.002
Matches : 8/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	***295.1441***	148.0757					F	1105.5710	553.2892	1088.5445	544.7759	1087.5605	544.2839	9
3	***455.1748***	228.0910					C	**958.5026**	479.7550	941.4761	471.2417	940.4921	470.7497	8
4	552.2275	276.6174					P	**798.4720**	399.7396	781.4454	391.2264	780.4614	390.7343	7
5	665.3116	333.1594					I	701.4192	351.2132	684.3927	342.7000	683.4087	342.2080	6
6	***764.3800***	382.6936					V	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
7	878.4229	439.7151	861.3964	431.2018			N	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	4
8	991.5070	496.2571	974.4804	487.7439			L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
9	***1106.5339***	553.7706	1089.5074	545.2573	1088.5234	544.7653	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FFCPIVNLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G23290.1

Score	Mr(calc)	Delta	Sequence
32.9	1251.6322	0.0012	FFCPIVNLDK
3.8	1251.6315	0.0019	MMKSLANAVGAK
0.1	1251.6347	-0.0013	KTDELSLDGFK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPTGALQAAK**
Found in **AT1G23310.1** in **TAIR_Arabidopsis**, Symbols: AOAT1, GGT1 | GGT1 (ALANINE-2-OXOGLUTARATE AMINOTRANSFERASE 1) | chr1:8268709-8271318 REVERSE

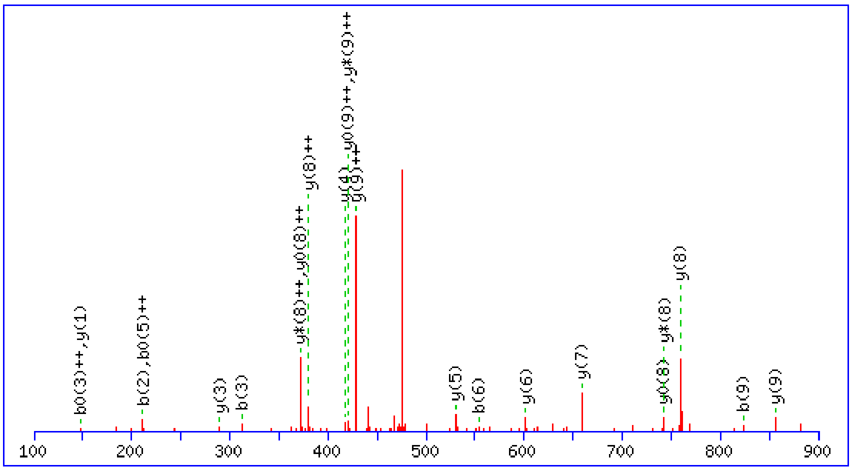
Match to Query 2131: 968.565944 from(485.290248,2+) index(2000)
Title: Elution from: 23.085 to 23.085 scan no 2557 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 900 Da Full range

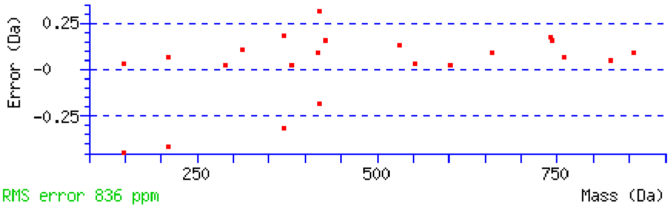
Label all possible matches ○ Label matches used for scoring ●

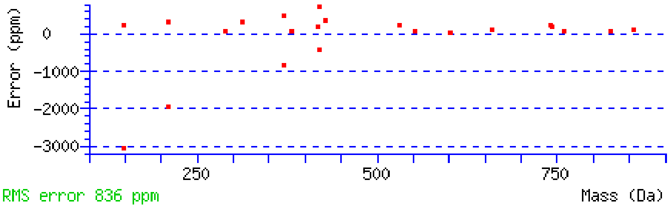
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.5655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 1.7e-005
Matches : 22/78 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							10
2	**211.1441**	106.0757					P	***856.4887***	428.7480	839.4621	420.2347	838.4781	419.7427	9
3	**312.1918**	156.5995			294.1812	147.5942	T	***759.4359***	380.2216	742.4094	371.7083	741.4254	371.2163	8
4	369.2132	185.1103			351.2027	176.1050	G	***658.3883***	329.6978	641.3617	321.1845			7
5	440.2504	220.6288			422.2398	211.6235	A	***601.3668***	301.1870	584.3402	292.6738			6
6	**553.3344**	277.1709			535.3239	268.1656	L	***530.3297***	265.6685	513.3031	257.1552			5
7	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	Q	***417.2456***	209.1264	400.2191	200.6132			4
8	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	A	***289.1870***	145.0972	272.1605	136.5839			3
9	**823.4672**	412.2373	806.4407	403.7240	805.4567	403.2320	A	218.1499	109.5786	201.1234	101.0653			2
10							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LPTGALQAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G23310.1

Score	Mr(calc)	Delta	Sequence
51.3	968.5655	0.0005	LPTGALQAAK
10.5	968.5655	0.0005	LTSLLASHK
8.3	968.5654	0.0005	IPKELQNK
6.9	968.5655	0.0005	SGPVKSVPAK
4.1	968.5668	-0.0009	IRQFLHR
2.5	968.5655	0.0005	LSHITTGIK
1.6	968.5655	0.0005	LLQNSPGLK
0.8	968.5655	0.0005	LREVLDPK

Mascot: http://www.matrixscience.com/

AT1G23410.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TITLEVESSDTIDNVK**
Found in **AT1G23410.1** in **TAIR_Arabidopsis**, Symbols: | ubiquitin extension protein, putative / 40S ribosomal protein S27A (RPS27aA) | chr1:8314929-8315399 FORWARD

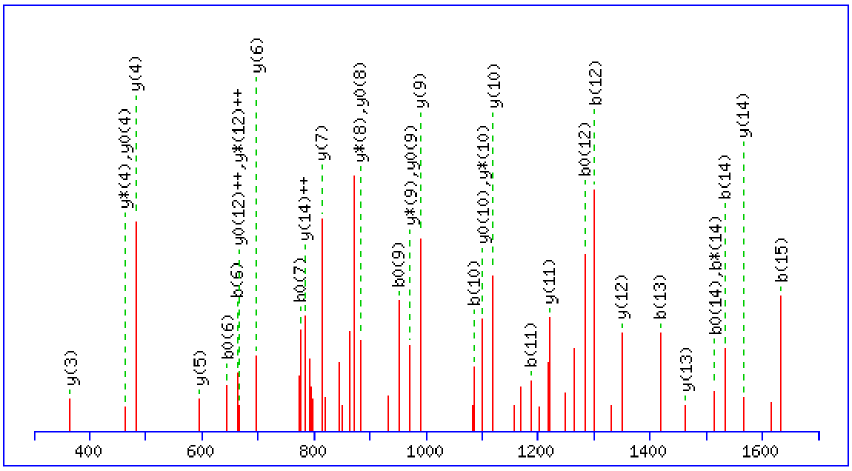
Match to Query 8101: 1780.829488 from(891.422020,2+) index(5835)
Title: Elution from: 54.560 to 54.560 scan no 7531 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

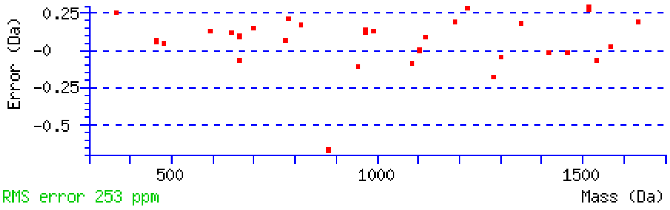
Show Y-axis ☐

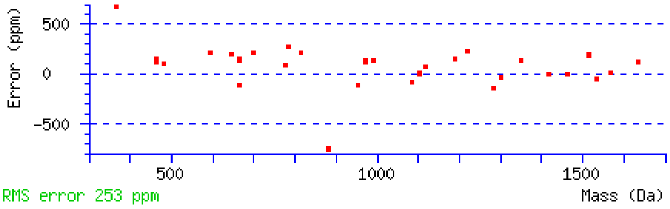


Monoisotopic mass of neutral peptide Mr(calc): 1780.8302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 114 **Expect:** 4.6e-011
Matches : 35/148 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	**T**							**16**
2	217.1331	109.0702			199.1225	100.0649	**I**	1679.7928	840.4001	1661.7692	831.3883	1661.7823	831.3948	**15**
3	319.1778	160.0925			301.1672	151.0873	**T**	***1565.7117***	783.3595	1547.6881	774.3477	1547.7012	774.3542	**14**
4	433.2589	217.1331			415.2483	208.1278	**L**	***1463.6670***	732.3371	1445.6434	723.3254	1445.6565	723.3319	**13**
5	563.2985	282.1529			545.2880	273.1476	**E**	***1349.5859***	675.2966	1331.5623	666.2848	1331.5754	666.2913	**12**
6	**663.3640**	332.1856			645.3534	323.1803	**V**	***1219.5463***	610.2768	1201.5227	601.2650	1201.5357	601.2715	**11**
7	793.4036	397.2054			775.3930	388.2002	**E**	***1119.4808***	560.2441	1101.4573	551.2323	1101.4703	551.2388	**10**
8	881.4327	441.2200			863.4221	432.2147	**S**	***989.4412***	495.2242	971.4176	486.2125	971.4306	486.2190	**9**
9	969.4617	485.2345			951.4512	476.2292	**S**	901.4122	451.2097	883.3886	442.1979	883.4016	442.2044	**8**
10	**1085.4857**	543.2465			1067.4751	534.2412	**D**	***813.3831***	407.1952	795.3595	398.1834	795.3725	398.1899	**7**
11	**1187.5304**	594.2688			1169.5199	585.2636	**T**	***697.3591***	349.1832	679.3355	340.1714	679.3485	340.1779	**6**
12	**1301.6115**	651.3094			1283.6010	642.3041	**I**	***595.3144***	298.1608	577.2908	289.1490	577.3038	289.1556	**5**
13	**1417.6355**	709.3214			1399.6249	700.3161	**D**	***481.2333***	241.1203	463.2097	232.1085	463.2227	232.1150	**4**
14	**1533.6725**	767.3399	1515.6489	758.3281	1515.6619	758.3346	**N**	***365.2093***	183.1083	347.1857	174.0965			**3**
15	**1633.7379**	817.3726	1615.7144	808.3608	1615.7274	808.3673	**V**	249.1723	125.0898	231.1487	116.0780			**2**
16							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT1G23410.1





NCBI **BLAST** search of TITLEVESSDTIDNVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
114.4	1780.8302	-0.0008	TITLEVESSDTIDNVK
12.1	1780.8282	0.0013	MKTESPERVVLPDSR
12.0	1780.8309	-0.0014	NHTLTNRMTGVGNTLK
9.8	1780.8277	0.0017	ELEGSLKWMVDVDVK
8.4	1780.8309	-0.0014	RQILQAACETLSNPR
7.5	1780.8311	-0.0017	SLEEVMTPSVVAMNLK
2.7	1780.8297	-0.0002	IGDFGLSNFYRGQRK
2.6	1780.8304	-0.0009	EGRYLLSRDYMTLK
2.1	1780.8255	0.0040	EEEENVVKAMETKVK
1.5	1780.8282	0.0013	LVAEGMRAANLEENVK

Mascot: http://www.matrixscience.com/

AT1G23730.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTFDLWELDFK**
Found in **AT1G23730.1** in **TAIR_Arabidopsis**, Symbols: | carbonic anhydrase, putative / carbonate dehydratase, putative | chr1:8395954-8398003 FORWARD

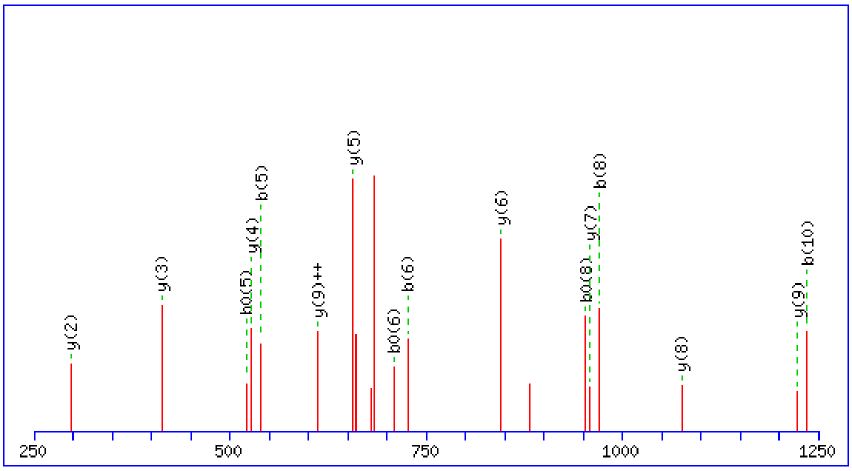
Match to Query 5151: 1382.614830 from(692.314691,2+) index(10468)
Title: Elution from: 100.716 to 100.716 scan no 14911 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1250 Da Full range

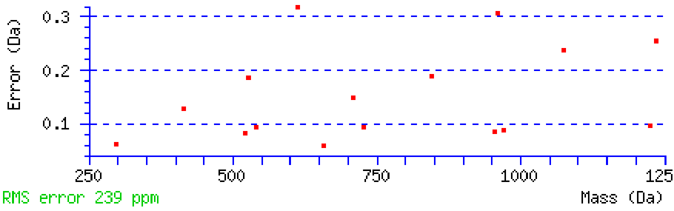
Label all possible matches ○ Label matches used for scoring ●

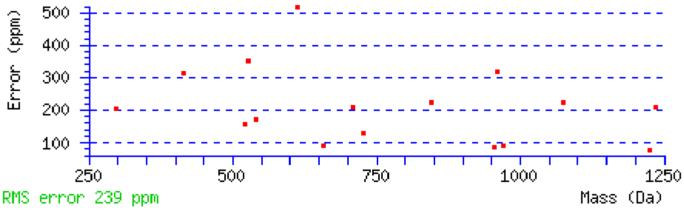
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.6168
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 1.5e-007
Matches : 16/94 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			**G**							**11**
2	161.0705	81.0389	143.0599	72.0336	**T**	1325.6057	663.3065	1307.5821	654.2947	1307.5951	654.3012	**10**
3	309.1359	155.0716	291.1254	146.0663	**F**	***1223.5609***	612.2841	1205.5374	603.2723	1205.5504	603.2788	**9**
4	425.1599	213.0836	407.1493	204.0783	**D**	***1075.4955***	538.2514	1057.4719	529.2396	1057.4849	529.2461	**8**
5	**539.2410**	270.1241	521.2304	261.1189	**L**	***959.4715***	480.2394	941.4479	471.2276	941.4609	471.2341	**7**
6	**727.3144**	364.1608	709.3038	355.1556	**W**	***845.3904***	423.1988	827.3668	414.1871	827.3798	414.1936	**6**
7	857.3540	429.1807	839.3435	420.1754	**E**	***657.3170***	329.1622	639.2934	320.1504	639.3065	320.1569	**5**
8	**971.4351**	486.2212	953.4246	477.2159	**L**	***527.2774***	264.1423	509.2538	255.1305	509.2668	255.1371	**4**
9	1087.4591	544.2332	1069.4485	535.2279	**D**	***413.1963***	207.1018	395.1727	198.0900	395.1857	198.0965	**3**
10	**1235.5246**	618.2659	1217.5140	609.2606	**F**	***297.1723***	149.0898	279.1487	140.0780			**2**
11					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of GTFDLWELDFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G23730.1

Score	Mr(calc)	Delta	Sequence
77.3	1382.6168	-0.0020	GTFDLWELDFK
9.0	1382.6124	0.0024	FSESAELITTDR
8.5	1382.6128	0.0020	ELSRTSDTGDRK
4.7	1382.6177	-0.0029	FRDANQRNDVK
4.4	1382.6180	-0.0032	IEELMDKSFNK
3.0	1382.6173	-0.0025	SFHSFLGQTNTK
1.8	1382.6146	0.0002	KEAEFNDFLEK
1.6	1382.6111	0.0038	ALMNGSMNLSSVK
1.6	1382.6111	0.0038	ALMNGSMNLSSVK
1.2	1382.6158	-0.0010	LNLSSTAMDSVSK

AT1G23740.1

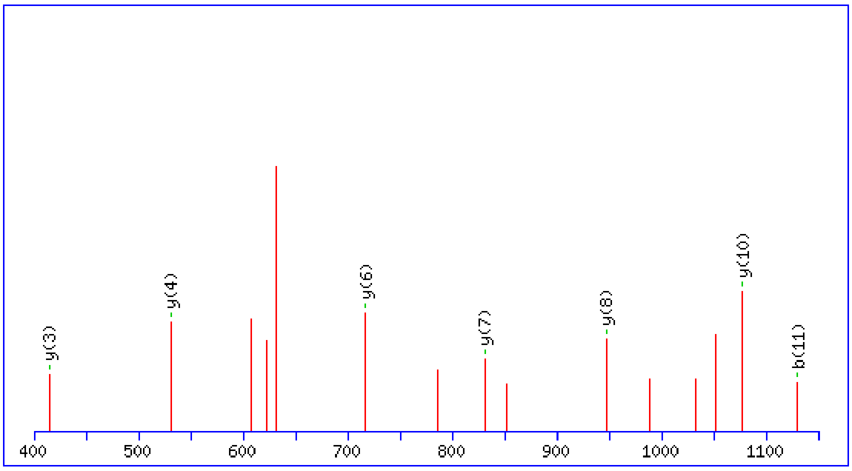
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLGADLAIDYTK**
Found in **AT1G23740.1** in **TAIR_Arabidopsis**, Symbols: | oxidoreductase, zinc-binding dehydrogenase family protein | chr1:8398234-8399645 REVERSE

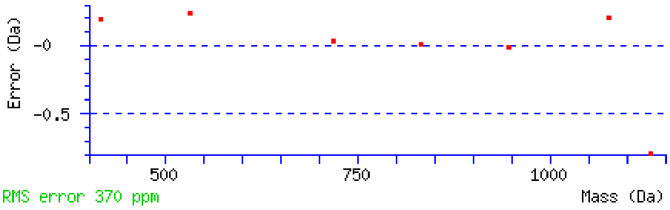
Match to Query 4935: 1278.611844 from(640.313198,2+) index(6496)
Title: Elution from: 56.680 to 56.680 scan no 8137 cid35.00 polarity:+
Data file 0-1_1.mgf

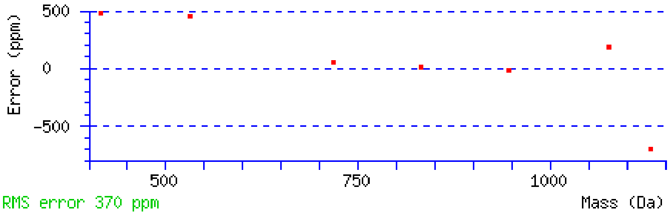
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1278.6118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00083
Matches : 7/108 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							12
2	203.1174	102.0624	185.1069	93.0571	L	1191.5900	596.2986	1173.5664	587.2868	1173.5794	587.2934	11
3	261.1359	131.0716	243.1254	122.0663	G	***1077.5089***	539.2581	1059.4853	530.2463	1059.4983	530.2528	10
4	333.1701	167.0887	315.1595	158.0834	A	1019.4904	510.2488	1001.4668	501.2370	1001.4798	501.2436	9
5	449.1941	225.1007	431.1835	216.0954	D	***947.4563***	474.2318	929.4327	465.2200	929.4457	465.2265	8
6	563.2752	282.1412	545.2646	273.1359	L	***831.4323***	416.2198	813.4087	407.2080	813.4217	407.2145	7
7	635.3093	318.1583	617.2987	309.1530	A	***717.3512***	359.1792	699.3276	350.1674	699.3406	350.1739	6
8	749.3904	375.1988	731.3798	366.1936	I	645.3170	323.1622	627.2934	314.1504	627.3065	314.1569	5
9	865.4144	433.2108	847.4038	424.2056	D	***531.2359***	266.1216	513.2123	257.1098	513.2254	257.1163	4
10	1029.4748	515.2410	1011.4642	506.2357	Y	***415.2120***	208.1096	397.1884	199.0978	397.2014	199.1043	3
11	1131.5195	566.2634	1113.5089	557.2581	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
12					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SLGADLAIDYTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G23740.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.4	1278.6118	0.0001	SLGADLAIDYTK
7.3	1278.6140	-0.0022	EGYYIGIEVPK
2.3	1278.6144	-0.0026	SLRVVDFEGNK
2.1	1278.6122	-0.0004	TVKRESEATGGK
1.7	1278.6122	-0.0004	AQKTDTSGVISR
1.7	1278.6131	-0.0012	KQARIMEMQK
1.5	1278.6118	0.0001	LLTETENATFK
1.4	1278.6131	-0.0012	TVVPSVRMSMR
1.3	1278.6145	-0.0026	AKSYSDHVKTK
0.9	1278.6149	-0.0031	KNQLPRSSSSR

Mascot: http://www.matrixscience.com/

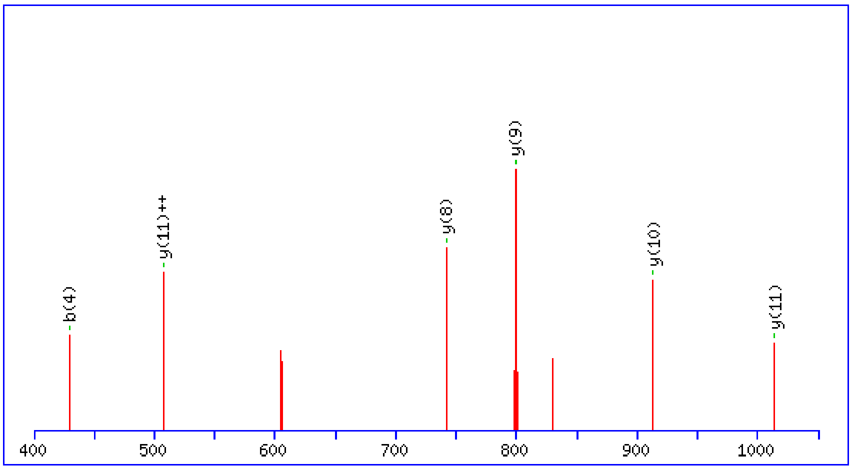
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLVIGGGDGGVLR**
Found in **AT1G23820.1** in **TAIR_Arabidopsis**, Symbols: SPDS1 | SPDS1 (SPERMIDINE SYNTHASE 1) | chr1:8420267-8422713 FORWARD

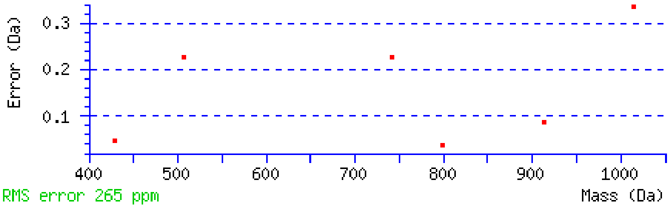
Match to Query 3794: 1226.656840 from(614.335696,2+) index(5259)
Title: Elution from: 48.515 to 48.515 scan no 6798 cid35.00 polarity:+
Data file D1d-2_3.mgf

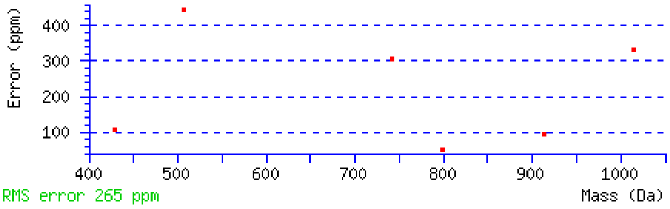
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1226.6559
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0048
Matches : 6/96 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400			V							13
2	215.1538	108.0805			L	1127.5978	564.3025	1109.5742	555.2907	1109.5872	555.2972	12
3	315.2193	158.1133			V	***1013.5167***	507.2620	995.4931	498.2502	995.5061	498.2567	11
4	429.3004	215.1538			I	***913.4512***	457.2292	895.4276	448.2175	895.4406	448.2240	10
5	487.3189	244.1631			G	***799.3701***	400.1887	781.3465	391.1769	781.3595	391.1834	9
6	545.3374	273.1723			G	***741.3516***	371.1794	723.3280	362.1677	723.3410	362.1742	8
7	603.3559	302.1816			G	683.3331	342.1702	665.3095	333.1584	665.3225	333.1649	7
8	719.3798	360.1936	701.3693	351.1883	D	625.3146	313.1609	607.2910	304.1492	607.3041	304.1557	6
9	777.3983	389.2028	759.3878	380.1975	G	509.2906	255.1490	491.2671	246.1372			5
10	835.4168	418.2121	817.4063	409.2068	G	451.2721	226.1397	433.2486	217.1279			4
11	935.4823	468.2448	917.4717	459.2395	V	393.2536	197.1305	375.2301	188.1187			3
12	1049.5634	525.2853	1031.5528	516.2801	L	293.1882	147.0977	275.1646	138.0859			2
13					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VLVIGGGDGGVLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G23820.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.0	1226.6559	0.0010	VLVIGGGDGGVLR

Mascot: http://www.matrixscience.com/

AT1G23900.1

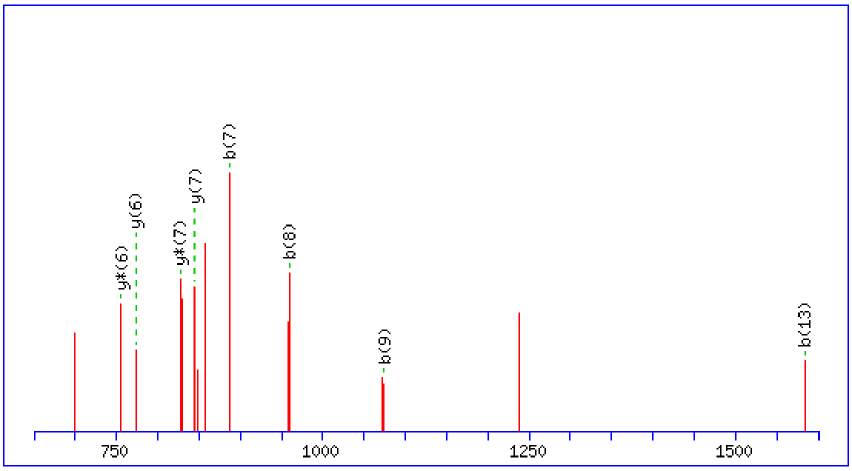
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNNIRYVALNMLMK**
Found in **AT1G23900.1** in **TAIR_Arabidopsis**, Symbols: GAMMA-ADR, GAMMA-ADAPTIN 1 | GAMMA-ADAPTIN 1; clathrin binding | chr1:8441368-8447141 FORWARD

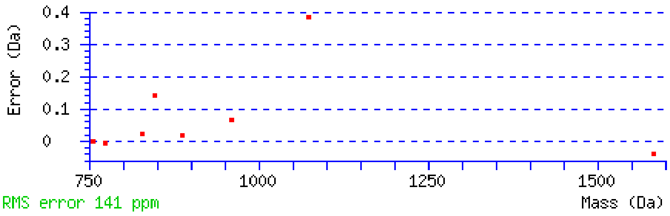
Match to Query 7867: 1730.793128 from(866.403840,2+) index(6043)
Title: Elution from: 52.880 to 52.880 scan no 7740 cid35.00 polarity:+
Data file D6h-3_3.mgf

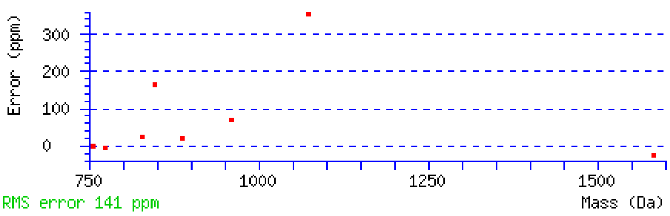
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1730.7970
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.041
Matches : 8/182 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	117.0313	59.0193			99.0207	50.0140	D					14
2	233.0683	117.0378	215.0447	108.0260	215.0577	108.0325	N	1615.7803	808.3938	1597.7567	799.3820	13
3	349.1052	175.0563	331.0817	166.0445	331.0947	166.0510	N	1499.7433	750.3753	1481.7197	741.3635	12
4	463.1863	232.0968	445.1628	223.0850	445.1758	223.0915	I	1383.7063	692.3568	1365.6828	683.3450	11
5	623.2756	312.1414	605.2520	303.1296	605.2650	303.1362	R	1269.6252	635.3163	1251.6017	626.3045	10
6	787.3360	394.1716	769.3124	385.1598	769.3254	385.1663	Y	1109.5360	555.2716	1091.5124	546.2598	9
7	***887.4014***	444.2043	869.3778	435.1926	869.3908	435.1991	V	945.4756	473.2414	927.4520	464.2297	8
8	***959.4356***	480.2214	941.4120	471.2096	941.4250	471.2161	A	**845.4102**	423.2087	827.3866	414.1969	7
9	***1073.5167***	537.2620	1055.4931	528.2502	1055.5061	528.2567	L	**773.3760**	387.1917	755.3524	378.1799	6
10	1189.5537	595.2805	1171.5301	586.2687	1171.5431	586.2752	N	659.2949	330.1511	641.2713	321.1393	5
11	1321.5912	661.2992	1303.5676	652.2874	1303.5806	652.2939	M	543.2579	272.1326	525.2343	263.1208	4
12	1435.6723	718.3398	1417.6487	709.3280	1417.6617	709.3345	L	411.2204	206.1138	393.1968	197.1020	3
13	***1583.7047***	792.3560	1565.6811	783.3442	1565.6941	783.3507	M	297.1393	149.0733	279.1157	140.0615	2
14							K	149.1069	75.0571	131.0833	66.0453	1





AT1G23900.1

NCBI **BLAST** search of DNNIRYVALNMLMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
23.1	1730.7970	-0.0039	DNNIRYVALNMLMK	Oxidation M13 50.00%
23.1	1730.7970	-0.0039	DNNIRYVALNMLMK	Oxidation M11 50.00%
6.5	1730.7957	-0.0026	VTSEFDSDSLLFLNK	
3.2	1730.7888	0.0044	NAPPPATGIEAVDSMVK	
2.8	1730.7962	-0.0030	VNDHPISTVESNLSAK	
1.1	1730.7888	0.0044	NSLLNMYVKSGETEK	
0.2	1730.7880	0.0051	QVRSYQGSEVWKDK	

AT1G24020.1

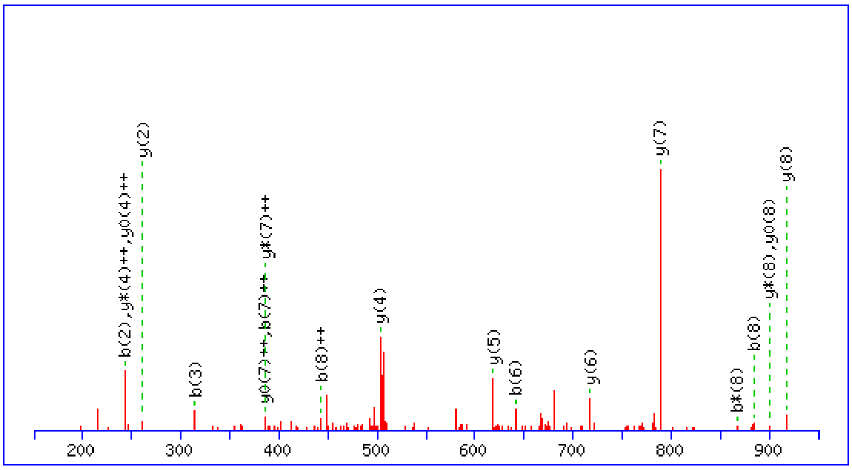
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEAVDLENK**
Found in **AT1G24020.1** in **TAIR_Arabidopsis**, Symbols: MLP423 | MLP423 (MLP-LIKE PROTEIN 423) | chr1:8500642-8501447 REVERSE

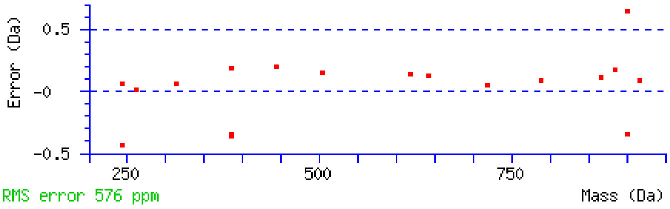
Match to Query 2658: 1029.534028 from(515.774290,2+) index(2540)
Title: Elution from: 26.697 to 26.697 scan no 3179 cid35.00 polarity:+
Data file D6h-3_2.mgf

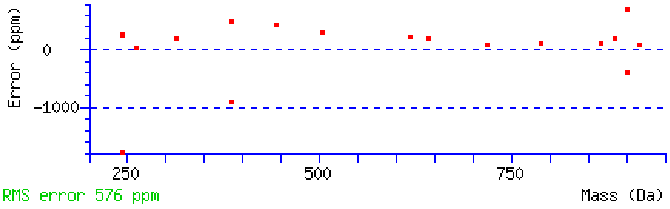
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1029.5342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 6.9e-005
Matches : 19/76 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							9
2	***243.1339***	122.0706			225.1234	113.0653	E	***917.4575***	459.2324	900.4309	450.7191	899.4469	450.2271	8
3	***314.1710***	157.5892			296.1605	148.5839	A	***788.4149***	394.7111	771.3883	386.1978	770.4043	385.7058	7
4	413.2395	207.1234			395.2289	198.1181	V	***717.3777***	359.1925	700.3512	350.6792	699.3672	350.1872	6
5	528.2664	264.6368			510.2558	255.6316	D	***618.3093***	309.6583	601.2828	301.1450	600.2988	300.6530	5
6	***641.3505***	321.1789			623.3399	312.1736	L	***503.2824***	252.1448	486.2558	243.6316	485.2718	243.1395	4
7	770.3931	**385.7002**			752.3825	376.6949	E	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
8	***884.4360***	**442.7216**	867.4094	434.2084	866.4254	433.7163	N	***261.1557***	131.0815	244.1292	122.5682			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IEAVDLENK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.1	1029.5342	-0.0002	IEAVDLENK

AT1G24020.1

6.2	1029.5342	-0.0002	IAEIDEVNK
4.5	1029.5315	0.0025	GQQQQASRK
2.7	1029.5342	-0.0002	IQEDITPSK

AT1G24100.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLPSLSYDELPSFVGR**
Found in **AT1G24100.1** in **TAIR_Arabidopsis**, Symbols: UGT74B1 | UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups | chr1:8525536-8526999 REVERSE

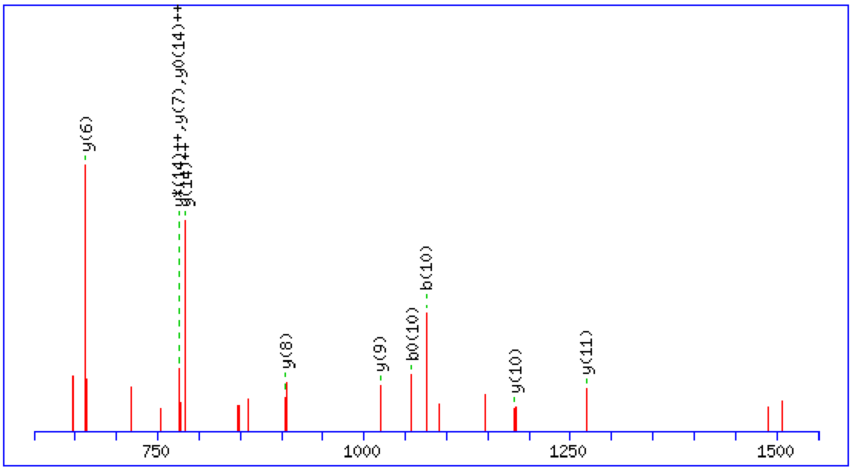
Match to Query 8427: 1735.875292 from(868.944922,2+) index(9790)
Title: Elution from: 89.901 to 89.901 scan no 13446 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 600 to 1550 Da Full range

Label all possible matches ○ Label matches used for scoring ●

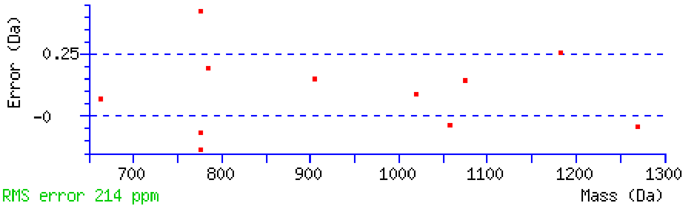
Show Y-axis ☐

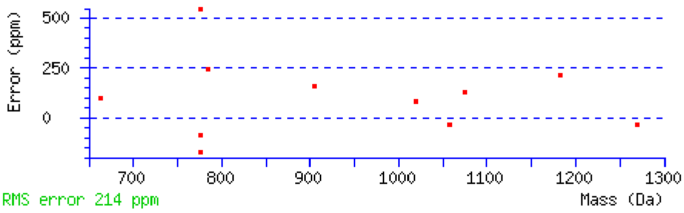


Monoisotopic mass of neutral peptide Mr(calc): 1735.8781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0055
Matches : 11/136 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180			**G**							**16**
2	171.1128	86.0600			**L**	1679.8639	840.4356	1662.8374	831.9223	1661.8533	831.4303	**15**
3	268.1656	134.5864			**P**	1566.7798	783.8936	1549.7533	775.3803	1548.7693	774.8883	**14**
4	355.1976	178.1024	337.1870	169.0972	**S**	1469.7271	735.3672	1452.7005	726.8539	1451.7165	726.3619	**13**
5	468.2817	234.6445	450.2711	225.6392	**L**	1382.6951	691.8512	1365.6685	683.3379	1364.6845	682.8459	**12**
6	555.3137	278.1605	537.3031	269.1552	**S**	***1269.6110***	635.3091	1252.5844	626.7959	1251.6004	626.3039	**11**
7	718.3770	359.6921	700.3665	350.6869	**Y**	***1182.5790***	591.7931	1165.5524	583.2798	1164.5684	582.7878	**10**
8	833.4040	417.2056	815.3934	408.2003	**D**	***1019.5156***	510.2615	1002.4891	501.7482	1001.5051	501.2562	**9**
9	962.4466	481.7269	944.4360	472.7216	**E**	***904.4887***	452.7480	887.4621	444.2347	886.4781	443.7427	**8**
10	1075.5306	538.2689	1057.5201	529.2637	**L**	***775.4461***	388.2267	758.4196	379.7134	757.4355	379.2214	**7**
11	1172.5834	586.7953	1154.5728	577.7900	**P**	***662.3620***	331.6847	645.3355	323.1714	644.3515	322.6794	**6**
12	1259.6154	630.3113	1241.6048	621.3061	**S**	565.3093	283.1583	548.2827	274.6450	547.2987	274.1530	**5**
13	1406.6838	703.8455	1388.6733	694.8403	**F**	478.2772	239.6423	461.2507	231.1290			**4**
14	1505.7522	753.3798	1487.7417	744.3745	**V**	331.2088	166.1081	314.1823	157.5948			**3**
15	1562.7737	781.8905	1544.7631	772.8852	**G**	232.1404	116.5738	215.1139	108.0606			**2**
16					**R**	175.1190	88.0631	158.0924	79.5498			**1**

AT1G24100.1





NCBI **BLAST** search of GLPSLSYDELPSFVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.9	1735.8781	-0.0028	GLPSLSYDELPSFVGR
6.8	1735.8740	0.0013	ERVDFAEETINASKK
1.1	1735.8749	0.0004	LQMSWMPSLLSQKR

Mascot: http://www.matrixscience.com/

AT1G24180.1

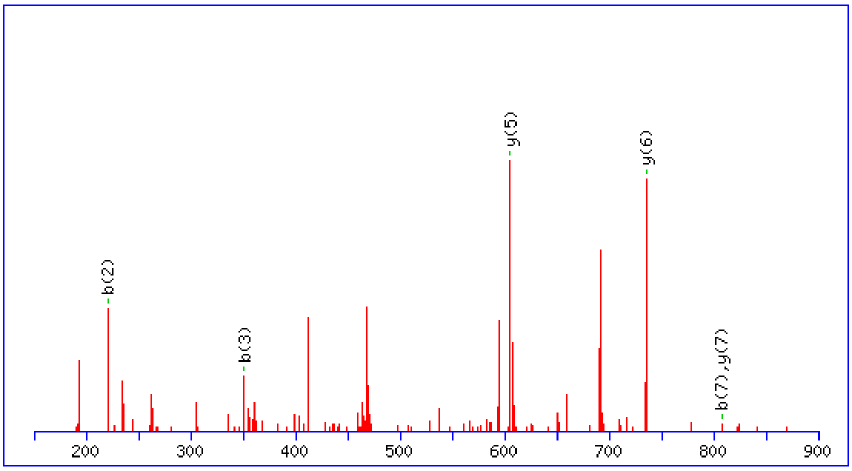
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAKEHALK**
Found in **AT1G24180.1** in **TAIR_Arabidopsis**, Symbols: IAR4 | IAR4 (IAA-conjugate-resistant 4); pyruvate dehydrogenase (acetyl-transferring) | chr1:8560766-8563371 REVERSE

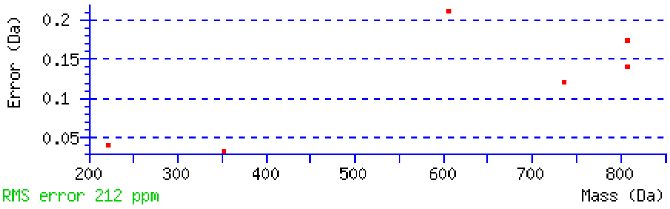
Match to Query 2108: 954.494594 from(478.254573,2+) index(4844)
Title: Elution from: 43.276 to 43.276 scan no 6026 cid35.00 polarity:+
Data file C7-1_1.mgf

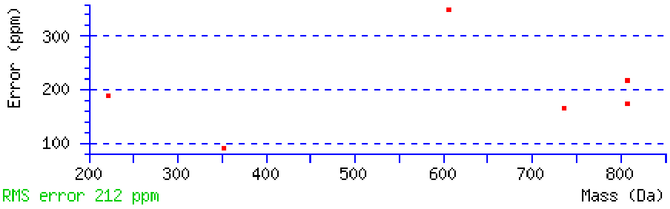
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 954.4931
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.024
Matches : 6/66 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							8
2	*221.1069*	111.0571					A	*807.4349*	404.2211	789.4114	395.2093	789.4244	395.2158	7
3	*351.1959*	176.1016	333.1723	167.0898			K	*735.4008*	368.2040	717.3772	359.1922	717.3902	359.1988	6
4	481.2355	241.1214	463.2120	232.1096	463.2250	232.1161	E	*605.3118*	303.1595	587.2882	294.1477	587.3012	294.1542	5
5	621.2856	311.1464	603.2620	302.1346	603.2750	302.1411	H	475.2721	238.1397	457.2486	229.1279			4
6	693.3197	347.1635	675.2961	338.1517	675.3091	338.1582	A	335.2221	168.1147	317.1985	159.1029			3
7	*807.4008*	404.2040	789.3772	395.1922	789.3902	395.1988	L	263.1880	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FAKEHALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.4	954.4931	0.0015	FAKEHALK

AT1G24180.1

19.3	954.4965	-0.0019	MISHKALK
10.3	954.4938	0.0008	SLMEIPLK
8.2	954.4931	0.0015	LLGHGTFAK
6.7	954.4965	-0.0019	MLGPSLLGR
6.3	954.4931	0.0015	FEAAKLHK
6.3	954.4965	-0.0019	MHVTLAKK
5.8	954.4965	-0.0019	CGVVVKGPK

AT1G24290.1

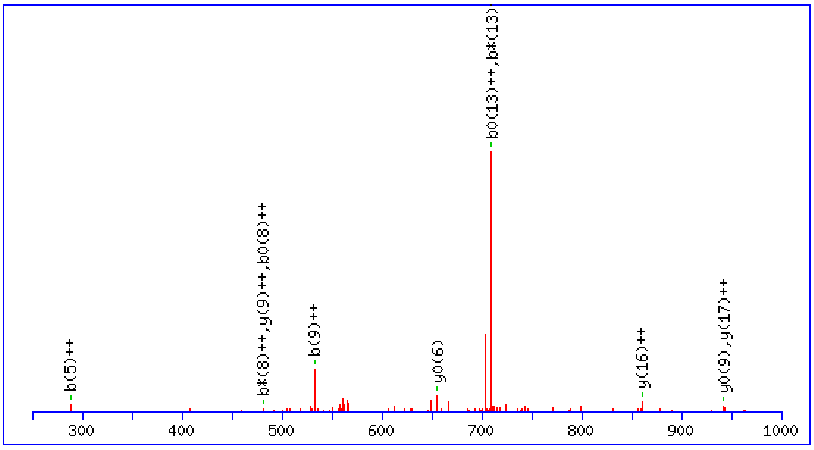
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPSLYRFVSLSAVTSGVKDVR**
Found in **AT1G24290.1** in **TAIR_Arabidopsis**, Symbols: | AAA-type ATPase family protein | chr1:8612639-8614216 REVERSE

Match to Query 10271: 2295.223168 from(574.813068,4+) index(3820)
Title: Elution from: 38.362 to 38.362 scan no 4855 cid35.00 polarity:+
Data file D1d-2_1.mgf

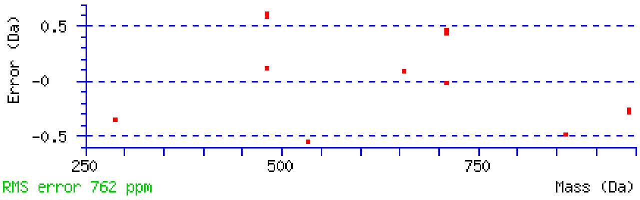
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

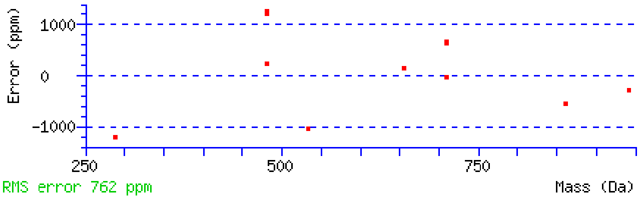


Monoisotopic mass of neutral peptide Mr(calc): 2295.2223
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.004
Matches : 12/226 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							21
2	213.0870	107.0471			195.0764	98.0418	P	2181.2026	1091.1050	2164.1761	1082.5917	2163.1921	1082.0997	20
3	300.1190	150.5631			282.1084	141.5579	S	2084.1499	1042.5786	2067.1233	1034.0653	2066.1393	1033.5733	19
4	413.2031	207.1052			395.1925	198.0999	L	1997.1178	999.0626	1980.0913	990.5493	1979.1073	990.0573	18
5	576.2664	**288.6368**			558.2558	279.6316	Y	1884.0338	942.5205	1867.0072	934.0073	1866.0232	933.5152	17
6	732.3675	366.6874	715.3410	358.1741	714.3569	357.6821	R	1720.9704	860.9889	1703.9439	852.4756	1702.9599	851.9836	16
7	879.4359	440.2216	862.4094	431.7083	861.4254	431.2163	F	1564.8693	782.9383	1547.8428	774.4250	1546.8588	773.9330	15
8	978.5043	489.7558	961.4778	481.2425	960.4938	480.7505	V	1417.8009	709.4041	1400.7744	700.8908	1399.7904	700.3988	14
9	1065.5364	**533.2718**	1048.5098	524.7585	1047.5258	524.2665	S	1318.7325	659.8699	1301.7060	651.3566	1300.7219	650.8646	13
10	1178.6204	589.8139	1161.5939	581.3006	1160.6099	580.8086	L	1231.7005	616.3539	1214.6739	607.8406	1213.6899	607.3486	12
11	1265.6525	633.3299	1248.6259	624.8166	1247.6419	624.3246	S	1118.6164	559.8118	1101.5899	551.2986	1100.6058	550.8066	11
12	1336.6896	668.8484	1319.6630	660.3352	1318.6790	659.8431	A	1031.5844	516.2958	1014.5578	507.7826	1013.5738	507.2905	10
13	1435.7580	718.3826	1418.7314	709.8694	1417.7474	709.3774	V	960.5473	480.7773	943.5207	472.2640	942.5367	471.7720	9
14	1536.8057	768.9065	1519.7791	760.3932	1518.7951	759.9012	T	861.4789	431.2431	844.4523	422.7298	843.4683	422.2378	8
15	1623.8377	812.4225	1606.8111	803.9092	1605.8271	803.4172	S	760.4312	380.7192	743.4046	372.2060	742.4206	371.7139	7
16	1680.8592	840.9332	1663.8326	832.4199	1662.8486	831.9279	G	673.3991	337.2032	656.3726	328.6899	655.3886	328.1979	6
17	1779.9276	890.4674	1762.9010	881.9542	1761.9170	881.4621	V	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
18	1908.0225	954.5149	1890.9960	946.0016	1890.0120	945.5096	K	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	4
19	2023.0495	1012.0284	2006.0229	1003.5151	2005.0389	1003.0231	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
20	2122.1179	1061.5626	2105.0913	1053.0493	2104.1073	1052.5573	V	274.1874	137.5973	257.1608	129.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1

AT1G24290.1





NCBI **BLAST** search of DPSLYRFVSLSAVTSGVKDVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.5	2295.2223	0.0009	DPSLYRFVSLSAVTSGVKDVR
4.4	2295.2263	-0.0032	TVPFVLSFDNLTYNVSVRPK
0.2	2295.2184	0.0047	ELQFSVEVLFTGEKIGIGMAK

Mascot: http://www.matrixscience.com/

AT1G24360.1

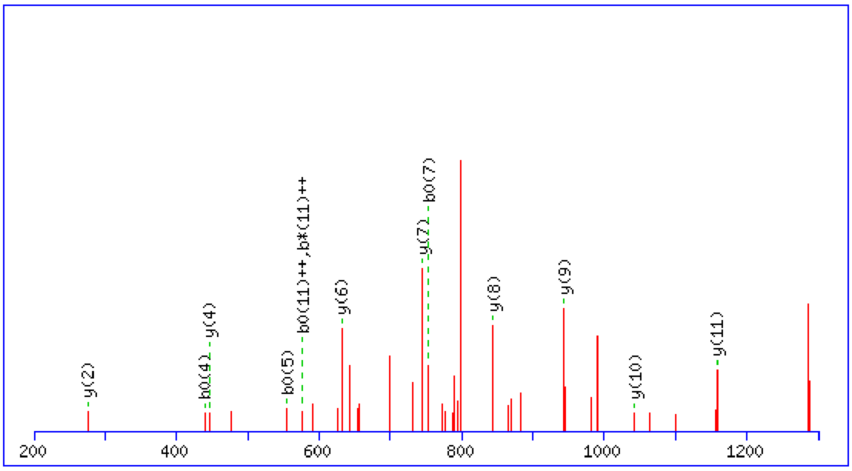
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **WGTIDVVVNNAGITR**
Found in **AT1G24360.1** in **TAIR_Arabidopsis**, Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640809-8643272 FORWARD

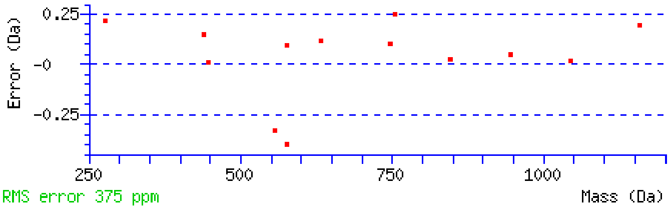
Match to Query 6877: 1613.849756 from(807.932154,2+) index(7327)
Title: Elution from: 67.498 to 67.498 scan no 9659 cid35.00 polarity:+
Data file D12h-2_2.mgf

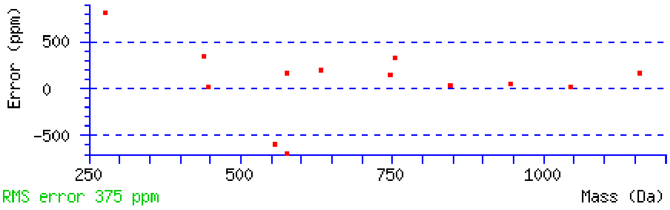
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1613.8526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0059
Matches : 13/146 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	187.0866	94.0469					**W**							**15**
2	244.1081	122.5577					**G**	1428.7805	714.8939	1411.7540	706.3806	1410.7700	705.8886	**14**
3	345.1557	173.0815			327.1452	164.0762	**T**	1371.7591	686.3832	1354.7325	677.8699	1353.7485	677.3779	**13**
4	458.2398	229.6235			440.2292	220.6183	**I**	1270.7114	635.8593	1253.6848	627.3461	1252.7008	626.8540	**12**
5	573.2667	287.1370			555.2562	278.1317	**D**	***1157.6273***	579.3173	1140.6008	570.8040	1139.6167	570.3120	**11**
6	672.3352	336.6712			654.3246	327.6659	**V**	***1042.6004***	521.8038	1025.5738	513.2905	1024.5898	512.7985	**10**
7	771.4036	386.2054			753.3930	377.2001	**V**	***943.5320***	472.2696	926.5054	463.7563	925.5214	463.2643	**9**
8	870.4720	435.7396			852.4614	426.7343	**V**	***844.4635***	422.7354	827.4370	414.2221	826.4530	413.7301	**8**
9	984.5149	492.7611	967.4884	484.2478	966.5043	483.7558	**N**	***745.3951***	373.2012	728.3686	364.6879	727.3846	364.1959	**7**
10	1098.5578	549.7826	1081.5313	541.2693	1080.5473	540.7773	**N**	***631.3522***	316.1797	614.3257	307.6665	613.3416	307.1745	**6**
11	1169.5949	585.3011	1152.5684	576.7878	1151.5844	576.2958	**A**	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	**5**
12	1226.6164	613.8118	1209.5899	605.2986	1208.6058	604.8066	**G**	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	**4**
13	1339.7005	670.3539	1322.6739	661.8406	1321.6899	661.3486	**I**	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	**3**
14	1440.7482	720.8777	1423.7216	712.3644	1422.7376	711.8724	**T**	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





AT1G24360.1

NCBI **BLAST** search of WGTIDVVVNNAGITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	1613.8526	-0.0028	WGTIDVVVNNAGITR

Mascot: http://www.matrixscience.com/

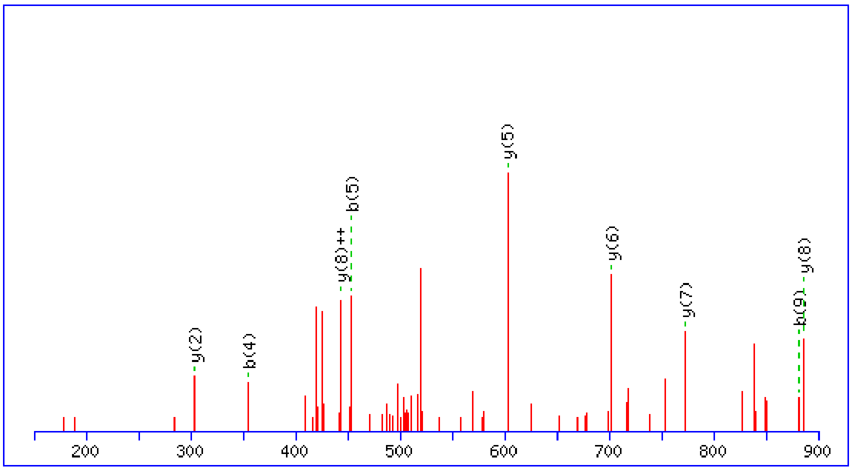
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVLAVADLER**
Found in **AT1G24510.1** in **TAIR_Arabidopsis**, Symbols: | T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative | chr1:8685492-8688089 REVERSE

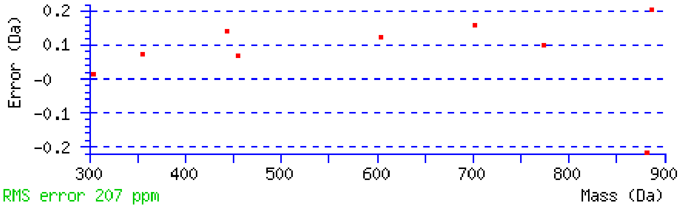
Match to Query 3051: 1055.597682 from(528.806117,2+) index(5245)
Title: Elution from: 45.610 to 45.610 scan no 6581 cid35.00 polarity:+
Data file D1d-3_3.mgf

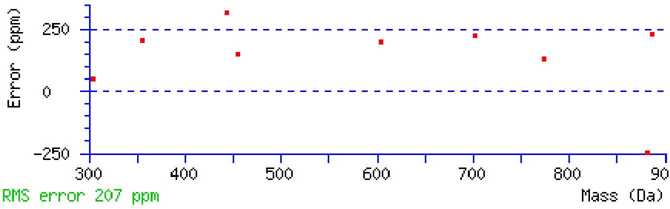
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1055.5975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0042
Matches : 9/76 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							10
2	171.1128	86.0600			V	985.5677	493.2875	968.5411	484.7742	967.5571	484.2822	9
3	284.1969	142.6021			L	***886.4993***	443.7533	869.4727	435.2400	868.4887	434.7480	8
4	**355.2340**	178.1206			A	***773.4152***	387.2112	756.3886	378.6980	755.4046	378.2060	7
5	**454.3024**	227.6548			V	***702.3781***	351.6927	685.3515	343.1794	684.3675	342.6874	6
6	525.3395	263.1734			A	***603.3097***	302.1585	586.2831	293.6452	585.2991	293.1532	5
7	640.3665	320.6869	622.3559	311.6816	D	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
8	753.4505	377.2289	735.4400	368.2236	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
9	**882.4931**	441.7502	864.4825	432.7449	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AVLAVADLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G24510.1

Score	Mr(calc)	Delta	Sequence
30.2	1055.5975	0.0002	AVLAVADLER
1.1	1055.5975	0.0002	AVLEDQLLR

Mascot: http://www.matrixscience.com/

AT1G26160.1

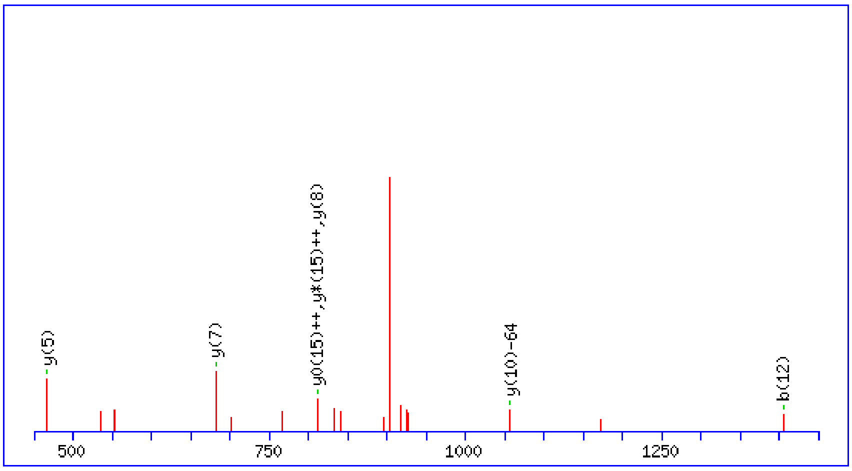
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAALKEMCEVLGGGLR**
Found in **AT1G26160.1** in **TAIR_Arabidopsis**, Symbols: | metal-dependent phosphohydrolase HD domain-containing protein | chr1:9044771-9046932 REVERSE

Match to Query 8688: 1870.839996 from(936.427274,2+) index(6849)
Title: Elution from: 60.703 to 60.703 scan no 8890 cid35.00 polarity:+
Data file D12h-3_2.mgf

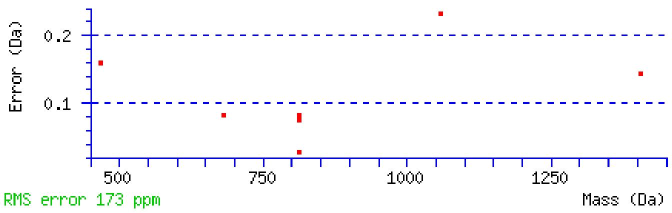
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

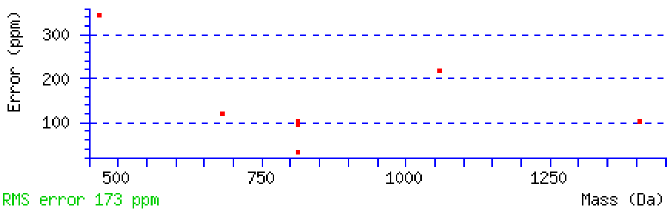


Monoisotopic mass of neutral peptide Mr(calc): 1870.8421
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.019
Matches : 7/264 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							17
2	233.0916	117.0494			215.0811	108.0442	T	1677.8115	839.4094	1659.7879	830.3976	1659.8009	830.4041	16
3	305.1258	153.0665			287.1152	144.0612	A	1575.7668	788.3870	1557.7432	779.3752	1557.7562	779.3818	15
4	377.1599	189.0836			359.1494	180.0783	A	1503.7326	752.3700	1485.7091	743.3582	1485.7221	743.3647	14
5	491.2410	246.1241			473.2304	237.1189	L	1431.6985	716.3529	1413.6749	707.3411	1413.6879	707.3476	13
6	621.3300	311.1687	603.3065	302.1569	603.3195	302.1634	K	1317.6174	659.3123	1299.5938	650.3005	1299.6068	650.3071	12
7	751.3697	376.1885	733.3461	367.1767	733.3591	367.1832	E	1187.5284	594.2678	1169.5048	585.2560	1169.5178	585.2625	11
8	835.4038	418.2056	817.3802	409.1938	817.3933	409.2003	M	***1057.4887***	529.2480	1039.4651	520.2362	1039.4782	520.2427	10
9	997.4285	499.2179	979.4050	490.2061	979.4180	490.2126	C	973.4546	487.2309	955.4310	478.2191	955.4440	478.2256	9
10	1127.4682	564.2377	1109.4446	555.2259	1109.4576	555.2324	E	***811.4299***	406.2186	793.4063	397.2068	793.4193	397.2133	8
11	1227.5336	614.2704	1209.5100	605.2587	1209.5231	605.2652	V	***681.3902***	341.1988	663.3667	332.1870			7
12	1341.6147	671.3110	1323.5911	662.2992	1323.6042	662.3057	L	581.3248	291.1660	563.3012	282.1542			6
13	1399.6332	700.3202	1381.6096	691.3085	1381.6227	691.3150	G	***467.2437***	234.1255	449.2201	225.1137			5
14	1457.6517	729.3295	1439.6281	720.3177	1439.6412	720.3242	G	409.2252	205.1162	391.2016	196.1044			4
15	1515.6702	758.3387	1497.6466	749.3270	1497.6597	749.3335	G	351.2067	176.1070	333.1831	167.0952			3
16	1629.7513	815.3793	1611.7277	806.3675	1611.7407	806.3740	L	293.1882	147.0977	275.1646	138.0859			2
17							R	179.1071	90.0572	161.0835	81.0454			1

AT1G26160.1





NCBI **BLAST** search of ETAALKEMCEVLGGGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.9	1870.8421	-0.0021	ETAALKEMCEVLGGGLR
11.2	1870.8410	-0.0010	AFDQVLGMEVAWNQVK
4.3	1870.8387	0.0013	KRTTLAELFMEDHDK
1.4	1870.8396	0.0004	HIVFCLCVMVVVDSR
0.4	1870.8437	-0.0037	TSFLHRLVCHTFDSK

Mascot: http://www.matrixscience.com/

AT1G26630.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYPQSAGNIR**
Found in **AT1G26630.1** in **TAIR_Arabidopsis**, Symbols: FBR12 | FBR12 (FUMONISIN B1-RESISTANT12); translation initiation factor | chr1:9205955-9207085 FORWARD

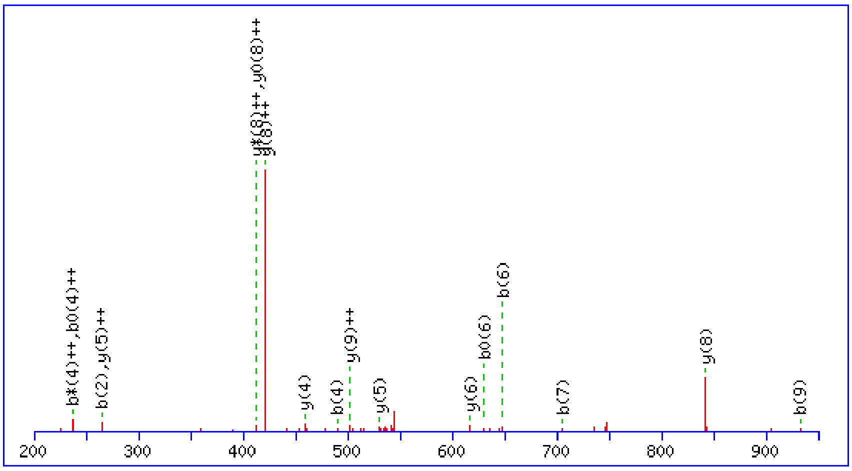
Match to Query 3601: 1105.551212 from(553.782882,2+) index(963)
Title: Elution from: 14.043 to 14.043 scan no 1308 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

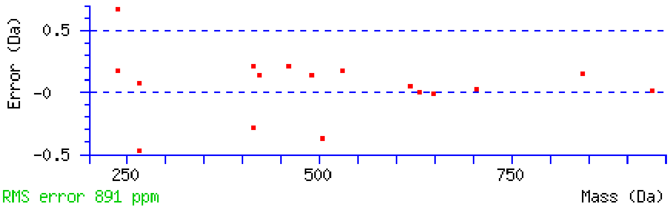
Label all possible matches ○ Label matches used for scoring ●

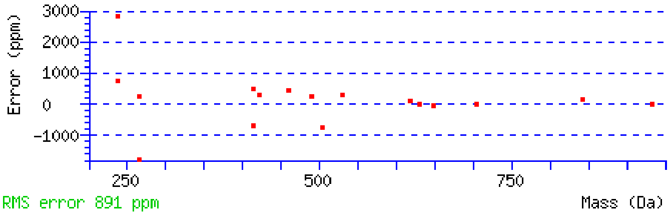
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1105.5516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0029
Matches : 17/92 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	***265.1183***	133.0628			247.1077	124.0575	Y	1005.5112	503.2592	988.4847	494.7460	987.5007	494.2540	9
3	362.1710	181.5892			344.1605	172.5839	P	***842.4479***	421.7276	825.4213	413.2143	824.4373	412.7223	8
4	***490.2296***	245.6185	473.2031	237.1052	472.2191	236.6132	Q	745.3951	373.2012	728.3686	364.6879	727.3846	364.1959	7
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	S	***617.3365***	309.1719	600.3100	300.6586	599.3260	300.1666	6
6	***648.2988***	324.6530	631.2722	316.1397	630.2882	315.6477	A	***530.3045***	265.6559	513.2780	257.1426			5
7	***705.3202***	353.1638	688.2937	344.6505	687.3097	344.1585	G	***459.2674***	230.1373	442.2409	221.6241			4
8	819.3632	410.1852	802.3366	401.6719	801.3526	401.1799	N	402.2459	201.6266	385.2194	193.1133			3
9	***932.4472***	466.7272	915.4207	458.2140	914.4367	457.7220	I	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TYPQSAGNIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G26630.1

Score	Mr(calc)	Delta	Sequence
27.9	1105.5516	-0.0004	TYPQSAGNIR
1.9	1105.5516	-0.0004	KASGSLDSWR
1.0	1105.5516	-0.0004	RYIPSEGER

AT1G26760.1

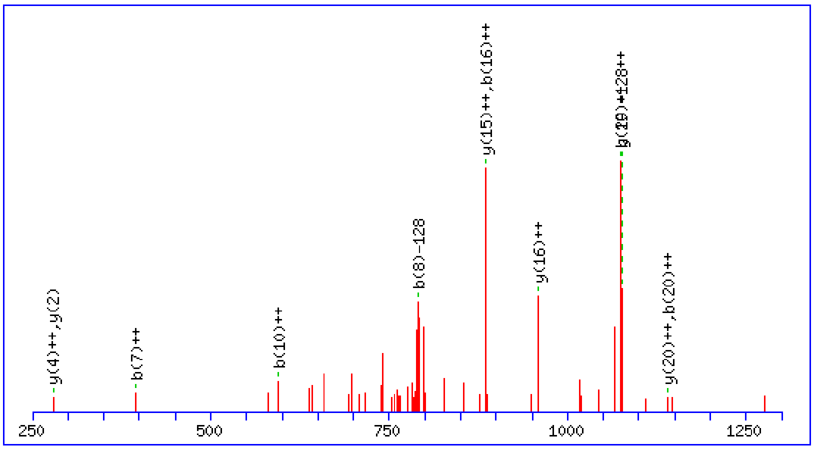
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAVEGMMKKHGGFSNIVEMEK**
Found in **AT1G26760.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr1:9248291-9249928 REVERSE

Match to Query 10276: 2427.012402 from(810.011410,3+) index(5891)
Title: Elution from: 52.204 to 52.204 scan no 7492 cid35.00 polarity:+
Data file 0-3_2.mgf

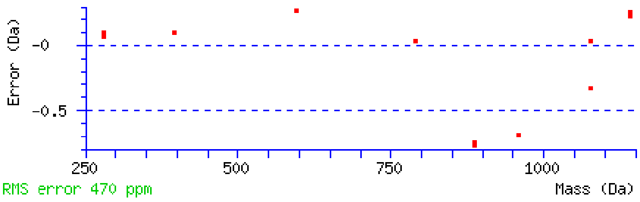
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

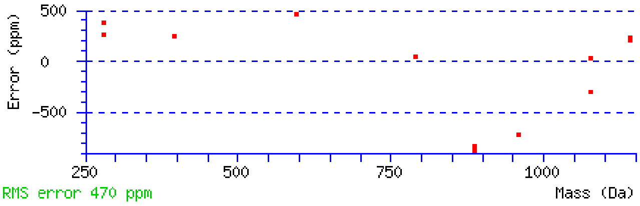


Monoisotopic mass of neutral peptide Mr(calc): 2427.0145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.015
Matches : 12/426 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235					M							21
2	221.0739	111.0406					A	2279.9894	1140.4983	2261.9658	1131.4865	2261.9788	1131.4930	20
3	321.1393	161.0733					V	2207.9552	1104.4813	2189.9316	1095.4695	2189.9447	1095.4760	19
4	451.1789	226.0931			433.1684	217.0878	E	2107.8898	1054.4485	2089.8662	1045.4367	2089.8792	1045.4432	18
5	509.1974	255.1024			491.1869	246.0971	G	1977.8502	989.4287	1959.8266	980.4169	1959.8396	980.4234	17
6	657.2299	329.1186			639.2193	320.1133	M	1919.8317	960.4195	1901.8081	951.4077	1901.8211	951.4142	16
7	789.2674	***395.1373***			771.2568	386.1321	M	1771.7992	886.4032	1753.7756	877.3915	1753.7887	877.3980	15
8	919.3564	460.1819	901.3328	451.1701	901.3459	451.1766	K	1639.7617	820.3845	1621.7381	811.3727	1621.7511	811.3792	14
9	1049.4455	525.2264	1031.4219	516.2146	1031.4349	516.2211	K	1509.6727	755.3400	1491.6491	746.3282	1491.6621	746.3347	13
10	1189.4955	***595.2514***	1171.4719	586.2396	1171.4849	586.2461	H	1379.5836	690.2955	1361.5601	681.2837	1361.5731	681.2902	12
11	1247.5140	624.2606	1229.4904	615.2488	1229.5034	615.2553	G	1239.5336	620.2704	1221.5100	611.2587	1221.5231	611.2652	11
12	1305.5325	653.2699	1287.5089	644.2581	1287.5219	644.2646	G	1181.5151	591.2612	1163.4915	582.2494	1163.5046	582.2559	10
13	1453.5979	727.3026	1435.5743	718.2908	1435.5874	718.2973	F	1123.4966	562.2519	1105.4730	553.2402	1105.4861	553.2467	9
14	1541.6270	771.3171	1523.6034	762.3053	1523.6164	762.3118	S	975.4312	488.2192	957.4076	479.2074	957.4206	479.2139	8
15	1657.6640	829.3356	1639.6404	820.3238	1639.6534	820.3303	N	887.4021	444.2047	869.3785	435.1929	869.3915	435.1994	7
16	1771.7451	***886.3762***	1753.7215	877.3644	1753.7345	877.3709	I	771.3651	386.1862	753.3415	377.1744	753.3545	377.1809	6
17	1871.8105	936.4089	1853.7869	927.3971	1853.8000	927.4036	V	657.2840	329.1456	639.2604	320.1339	639.2734	320.1404	5
18	2001.8502	1001.4287	1983.8266	992.4169	1983.8396	992.4234	E	557.2186	279.1129	539.1950	270.1011	539.2080	270.1076	4
19	2149.8826	***1075.4449***	2131.8590	1066.4331	2131.8720	1066.4397	M	427.1789	214.0931	409.1554	205.0813	409.1684	205.0878	3
20	2279.9222	***1140.4647***	2261.8986	1131.4530	2261.9117	1131.4595	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
21							K	149.1069	75.0571	131.0833	66.0453			1

AT1G26760.1





NCBI **BLAST** search of MAVEGMMKKHGGFSNIVEMEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
24.0	2427.0145	-0.0021	MAVEGMMKKHGGFSNIVEMEK	Oxidation M1, M6, M19 49.91%
22.5	2427.0145	-0.0021	MAVEGMMKKHGGFSNIVEMEK	Oxidation M1, M7, M19 34.93%
18.4	2427.0145	-0.0021	MAVEGMMKKHGGFSNIVEMEK	Oxidation M6, M7, M19 13.65%
13.6	2427.0058	0.0066	KNESTAGGSKMENGSVSSENIEK	
9.5	2427.0150	-0.0026	NDGFSLTSGDFPSLGAEKDTSEK	
8.8	2427.0145	-0.0021	MAVEGMMKKHGGFSNIVEMEK	Oxidation M1, M6, M7 1.52%
7.9	2427.0062	0.0062	GLCYEMRIEDAESVVLDMEK	
5.8	2427.0078	0.0046	APSWMATQSSWIGYVAVCQDK	
2.2	2427.0082	0.0042	EDFHVTSMTTAGNRWGVVMSR	
1.6	2427.0184	-0.0060	MDYKVSRSGEIVEGEVEDSEK	

Mascot: http://www.matrixscience.com/

AT1G26880.1

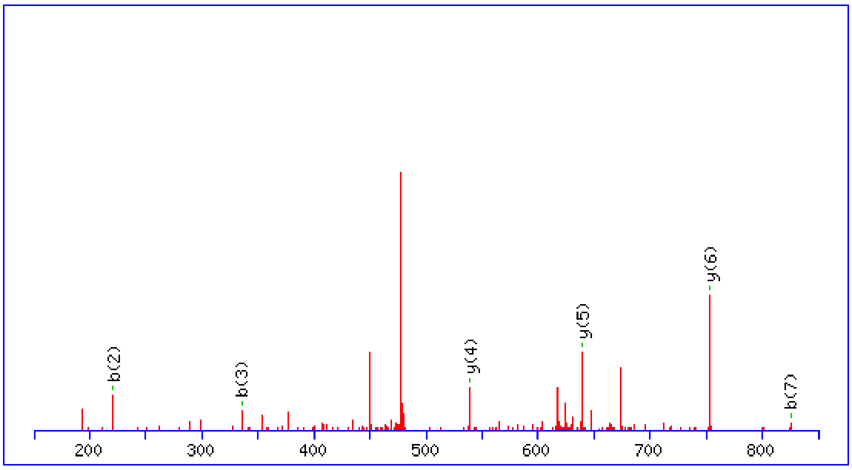
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFLVEEQK**
Found in **AT1G26880.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L34 (RPL34A) | chr1:9315627-9316668 REVERSE

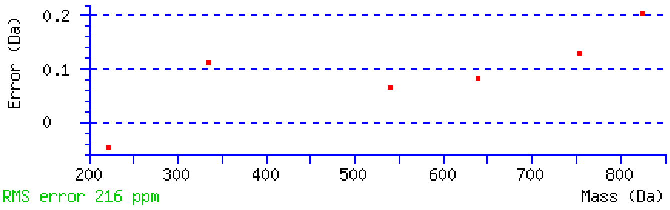
Match to Query 2435: 972.475280 from(487.244916,2+) index(2840)
Title: Elution from: 29.484 to 29.484 scan no 3560 cid35.00 polarity:+
Data file D12h-1_1.mgf

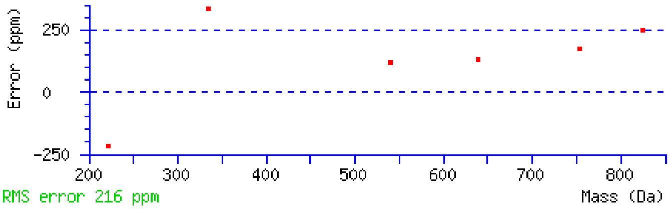
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0066
Matches : 6/60 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							8
2	*221.1069*	111.0571					F	901.4508	451.2290	883.4272	442.2172	883.4402	442.2237	7
3	*335.1880*	168.0976					L	*753.3853*	377.1963	735.3617	368.1845	735.3748	368.1910	6
4	435.2534	218.1303					V	*639.3042*	320.1558	621.2806	311.1440	621.2937	311.1505	5
5	565.2930	283.1502			547.2825	274.1449	E	*539.2388*	270.1230	521.2152	261.1112	521.2282	261.1177	4
6	695.3327	348.1700			677.3221	339.1647	E	409.1991	205.1032	391.1756	196.0914	391.1886	196.0979	3
7	*825.3853*	413.1963	807.3617	404.1845	807.3748	404.1910	Q	279.1595	140.0834	261.1359	131.0716			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AFLVEEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.2	972.4776	-0.0024	AFLVEEQK
22.5	972.4754	-0.0001	DQTSISLAK

AT1G26880.1

22.5	972.4776	-0.0024	EGEFLGIAK
22.5	972.4754	-0.0001	TEKESGIAK
22.5	972.4776	-0.0024	YEDPKLAK
16.3	972.4754	-0.0001	KDSLSTPSK
14.4	972.4754	-0.0001	ESAKQSLLS
13.3	972.4754	-0.0001	DTNTTIAVK
12.4	972.4781	-0.0028	QENVSRVK
12.1	972.4754	-0.0002	GISSLSSPSK

AT1G26960.1

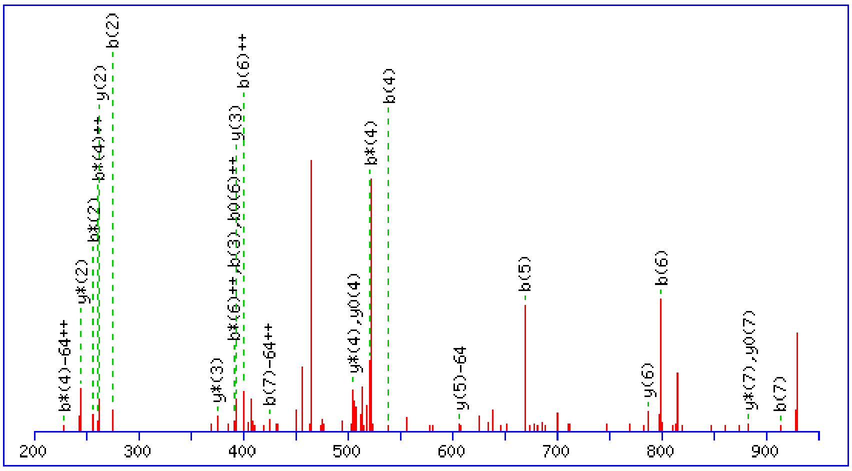
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RLNMEQLK**
Found in **AT1G26960.1** in **TAIR_Arabidopsis**, Symbols: ATHB23 | ATHB23 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 23); DNA binding / transcription factor | chr1:9356113-9357226 FORWARD

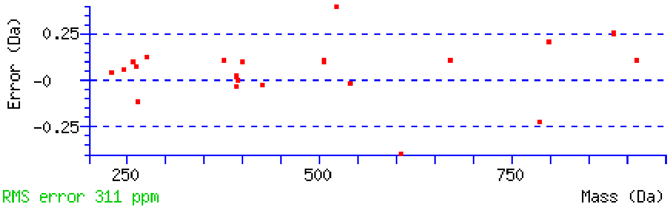
Match to Query 3041: 1060.514198 from(531.264375,2+) index(4985)
Title: Elution from: 43.872 to 43.872 scan no 6236 cid35.00 polarity:+
Data file C7-2_3.mgf

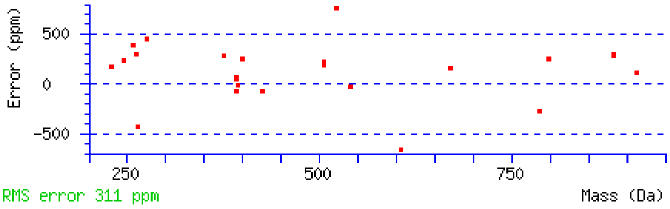
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1060.5128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.029
Matches : 24/110 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			**R**							**8**
2	***275.1776***	138.0925	257.1540	129.0807			**L**	901.4308	451.2190	883.4072	442.2072	883.4202	442.2137	**7**
3	***391.2146***	196.1109	373.1910	187.0992			**N**	**787.3497**	394.1785	769.3261	385.1667	769.3391	385.1732	**6**
4	***539.2471***	270.1272	521.2235	261.1154			**M**	671.3127	336.1600	653.2891	327.1482	653.3021	327.1547	**5**
5	***669.2867***	335.1470	651.2631	326.1352	651.2761	326.1417	**E**	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	**4**
6	***799.3393***	400.1733	781.3157	391.1615	781.3288	391.1680	**Q**	**393.2406**	197.1239	375.2170	188.1122			**3**
7	***913.4204***	457.2139	895.3968	448.2021	895.4099	448.2086	**L**	**263.1880**	132.0976	245.1644	123.0858			**2**
8							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of RLNMEQLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G26960.1

24.7	1060.5128	0.0014	RLNMEQLK
20.2	1060.5127	0.0015	MAARETGALK
19.4	1060.5127	0.0015	MEQQKQKK
11.5	1060.5127	0.0015	QMIQDRIK
11.5	1060.5150	-0.0008	MIKWDALR
11.4	1060.5127	0.0015	MDVSRVNVK
11.0	1060.5128	0.0014	KMEERNIK
9.8	1060.5116	0.0026	DVGFGWVIR
8.2	1060.5127	0.0015	KMSADVLQR
7.4	1060.5127	0.0015	MRKDLEQK

AT1G27400.1

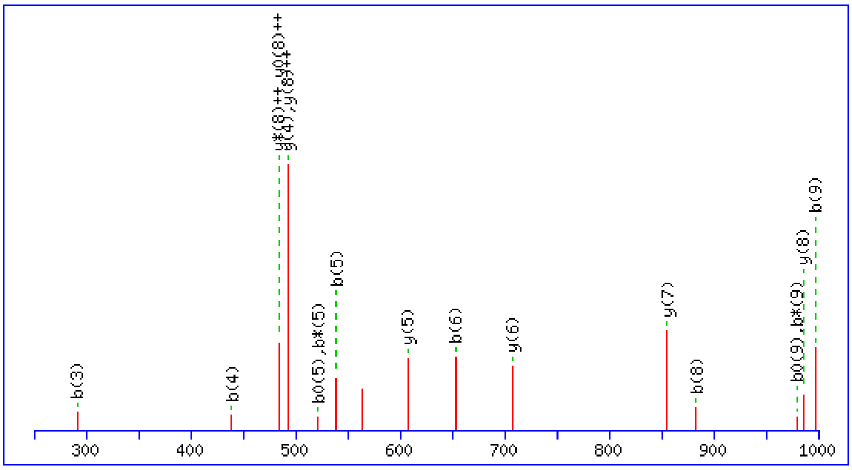
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAQFVLDLLK**
Found in **AT1G27400.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L17 (RPL17A) | chr1:9515217-9516712 FORWARD

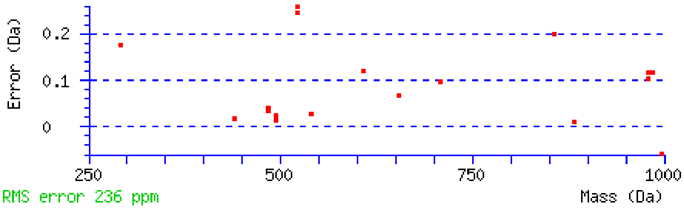
Match to Query 3662: 1144.615854 from(573.315203,2+) index(9241)
Title: Elution from: 83.180 to 83.180 scan no 12534 cid35.00 polarity:+
Data file 0-3_2.mgf

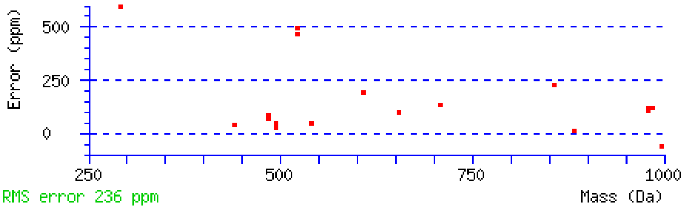
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.6136
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 1e-006
Matches : 18/98 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							10
2	161.0705	81.0389			143.0599	72.0336	A	1057.5918	529.2996	1039.5683	520.2878	1039.5813	520.2943	9
3	***291.1231***	146.0652	273.0996	137.0534	273.1126	137.0599	Q	***985.5577***	493.2825	967.5341	484.2707	967.5471	484.2772	8
4	***439.1886***	220.0979	421.1650	211.0861	421.1780	211.0926	F	***855.5050***	428.2562	837.4815	419.2444	837.4945	419.2509	7
5	***539.2540***	270.1307	521.2304	261.1189	521.2435	261.1254	V	***707.4396***	354.2234	689.4160	345.2116	689.4290	345.2182	6
6	***653.3351***	327.1712	635.3115	318.1594	635.3246	318.1659	L	***607.3741***	304.1907	589.3506	295.1789	589.3636	295.1854	5
7	769.3591	385.1832	751.3355	376.1714	751.3485	376.1779	D	***493.2930***	247.1502	475.2695	238.1384	475.2825	238.1449	4
8	***883.4402***	442.2237	865.4166	433.2120	865.4296	433.2185	L	377.2691	189.1382	359.2455	180.1264			3
9	***997.5213***	499.2643	979.4977	490.2525	979.5107	490.2590	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SAQFVLDLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G27400.1

68.9	1144.6136	0.0022	SAQFVLDLLK
22.9	1144.6141	0.0018	TDARAKNLLK
15.5	1144.6141	0.0018	REQIKTLNK
9.0	1144.6190	-0.0031	LRHHPNILK
7.5	1144.6190	-0.0031	RTGRHLFLK
6.3	1144.6136	0.0022	YLQEVAAVLK
5.3	1144.6163	-0.0004	NTAFAPLKIR
4.5	1144.6167	-0.0009	ARRVIDQIR
3.6	1144.6167	-0.0009	RVTQTLPRR
2.7	1144.6136	0.0022	EFTATPIKVK

AT1G27450.1

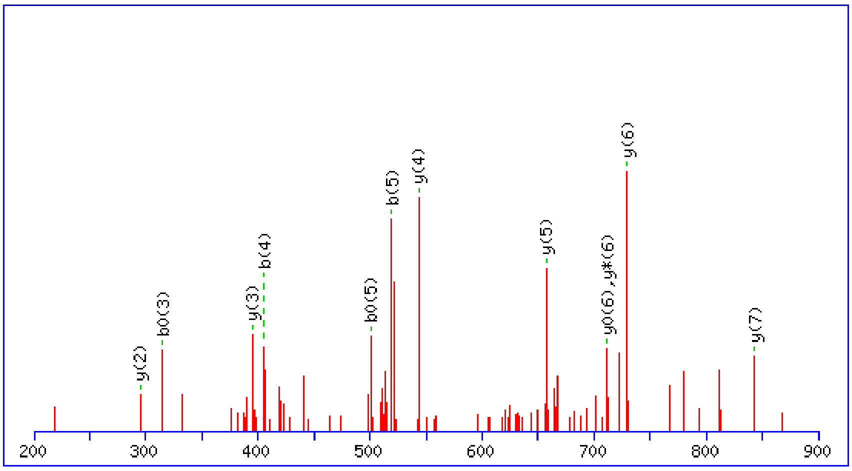
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTIALFVDR**
Found in **AT1G27450.1** in **TAIR_Arabidopsis**, Symbols: APT1, ATAPT1, APRT | APT1; adenine phosphoribosyltransferase | chr1:9532029-9533794 FORWARD

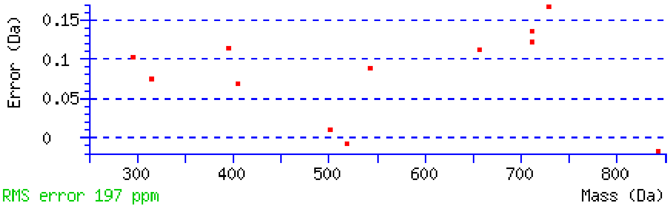
Match to Query 2574: 1060.517488 from(531.266020,2+) index(6780)
Title: Elution from: 61.246 to 61.246 scan no 8898 cid35.00 polarity:+
Data file D12h-2_3.mgf

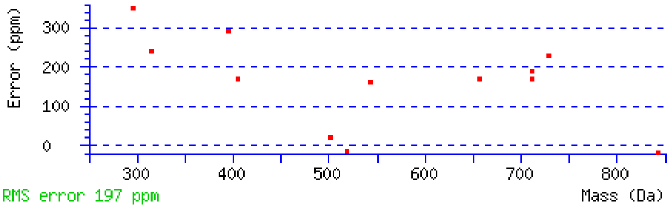
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1060.5197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 4.8e-005
Matches : 12/78 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							9
2	219.0760	110.0416	201.0654	101.0363	T	945.5030	473.2552	927.4794	464.2434	927.4925	464.2499	8
3	333.1571	167.0822	315.1465	158.0769	I	***843.4583***	422.2328	825.4347	413.2210	825.4478	413.2275	7
4	**405.1912**	203.0992	387.1807	194.0940	A	***729.3772***	365.1922	711.3536	356.1805	711.3667	356.1870	6
5	**519.2723**	260.1398	501.2617	251.1345	L	***657.3431***	329.1752	639.3195	320.1634	639.3325	320.1699	5
6	667.3378	334.1725	649.3272	325.1672	F	***543.2620***	272.1346	525.2384	263.1228	525.2514	263.1293	4
7	767.4032	384.2052	749.3926	375.2000	V	***395.1965***	198.1019	377.1729	189.0901	377.1860	189.0966	3
8	883.4272	442.2172	865.4166	433.2120	D	***295.1311***	148.0692	277.1075	139.0574	277.1205	139.0639	2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DTIALFVDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G27450.1

53.9	1060.5197	-0.0022	DTIALFVDR
6.8	1060.5197	-0.0022	ESLFGPKSGK
6.0	1060.5175	0.0000	AEQSEKKTK
5.0	1060.5175	0.0000	EAKASVSQTK
3.8	1060.5202	-0.0027	SELRSNIAR
1.9	1060.5202	-0.0027	SELGKARER
1.0	1060.5197	-0.0022	DIVVSFDVR
0.4	1060.5197	-0.0022	LGVGGKFDEK

AT1G27520.1

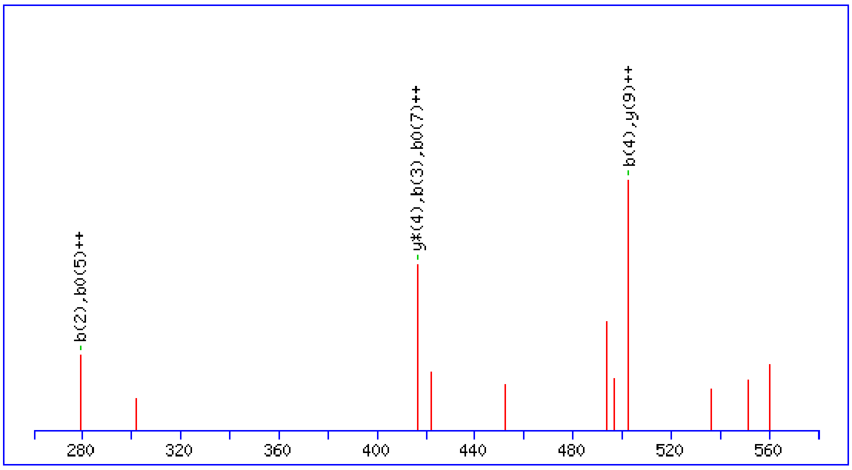
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MFHSAYLASQK**
Found in **AT1G27520.1** in **TAIR_Arabidopsis**, Symbols: | glycoside hydrolase family 47 protein | chr1:9558739-9562078 FORWARD

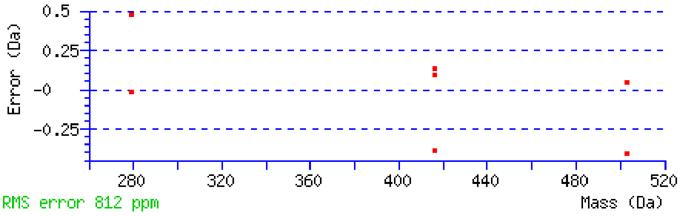
Match to Query 4790: 1281.614871 from(428.212233,3+) index(7093)
Title: Elution from: 61.526 to 61.526 scan no 9159 cid35.00 polarity:+
Data file D1d-3_2.mgf

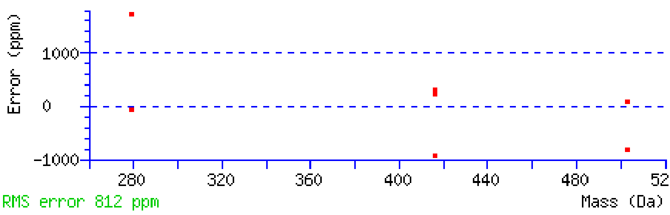
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 260 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1281.6176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.013
Matches : 7/92 fragment ions using 3 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					M							11
2	***279.1162***	140.0617					F	1151.5844	576.2958	1134.5578	567.7826	1133.5738	567.2905	10
3	***416.1751***	208.5912					H	1004.5160	502.7616	987.4894	494.2483	986.5054	493.7563	9
4	***503.2071***	252.1072			485.1965	243.1019	S	867.4571	434.2322	850.4305	425.7189	849.4465	425.2269	8
5	574.2442	287.6258			556.2337	278.6205	A	780.4250	390.7162	763.3985	382.2029	762.4145	381.7109	7
6	737.3076	369.1574			719.2970	360.1521	Y	709.3879	355.1976	692.3614	346.6843	691.3774	346.1923	6
7	850.3916	425.6994			832.3811	416.6942	L	546.3246	273.6659	529.2980	265.1527	528.3140	264.6606	5
8	921.4287	461.2180			903.4182	452.2127	A	433.2405	217.1239	416.2140	208.6106	415.2300	208.1186	4
9	1008.4608	504.7340			990.4502	495.7287	S	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
10	1136.5193	568.7633	1119.4928	560.2500	1118.5088	559.7580	Q	275.1714	138.0893	258.1448	129.5761			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of MFHSAYLASQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G27520.1

Score	Mr(calc)	Delta	Sequence
25.0	1281.6176	-0.0027	MFHSAYLASQK
14.3	1281.6136	0.0013	EARQVFNGMSK
13.2	1281.6142	0.0006	YDTPFHSLFR

Mascot: http://www.matrixscience.com/

AT1G28590.1

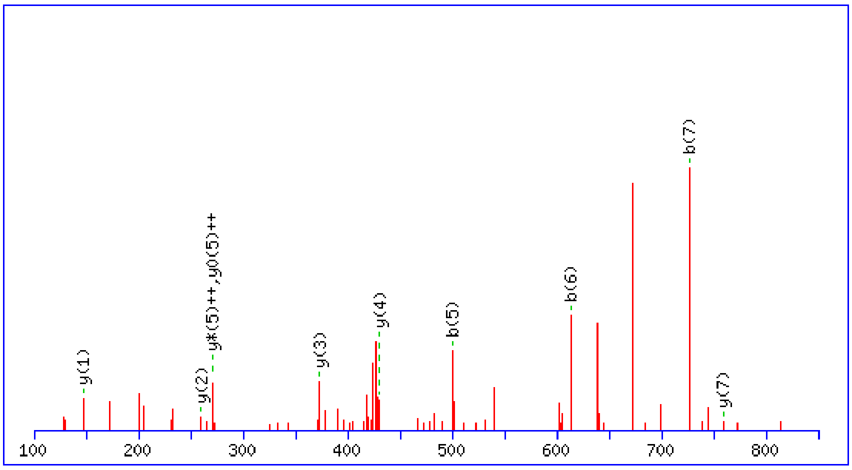
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LISEGLLK**
Found in **AT1G28590.1** in **TAIR_Arabidopsis**, Symbols: | lipase, putative | chr1:10047495-10049286 REVERSE

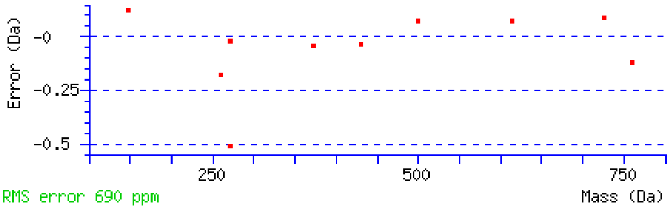
Match to Query 1424: 871.539660 from(436.777106,2+) index(1959)
Title: Elution from: 21.917 to 21.917 scan no 2472 cid35.00 polarity:+
Data file C7-2_3.mgf

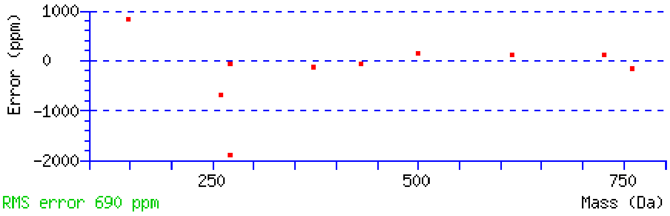
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 871.5378
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0056
Matches : 10/58 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							8
2	227.1754	114.0913			I	***759.4611***	380.2342	742.4345	371.7209	741.4505	371.2289	7
3	314.2074	157.6074	296.1969	148.6021	S	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
4	443.2500	222.1287	425.2395	213.1234	E	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
5	**500.2715**	250.6394	482.2609	241.6341	G	***430.3024***	215.6548	413.2758	207.1416			4
6	**613.3556**	307.1814	595.3450	298.1761	L	***373.2809***	187.1441	356.2544	178.6308			3
7	**726.4396**	363.7234	708.4291	354.7182	L	***260.1969***	130.6021	243.1703	122.0888			2
8					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LISEGLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	871.5378	0.0018	LISEGLLK
25.1	871.5378	0.0018	KELELIK

AT1G28590.1

20.4	871.5378	0.0018	LEEKLLK
16.5	871.5379	0.0018	ITVADIIK
15.9	871.5378	0.0018	IKEIELK
15.9	871.5378	0.0018	IKELEIK
15.9	871.5378	0.0018	LKELELK
15.1	871.5378	0.0018	EEKLLLK
15.0	871.5378	0.0018	EKIELLK
15.0	871.5378	0.0018	ELKELLK

AT1G29020.1

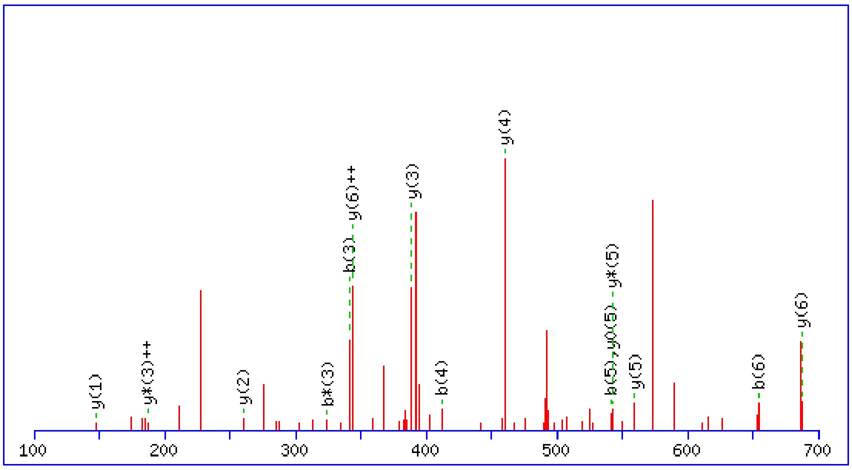
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQVAELK**
Found in **AT1G29020.1** in **TAIR_Arabidopsis**, Symbols: | calcium-binding EF hand family protein | chr1:10120483-10126861 REVERSE

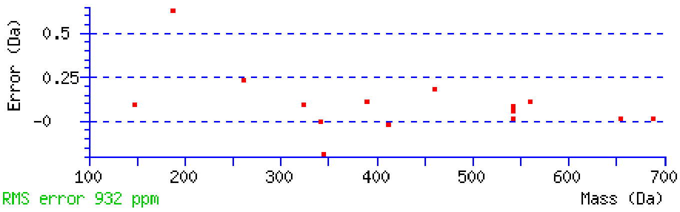
Match to Query 987: 799.480068 from(400.747310,2+) index(3219)
Title: Elution from: 33.407 to 33.407 scan no 4072 cid35.00 polarity:+
Data file D6h-2_1.mgf

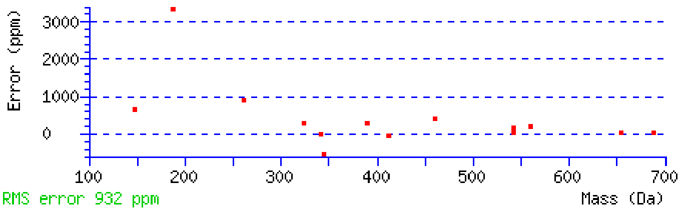
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 799.4803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0069
Matches : 15/58 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							7
2	242.1499	121.5786	225.1234	113.0653			Q	***687.4036***	344.2054	670.3770	335.6921	669.3930	335.2001	6
3	**341.2183**	171.1128	324.1918	162.5995			V	***559.3450***	280.1761	542.3184	271.6629	541.3344	271.1709	5
4	**412.2554**	206.6314	395.2289	198.1181			A	***460.2766***	230.6419	443.2500	222.1287	442.2660	221.6366	4
5	**541.2980**	271.1527	524.2715	262.6394	523.2875	262.1474	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
6	**654.3821**	327.6947	637.3556	319.1814	636.3715	318.6894	L	***260.1969***	130.6021	243.1703	122.0888			2
7							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IQVAELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	799.4803	-0.0003	IQVAELK
14.8	799.4803	-0.0003	LLLGGAEK
11.8	799.4803	-0.0003	ALVGIAEK

AT1G29020.1

8.9	799.4803	-0.0003	ILGSSPVK
8.5	799.4803	-0.0003	IVQEAIK
6.9	799.4803	-0.0002	LIAELNK
6.4	799.4803	-0.0003	TAAPTVLK
6.1	799.4803	-0.0003	VNVVEIK
5.5	799.4817	-0.0016	AIRVWR
5.1	799.4803	-0.0003	LIDSPKK

AT1G29250.1

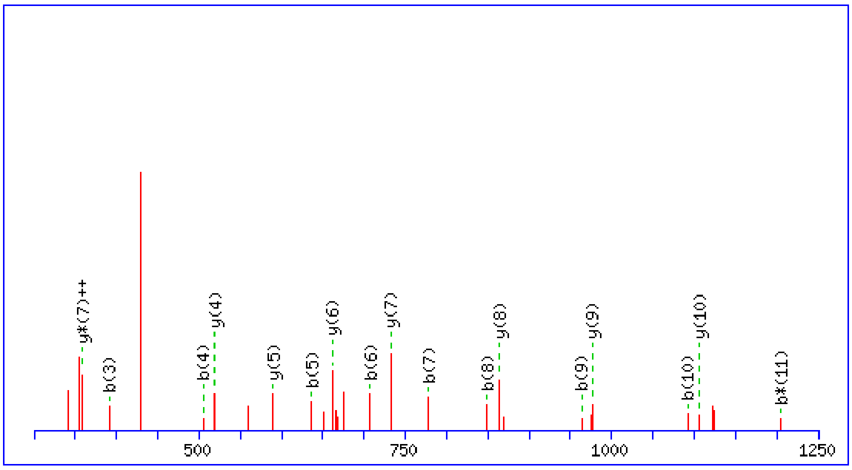
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDELMAAANEEK**
Found in **AT1G29250.1** in **TAIR_Arabidopsis**, Symbols: | nucleic acid binding | chr1:10223447-10224578 REVERSE

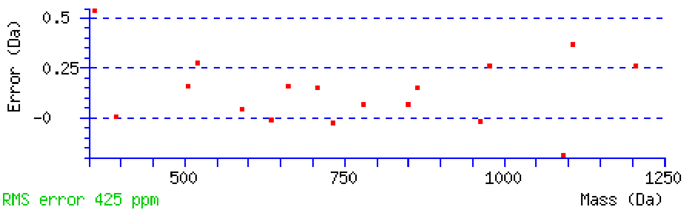
Match to Query 5598: 1366.606550 from(684.310551,2+) index(4689)
Title: Elution from: 42.432 to 42.432 scan no 5859 cid35.00 polarity:+
Data file D6h-1_1.mgf

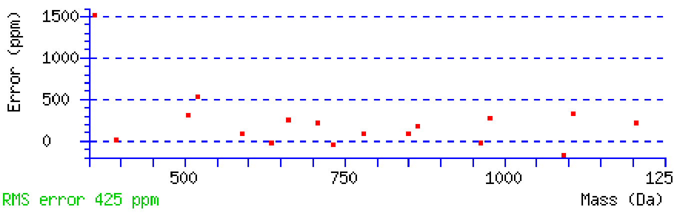
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1366.6074
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 1.1e-006
Matches : 17/112 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							12
2	263.1026	132.0550			245.0921	123.0497	D	1220.5463	610.7768	1203.5198	602.2635	1202.5358	601.7715	11
3	***392.1452***	196.5763			374.1347	187.5710	E	***1105.5194***	553.2633	1088.4929	544.7501	1087.5088	544.2581	10
4	***505.2293***	253.1183			487.2187	244.1130	L	***976.4768***	488.7420	959.4503	480.2288	958.4662	479.7368	9
5	***636.2698***	318.6385			618.2592	309.6332	M	***863.3927***	432.2000	846.3662	423.6867	845.3822	423.1947	8
6	***707.3069***	354.1571			689.2963	345.1518	A	***732.3523***	366.6798	715.3257	358.1665	714.3417	357.6745	7
7	***778.3440***	389.6756			760.3334	380.6704	A	***661.3151***	331.1612	644.2886	322.6479	643.3046	322.1559	6
8	***849.3811***	425.1942			831.3706	416.1889	A	***590.2780***	295.6427	573.2515	287.1294	572.2675	286.6374	5
9	***963.4240***	482.2157	946.3975	473.7024	945.4135	473.2104	N	***519.2409***	260.1241	502.2144	251.6108	501.2304	251.1188	4
10	***1092.4666***	546.7370	1075.4401	538.2237	1074.4561	537.7317	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
11	1221.5092	611.2583	1204.4827	602.7450	1203.4987	602.2530	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FDELMAAANEEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G29250.1

Score	Mr(calc)	Delta	Sequence
61.5	1366.6074	-0.0009	FDELMAAANEEK
4.1	1366.6034	0.0031	CSKEGLSSDEGAK

Mascot: http://www.matrixscience.com/

AT1G29880.1

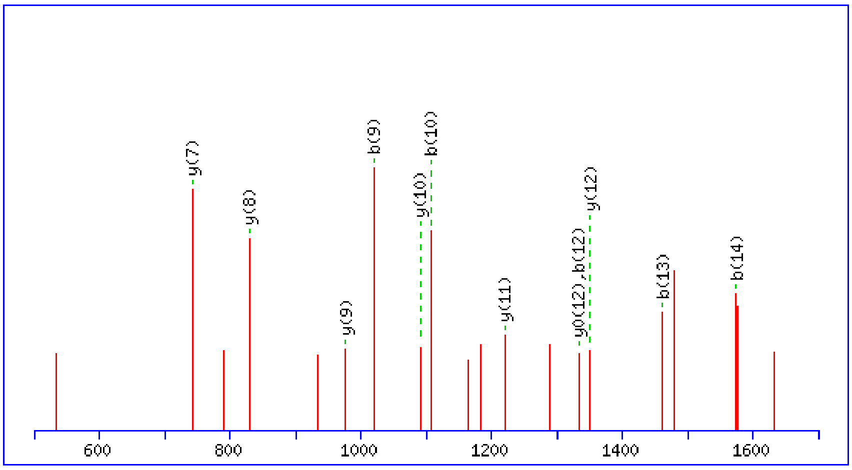
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVLAVMEDFSPEQLGAK**
Found in **AT1G29880.1** in **TAIR_Arabidopsis**, Symbols: | glycyl-tRNA synthetase / glycine--tRNA ligase | chr1:10459646-10462765 REVERSE

Match to Query 9176: 1847.897414 from(924.955983,2+) index(11074)
Title: Elution from: 105.123 to 105.123 scan no 15712 cid35.00 polarity:+
Data file C7-1_1.mgf

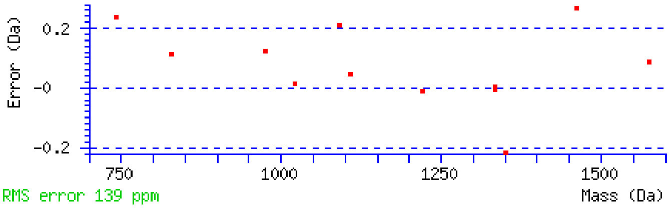
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

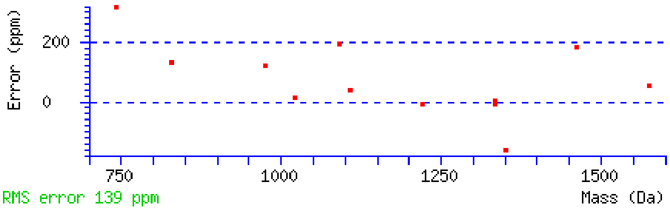


Monoisotopic mass of neutral peptide Mr(calc): 1847.8975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00011
Matches : 12/158 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							17
2	215.1026	108.0550			197.0921	99.0497	V	1733.8778	867.4426	1716.8513	858.9293	1715.8673	858.4373	16
3	328.1867	164.5970			310.1761	155.5917	L	1634.8094	817.9084	1617.7829	809.3951	1616.7989	808.9031	15
4	399.2238	200.1155			381.2132	191.1103	A	1521.7254	761.3663	1504.6988	752.8530	1503.7148	752.3610	14
5	498.2922	249.6498			480.2817	240.6445	V	1450.6883	725.8478	1433.6617	717.3345	1432.6777	716.8425	13
6	629.3327	315.1700			611.3221	306.1647	M	***1351.6198***	676.3136	1334.5933	667.8003	1333.6093	667.3083	12
7	758.3753	379.6913			740.3647	370.6860	E	***1220.5794***	610.7933	1203.5528	602.2800	1202.5688	601.7880	11
8	873.4022	437.2048			855.3917	428.1995	D	***1091.5368***	546.2720	1074.5102	537.7587	1073.5262	537.2667	10
9	***1020.4707***	510.7390			1002.4601	501.7337	F	***976.5098***	488.7585	959.4833	480.2453	958.4993	479.7533	9
10	***1107.5027***	554.2550			1089.4921	545.2497	S	***829.4414***	415.2243	812.4149	406.7111	811.4308	406.2191	8
11	1204.5555	602.7814			1186.5449	593.7761	P	***742.4094***	371.7083	725.3828	363.1951	724.3988	362.7030	7
12	***1333.5980***	667.3027			1315.5875	658.2974	E	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	6
13	***1461.6566***	731.3319	1444.6301	722.8187	1443.6461	722.3267	Q	516.3140	258.6607	499.2875	250.1474			5
14	***1574.7407***	787.8740	1557.7141	779.3607	1556.7301	778.8687	L	388.2554	194.6314	371.2289	186.1181			4
15	1631.7622	816.3847	1614.7356	807.8714	1613.7516	807.3794	G	275.1714	138.0893	258.1448	129.5761			3
16	1702.7993	851.9033	1685.7727	843.3900	1684.7887	842.8980	A	218.1499	109.5786	201.1234	101.0653			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT1G29880.1





NCBI **BLAST** search of DVLAVMEDFSPEQLGAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.3	1847.8975	-0.0001	DVLAVMEDFSPEQLGAK
1.1	1847.8935	0.0039	NPSVESQSEKMVGVVDK

Mascot: http://www.matrixscience.com/

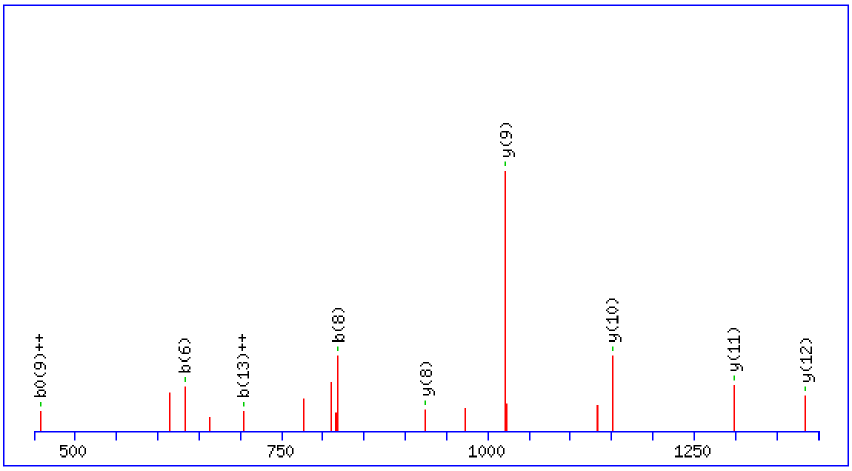
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPASFEPSIDYVVTK**
Found in **AT1G29900.1** in **TAIR_Arabidopsis**, Symbols: CARB | CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / carbamoyl-phosphate synthase | chr1:10468148-10471960 FORWARD

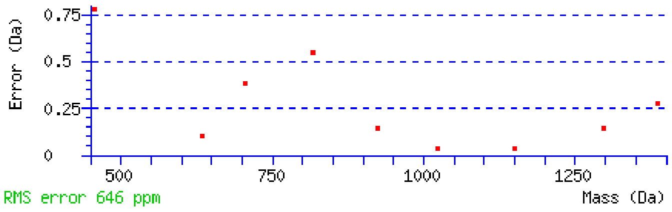
Match to Query 7649: 1652.828118 from(827.421335,2+) index(6946)
Title: Elution from: 63.624 to 63.624 scan no 9096 cid35.00 polarity:+
Data file D1d-2_1.mgf

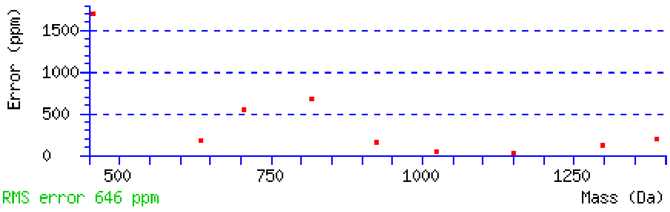
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1652.8298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00026
Matches : 9/138 fragment ions using 9 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	84.0444	42.5258	T							15
2	199.1077	100.0575	181.0972	91.0522	P	1552.7894	776.8983	1535.7628	768.3850	1534.7788	767.8930	14
3	270.1448	135.5761	252.1343	126.5708	A	1455.7366	728.3719	1438.7100	719.8587	1437.7260	719.3666	13
4	357.1769	179.0921	339.1663	170.0868	S	***1384.6995***	692.8534	1367.6729	684.3401	1366.6889	683.8481	12
5	504.2453	252.6263	486.2347	243.6210	F	***1297.6674***	649.3374	1280.6409	640.8241	1279.6569	640.3321	11
6	**633.2879**	317.1476	615.2773	308.1423	E	***1150.5990***	575.8032	1133.5725	567.2899	1132.5885	566.7979	10
7	730.3406	365.6740	712.3301	356.6687	P	***1021.5564***	511.2819	1004.5299	502.7686	1003.5459	502.2766	9
8	**817.3727**	409.1900	799.3621	400.1847	S	***924.5037***	462.7555	907.4771	454.2422	906.4931	453.7502	8
9	930.4567	465.7320	912.4462	456.7267	I	837.4716	419.2395	820.4451	410.7262	819.4611	410.2342	7
10	1045.4837	523.2455	1027.4731	514.2402	D	724.3876	362.6974	707.3610	354.1842	706.3770	353.6921	6
11	1208.5470	604.7771	1190.5364	595.7719	Y	609.3606	305.1840	592.3341	296.6707	591.3501	296.1787	5
12	1307.6154	654.3113	1289.6048	645.3061	V	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
13	1406.6838	703.8456	1388.6733	694.8403	V	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
14	1507.7315	754.3694	1489.7209	745.3641	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
15					K	147.1128	74.0600	130.0863	65.5468			1





AT1G29900.1

NCBI **BLAST** search of TPASFEPSIDYVVTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.4	1652.8298	-0.0016	TPASFEPSIDYVVTK
8.7	1652.8266	0.0015	EVMKKMVAFAENPK
1.9	1652.8299	-0.0018	NCSSTVKMLMEILK

AT1G29910.1

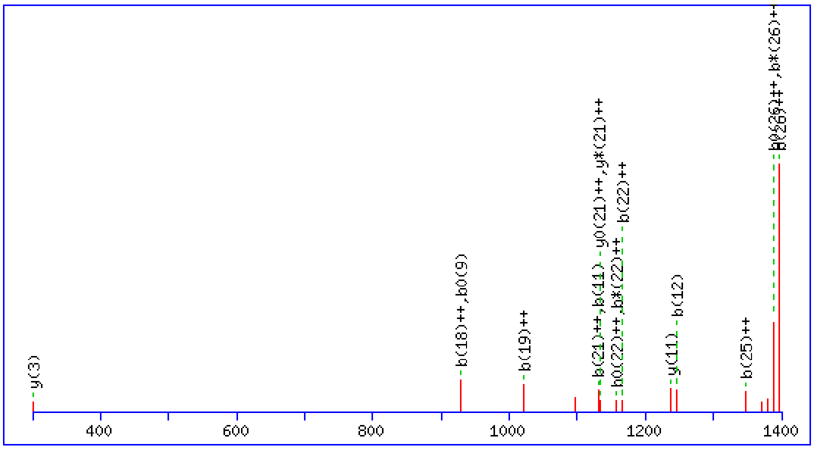
Mascot Search Results

Peptide View

MS/MS Fragmentation of GPIENLADHLADPVNNNAWAFATNFVPGK
Found in AT1G29910.1 in TAIR_Arabidopsis, Symbols: AB180, LHCB1.2, CAB3 | CAB3 (CHLOROPHYLL A/B BINDING PROTEIN 3); chlorophyll binding | chr1:10472427-10473230 REVERSE

Match to Query 10928: 3091.524051 from(1031.515293,3+) index(10923)
Title: Elution from: 110.752 to 110.752 scan no 15860 cid35.00 polarity:+
Data file C7-2_2.mgf

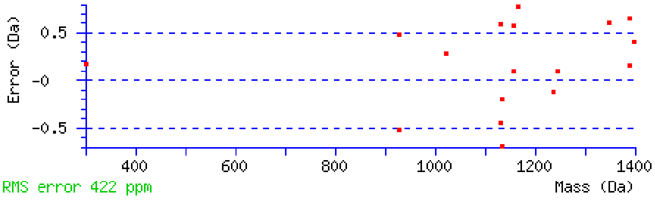
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

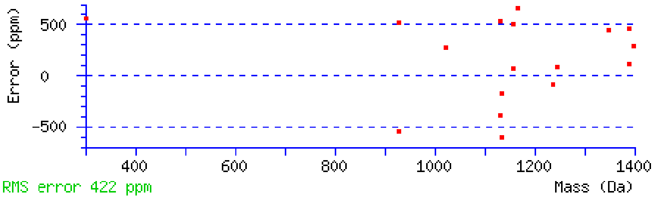


Monoisotopic mass of neutral peptide Mr(calc): 3091.5152
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00049
Matches : 17/310 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							29
2	155.0815	78.0444					P	3035.5010	1518.2541	3018.4744	1509.7409	3017.4904	1509.2489	28
3	268.1656	134.5864					I	2938.4482	1469.7278	2921.4217	1461.2145	2920.4377	1460.7225	27
4	397.2082	199.1077			379.1976	190.1024	E	2825.3642	1413.1857	2808.3376	1404.6724	2807.3536	1404.1804	26
5	511.2511	256.1292	494.2245	247.6159	493.2405	247.1239	N	2696.3216	1348.6644	2679.2950	1340.1512	2678.3110	1339.6591	25
6	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	L	2582.2786	1291.6430	2565.2521	1283.1297	2564.2681	1282.6377	24
7	695.3723	348.1898	678.3457	339.6765	677.3617	339.1845	A	2469.1946	1235.1009	2452.1680	1226.5877	2451.1840	1226.0956	23
8	810.3992	405.7032	793.3727	397.1900	792.3886	396.6980	D	2398.1575	1199.5824	2381.1309	1191.0691	2380.1469	1190.5771	22
9	947.4581	474.2327	930.4316	465.7194	929.4476	465.2274	H	2283.1305	1142.0689	2266.1040	1133.5556	2265.1200	1133.0636	21
10	1060.5422	530.7747	1043.5156	522.2615	1042.5316	521.7694	L	2146.0716	1073.5394	2129.0451	1065.0262	2128.0610	1064.5342	20
11	**1131.5793**	566.2933	1114.5528	557.7800	1113.5687	557.2880	A	2032.9876	1016.9974	2015.9610	1008.4841	2014.9770	1007.9921	19
12	**1246.6062**	623.8068	1229.5797	615.2935	1228.5957	614.8015	D	1961.9504	981.4789	1944.9239	972.9656	1943.9399	972.4736	18
13	1343.6590	672.3331	1326.6325	663.8199	1325.6484	663.3279	P	1846.9235	923.9654	1829.8969	915.4521	1828.9129	914.9601	17
14	1442.7274	721.8673	1425.7009	713.3541	1424.7169	712.8621	V	1749.8707	875.4390	1732.8442	866.9257	1731.8602	866.4337	16
15	1556.7703	778.8888	1539.7438	770.3755	1538.7598	769.8835	N	1650.8023	825.9048	1633.7758	817.3915	1632.7918	816.8995	15
16	1670.8133	835.9103	1653.7867	827.3970	1652.8027	826.9050	N	1536.7594	768.8833	1519.7328	760.3701	1518.7488	759.8780	14
17	1784.8562	892.9317	1767.8297	884.4185	1766.8456	883.9265	N	1422.7165	711.8619	1405.6899	703.3486	1404.7059	702.8566	13
18	1855.8933	***928.4503***	1838.8668	919.9370	1837.8828	919.4450	A	1308.6735	654.8404	1291.6470	646.3271	1290.6630	645.8351	12
19	2041.9726	***1021.4900***	2024.9461	1012.9767	2023.9621	1012.4847	W	**1237.6364**	619.3218	1220.6099	610.8086	1219.6259	610.3166	11
20	2113.0097	1057.0085	2095.9832	1048.4952	2094.9992	1048.0032	A	1051.5571	526.2822	1034.5306	517.7689	1033.5465	517.2769	10
21	2260.0782	***1130.5427***	2243.0516	1122.0294	2242.0676	1121.5374	F	980.5200	490.7636	963.4934	482.2504	962.5094	481.7584	9
22	2331.1153	***1166.0613***	2314.0887	1157.5480	2313.1047	1157.0560	A	833.4516	417.2294	816.4250	408.7162	815.4410	408.2241	8
23	2432.1629	1216.5851	2415.1364	1208.0718	2414.1524	1207.5798	T	762.4145	381.7109	745.3879	373.1976	744.4039	372.7056	7
24	2546.2059	1273.6066	2529.1793	1265.0933	2528.1953	1264.6013	N	661.3668	331.1870	644.3402	322.6738			6

25	2693.2743	***1347.1408***	2676.2477	1338.6275	2675.2637	1338.1355	**F**	547.3239	274.1656	530.2973	265.6523			**5**
26	2792.3427	***1396.6750***	2775.3162	1388.1617	2774.3321	1387.6697	**V**	400.2554	200.6314	383.2289	192.1181			**4**
27	2889.3955	1445.2014	2872.3689	1436.6881	2871.3849	1436.1961	**P**	**301.1870**	151.0972	284.1605	142.5839			**3**
28	2946.4169	1473.7121	2929.3904	1465.1988	2928.4064	1464.7068	**G**	204.1343	102.5708	187.1077	94.0575			**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GPIENLADHLADPVNNNAWAFATNFVPGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.4	3091.5152	0.0089	GPIENLADHLADPVNNNAWAFATNFVPGK
38.4	3091.5152	0.0089	GPLENLADHLADPVNNNAWAFATNFVPGK
6.0	3091.5300	-0.0059	FGLMWYDSELMLWRVVYGLDLDKAR
3.1	3091.5324	-0.0084	IWLWGDESGASPELVAGMVEYLAVESRK
0.1	3091.5300	-0.0059	FGLMWYDSELMLWRVVYGLDLDKAR

Mascot: http://www.matrixscience.com/

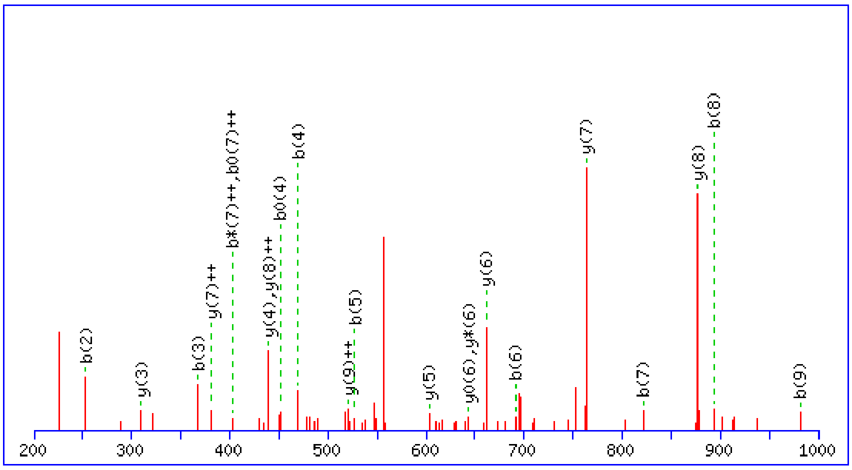
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYITGYQASK**
Found in **AT1G30230.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1-beta / EF-1-beta | chr1:10639270-10640499 FORWARD

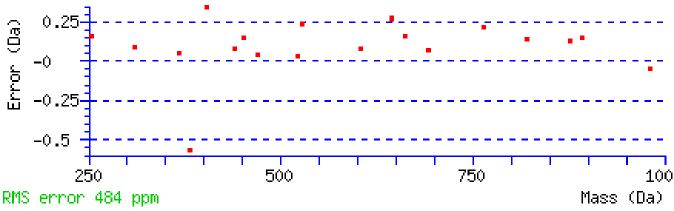
Match to Query 3828: 1128.512314 from(565.263433,2+) index(2077)
Title: Elution from: 24.700 to 24.700 scan no 2692 cid35.00 polarity:+
Data file 0-1_1.mgf

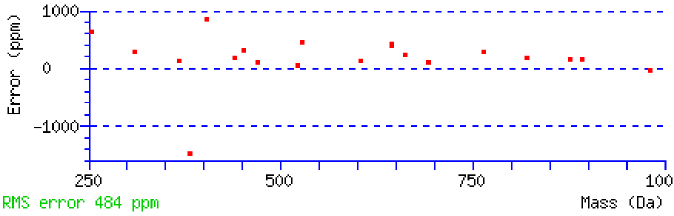
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1128.5096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 5.1e-006
Matches : 22/94 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							10
2	***253.0967***	127.0520			235.0861	118.0467	Y	1041.4878	521.2475	1023.4642	512.2357	1023.4772	512.2422	9
3	***367.1778***	184.0925			349.1672	175.0873	I	**877.4274**	439.2173	859.4038	430.2056	859.4168	430.2121	8
4	***469.2225***	235.1149			451.2120	226.1096	T	**763.3463**	382.1768	745.3227	373.1650	745.3357	373.1715	7
5	***527.2410***	264.1241			509.2304	255.1189	G	**661.3016**	331.1544	643.2780	322.1426	643.2910	322.1492	6
6	***691.3014***	346.1543			673.2908	337.1490	Y	**603.2831**	302.1452	585.2595	293.1334	585.2725	293.1399	5
7	***821.3540***	411.1807	803.3304	402.1689	803.3435	402.1754	Q	**439.2227**	220.1150	421.1991	211.1032	421.2122	211.1097	4
8	***893.3882***	447.1977	875.3646	438.1859	875.3776	438.1924	A	**309.1701**	155.0887	291.1465	146.0769	291.1595	146.0834	3
9	***981.4172***	491.2123	963.3937	482.2005	963.4067	482.2070	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SYITGYQASK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G30230.1

60.9	1128.5096	0.0028	SYITGYQASK
15.3	1128.5096	0.0028	AYETSQKYK
7.8	1128.5104	0.0019	KIMGFCFSK
4.2	1128.5152	-0.0029	KFSYSEVMK
3.1	1128.5156	-0.0033	IVSDMHERK
2.2	1128.5156	-0.0033	MHAVDVTVSR
0.7	1128.5129	-0.0006	KYTSKMSEK
0.7	1128.5100	0.0023	SSSYGRNSKK
0.7	1128.5152	-0.0029	WMVLEPSEK

AT1G30380.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGLAPSANRK**
Found in **AT1G30380.1** in **TAIR_Arabidopsis**, Symbols: PSAK | PSAK (PHOTOSYSTEM I SUBUNIT K) | chr1:10722307-10722995 FORWARD

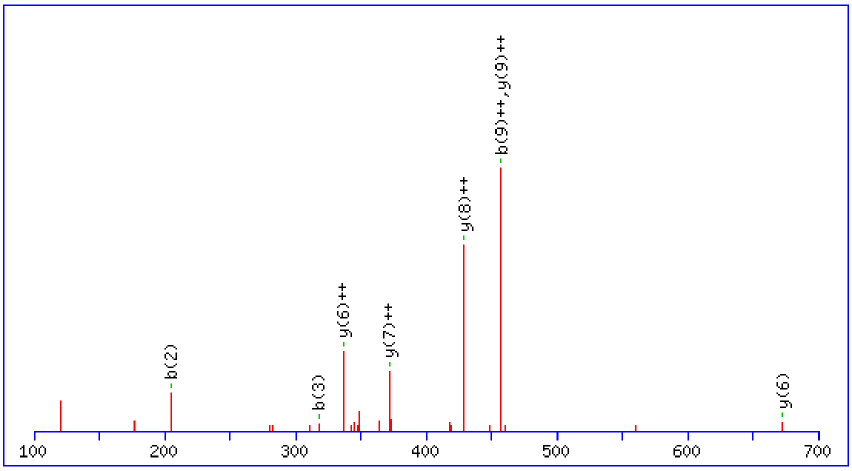
Match to Query 3011: 1059.582585 from(354.201471,3+) index(1004)
Title: Elution from: 15.903 to 15.903 scan no 1419 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

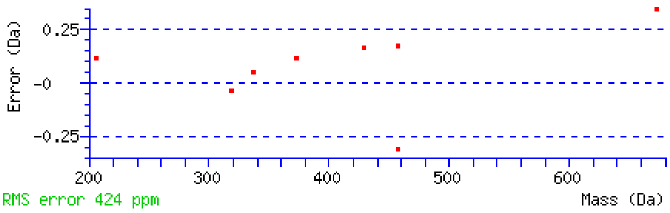
Label all possible matches ○ Label matches used for scoring ●

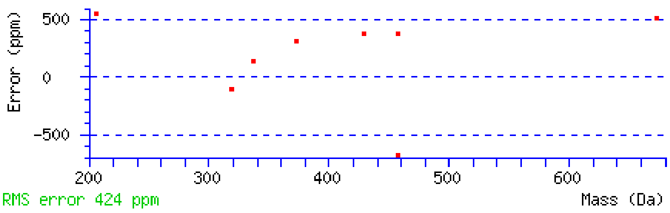
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1059.5825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0069
Matches : 8/76 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	**205.0972**	103.0522					G	913.5214	457.2643	896.4948	448.7511	895.5108	448.2591	9
3	**318.1812**	159.5942					L	856.4999	428.7536	839.4734	420.2403	838.4894	419.7483	8
4	389.2183	195.1128					A	743.4159	372.2116	726.3893	363.6983	725.4053	363.2063	7
5	486.2711	243.6392					P	672.3787	336.6930	655.3522	328.1797	654.3682	327.6877	6
6	573.3031	287.1552			555.2926	278.1499	S	575.3260	288.1666	558.2994	279.6534	557.3154	279.1613	5
7	644.3402	322.6738			626.3297	313.6685	A	488.2940	244.6506	471.2674	236.1373			4
8	758.3832	379.6952	741.3566	371.1819	740.3726	370.6899	N	417.2568	209.1321	400.2303	200.6188			3
9	914.4843	457.7458	897.4577	449.2325	896.4737	448.7405	R	303.2139	152.1106	286.1874	143.5973			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FGLAPSANRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G30380.1

Score	Mr(calc)	Delta	Sequence
26.8	1059.5825	0.0001	FGLAPSANRK
4.7	1059.5811	0.0014	EEEIAKTLK
4.6	1059.5812	0.0014	LTEASVALEK
3.9	1059.5812	0.0014	EKVIDSELK
3.9	1059.5812	0.0014	LSELETQLK
3.8	1059.5825	0.0001	ASVHIYSRK
3.8	1059.5825	0.0001	RTWKVNEK
3.0	1059.5825	0.0001	QGWIKTATR
3.0	1059.5825	0.0001	SRVWLQSGK

AT1G30580.1

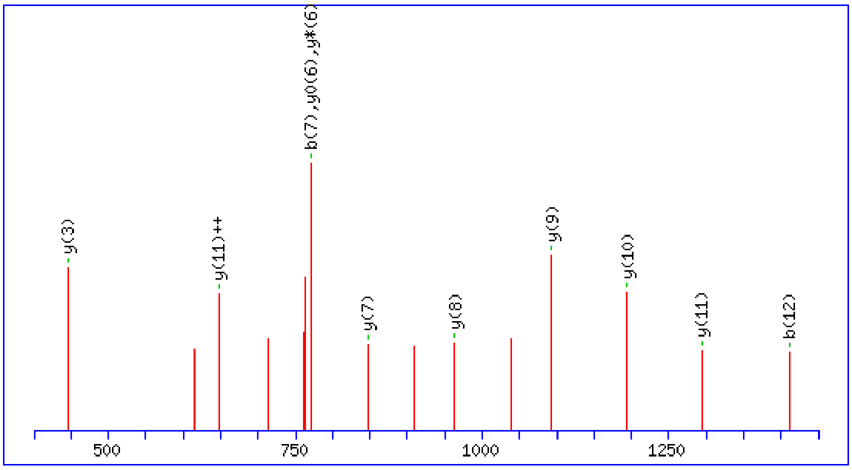
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYVVQDGDIIFFK**
Found in **AT1G30580.1** in **TAIR_Arabidopsis**, Symbols: | GTP binding | chr1:10831935-10835436 REVERSE

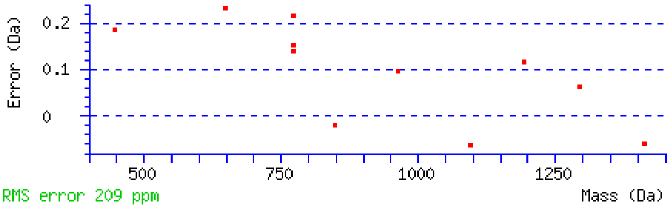
Match to Query 6794: 1558.749602 from(780.382077,2+) index(8462)
Title: Elution from: 76.041 to 76.041 scan no 11376 cid35.00 polarity:+
Data file 0-2_2.mgf

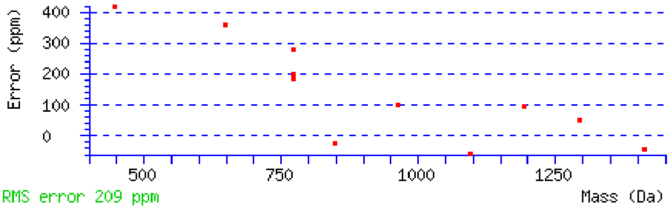
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1558.7477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00059
Matches : 11/126 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							13
2	267.1124	134.0598			249.1018	125.0545	Y	1457.7103	729.3588	1439.6867	720.3470	1439.6998	720.3535	12
3	367.1778	184.0925			349.1672	175.0873	V	***1293.6500***	647.3286	1275.6264	638.3168	1275.6394	638.3233	11
4	467.2433	234.1253			449.2327	225.1200	V	***1193.5845***	597.2959	1175.5609	588.2841	1175.5740	588.2906	10
5	597.2959	299.1516	579.2723	290.1398	579.2853	290.1463	Q	***1093.5191***	547.2632	1075.4955	538.2514	1075.5085	538.2579	9
6	713.3199	357.1636	695.2963	348.1518	695.3093	348.1583	D	***963.4664***	482.2369	945.4428	473.2251	945.4559	473.2316	8
7	**771.3384**	386.1728	753.3148	377.1610	753.3278	377.1675	G	***847.4424***	424.2249	829.4189	415.2131	829.4319	415.2196	7
8	887.3624	444.1848	869.3388	435.1730	869.3518	435.1795	D	789.4239	395.2156	771.4004	386.2038	771.4134	386.2103	6
9	1001.4435	501.2254	983.4199	492.2136	983.4329	492.2201	I	673.4000	337.2036	655.3764	328.1918			5
10	1115.5246	558.2659	1097.5010	549.2541	1097.5140	549.2606	I	559.3189	280.1631	541.2953	271.1513			4
11	1263.5900	632.2986	1245.5664	623.2868	1245.5794	623.2934	F	***445.2378***	223.1225	427.2142	214.1107			3
12	**1411.6554**	706.3314	1393.6319	697.3196	1393.6449	697.3261	F	297.1723	149.0898	279.1487	140.0780			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TYVVQDGDIIFFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G30580.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	1558.7477	0.0019	TYVVQDGDIIFFK
22.8	1558.7542	-0.0046	MTNKVNRAFTIAR
10.9	1558.7482	0.0014	VASYNVYGVEGRVK
10.0	1558.7460	0.0036	TTNVNHLVISAQDK
4.9	1558.7534	-0.0038	FMFEAEISFLLAK
4.4	1558.7538	-0.0042	FMALQPPGQPSQLK
3.5	1558.7455	0.0041	SFKVIATSDIYGDK
2.5	1558.7455	0.0041	VFSKQEYSESVIK
2.5	1558.7542	-0.0046	ERFMLLSQRVSR
2.3	1558.7486	0.0010	MPVSKMYLPGFFK

AT1G30660.1

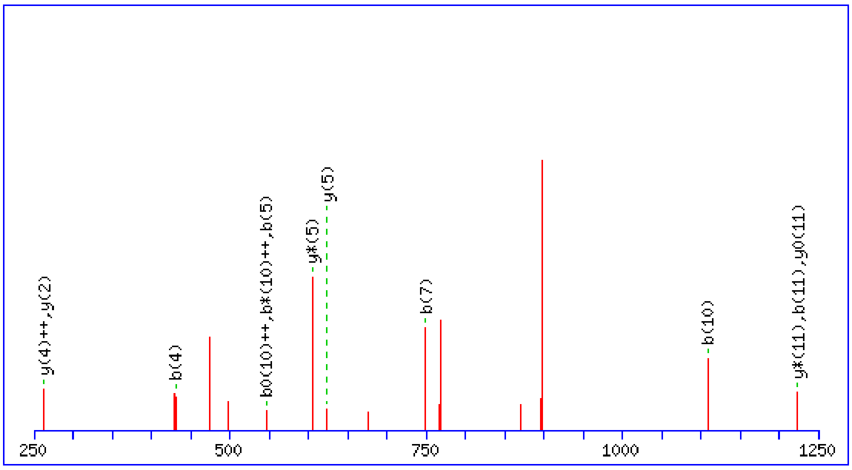
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAILNAEPYPLK**
Found in **AT1G30660.1** in **TAIR_Arabidopsis**, Symbols: | toprim domain-containing protein | chr1:10876835-10878999 FORWARD

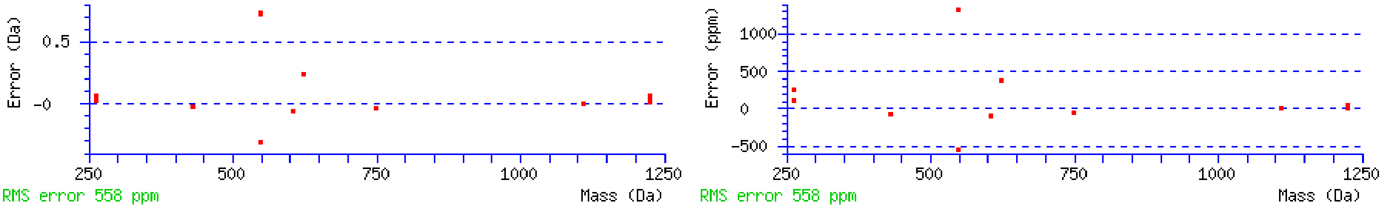
Match to Query 5303: 1370.690552 from(686.352552,2+) index(10153)
Title: Elution from: 94.203 to 94.203 scan no 14110 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1370.6874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.021
Matches : 13/114 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							12
2	203.0811	102.0442			185.0705	93.0389	A	1241.6551	621.3312	1223.6315	612.3194	1223.6445	612.3259	11
3	317.1622	159.0847			299.1516	150.0794	I	1169.6209	585.3141	1151.5973	576.3023	1151.6103	576.3088	10
4	***431.2433***	216.1253			413.2327	207.1200	L	1055.5398	528.2735	1037.5162	519.2617	1037.5292	519.2683	9
5	***547.2802***	274.1438	529.2567	265.1320	529.2697	265.1385	N	941.4587	471.2330	923.4351	462.2212	923.4481	462.2277	8
6	619.3144	310.1608	601.2908	301.1490	601.3038	301.1556	A	825.4217	413.2145	807.3981	404.2027	807.4111	404.2092	7
7	***749.3540***	375.1807	731.3304	366.1689	731.3435	366.1754	E	753.3876	377.1974	735.3640	368.1856	735.3770	368.1921	6
8	847.4038	424.2056	829.3802	415.1938	829.3933	415.2003	P	**623.3479**	312.1776	605.3244	303.1658			5
9	1011.4642	506.2357	993.4406	497.2239	993.4536	497.2304	Y	525.2981	263.1527	507.2746	254.1409			4
10	***1109.5140***	555.2606	1091.4904	546.2488	1091.5034	546.2553	P	361.2378	181.1225	343.2142	172.1107			3
11	***1223.5951***	612.3012	1205.5715	603.2894	1205.5845	603.2959	L	**263.1880**	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of EAILNAEPYPLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G30660.1

Score	Mr(calc)	Delta	Sequence
23.8	1370.6874	0.0031	EAILNAEPYPLK
13.6	1370.6908	-0.0002	MKLPLDIDSPTK
3.3	1370.6935	-0.0029	SLSRMTQKFIK
2.3	1370.6901	0.0005	LYKDQGFRSIK

AT1G30890.1

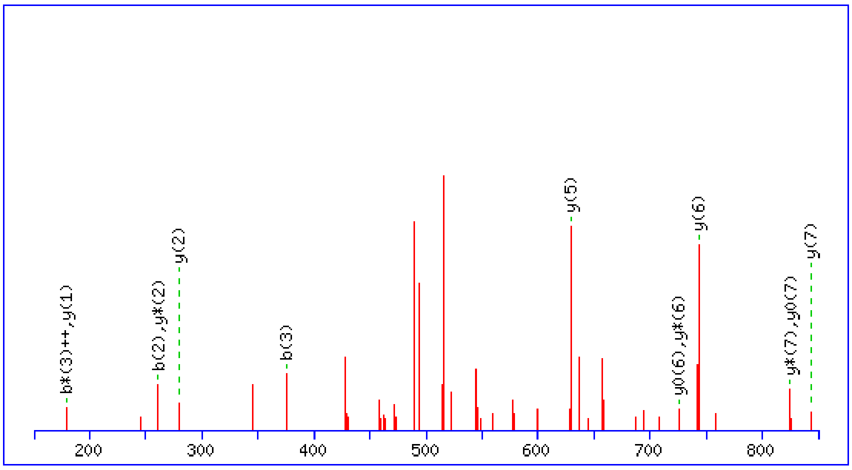
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RVLFAEVR**
Found in **AT1G30890.1** in **TAIR_Arabidopsis**, Symbols: | integral membrane HRF1 family protein | chr1:10994871-10995980 FORWARD

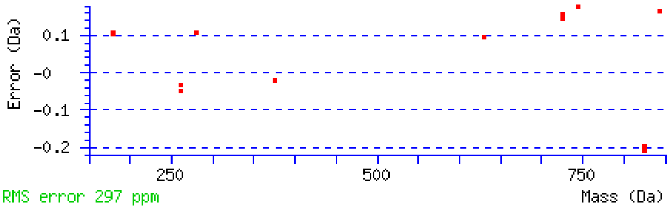
Match to Query 2716: 1002.540624 from(502.277588,2+) index(8233)
Title: Elution from: 71.746 to 71.746 scan no 10760 cid35.00 polarity:+
Data file D1d-3_1.mgf

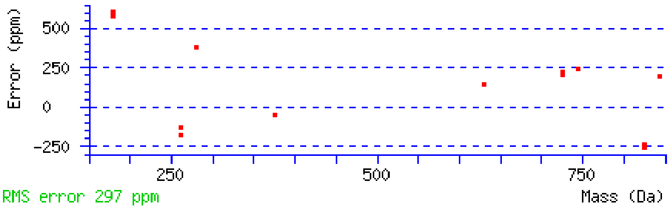
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1002.5403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.015
Matches : 15/70 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							8
2	**261.1620**	131.0846	243.1384	122.0728			V	***843.4583***	422.2328	825.4347	413.2210	825.4478	413.2275	7
3	**375.2431**	188.1252	357.2195	179.1134			L	***743.3929***	372.2001	725.3693	363.1883	725.3823	363.1948	6
4	523.3085	262.1579	505.2849	253.1461			F	***629.3118***	315.1595	611.2882	306.1477	611.3012	306.1542	5
5	595.3427	298.1750	577.3191	289.1632			A	481.2463	241.1268	463.2227	232.1150	463.2358	232.1215	4
6	**725.3823**	363.1948	707.3587	354.1830	707.3717	354.1895	E	409.2122	205.1097	391.1886	196.0979	391.2016	196.1044	3
7	**825.4478**	413.2275	807.4242	404.2157	807.4372	404.2222	V	***279.1725***	140.0899	261.1490	131.0781			2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RVLFAEVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.7	1002.5403	0.0004	RVLFAEVR
10.3	1002.5376	0.0030	KLQIESFK

AT1G30890.1

9.2	1002.5407	-0.0001	RAILNSRR
9.1	1002.5381	0.0026	LKLESSRR
8.8	1002.5407	-0.0001	RVRSAALGR
8.3	1002.5376	0.0030	ELKLFTNK
8.2	1002.5380	0.0026	LKTERSVR
7.7	1002.5429	-0.0023	VRPGFRVR
7.1	1002.5410	-0.0004	EKLTKVMK
7.1	1002.5410	-0.0004	KKIEMLSK

AT1G31160.1

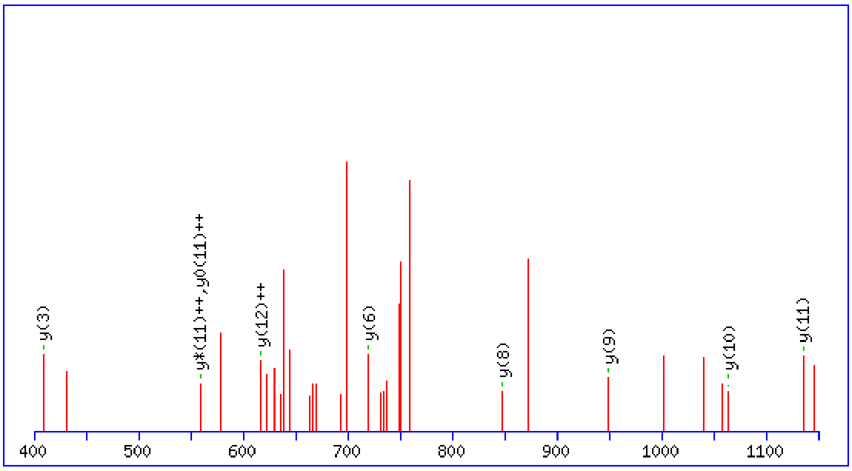
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAASVADTGAPTIFDK**
Found in **AT1G31160.1** in **TAIR_Arabidopsis**, Symbols: | zinc-binding protein, putative / protein kinase C inhibitor, putative | chr1:11122861-11124087 REVERSE

Match to Query 6183: 1533.769194 from(767.891873,2+) index(4771)
Title: Elution from: 46.338 to 46.338 scan no 6132 cid35.00 polarity:+
Data file D1d-2_2.mgf

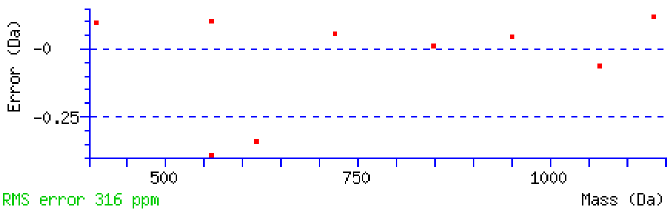
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

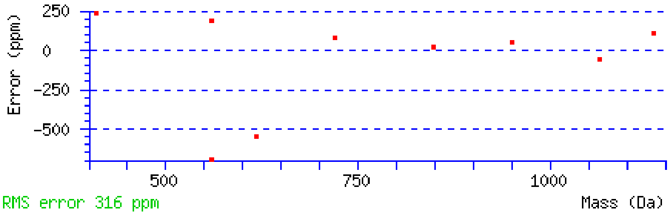


Monoisotopic mass of neutral peptide Mr(calc): 1533.7675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.036
Matches : 9/142 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			**A**							**16**
2	143.0815	72.0444			**A**	1463.7377	732.3725	1446.7111	723.8592	1445.7271	723.3672	**15**
3	214.1186	107.5629			**A**	1392.7005	696.8539	1375.6740	688.3406	1374.6900	687.8486	**14**
4	301.1506	151.0790	283.1401	142.0737	**S**	1321.6634	661.3354	1304.6369	652.8221	1303.6529	652.3301	**13**
5	400.2191	200.6132	382.2085	191.6079	**V**	1234.6314	617.8193	1217.6048	609.3061	1216.6208	608.8141	**12**
6	471.2562	236.1317	453.2456	227.1264	**A**	***1135.5630***	568.2851	1118.5364	559.7719	1117.5524	559.2798	**11**
7	586.2831	293.6452	568.2726	284.6399	**D**	***1064.5259***	532.7666	1047.4993	524.2533	1046.5153	523.7613	**10**
8	687.3308	344.1690	669.3202	335.1638	**T**	***949.4989***	475.2531	932.4724	466.7398	931.4884	466.2478	**9**
9	744.3523	372.6798	726.3417	363.6745	**G**	***848.4512***	424.7293	831.4247	416.2160	830.4407	415.7240	**8**
10	815.3894	408.1983	797.3788	399.1930	**A**	791.4298	396.2185	774.4032	387.7053	773.4192	387.2132	**7**
11	912.4421	456.7247	894.4316	447.7194	**P**	***720.3927***	360.7000	703.3661	352.1867	702.3821	351.6947	**6**
12	1013.4898	507.2485	995.4793	498.2433	**T**	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
13	1126.5739	563.7906	1108.5633	554.7853	**I**	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	**4**
14	1273.6423	637.3248	1255.6317	628.3195	**F**	***409.2082***	205.1077	392.1816	196.5944	391.1976	196.1024	**3**
15	1388.6692	694.8383	1370.6587	685.8330	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
16					**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT1G31160.1





NCBI **BLAST** search of AAASVADTGAPTIFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.9	1533.7675	0.0017	AAASVADTGAPTIFDK
10.3	1533.7675	0.0017	TELSDSSPIKSWGK
2.9	1533.7722	-0.0030	VRNMLWQNTAGTK
0.2	1533.7648	0.0044	DESVNDGKRLHHK

Mascot: http://www.matrixscience.com/

AT1G31330.1

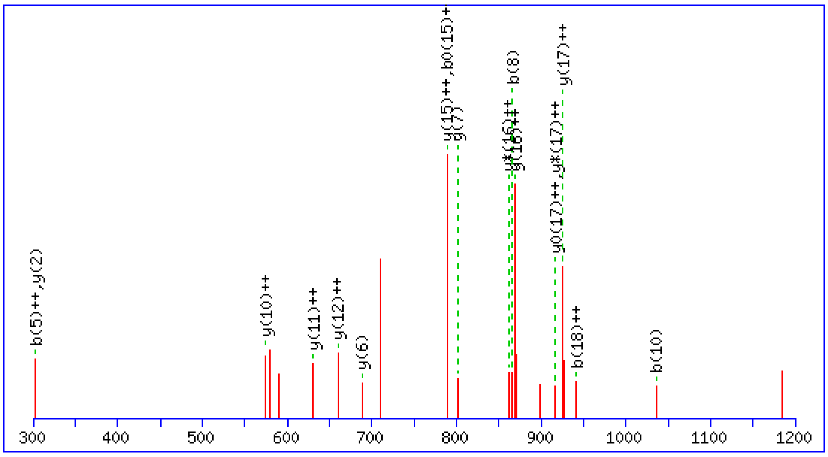
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGLLCGSDGLPHLIVNGDQR**
Found in **AT1G31330.1** in **TAIR_Arabidopsis**, Symbols: PSAF | PSAF (photosystem I subunit F) | chr1:11214992-11215920 REVERSE

Match to Query 9820: 2183.077785 from(728.699871,3+) index(8529)
Title: Elution from: 75.073 to 75.073 scan no 11312 cid35.00 polarity:+
Data file C7-3_2.mgf

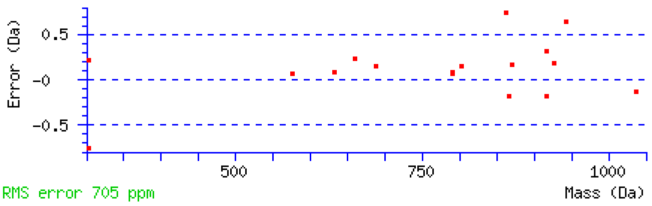
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

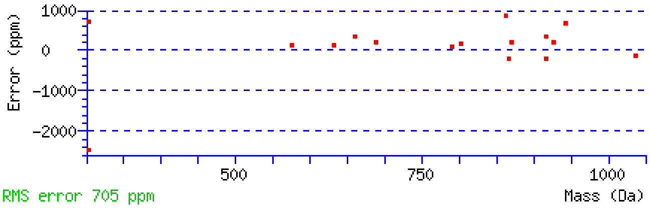


Monoisotopic mass of neutral peptide Mr(calc): 2183.0793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00042
Matches : 17/182 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							20
2	221.0921	111.0497					G	2021.0233	1011.0153	2003.9967	1002.5020	2003.0127	1002.0100	19
3	334.1761	167.5917					L	1964.0018	982.5045	1946.9753	973.9913	1945.9913	973.4993	18
4	447.2602	224.1337					L	1850.9178	925.9625	1833.8912	917.4492	1832.9072	916.9572	17
5	607.2908	**304.1491**					C	1737.8337	869.4205	1720.8071	860.9072	1719.8231	860.4152	16
6	664.3123	332.6598					G	1577.8030	789.4052	1560.7765	780.8919	1559.7925	780.3999	15
7	751.3443	376.1758			733.3338	367.1705	S	1520.7816	760.8944	1503.7550	752.3812	1502.7710	751.8891	14
8	**866.3713**	433.6893			848.3607	424.6840	D	1433.7496	717.3784	1416.7230	708.8651	1415.7390	708.3731	13
9	923.3927	462.2000			905.3822	453.1947	G	1318.7226	659.8649	1301.6961	651.3517	1300.7120	650.8597	12
10	**1036.4768**	518.7420			1018.4662	509.7368	L	1261.7011	631.3542	1244.6746	622.8409	1243.6906	622.3489	11
11	1133.5296	567.2684			1115.5190	558.2631	P	1148.6171	574.8122	1131.5905	566.2989	1130.6065	565.8069	10
12	1270.5885	635.7979			1252.5779	626.7926	H	1051.5643	526.2858	1034.5378	517.7725	1033.5538	517.2805	9
13	1383.6725	692.3399			1365.6620	683.3346	L	914.5054	457.7563	897.4789	449.2431	896.4948	448.7511	8
14	1496.7566	748.8819			1478.7460	739.8767	I	***801.4213***	401.2143	784.3948	392.7010	783.4108	392.2090	7
15	1595.8250	798.4162			1577.8145	789.4109	V	***688.3373***	344.6723	671.3107	336.1590	670.3267	335.6670	6
16	1709.8680	855.4376	1692.8414	846.9243	1691.8574	846.4323	N	589.2689	295.1381	572.2423	286.6248	571.2583	286.1328	5
17	1766.8894	883.9483	1749.8629	875.4351	1748.8789	874.9431	G	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	4
18	1881.9164	**941.4618**	1864.8898	932.9485	1863.9058	932.4565	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
19	2009.9749	1005.4911	1992.9484	996.9778	1991.9644	996.4858	Q	***303.1775***	152.0924	286.1510	143.5791			2
20							R	175.1190	88.0631	158.0924	79.5498			1

AT1G31330.1





NCBI **BLAST** search of YGLLCGSDGLPHLIVNGDQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.7	2183.0793	-0.0016	YGLLCGSDGLPHLIVNGDQR
9.1	2183.0827	-0.0049	LQKIRPEAVNEMESCVHK
4.8	2183.0793	-0.0016	MNFPTIPHESNVVSINVGGR
3.8	2183.0818	-0.0040	RSSDVISYESSVANLSREGK
3.4	2183.0754	0.0023	KLMEEFLEIWQEAMSKR
1.8	2183.0775	0.0003	GYNFLFWIFKMNFERR
0.5	2183.0740	0.0038	DTMTTTTTGSELAVVVSRNGK
0.1	2183.0768	0.0009	VSLPFSDFIRFCKQHMR

Mascot: http://www.matrixscience.com/

AT1G31360.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLIAELK**
Found in **AT1G31360.1** in **TAIR_Arabidopsis**, Symbols: RECQL2 | RECQL2 (Arabidopsis RecQ helicase l2); ATP-dependent helicase/ protein binding | chr1:11232403-11237393 FORWARD

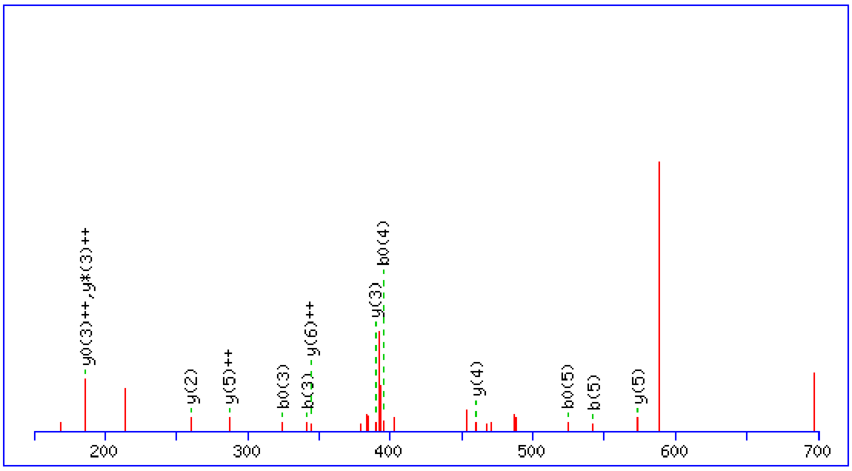
Match to Query 1043: 800.465458 from(401.240005,2+) index(2292)
Title: Elution from: 26.026 to 26.026 scan no 2923 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 700 Da Full range

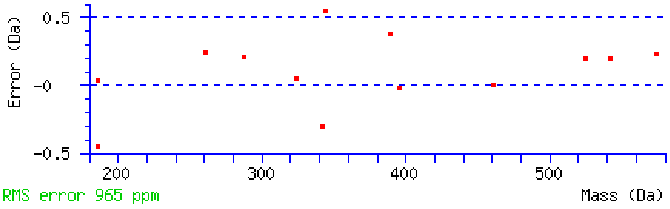
Label all possible matches ○ Label matches used for scoring ●

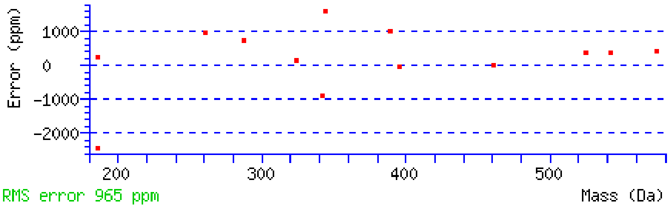
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 800.4643
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.028
Matches : 13/56 fragment ions using 25 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	98.0237	49.5155	D							7
2	229.1183	115.0628	211.1077	106.0575	L	686.4447	343.7260	669.4182	335.2127	668.4341	334.7207	6
3	**342.2023**	171.6048	324.1918	162.5995	I	***573.3606***	287.1840	556.3341	278.6707	555.3501	278.1787	5
4	413.2395	207.1234	395.2289	198.1181	A	***460.2766***	230.6419	443.2500	222.1287	442.2660	221.6366	4
5	**542.2821**	271.6447	524.2715	262.6394	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
6	655.3661	328.1867	637.3556	319.1814	L	***260.1969***	130.6021	243.1703	122.0888			2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DLIAELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.0	800.4643	0.0011	DLIAELK
22.0	800.4643	0.0011	IDLAELK

AT1G31360.1

19.7	800.4643	0.0011	EVIAELK
17.0	800.4643	0.0011	LLDAEIK

Mascot: http://www.matrixscience.com/

AT1G31810.1

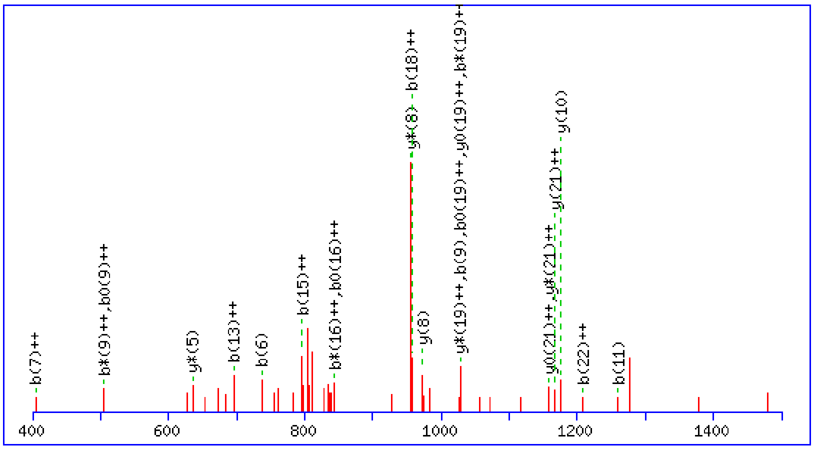
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEQELMASENDGAISLGFRKVLK**
Found in **AT1G31810.1** in **TAIR_Arabidopsis**, Symbols: | actin binding | chr1:11399903-11405742 REVERSE

Match to Query 10300: 2563.227174 from(855.416334,3+) index(6988)
Title: Elution from: 61.641 to 61.641 scan no 9097 cid35.00 polarity:+
Data file D12h-1_3.mgf

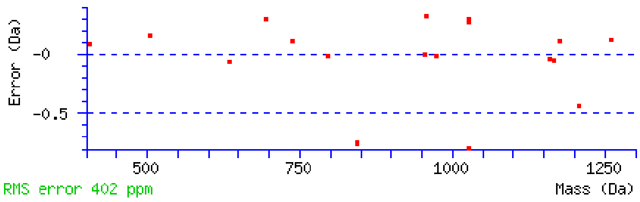
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

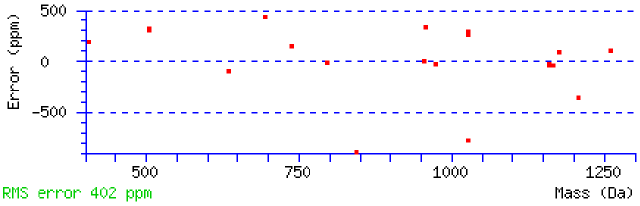


Monoisotopic mass of neutral peptide Mr(calc): 2563.2321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.014
Matches : 23/242 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							23
2	231.1124	116.0598			213.1018	107.0545	E	2464.1739	1232.5906	2446.1503	1223.5788	2446.1633	1223.5853	22
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	Q	2334.1343	1167.5708	2316.1107	1158.5590	2316.1237	1158.5655	21
4	491.2046	246.1060	473.1810	237.0942	473.1941	237.1007	E	2204.0816	1102.5445	2186.0580	1093.5327	2186.0711	1093.5392	20
5	605.2857	303.1465	587.2621	294.1347	587.2752	294.1412	L	2074.0420	1037.5246	2056.0184	1028.5128	2056.0314	1028.5194	19
6	***737.3232***	369.1653	719.2997	360.1535	719.3127	360.1600	M	1959.9609	980.4841	1941.9373	971.4723	1941.9503	971.4788	18
7	809.3574	***405.1823***	791.3338	396.1705	791.3468	396.1771	A	1827.9234	914.4653	1809.8998	905.4535	1809.9128	905.4600	17
8	897.3865	449.1969	879.3629	440.1851	879.3759	440.1916	S	1755.8892	878.4483	1737.8656	869.4365	1737.8787	869.4430	16
9	***1027.4261***	514.2167	1009.4025	505.2049	1009.4155	505.2114	E	1667.8602	834.4337	1649.8366	825.4219	1649.8496	825.4284	15
10	1143.4631	572.2352	1125.4395	563.2234	1125.4525	563.2299	N	1537.8205	769.4139	1519.7970	760.4021	1519.8100	760.4086	14
11	***1259.4871***	630.2472	1241.4635	621.2354	1241.4765	621.2419	D	1421.7835	711.3954	1403.7600	702.3836	1403.7730	702.3901	13
12	1317.5056	659.2564	1299.4820	650.2446	1299.4950	650.2511	G	1305.7596	653.3834	1287.7360	644.3716	1287.7490	644.3781	12
13	1389.5397	***695.2735***	1371.5161	686.2617	1371.5291	686.2682	A	1247.7411	624.3742	1229.7175	615.3624	1229.7305	615.3689	11
14	1503.6208	752.3140	1485.5972	743.3023	1485.6102	743.3088	I	**1175.7069**	588.3571	1157.6833	579.3453	1157.6964	579.3518	10
15	1591.6499	***796.3286***	1573.6263	787.3168	1573.6393	787.3233	S	1061.6258	531.3165	1043.6022	522.3048	1043.6153	522.3113	9
16	1705.7310	853.3691	1687.7074	844.3573	1687.7204	844.3638	L	**973.5968**	487.3020	955.5732	478.2902			8
17	1763.7495	882.3784	1745.7259	873.3666	1745.7389	873.3731	G	859.5157	430.2615	841.4921	421.2497			7
18	1911.8149	***956.4111***	1893.7913	947.3993	1893.8044	947.4058	F	801.4972	401.2522	783.4736	392.2404			6
19	2071.9042	1036.4557	2053.8806	1027.4439	2053.8936	1027.4504	R	653.4317	327.2195	635.4081	318.2077			5
20	2201.9932	1101.5002	2183.9696	1092.4884	2183.9826	1092.4950	K	493.3425	247.1749	475.3189	238.1631			4
21	2302.0587	1151.5330	2284.0351	1142.5212	2284.0481	1142.5277	V	363.2534	182.1303	345.2298	173.1186			3
22	2416.1398	***1208.5735***	2398.1162	1199.5617	2398.1292	1199.5682	L	263.1880	132.0976	245.1644	123.0858			2
23							K	149.1069	75.0571	131.0833	66.0453			1

AT1G31810.1





NCBI **BLAST** search of VEQELMASENDGAISLGFRKVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.2	2563.2321	-0.0049	VEQELMASENDGAISLGFRKVLK
11.4	2563.2343	-0.0071	GLQFLVAESMSKNAPVFNDNLLK
3.1	2563.2199	0.0073	YMIKICKILGMATLVEVHDER
1.2	2563.2305	-0.0033	AFSALVGEFPIGEYIPSLSWIDK
0.7	2563.2247	0.0025	IPVPKIELASMDFTVQNITMTR
0.2	2563.2343	-0.0071	SLDFHALCALYAVTDVALVTSLR
0.1	2563.2291	-0.0020	AEESRVPSSVSVTVAHDLLLAGHR

Mascot: http://www.matrixscience.com/

AT1G31812.1

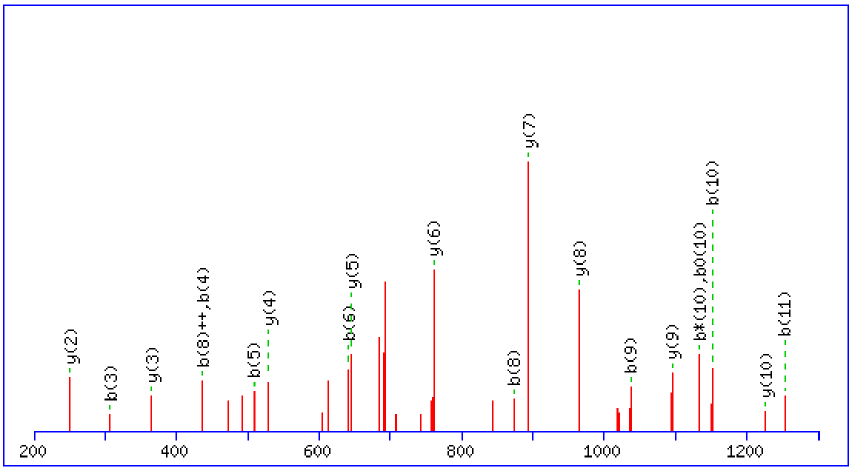
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSEEAMNDYITK**
Found in **AT1G31812.1** in **TAIR_Arabidopsis**, Symbols: ACBP | ACBP (ACYL-COA-BINDING PROTEIN); acyl-CoA binding | chr1:11411113-11412080 REVERSE

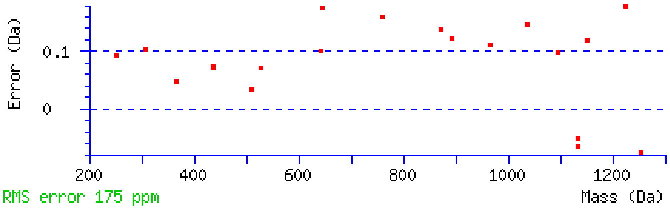
Match to Query 5400: 1400.556330 from(701.285441,2+) index(3010)
Title: Elution from: 30.088 to 30.088 scan no 3758 cid35.00 polarity:+
Data file D6h-3_2.mgf

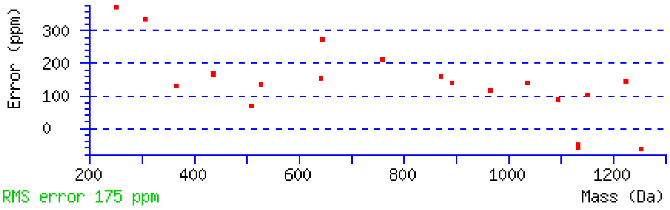
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1400.5558
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 106 **Expect:** 6.2e-011
Matches : 20/118 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	177.0654	89.0363			159.0548	80.0311	S	1313.5340	657.2706	1295.5104	648.2589	1295.5234	648.2654	11
3	***307.1050***	154.0562			289.0945	145.0509	E	***1225.5050***	613.2561	1207.4814	604.2443	1207.4944	604.2508	10
4	***437.1447***	219.0760			419.1341	210.0707	E	***1095.4653***	548.2363	1077.4417	539.2245	1077.4548	539.2310	9
5	***509.1788***	255.0930			491.1682	246.0878	A	***965.4257***	483.2165	947.4021	474.2047	947.4151	474.2112	8
6	***641.2163***	321.1118			623.2058	312.1065	M	***893.3915***	447.1994	875.3680	438.1876	875.3810	438.1941	7
7	757.2533	379.1303	739.2297	370.1185	739.2428	370.1250	N	***761.3540***	381.1807	743.3304	372.1689	743.3435	372.1754	6
8	***873.2773***	***437.1423***	855.2537	428.1305	855.2667	428.1370	D	***645.3170***	323.1622	627.2934	314.1504	627.3065	314.1569	5
9	***1037.3377***	519.1725	1019.3141	510.1607	1019.3271	510.1672	Y	***529.2930***	265.1502	511.2695	256.1384	511.2825	256.1449	4
10	***1151.4188***	576.2130	1133.3952	567.2012	1133.4082	567.2077	I	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
11	***1253.4635***	627.2354	1235.4399	618.2236	1235.4529	618.2301	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SSEEAMNDYITK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G31812.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
106.3	1400.5558	0.0005	SSEEAMNDYITK
5.8	1400.5537	0.0026	FNMQDPNKAMR
0.0	1400.5567	-0.0004	CGIAMMPSYPTK

AT1G32060.1

Mascot Search Results

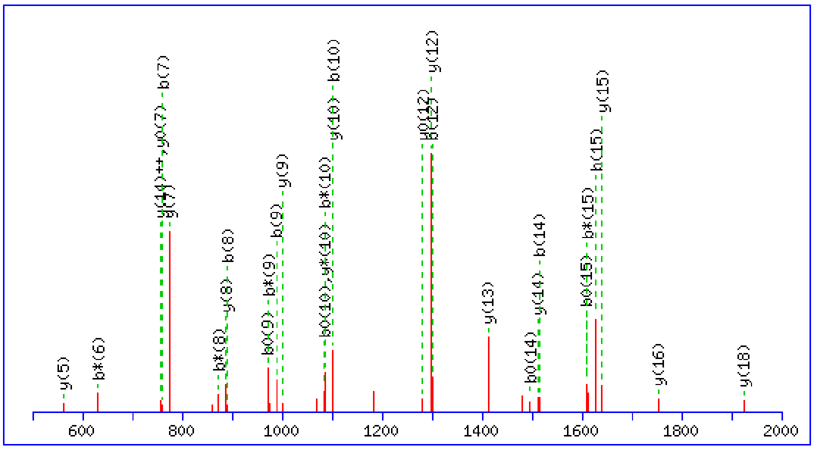
Peptide View

MS/MS Fragmentation of **QYADAVIEVLPTTLIPDDNEGK**
Found in **AT1G32060.1** in **TAIR_Arabidopsis**, Symbols: PRK | PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein binding | chr1:11532648-11534386 FORWARD

Match to Query 10331: 2400.206520 from(1201.110536,2+) index(10201)
Title: Elution from: 94.798 to 94.798 scan no 14349 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

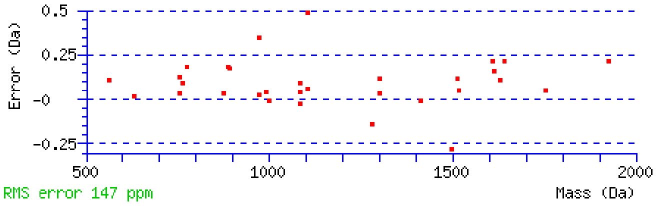
Or, Plot from 500 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

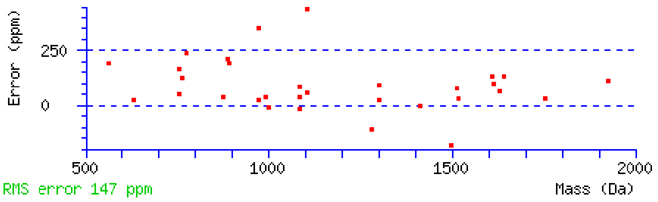


Monoisotopic mass of neutral peptide Mr(calc): 2400.2060
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 89 **Expect:** 5.4e-009
Matches : 31/242 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							22
2	292.1292	146.5682	275.1026	138.0550			Y	2273.1547	1137.0810	2256.1282	1128.5677	2255.1442	1128.0757	21
3	363.1663	182.0868	346.1397	173.5735			A	2110.0914	1055.5493	2093.0649	1047.0361	2092.0808	1046.5441	20
4	478.1932	239.6003	461.1667	231.0870	460.1827	230.5950	D	2039.0543	1020.0308	2022.0277	1011.5175	2021.0437	1011.0255	19
5	549.2304	275.1188	532.2038	266.6055	531.2198	266.1135	A	***1924.0274***	962.5173	1907.0008	954.0040	1906.0168	953.5120	18
6	648.2988	324.6530	631.2722	316.1397	630.2882	315.6477	V	1852.9902	926.9988	1835.9637	918.4855	1834.9797	917.9935	17
7	**761.3828**	381.1951	744.3563	372.6818	743.3723	372.1898	I	***1753.9218***	877.4645	1736.8953	868.9513	1735.9113	868.4593	16
8	**890.4254**	445.7164	873.3989	437.2031	872.4149	436.7111	E	***1640.8378***	820.9225	1623.8112	812.4092	1622.8272	811.9172	15
9	**989.4938**	495.2506	972.4673	486.7373	971.4833	486.2453	V	***1511.7952***	756.4012	1494.7686	747.8879	1493.7846	747.3959	14
10	**1102.5779**	551.7926	1085.5514	543.2793	1084.5673	542.7873	L	***1412.7268***	706.8670	1395.7002	698.3537	1394.7162	697.8617	13
11	1199.6307	600.3190	1182.6041	591.8057	1181.6201	591.3137	P	***1299.6427***	650.3250	1282.6161	641.8117	1281.6321	641.3197	12
12	**1300.6783**	650.8428	1283.6518	642.3295	1282.6678	641.8375	T	1202.5899	601.7986	1185.5634	593.2853	1184.5794	592.7933	11
13	1401.7260	701.3667	1384.6995	692.8534	1383.7155	692.3614	T	***1101.5422***	551.2748	1084.5157	542.7615	1083.5317	542.2695	10
14	**1514.8101**	757.9087	1497.7835	749.3954	1496.7995	748.9034	L	***1000.4946***	500.7509	983.4680	492.2376	982.4840	491.7456	9
15	**1627.8942**	814.4507	1610.8676	805.9374	1609.8836	805.4454	I	***887.4105***	444.2089	870.3840	435.6956	869.3999	435.2036	8
16	1724.9469	862.9771	1707.9204	854.4638	1706.9364	853.9718	P	***774.3264***	387.6669	757.2999	379.1536	756.3159	378.6616	7
17	1839.9739	920.4906	1822.9473	911.9773	1821.9633	911.4853	D	677.2737	339.1405	660.2471	330.6272	659.2631	330.1352	6
18	1955.0008	978.0040	1937.9743	969.4908	1936.9902	968.9988	D	***562.2467***	281.6270	545.2202	273.1137	544.2362	272.6217	5
19	2069.0437	1035.0255	2052.0172	1026.5122	2051.0332	1026.0202	N	447.2198	224.1135	430.1932	215.6003	429.2092	215.1082	4
20	2198.0863	1099.5468	2181.0598	1091.0335	2180.0758	1090.5415	E	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
21	2255.1078	1128.0575	2238.0812	1119.5443	2237.0972	1119.0522	G	204.1343	102.5708	187.1077	94.0575			2
22							K	147.1128	74.0600	130.0863	65.5468			1

AT1G32060.1





NCBI **BLAST** search of QYADAVIEVLPTTLIPDDNEGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
89.2	2400.2060	0.0005	QYADAVIEVLPTTLIPDDNEGK

Mascot: http://www.matrixscience.com/

AT1G32220.1

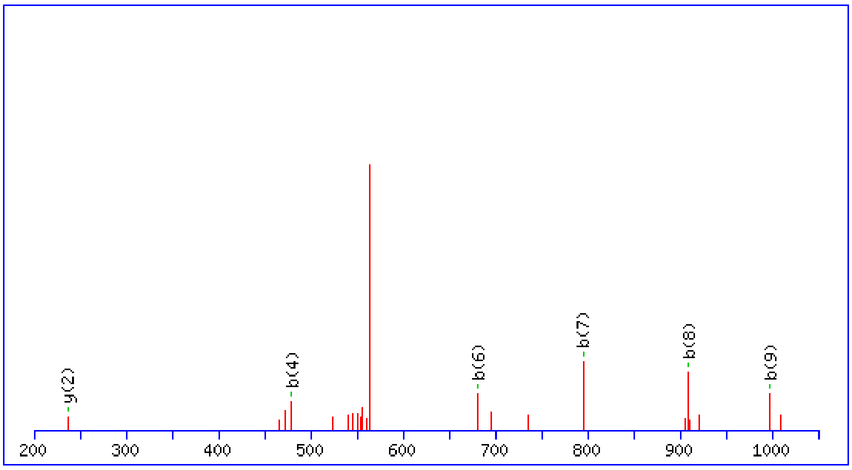
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNAEAELLSK**
Found in **AT1G32220.1** in **TAIR_Arabidopsis**, Symbols: | binding / catalytic/ coenzyme binding | chr1:11608018-11609571 FORWARD

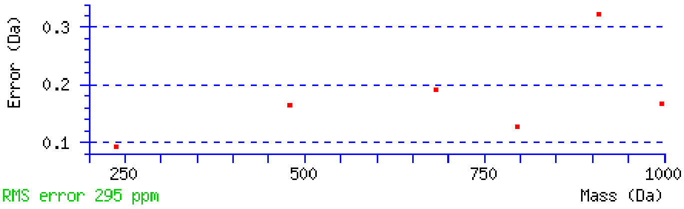
Match to Query 3631: 1144.562720 from(573.288636,2+) index(1374)
Title: Elution from: 18.891 to 18.891 scan no 1854 cid35.00 polarity:+
Data file D12h-1_3.mgf

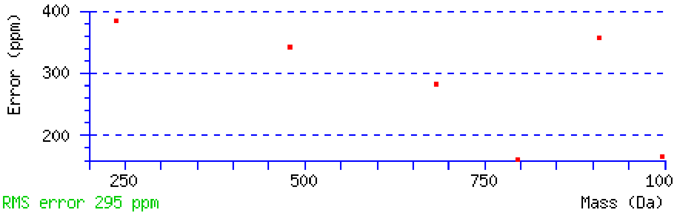
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.5647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0011
Matches : 6/100 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							10
2	277.1335	139.0704	259.1099	130.0586			N	985.4827	493.2450	967.4591	484.2332	967.4721	484.2397	9
3	349.1677	175.0875	331.1441	166.0757			A	869.4457	435.2265	851.4221	426.2147	851.4351	426.2212	8
4	*479.2073*	240.1073	461.1837	231.0955	461.1967	231.1020	E	797.4115	399.2094	779.3880	390.1976	779.4010	390.2041	7
5	551.2414	276.1244	533.2179	267.1126	533.2309	267.1191	A	667.3719	334.1896	649.3483	325.1778	649.3613	325.1843	6
6	*681.2811*	341.1442	663.2575	332.1324	663.2705	332.1389	E	595.3378	298.1725	577.3142	289.1607	577.3272	289.1672	5
7	*795.3622*	398.1847	777.3386	389.1729	777.3516	389.1794	L	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
8	*909.4433*	455.2253	891.4197	446.2135	891.4327	446.2200	L	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
9	*997.4723*	499.2398	979.4488	490.2280	979.4618	490.2345	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RNAEAELLSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G32220.1

39.6	1144.5647	-0.0019	RNAEAELLSK
18.1	1144.5646	-0.0019	EVRDGLGGISK
11.6	1144.5642	-0.0015	ELFAEVGELK
10.3	1144.5647	-0.0019	LSSNVEGVLGR
8.0	1144.5642	-0.0015	EIGFLEGEIK
6.0	1144.5642	-0.0015	IYGLELSDPK
5.3	1144.5647	-0.0019	SRSEPLDAKK
4.7	1144.5647	-0.0019	AGKGKDKPSDK
4.2	1144.5655	-0.0028	HRGILMMLK
4.0	1144.5647	-0.0019	REKEQAELK

Mascot: http://www.matrixscience.com/

AT1G32470.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VKPSSPAELEALMGPK**
Found in **AT1G32470.1** in **TAIR_Arabidopsis**, Symbols: | glycine cleavage system H protein, mitochondrial, putative | chr1:11739459-11740226 REVERSE

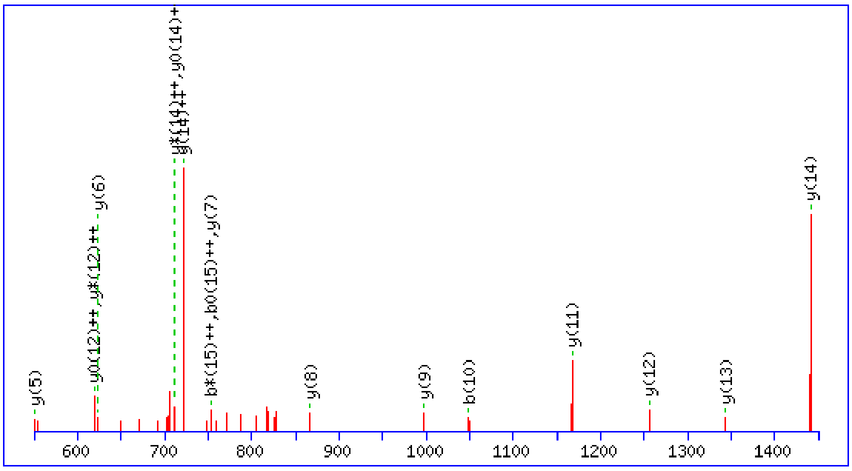
Match to Query 8299: 1670.827272 from(836.420912,2+) index(6369)
Title: Elution from: 55.488 to 55.488 scan no 8068 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1450 Da Full range

Label all possible matches ○ Label matches used for scoring ●

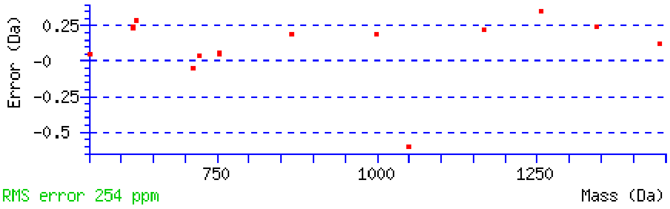
Show Y-axis ☐

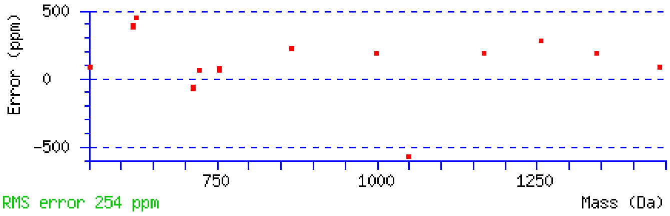


Monoisotopic mass of neutral peptide Mr(calc): 1670.8274
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 6.3e-007
Matches : 17/160 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					**V**							**16**
2	231.1618	116.0845	213.1382	107.0727			**K**	1571.7692	786.3882	1553.7456	777.3764	1553.7586	777.3830	**15**
3	329.2116	165.1094	311.1880	156.0976			**P**	***1441.6802***	721.3437	1423.6566	712.3319	1423.6696	712.3384	**14**
4	417.2406	209.1239	399.2170	200.1122	399.2301	200.1187	**S**	***1343.6304***	672.3188	1325.6068	663.3070	1325.6198	663.3135	**13**
5	505.2697	253.1385	487.2461	244.1267	487.2591	244.1332	**S**	***1255.6013***	628.3043	1237.5777	619.2925	1237.5907	619.2990	**12**
6	603.3195	302.1634	585.2959	293.1516	585.3089	293.1581	**P**	***1167.5722***	584.2898	1149.5487	575.2780	1149.5617	575.2845	**11**
7	675.3536	338.1805	657.3300	329.1687	657.3431	329.1752	**A**	1069.5224	535.2649	1051.4989	526.2531	1051.5119	526.2596	**10**
8	805.3933	403.2003	787.3697	394.1885	787.3827	394.1950	**E**	***997.4883***	499.2478	979.4647	490.2360	979.4777	490.2425	**9**
9	919.4744	460.2408	901.4508	451.2290	901.4638	451.2355	**L**	***867.4487***	434.2280	849.4251	425.2162	849.4381	425.2227	**8**
10	1049.5140	525.2606	1031.4904	516.2488	1031.5034	516.2553	**E**	***753.3676***	377.1874	735.3440	368.1756	735.3570	368.1821	**7**
11	1121.5481	561.2777	1103.5246	552.2659	1103.5376	552.2724	**A**	***623.3279***	312.1676	605.3044	303.1558			**6**
12	1235.6292	618.3183	1217.6057	609.3065	1217.6187	609.3130	**L**	***551.2938***	276.1505	533.2702	267.1387			**5**
13	1367.6668	684.3370	1349.6432	675.3252	1349.6562	675.3317	**M**	437.2127	219.1100	419.1891	210.0982			**4**
14	1425.6853	713.3463	1407.6617	704.3345	1407.6747	704.3410	**G**	305.1752	153.0912	287.1516	144.0794			**3**
15	1523.7351	762.3712	1505.7115	753.3594	1505.7245	753.3659	**P**	247.1567	124.0820	229.1331	115.0702			**2**
16							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT1G32470.1





NCBI **BLAST** search of VKPSSPAELEALMGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.5	1670.8274	-0.0001	VKPSSPAELEALMGPK
7.2	1670.8274	-0.0001	SVYSEAPMKKVSALK
4.2	1670.8248	0.0024	VKVMVMPGFYVLDR
1.4	1670.8271	0.0002	LQVATELNAYGRRR

Mascot: http://www.matrixscience.com/

AT1G32530.1

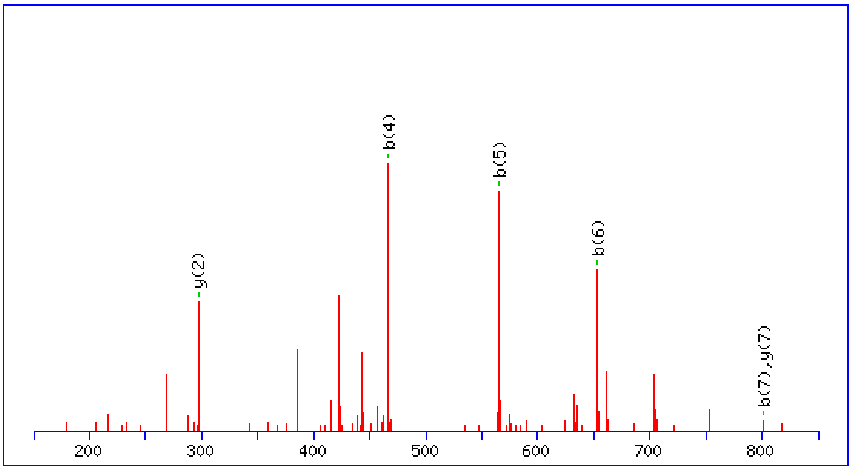
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNLSPSMK**
Found in **AT1G32530.1** in **TAIR_Arabidopsis**, Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:11759646-11762366 REVERSE

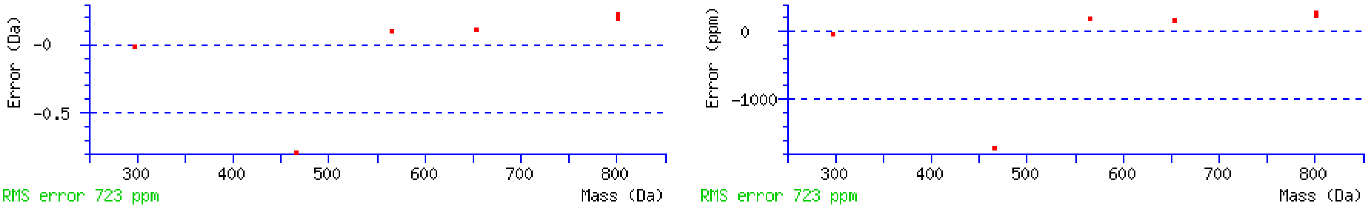
Match to Query 1649: 948.421824 from(475.218188,2+) index(1981)
Title: Elution from: 26.406 to 26.406 scan no 2651 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 948.4235
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 29 **Expect:** 0.011
Matches : 6/112 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							8
2	265.1097	133.0585	247.0861	124.0467			N	**801.3653**	401.1863	783.3417	392.1745	783.3548	392.1810	7
3	379.1908	190.0990	361.1672	181.0873			L	685.3283	343.1678	667.3047	334.1560	667.3178	334.1625	6
4	***467.2199***	234.1136	449.1963	225.1018	449.2093	225.1083	S	571.2472	286.1273	553.2236	277.1155	553.2367	277.1220	5
5	***565.2697***	283.1385	547.2461	274.1267	547.2591	274.1332	P	483.2182	242.1127	465.1946	233.1009	465.2076	233.1074	4
6	***653.2987***	327.1530	635.2752	318.1412	635.2882	318.1477	S	385.1684	193.0878	367.1448	184.0760	367.1578	184.0825	3
7	***801.3312***	401.1692	783.3076	392.1574	783.3206	392.1639	M	**297.1393**	149.0733	279.1157	140.0615			2
8							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of FNLSPSMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G32530.1

29.4	948.4235	-0.0017	FNLSPSMK
18.3	948.4235	-0.0017	EQIMGSFK
15.9	948.4201	0.0017	SPWTSSFK
10.7	948.4235	-0.0017	QLQEMFK
8.9	948.4235	-0.0017	MVDGLNFK
6.9	948.4235	-0.0017	LNGFVDMK
5.5	948.4235	-0.0017	MYDQAALK
4.1	948.4235	-0.0017	FEMEVIR
4.0	948.4235	-0.0017	IQGMEAFK
3.4	948.4213	0.0005	ELLSSMSR

AT1G32850.1

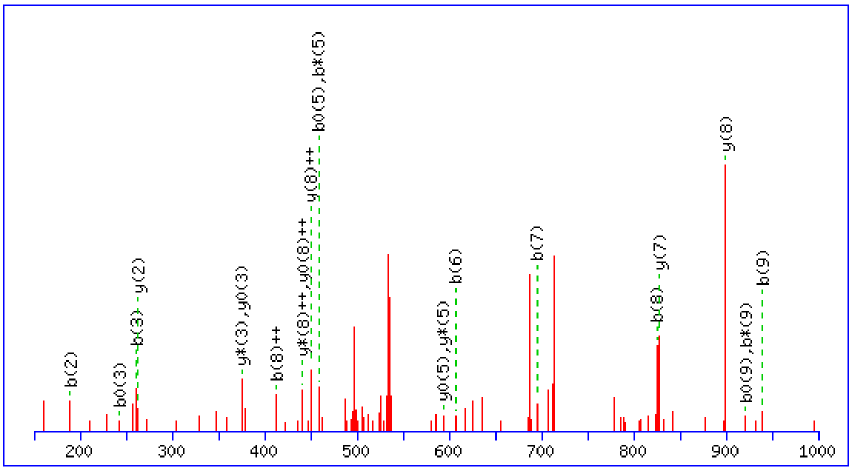
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSAVNESEIK**
Found in **AT1G32850.1** in **TAIR_Arabidopsis**, Symbols: | ubiquitin carboxyl-terminal hydrolase family protein | chr1:11902609-11906880 FORWARD

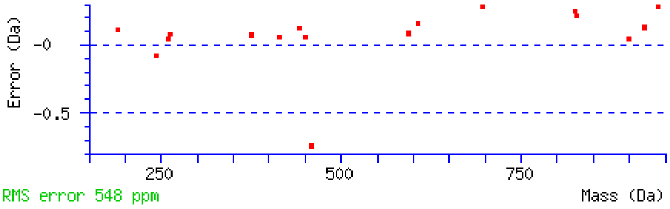
Match to Query 3376: 1086.518002 from(544.266277,2+) index(2631)
Title: Elution from: 28.089 to 28.089 scan no 3308 cid35.00 polarity:+
Data file 0-2_1.mgf

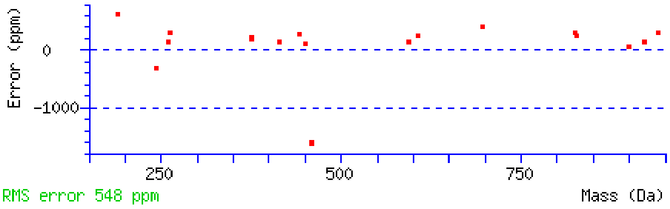
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1086.5201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.018
Matches : 22/94 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							10
2	***189.1018***	95.0545			171.0912	86.0492	S	987.4620	494.2346	969.4384	485.2228	969.4514	485.2293	9
3	***261.1359***	131.0716			243.1254	122.0663	A	**899.4329**	450.2201	881.4093	441.2083	881.4223	441.2148	8
4	361.2014	181.1043			343.1908	172.0990	V	**827.3987**	414.2030	809.3752	405.1912	809.3882	405.1977	7
5	477.2384	239.1228	459.2148	230.1110	459.2278	230.1175	N	727.3333	364.1703	709.3097	355.1585	709.3227	355.1650	6
6	***607.2780***	304.1426	589.2544	295.1309	589.2674	295.1374	E	611.2963	306.1518	593.2727	297.1400	593.2857	297.1465	5
7	***695.3071***	348.1572	677.2835	339.1454	677.2965	339.1519	S	481.2567	241.1320	463.2331	232.1202	463.2461	232.1267	4
8	***825.3467***	413.1770	807.3231	404.1652	807.3361	404.1717	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
9	***939.4278***	470.2175	921.4042	461.2057	921.4172	461.2123	I	**263.1880**	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VSAVNESEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G32850.1

Score	Mr(calc)	Delta	Sequence
25.9	1086.5201	-0.0021	VSAVNESEIK
21.9	1086.5201	-0.0021	EQLSASEALK
13.8	1086.5176	0.0004	WCLTGTPIK
7.7	1086.5201	-0.0021	SVKDVVDDAK
5.9	1086.5199	-0.0019	FCFFSKLK
4.7	1086.5154	0.0026	SAPSPKSCLK
3.5	1086.5154	0.0026	TMGHSSVVLK
2.5	1086.5201	-0.0021	SLGNLSLEDK

AT1G32900.1

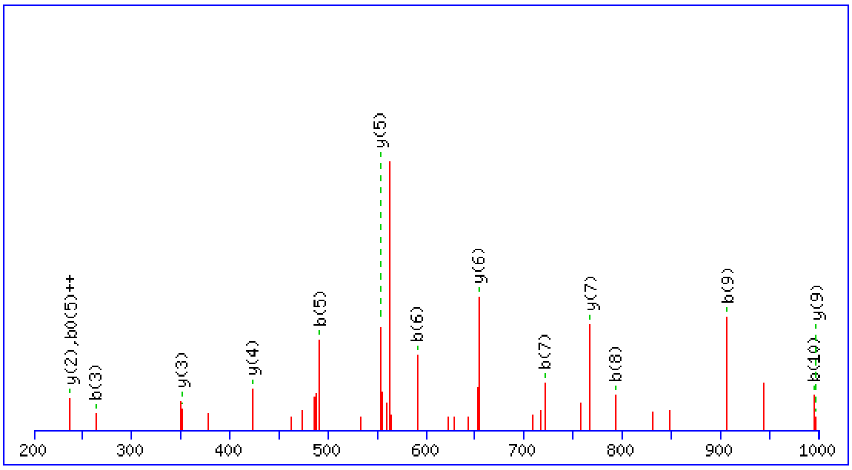
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSDILVEAISK**
Found in **AT1G32900.1** in **TAIR_Arabidopsis**, Symbols: | starch synthase, putative | chr1:11920562-11923486 REVERSE

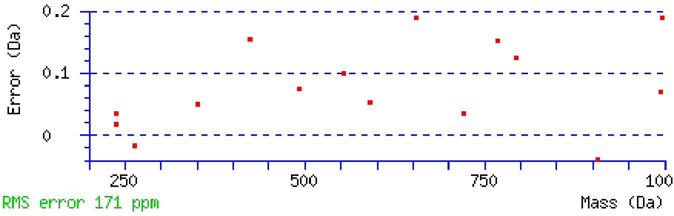
Match to Query 3197: 1142.583830 from(572.299191,2+) index(5432)
Title: Elution from: 52.305 to 52.305 scan no 7054 cid35.00 polarity:+
Data file D1d-1-2.mgf

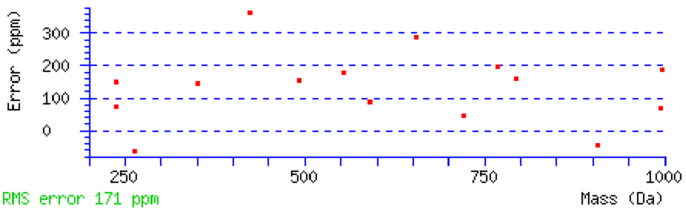
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1142.5827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.7e-006
Matches : 15/96 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			**G**							**11**
2	147.0548	74.0311	129.0443	65.0258	**S**	1085.5715	543.2894	1067.5479	534.2776	1067.5609	534.2841	**10**
3	***263.0788***	132.0430	245.0683	123.0378	**D**	***997.5424***	499.2749	979.5189	490.2631	979.5319	490.2696	**9**
4	377.1599	189.0836	359.1494	180.0783	**I**	881.5185	441.2629	863.4949	432.2511	863.5079	432.2576	**8**
5	***491.2410***	246.1241	473.2304	237.1189	**L**	***767.4374***	384.2223	749.4138	375.2105	749.4268	375.2170	**7**
6	***591.3065***	296.1569	573.2959	287.1516	**V**	***653.3563***	327.1818	635.3327	318.1700	635.3457	318.1765	**6**
7	***721.3461***	361.1767	703.3355	352.1714	**E**	***553.2908***	277.1490	535.2672	268.1373	535.2802	268.1438	**5**
8	***793.3802***	397.1938	775.3697	388.1885	**A**	***423.2512***	212.1292	405.2276	203.1174	405.2406	203.1239	**4**
9	***907.4613***	454.2343	889.4508	445.2290	**I**	***351.2170***	176.1122	333.1935	167.1004	333.2065	167.1069	**3**
10	***995.4904***	498.2488	977.4798	489.2436	**S**	***237.1359***	119.0716	219.1124	110.0598	219.1254	110.0663	**2**
11					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of GSDILVEAISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G32900.1

Score	Mr(calc)	Delta	Sequence
66.7	1142.5827	0.0011	GSDILVEAISK
21.7	1142.5854	-0.0016	LNEEVQRLK
15.8	1142.5827	0.0011	KVELEDALSK
10.7	1142.5827	0.0011	DSGVILAESLK
10.2	1142.5827	0.0011	ELSGVASVELK
10.0	1142.5854	-0.0016	TRTPVPSVSGK
9.6	1142.5829	0.0009	MLRRVFYK
9.4	1142.5807	0.0032	TMLRPLPSGR
8.7	1142.5854	-0.0015	GSVLEVGNVVR
8.2	1142.5854	-0.0016	KETPQERLK

AT1G32990.1

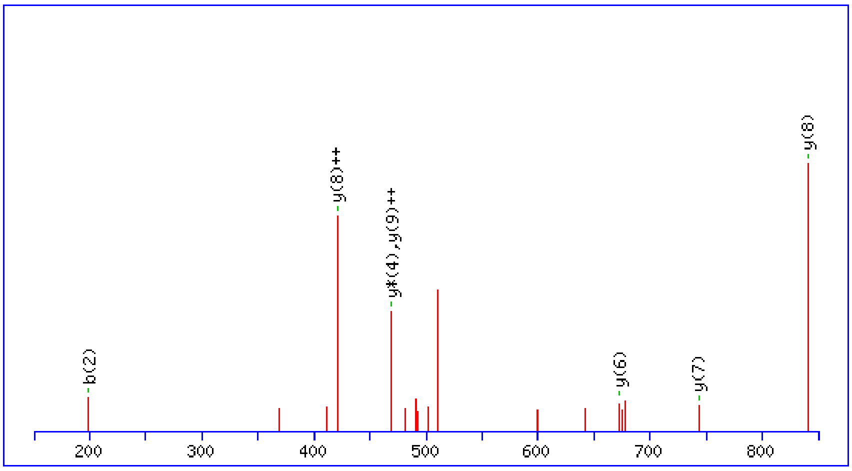
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPPASVLLLK**
Found in **AT1G32990.1** in **TAIR_Arabidopsis**, Symbols: PRPL11 | PRPL11 (PLASTID RIBOSOMAL PROTEIN L11); structural constituent of ribosome | chr1:11955807-11957119 FORWARD

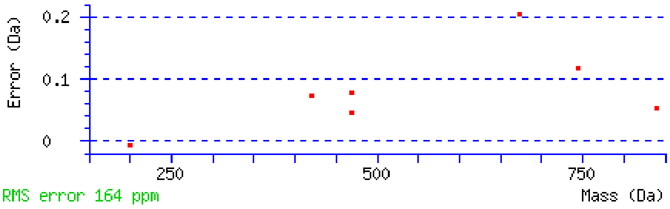
Match to Query 2393: 1037.649326 from(519.831939,2+) index(5157)
Title: Elution from: 49.409 to 49.409 scan no 6652 cid35.00 polarity:+
Data file D1d-2_2.mgf

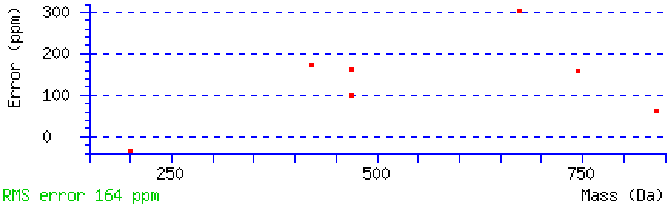
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1037.6485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.012
Matches : 7/80 fragment ions using 10 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	199.1077	100.0575	181.0972	91.0522	P	937.6081	469.3077	920.5815	460.7944	919.5975	460.3024	9
3	296.1605	148.5839	278.1499	139.5786	P	***840.5553***	420.7813	823.5288	412.2680	822.5448	411.7760	8
4	367.1976	184.1024	349.1870	175.0972	A	***743.5026***	372.2549	726.4760	363.7416	725.4920	363.2496	7
5	454.2296	227.6185	436.2191	218.6132	S	***672.4654***	336.7364	655.4389	328.2231	654.4549	327.7311	6
6	553.2980	277.1527	535.2875	268.1474	V	585.4334	293.2203	568.4069	284.7071			5
7	666.3821	333.6947	648.3715	324.6894	L	486.3650	243.6861	469.3384	235.1729			4
8	779.4662	390.2367	761.4556	381.2314	L	373.2809	187.1441	356.2544	178.6308			3
9	892.5502	446.7788	874.5397	437.7735	L	260.1969	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TPPASVLLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G32990.1

Score	Mr(calc)	Delta	Sequence
19.1	1037.6485	0.0009	TPPASVLLLK

Mascot: http://www.matrixscience.com/

AT1G33120.1

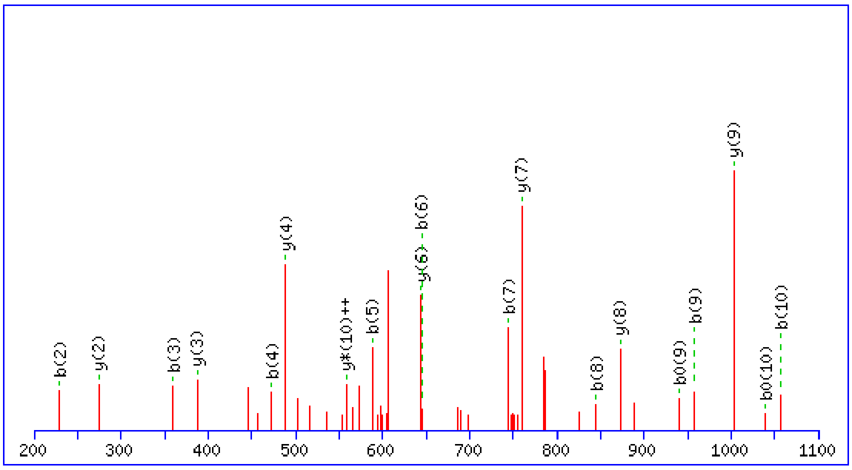
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEMLDGVTIVR**
Found in **AT1G33120.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L9 (RPL90B) | chr1:12010966-12012203 FORWARD

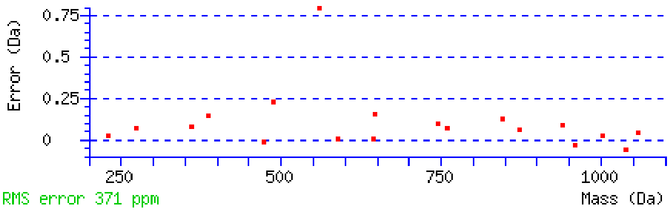
Match to Query 4084: 1230.664294 from(616.339423,2+) index(6390)
Title: Elution from: 56.660 to 56.660 scan no 8264 cid35.00 polarity:+
Data file D6h-2_3.mgf

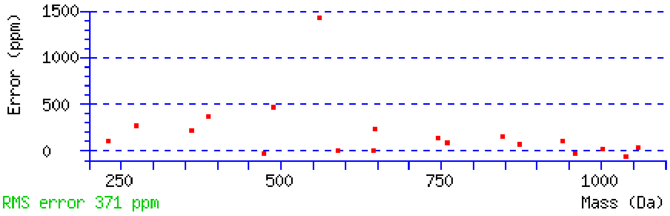
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1230.6642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 2.8e-008
Matches : 19/92 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			**V**							**11**
2	***229.1183***	115.0628	211.1077	106.0575	**E**	1132.6031	566.8052	1115.5765	558.2919	1114.5925	557.7999	**10**
3	***360.1588***	180.5830	342.1482	171.5777	**M**	**1003.5605**	502.2839	986.5339	493.7706	985.5499	493.2786	**9**
4	***473.2428***	237.1251	455.2323	228.1198	**L**	**872.5200**	436.7636	855.4934	428.2504	854.5094	427.7584	**8**
5	***588.2698***	294.6385	570.2592	285.6332	**D**	**759.4359**	380.2216	742.4094	371.7083	741.4254	371.2163	**7**
6	***645.2912***	323.1493	627.2807	314.1440	**G**	**644.4090**	322.7081	627.3824	314.1949	626.3984	313.7028	**6**
7	***744.3597***	372.6835	726.3491	363.6782	**V**	587.3875	294.1974	570.3610	285.6841	569.3770	285.1921	**5**
8	***845.4073***	423.2073	827.3968	414.2020	**T**	**488.3191**	244.6632	471.2926	236.1499	470.3085	235.6579	**4**
9	***958.4914***	479.7493	940.4808	470.7441	**I**	**387.2714**	194.1394	370.2449	185.6261			**3**
10	***1057.5598***	529.2835	1039.5492	520.2783	**V**	**274.1874**	137.5973	257.1608	129.0840			**2**
11					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VEMLDGVTIVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G33120.1

Score	Mr(calc)	Delta	Sequence
82.6	1230.6642	0.0001	VEMLDGVTIVR

Mascot: http://www.matrixscience.com/

AT1G33360.1

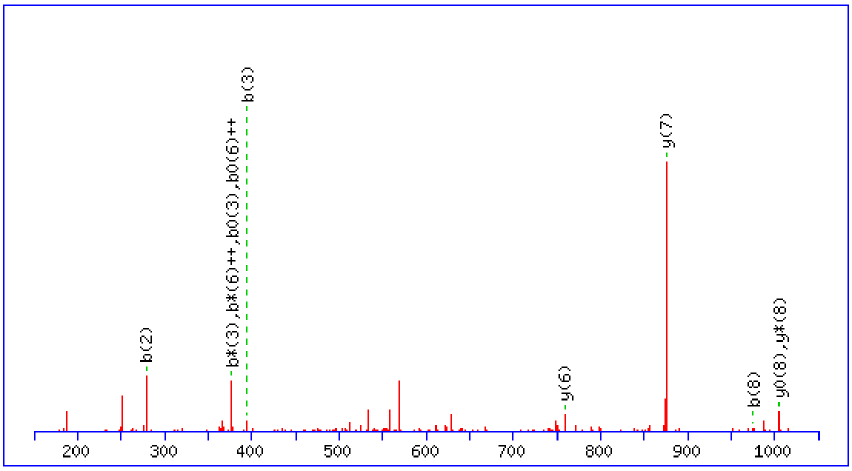
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QMDLLFSNR**
Found in **AT1G33360.1** in **TAIR_Arabidopsis**, Symbols: | ATP-dependent Clp protease ATP-binding subunit ClpX, putative | chr1:12092091-12095769 FORWARD

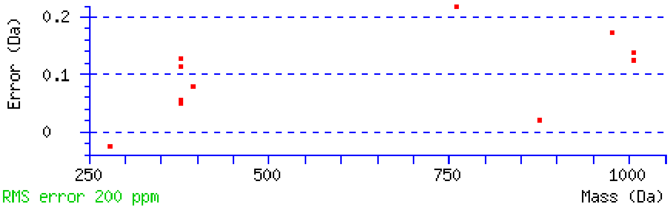
Match to Query 3644: 1152.501704 from(577.258128,2+) index(4414)
Title: Elution from: 39.868 to 39.868 scan no 5543 cid35.00 polarity:+
Data file D6h-3_3.mgf

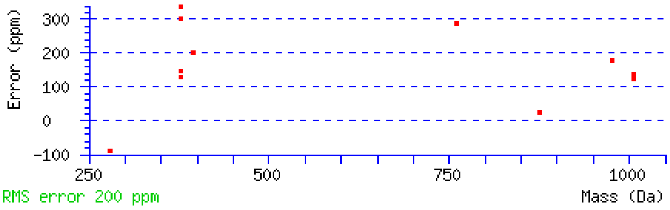
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1152.5026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.045
Matches : 11/134 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			**Q**							9
2	***279.0924***	140.0498	261.0688	131.0380			**M**	1023.4572	512.2322	1005.4336	503.2205	1005.4466	503.2270	8
3	***395.1163***	198.0618	377.0928	189.0500	377.1058	189.0565	**D**	**875.4248**	438.2160	857.4012	429.2042	857.4142	429.2107	7
4	509.1974	255.1024	491.1739	246.0906	491.1869	246.0971	**L**	**759.4008**	380.2040	741.3772	371.1922	741.3902	371.1988	6
5	623.2785	312.1429	605.2550	303.1311	605.2680	303.1376	**L**	645.3197	323.1635	627.2961	314.1517	627.3091	314.1582	5
6	771.3440	386.1756	753.3204	377.1638	753.3334	377.1703	**F**	531.2386	266.1229	513.2150	257.1111	513.2280	257.1177	4
7	859.3730	430.1902	841.3495	421.1784	841.3625	421.1849	**S**	383.1732	192.0902	365.1496	183.0784	365.1626	183.0849	3
8	***975.4100***	488.2087	957.3865	479.1969	957.3995	479.2034	**N**	295.1441	148.0757	277.1205	139.0639			2
9							**R**	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of QMDLLFSNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G33360.1

Score	Mr(calc)	Delta	Sequence
22.3	1152.5026	-0.0009	QMDLLFSNR
21.9	1152.5030	-0.0013	MNQGSGGGRKK
18.3	1152.4996	0.0021	FQEDRRER
11.4	1152.5026	-0.0009	FEMKGGEVAR
11.3	1152.5026	-0.0009	EAETRMFQK
11.0	1152.5030	-0.0013	AMASSRNGAVR
10.7	1152.4992	0.0025	FAGAFDNLER
9.9	1152.5033	-0.0016	MESLSSITMK
7.1	1152.4986	0.0032	MMTINMKEK
7.1	1152.4999	0.0018	KMLESDEFK

Mascot: http://www.matrixscience.com/

AT1G34360.1

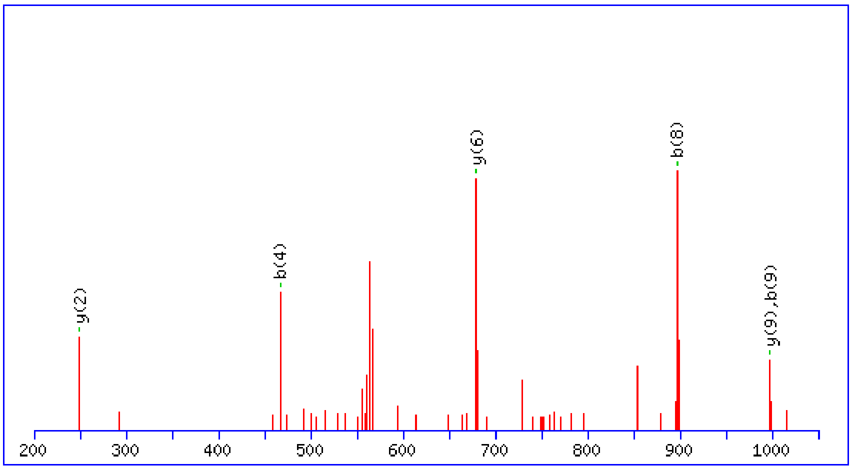
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSVEQAQPVK**
Found in **AT1G34360.1** in **TAIR_Arabidopsis**, Symbols: | translation initiation factor 3 (IF-3) family protein | chr1:12542964-12546003 FORWARD

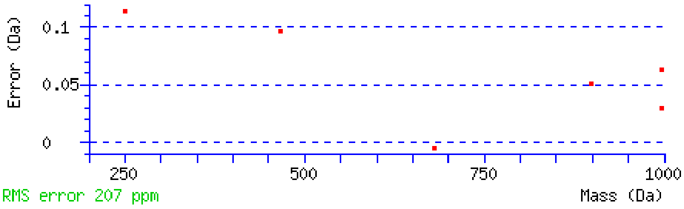
Match to Query 3766: 1144.550542 from(573.282547,2+) index(2708)
Title: Elution from: 26.857 to 26.857 scan no 3328 cid35.00 polarity:+
Data file C7-2_3.mgf

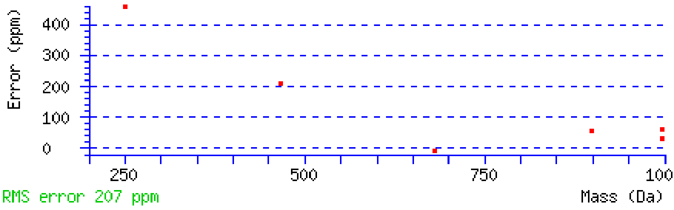
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.5539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.033
Matches : 6/86 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							10
2	237.1018	119.0545			219.0912	110.0492	S	***997.4957***	499.2515	979.4721	490.2397	979.4851	490.2462	9
3	337.1672	169.0873			319.1567	160.0820	V	909.4666	455.2370	891.4431	446.2252	891.4561	446.2317	8
4	***467.2069***	234.1071			449.1963	225.1018	E	809.4012	405.2042	791.3776	396.1924	791.3906	396.1990	7
5	597.2595	299.1334	579.2359	290.1216	579.2489	290.1281	Q	***679.3616***	340.1844	661.3380	331.1726			6
6	669.2937	335.1505	651.2701	326.1387	651.2831	326.1452	A	549.3089	275.1581	531.2853	266.1463			5
7	799.3463	400.1768	781.3227	391.1650	781.3357	391.1715	Q	477.2748	239.1410	459.2512	230.1292			4
8	***897.3961***	449.2017	879.3725	440.1899	879.3855	440.1964	P	347.2221	174.1147	329.1985	165.1029			3
9	***997.4616***	499.2344	979.4380	490.2226	979.4510	490.2291	V	***249.1723***	125.0898	231.1487	116.0780			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FSVEQAQPVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G34360.1

23.9	1144.5539	-0.0033	FSVEQAQPVK
9.7	1144.5516	-0.0011	EAIVSRDDVK
8.4	1144.5516	-0.0011	EGRDLTIAEK
8.1	1144.5517	-0.0011	NLNTELSNVK
7.8	1144.5539	-0.0033	YSPPEVVSVR
7.6	1144.5516	-0.0011	AKKTETPDNK
6.7	1144.5516	-0.0011	GTISGGENVAVK
5.3	1144.5512	-0.0007	FVEEEILEK
3.1	1144.5516	-0.0011	EKSPGGTVQTK
1.9	1144.5516	-0.0011	IQRELDETK

AT1G35160.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAQDIANAELAPTHPIR**
Found in **AT1G35160.1** in **TAIR_Arabidopsis**, Symbols: GF14 PHI, GRF4 | GRF4 (GENERAL REGULATORY FACTOR 4); protein phosphorylated amino acid binding | chr1:12867242-12868492 FORWARD

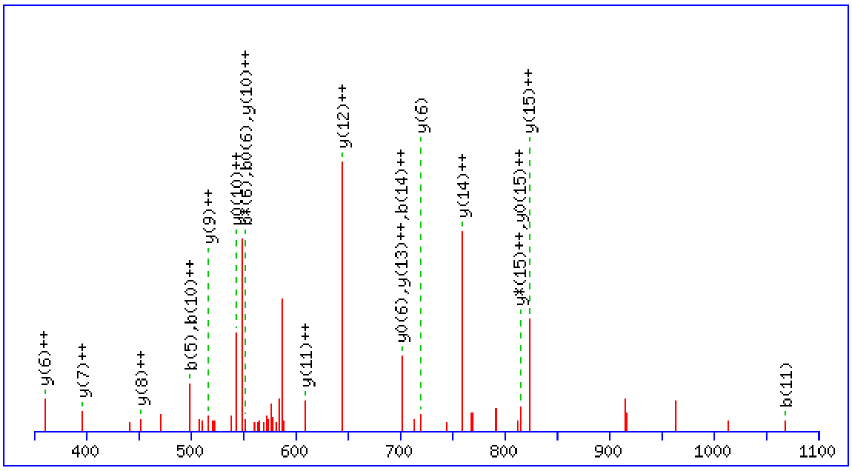
Match to Query 8046: 1786.932075 from(596.651301,3+) index(3568)
Title: Elution from: 37.811 to 37.811 scan no 4595 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●

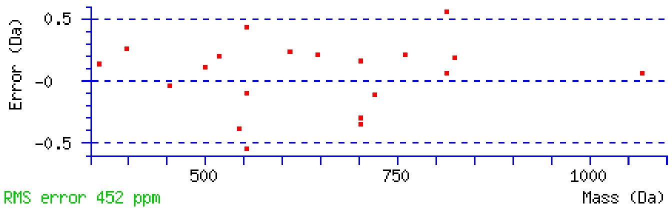
Show Y-axis ☐

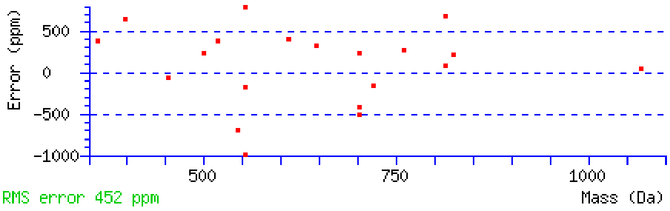


Monoisotopic mass of neutral peptide Mr(calc): 1786.9326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.0002
Matches : 21/174 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							17
2	143.0815	72.0444					A	1716.9028	858.9550	1699.8762	850.4417	1698.8922	849.9497	16
3	271.1401	136.0737	254.1135	127.5604			Q	1645.8656	823.4365	1628.8391	814.9232	1627.8551	814.4312	15
4	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	D	1517.8071	759.4072	1500.7805	750.8939	1499.7965	750.4019	14
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	I	1402.7801	701.8937	1385.7536	693.3804	1384.7696	692.8884	13
6	570.2882	285.6477	553.2617	277.1345	552.2776	276.6425	A	1289.6961	645.3517	1272.6695	636.8384	1271.6855	636.3464	12
7	684.3311	342.6692	667.3046	334.1559	666.3206	333.6639	N	1218.6589	609.8331	1201.6324	601.3198	1200.6484	600.8278	11
8	755.3682	378.1878	738.3417	369.6745	737.3577	369.1825	A	1104.6160	552.8116	1087.5895	544.2984	1086.6055	543.8064	10
9	884.4108	442.7091	867.3843	434.1958	866.4003	433.7038	E	1033.5789	517.2931	1016.5524	508.7798	1015.5683	508.2878	9
10	997.4949	499.2511	980.4684	490.7378	979.4843	490.2458	L	904.5363	452.7718	887.5098	444.2585	886.5257	443.7665	8
11	1068.5320	534.7696	1051.5055	526.2564	1050.5215	525.7644	A	791.4522	396.2298	774.4257	387.7165	773.4417	387.2245	7
12	1165.5848	583.2960	1148.5582	574.7828	1147.5742	574.2907	P	720.4151	360.7112	703.3886	352.1979	702.4046	351.7059	6
13	1266.6325	633.8199	1249.6059	625.3066	1248.6219	624.8146	T	623.3624	312.1848	606.3358	303.6715	605.3518	303.1795	5
14	1403.6914	702.3493	1386.6648	693.8360	1385.6808	693.3440	H	522.3147	261.6610	505.2881	253.1477			4
15	1500.7441	750.8757	1483.7176	742.3624	1482.7336	741.8704	P	385.2558	193.1315	368.2292	184.6183			3
16	1613.8282	807.4177	1596.8016	798.9045	1595.8176	798.4125	I	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1

AT1G35160.1





NCBI **BLAST** search of AAQDIANAELAPTHPIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.5	1786.9326	-0.0005	AAQDIANAELAPTHPIR
5.6	1786.9286	0.0035	RLGSGLDDAETTGLARR
2.4	1786.9359	-0.0038	LASLLRRENDPSAAMK
0.9	1786.9294	0.0027	IAAECTRLMGKERPR
0.7	1786.9326	-0.0005	LGNGLTASGISLNGFNPR
0.7	1786.9360	-0.0039	GLTVKCEVVEVARGDR
0.7	1786.9359	-0.0038	LVLEDAEKMLNRSNR
0.4	1786.9360	-0.0039	QGGTVKAIQEASACIVR

Mascot: http://www.matrixscience.com/

AT1G35340.1

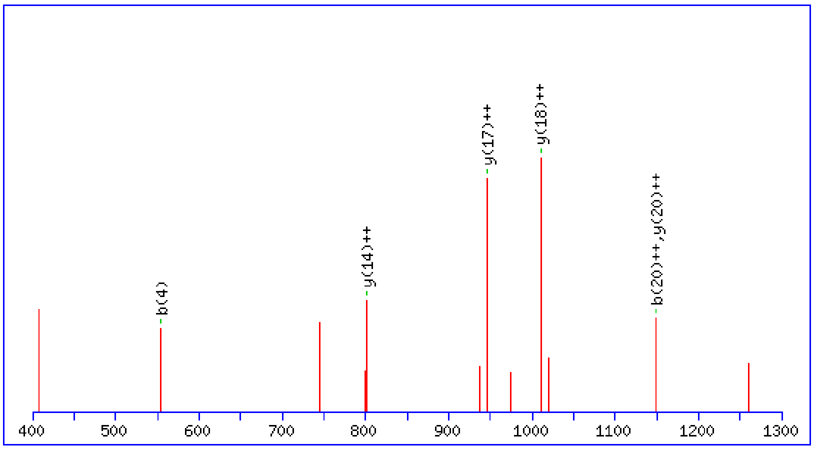
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MNYESSNELTSKISQLKESIK**
Found in **AT1G35340.1** in **TAIR_Arabidopsis**, Symbols: | ATP-dependent protease La (LON) domain-containing protein | chr1:12977746-12979727 FORWARD

Match to Query 10225: 2444.204154 from(815.741994,3+) index(10691)
Title: Elution from: 111.298 to 111.298 scan no 15805 cid35.00 polarity:+
Data file 0-1_3.mgf

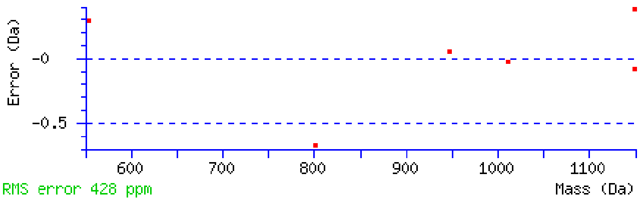
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

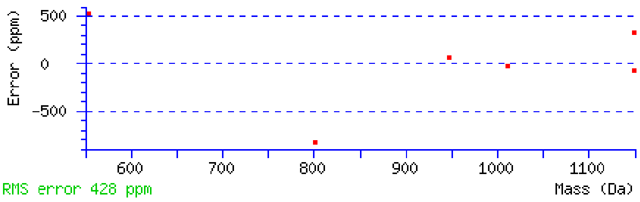


Monoisotopic mass of neutral peptide Mr(calc): 2444.2104
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.024
Matches : 6/340 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							21
2	262.0856	131.5464	245.0591	123.0332			N	2298.1823	1149.5948	2281.1558	1141.0815	2280.1718	1140.5895	20
3	425.1489	213.0781	408.1224	204.5648			Y	2184.1394	1092.5733	2167.1129	1084.0601	2166.1289	1083.5681	19
4	554.1915	277.5994	537.1650	269.0861	536.1810	268.5941	E	2021.0761	1011.0417	2004.0495	1002.5284	2003.0655	1002.0364	18
5	641.2236	321.1154	624.1970	312.6021	623.2130	312.1101	S	1892.0335	946.5204	1875.0069	938.0071	1874.0229	937.5151	17
6	728.2556	364.6314	711.2290	356.1182	710.2450	355.6261	S	1805.0015	903.0044	1787.9749	894.4911	1786.9909	893.9991	16
7	842.2985	421.6529	825.2720	413.1396	824.2879	412.6476	N	1717.9694	859.4884	1700.9429	850.9751	1699.9589	850.4831	15
8	971.3411	486.1742	954.3146	477.6609	953.3305	477.1689	E	1603.9265	802.4669	1586.9000	793.9536	1585.9159	793.4616	14
9	1084.4252	542.7162	1067.3986	534.2029	1066.4146	533.7109	L	1474.8839	737.9456	1457.8574	729.4323	1456.8734	728.9403	13
10	1185.4728	593.2401	1168.4463	584.7268	1167.4623	584.2348	T	1361.7999	681.4036	1344.7733	672.8903	1343.7893	672.3983	12
11	1272.5049	636.7561	1255.4783	628.2428	1254.4943	627.7508	S	1260.7522	630.8797	1243.7256	622.3665	1242.7416	621.8744	11
12	1400.5998	700.8036	1383.5733	692.2903	1382.5893	691.7983	K	1173.7201	587.3637	1156.6936	578.8504	1155.7096	578.3584	10
13	1513.6839	757.3456	1496.6574	748.8323	1495.6733	748.3403	I	1045.6252	523.3162	1028.5986	514.8030	1027.6146	514.3109	9
14	1600.7159	800.8616	1583.6894	792.3483	1582.7054	791.8563	S	932.5411	466.7742	915.5146	458.2609	914.5306	457.7689	8
15	1728.7745	864.8909	1711.7480	856.3776	1710.7639	855.8856	Q	845.5091	423.2582	828.4825	414.7449	827.4985	414.2529	7
16	1841.8586	921.4329	1824.8320	912.9196	1823.8480	912.4276	L	717.4505	359.2289	700.4240	350.7156	699.4400	350.2236	6
17	1969.9535	985.4804	1952.9270	976.9671	1951.9430	976.4751	K	604.3665	302.6869	587.3399	294.1736	586.3559	293.6816	5
18	2098.9961	1050.0017	2081.9696	1041.4884	2080.9856	1040.9964	E	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
19	2186.0282	1093.5177	2169.0016	1085.0044	2168.0176	1084.5124	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
20	2299.1122	1150.0597	2282.0857	1141.5465	2281.1017	1141.0545	I	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT1G35340.1





NCBI **BLAST** search of MNYESSNELTSKISQLKESIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.4	2444.2104	-0.0062	MNYESSNELTSKISQLKESIK
4.9	2444.2005	0.0036	EEISDRLNPGITPEFDPKTMR
1.1	2444.2001	0.0041	MECLEVVKVYLATEMNDLKK
0.0	2444.2044	-0.0002	NGIWEVSKPNTNGLSSSNRQEK

Mascot: http://www.matrixscience.com/

AT1G35680.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYIVFPGR**
Found in **AT1G35680.1** in **TAIR_Arabidopsis**, Symbols: | 50S ribosomal protein L21, chloroplast / CL21 (RPL21) | chr1:13209989-13211458 FORWARD

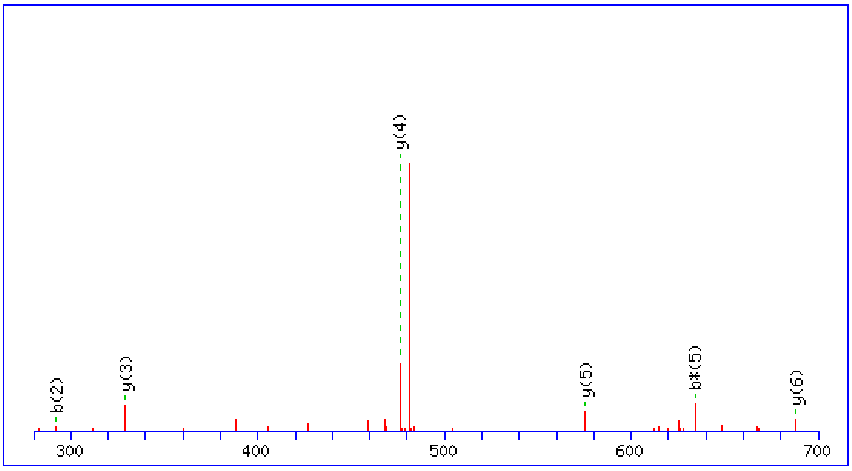
Match to Query 2201: 978.531644 from(490.273098,2+) index(4826)
Title: Elution from: 43.644 to 43.644 scan no 6084 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 280 to 700 Da Full range

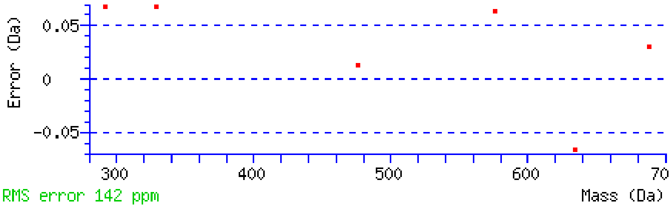
Label all possible matches ○ Label matches used for scoring ●

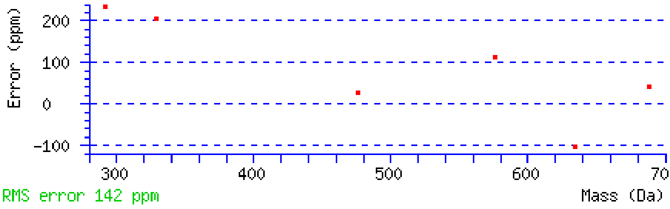
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 978.5287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0051
Matches : 6/56 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.0659	65.0366	112.0393	56.5233	Q					8
2	292.1292	146.5682	275.1026	138.0550	Y	851.4774	426.2423	834.4509	417.7291	7
3	405.2132	203.1103	388.1867	194.5970	I	***688.4141***	344.7107	671.3875	336.1974	6
4	504.2817	252.6445	487.2551	244.1312	V	***575.3300***	288.1686	558.3035	279.6554	5
5	651.3501	326.1787	634.3235	317.6654	F	***476.2616***	238.6344	459.2350	230.1212	4
6	748.4028	374.7051	731.3763	366.1918	P	***329.1932***	165.1002	312.1666	156.5870	3
7	805.4243	403.2158	788.3978	394.7025	G	232.1404	116.5738	215.1139	108.0606	2
8					R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of QYIVFPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.1	978.5287	0.0029	QYIVFPGR

AT1G35680.1

Mascot: http://www.matrixscience.com/

AT1G35720.1

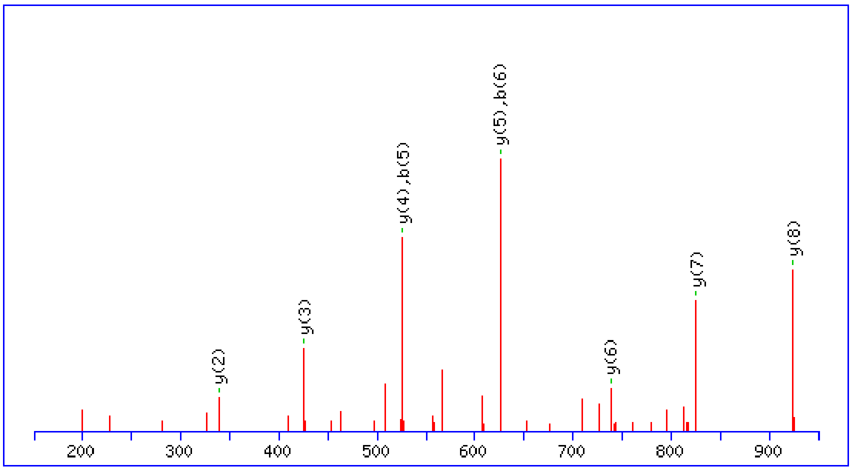
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLVSLVTSYR**
Found in **AT1G35720.1** in **TAIR_Arabidopsis**, Symbols: OXY5, ATOXY5, ANNAT1 | ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding | chr1:13226516-13228151 FORWARD

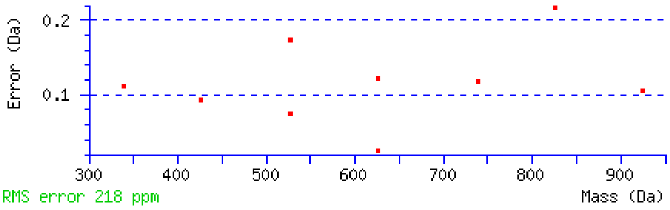
Match to Query 3877: 1149.675248 from(575.844900,2+) index(7389)
Title: Elution from: 66.463 to 66.463 scan no 9642 cid35.00 polarity:+
Data file D6h-2_1.mgf

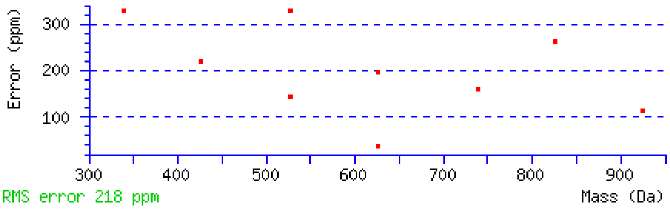
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1149.6758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 1.9e-007
Matches : 9/80 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							10
2	227.1754	114.0913			L	1037.5990	519.3031	1020.5724	510.7898	1019.5884	510.2978	9
3	326.2438	163.6255			V	***924.5149***	462.7611	907.4884	454.2478	906.5043	453.7558	8
4	413.2758	207.1416	395.2653	198.1363	S	***825.4465***	413.2269	808.4199	404.7136	807.4359	404.2216	7
5	**526.3599**	263.6836	508.3493	254.6783	L	***738.4145***	369.7109	721.3879	361.1976	720.4039	360.7056	6
6	**625.4283**	313.2178	607.4178	304.2125	V	***625.3304***	313.1688	608.3039	304.6556	607.3198	304.1636	5
7	726.4760	363.7416	708.4654	354.7364	T	***526.2620***	263.6346	509.2354	255.1214	508.2514	254.6293	4
8	813.5080	407.2577	795.4975	398.2524	S	***425.2143***	213.1108	408.1878	204.5975	407.2037	204.1055	3
9	976.5714	488.7893	958.5608	479.7840	Y	***338.1823***	169.5948	321.1557	161.0815			2
10					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LLVSLVTSYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G35720.1

Score	Mr(calc)	Delta	Sequence
69.3	1149.6758	-0.0005	LLVSLVTSYR
0.0	1149.6731	0.0022	GVAARALHLSR

AT1G41830.1

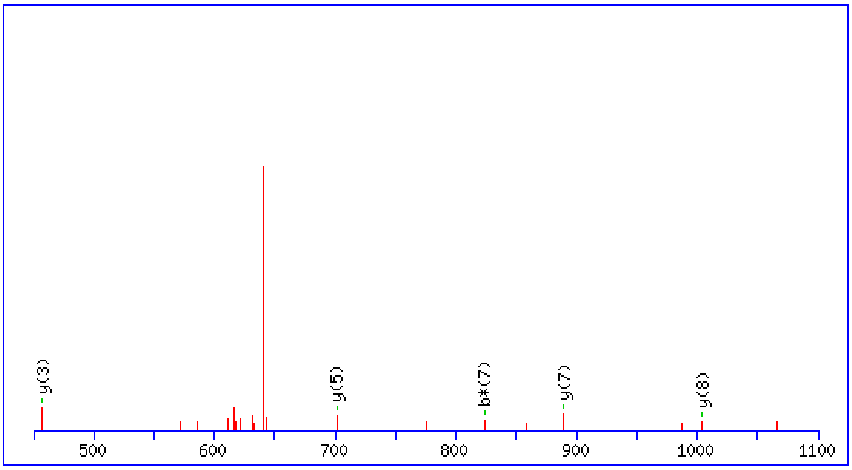
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYLGQQLYLR**
Found in **AT1G41830.1** in **TAIR_Arabidopsis**, Symbols: SKS6 | SKS6 (SKU5 Similar 6); pectinesterase | chr1:15606333-15610243 REVERSE

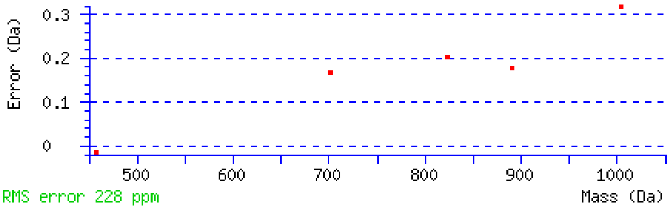
Match to Query 4784: 1296.640156 from(649.327354,2+) index(5673)
Title: Elution from: 50.768 to 50.768 scan no 7217 cid35.00 polarity:+
Data file D6h-3_1.mgf

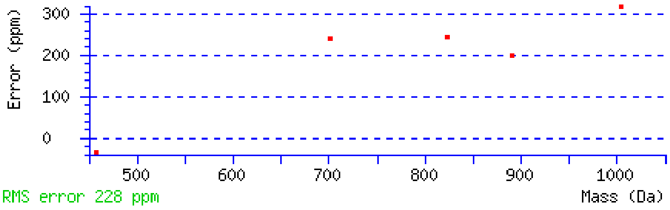
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1296.6403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.009
Matches : 5/72 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	131.0599	66.0336	113.0363	57.0218	Q					10
2	295.1203	148.0638	277.0967	139.0520	Y	1167.5949	584.3011	1149.5713	575.2893	9
3	409.2014	205.1043	391.1778	196.0925	L	***1003.5345***	502.2709	985.5110	493.2591	8
4	467.2199	234.1136	449.1963	225.1018	G	***889.4534***	445.2304	871.4299	436.2186	7
5	597.2725	299.1399	579.2489	290.1281	Q	831.4349	416.2211	813.4114	407.2093	6
6	727.3252	364.1662	709.3016	355.1544	Q	***701.3823***	351.1948	683.3587	342.1830	5
7	841.4063	421.2068	823.3827	412.1950	L	571.3297	286.1685	553.3061	277.1567	4
8	1005.4666	503.2370	987.4431	494.2252	Y	***457.2486***	229.1279	439.2250	220.1161	3
9	1119.5477	560.2775	1101.5242	551.2657	L	293.1882	147.0977	275.1646	138.0859	2
10					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of QYLGQQLYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G41830.1

29.0	1296.6403	-0.0001	QYLGQQLYLR
5.3	1296.6437	-0.0035	YKLAERNMLK
4.9	1296.6403	-0.0001	FGAKLSDFGLAR
4.7	1296.6381	0.0021	IAAPINPSDINR
4.7	1296.6437	-0.0035	LGLYMAKSLNR
3.7	1296.6380	0.0021	VEDHLTALNLR
3.4	1296.6436	-0.0035	GMLSLFERGKK
3.1	1296.6380	0.0021	KSFARSSELGAK
3.0	1296.6380	0.0021	HVVDDGLELRK
2.9	1296.6436	-0.0035	GTMQTLFKIAR

AT1G41880.1

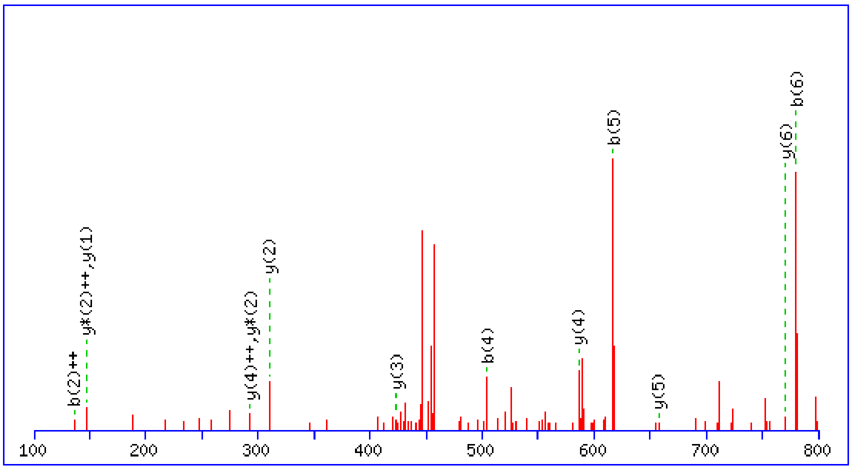
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RLAYIYK**
Found in **AT1G41880.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L35a (RPL35aB) | chr1:15654026-15654868 REVERSE

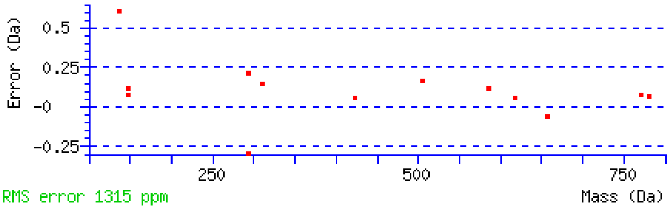
Match to Query 1612: 925.538250 from(463.776401,2+) index(1557)
Title: Elution from: 23.188 to 23.188 scan no 2183 cid35.00 polarity:+
Data file D12h-2_1.mgf

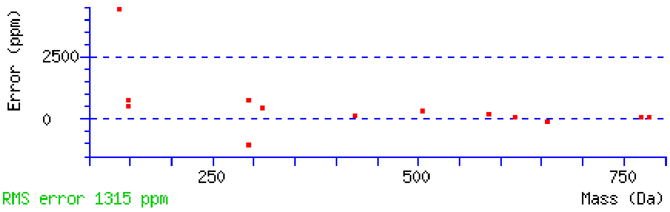
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 925.5385
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.033
Matches : 13/48 fragment ions using 47 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	157.1084	79.0578	140.0818	70.5446	R					7
2	270.1925	135.5999	253.1659	127.0866	L	***770.4447***	385.7260	753.4182	377.2127	6
3	341.2296	171.1184	324.2030	162.6051	A	***657.3606***	329.1840	640.3341	320.6707	5
4	**504.2929**	252.6501	487.2663	244.1368	Y	***586.3235***	293.6654	569.2970	285.1521	4
5	**617.3770**	309.1921	600.3504	300.6788	I	***423.2602***	212.1337	406.2336	203.6205	3
6	**780.4403**	390.7238	763.4137	382.2105	Y	***310.1761***	155.5917	293.1496	147.0784	2
7					K	***147.1128***	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of RLAYIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	925.5385	-0.0002	RLAYIYK
11.1	925.5385	-0.0003	FLRSIYK

AT1G41880.1

Mascot: http://www.matrixscience.com/

AT1G42960.1

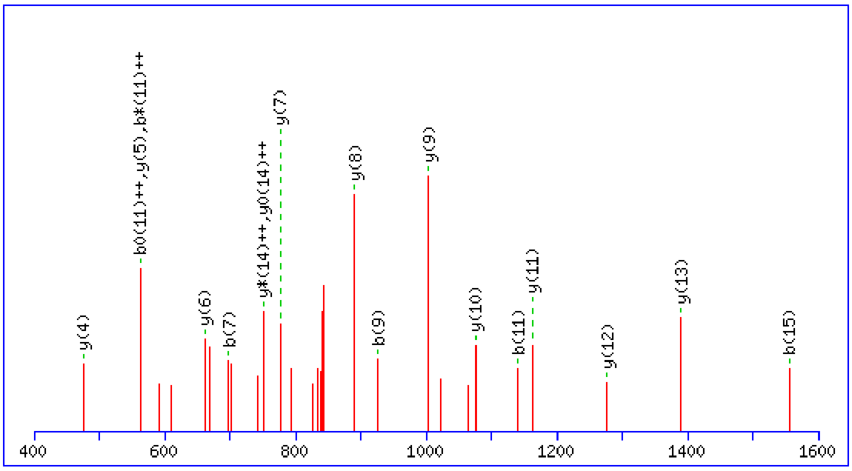
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAQLNSAIDDVSSQLK**
Found in **AT1G42960.1** in **TAIR_Arabidopsis**, Symbols: | expressed protein localized to the inner membrane of the chloroplast. | chr1:16128303-16129520 FORWARD

Match to Query 8094: 1700.891362 from(851.452957,2+) index(7841)
Title: Elution from: 70.270 to 70.270 scan no 10375 cid35.00 polarity:+
Data file 0-1_2.mgf

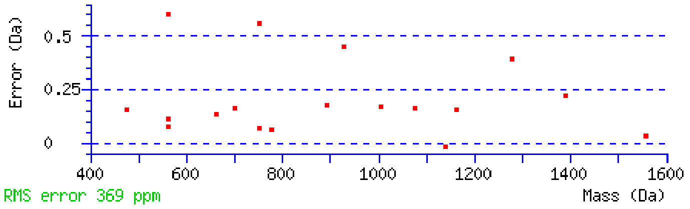
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

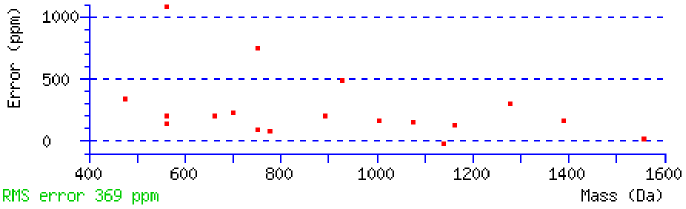


Monoisotopic mass of neutral peptide Mr(calc): 1700.8945
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 1.2e-008
Matches : 18/160 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							16
2	185.1285	93.0679					A	1588.8177	794.9125	1571.7911	786.3992	1570.8071	785.9072	15
3	313.1870	157.0972	296.1605	148.5839			Q	1517.7806	759.3939	1500.7540	750.8807	1499.7700	750.3886	14
4	426.2711	213.6392	409.2445	205.1259			L	***1389.7220***	695.3646	1372.6955	686.8514	1371.7114	686.3594	13
5	540.3140	270.6606	523.2875	262.1474			N	***1276.6379***	638.8226	1259.6114	630.3093	1258.6274	629.8173	12
6	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	S	***1162.5950***	581.8011	1145.5685	573.2879	1144.5844	572.7959	11
7	**698.3832**	349.6952	681.3566	341.1819	680.3726	340.6899	A	***1075.5630***	538.2851	1058.5364	529.7719	1057.5524	529.2798	10
8	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	I	***1004.5259***	502.7666	987.4993	494.2533	986.5153	493.7613	9
9	**926.4942**	463.7507	909.4676	455.2374	908.4836	454.7454	D	***891.4418***	446.2245	874.4153	437.7113	873.4312	437.2193	8
10	1041.5211	521.2642	1024.4946	512.7509	1023.5106	512.2589	D	***776.4149***	388.7111	759.3883	380.1978	758.4043	379.7058	7
11	**1140.5895**	570.7984	1123.5630	562.2851	1122.5790	561.7931	V	***661.3879***	331.1976	644.3614	322.6843	643.3774	322.1923	6
12	1227.6216	614.3144	1210.5950	605.8011	1209.6110	605.3091	S	***562.3195***	281.6634	545.2930	273.1501	544.3089	272.6581	5
13	1314.6536	657.8304	1297.6270	649.3172	1296.6430	648.8251	S	***475.2875***	238.1474	458.2609	229.6341	457.2769	229.1421	4
14	1442.7122	721.8597	1425.6856	713.3464	1424.7016	712.8544	Q	388.2554	194.6314	371.2289	186.1181			3
15	**1555.7962**	778.4018	1538.7697	769.8885	1537.7857	769.3965	L	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT1G42960.1





NCBI **BLAST** search of IAQLNSAIDDVSSQLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.1	1700.8945	-0.0031	IAQLNSAIDDVSSQLK
2.9	1700.8880	0.0034	VQISQAALGDGITICR
2.3	1700.8933	-0.0019	YVKGGGVHGWNLMRK

AT1G42970.1

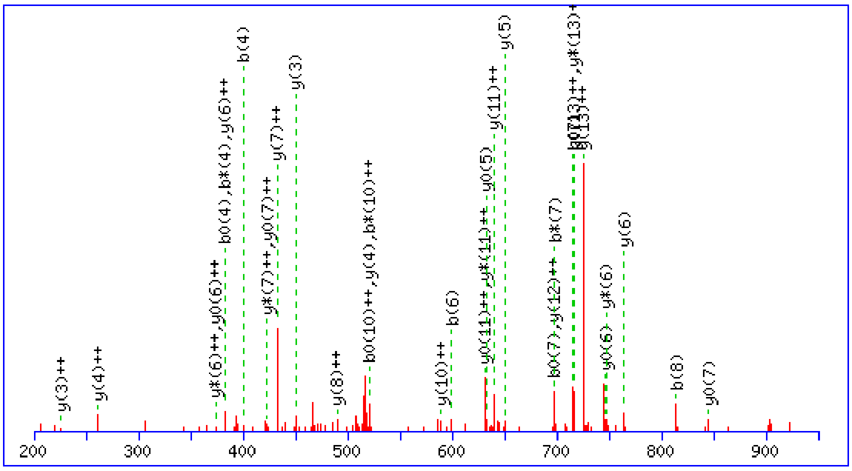
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGLTAEDVNEAFRK**
Found in **AT1G42970.1** in **TAIR_Arabidopsis**, Symbols: GAPB | GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase | chr1:16129992-16132024 FORWARD

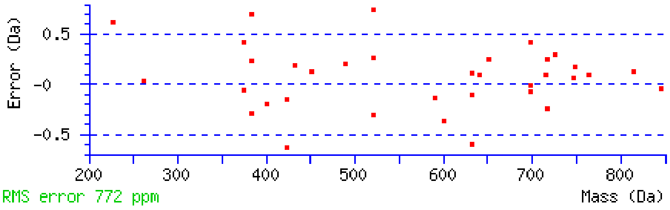
Match to Query 6718: 1576.819443 from(526.613757,3+) index(3152)
Title: Elution from: 31.538 to 31.538 scan no 3917 cid35.00 polarity:+
Data file C7-1_3.mgf

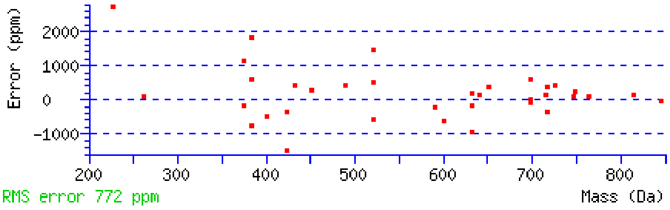
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1576.8209
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 6.8e-005
Matches : 36/142 fragment ions using 53 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	186.1237	93.5655	169.0972	85.0522			G	1449.7332	725.3703	1432.7067	716.8570	1431.7227	716.3650	13
3	299.2078	150.1075	282.1812	141.5942			L	1392.7118	696.8595	1375.6852	688.3462	1374.7012	687.8542	12
4	**400.2554**	200.6314	383.2289	192.1181	382.2449	191.6261	T	1279.6277	640.3175	1262.6012	631.8042	1261.6171	631.3122	11
5	471.2926	236.1499	454.2660	227.6366	453.2820	227.1446	A	1178.5800	589.7937	1161.5535	581.2804	1160.5695	580.7884	10
6	**600.3352**	300.6712	583.3086	292.1579	582.3246	291.6659	E	1107.5429	554.2751	1090.5164	545.7618	1089.5323	545.2698	9
7	**715.3621**	358.1847	698.3355	349.6714	697.3515	349.1794	D	978.5003	489.7538	961.4738	481.2405	960.4898	480.7485	8
8	**814.4305**	407.7189	797.4040	399.2056	796.4199	398.7136	V	863.4734	432.2403	846.4468	423.7271	845.4628	423.2350	7
9	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	N	**764.4050**	382.7061	747.3784	374.1928	746.3944	373.7008	6
10	1057.5160	529.2617	1040.4895	520.7484	1039.5055	520.2564	E	**650.3620**	325.6847	633.3355	317.1714	632.3515	316.6794	5
11	1128.5531	564.7802	1111.5266	556.2669	1110.5426	555.7749	A	**521.3194**	261.1634	504.2929	252.6501			4
12	1275.6216	638.3144	1258.5950	629.8011	1257.6110	629.3091	F	**450.2823**	225.6448	433.2558	217.1315			3
13	1431.7227	716.3650	1414.6961	707.8517	1413.7121	707.3597	R	303.2139	152.1106	286.1874	143.5973			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KGLTAEDVNEAFRK

AT1G42970.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.0	1576.8209	-0.0014	KGLTAEDVNEAFRK
6.9	1576.8222	-0.0028	WVQATFRRTNGNK

AT1G43170.1

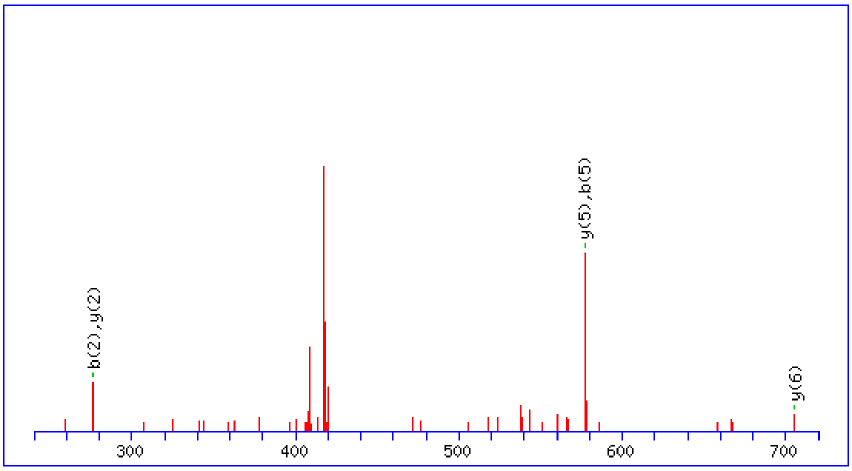
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQTSLEK**
Found in **AT1G43170.1** in **TAIR_Arabidopsis**, Symbols: EMB2207, RPL3A | ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome | chr1:16269432-16271071 FORWARD

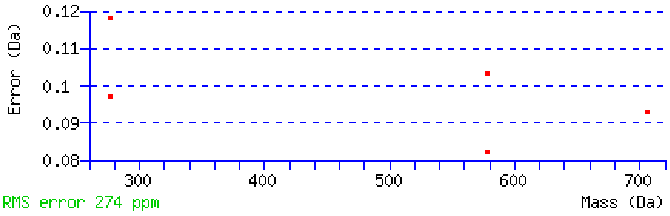
Match to Query 1222: 851.439270 from(426.726911,2+) index(1319)
Title: Elution from: 18.221 to 18.221 scan no 1791 cid35.00 polarity:+
Data file 0-3_3.mgf

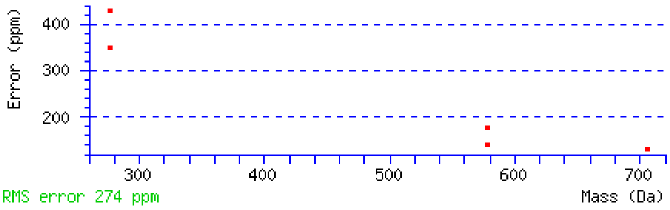
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 240 to 720 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 851.4389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.029
Matches : 5/64 fragment ions using 5 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							7
2	**276.1343**	138.5708	259.1077	130.0575			Q	***705.3777***	353.1925	688.3512	344.6792	687.3672	344.1872	6
3	377.1819	189.0946	360.1554	180.5813	359.1714	180.0893	T	***577.3192***	289.1632	560.2926	280.6499	559.3086	280.1579	5
4	464.2140	232.6106	447.1874	224.0974	446.2034	223.6053	S	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
5	**577.2980**	289.1527	560.2715	280.6394	559.2875	280.1474	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
6	706.3406	353.6740	689.3141	345.1607	688.3301	344.6687	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
7							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FQTSLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.8	851.4389	0.0004	FQTSLEK
10.4	851.4389	0.0004	FAATVSEK

AT1G43170.1

10.4	851.4389	0.0004	FQETISK
9.6	851.4389	0.0004	EGVYKEK
2.5	851.4389	0.0004	GLGTFTEK
2.4	851.4389	0.0004	NLTFTEK
2.2	851.4389	0.0004	GYESIVGK
0.6	851.4389	0.0004	ELTYAQK
0.5	851.4389	0.0004	FATLDTGK

AT1G43560.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEGALPANQLVER**
Found in **AT1G43560.1** in **TAIR_Arabidopsis**, Symbols: ATY2 | ATY2 (Arabidopsis thioredoxin y2); thiol-disulfide exchange intermediate | chr1:16400799-16402268 REVERSE

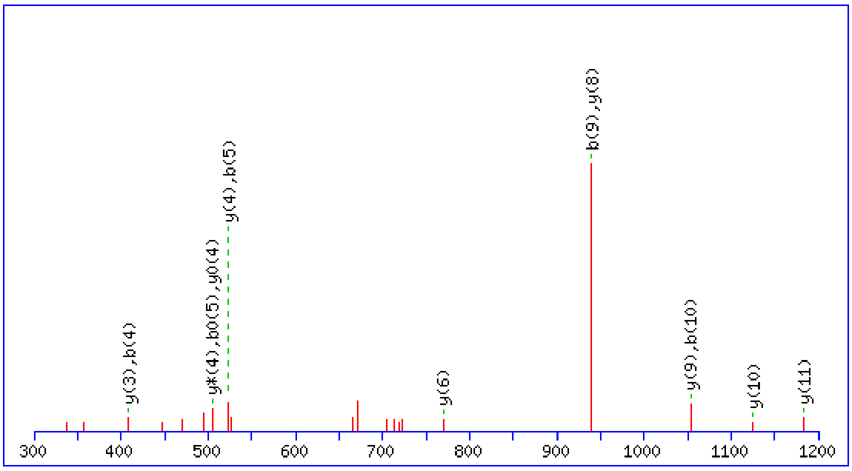
Match to Query 6371: 1460.695716 from(731.355134,2+) index(5604)
Title: Elution from: 49.312 to 49.312 scan no 7022 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1200 Da Full range

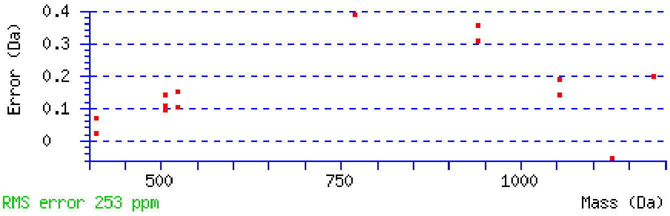
Label all possible matches ○ Label matches used for scoring ●

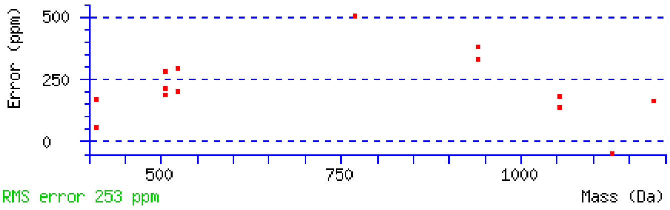
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1460.6984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.4e-005
Matches : 14/126 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					F							13
2	279.1124	140.0598			261.1018	131.0545	E	1313.6402	657.3238	1295.6167	648.3120	1295.6297	648.3185	12
3	337.1309	169.0691			319.1203	160.0638	G	***1183.6006***	592.3039	1165.5770	583.2921	1165.5900	583.2987	11
4	**409.1650**	205.0861			391.1544	196.0809	A	***1125.5821***	563.2947	1107.5585	554.2829	1107.5715	554.2894	10
5	**523.2461**	262.1267			505.2355	253.1214	L	***1053.5480***	527.2776	1035.5244	518.2658	1035.5374	518.2723	9
6	621.2959	311.1516			603.2853	302.1463	P	***939.4669***	470.2371	921.4433	461.2253	921.4563	461.2318	8
7	693.3300	347.1687			675.3195	338.1634	A	841.4171	421.2122	823.3935	412.2004	823.4065	412.2069	7
8	809.3670	405.1872	791.3435	396.1754	791.3565	396.1819	N	***769.3829***	385.1951	751.3593	376.1833	751.3723	376.1898	6
9	**939.4197**	470.2135	921.3961	461.2017	921.4091	461.2082	Q	653.3459	327.1766	635.3223	318.1648	635.3354	318.1713	5
10	**1053.5008**	527.2540	1035.4772	518.2422	1035.4902	518.2488	L	***523.2933***	262.1503	505.2697	253.1385	505.2827	253.1450	4
11	1153.5662	577.2868	1135.5427	568.2750	1135.5557	568.2815	V	***409.2122***	205.1097	391.1886	196.0979	391.2016	196.1044	3
12	1283.6059	642.3066	1265.5823	633.2948	1265.5953	633.3013	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FEGALPANQLVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G43560.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.5	1460.6984	-0.0027	FEGALPANQLVER
17.7	1460.6993	-0.0036	FPCLHALAVCKK
9.8	1460.6962	-0.0004	AVLSQRGPDSVGEK
9.0	1460.6932	0.0025	LYKMFKGTEWK
4.5	1460.6962	-0.0004	EDVVNRVNAGELK
4.1	1460.6935	0.0022	EVNDVELDEKKK
4.1	1460.6935	0.0022	KEVNDVELDEKK
3.7	1460.6984	-0.0027	ANHETIFDQLKK
3.6	1460.6962	-0.0004	LQEQDNEAVLRK
3.4	1460.6914	0.0043	LTAGSSKGYRMVR

AT1G43670.1

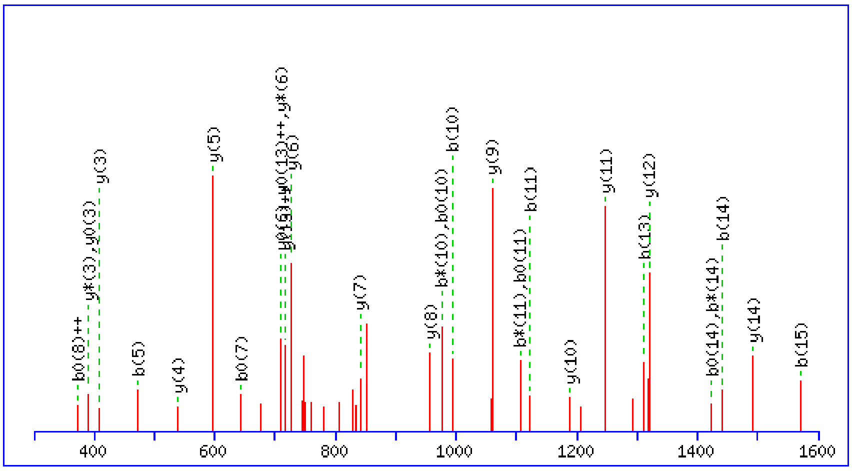
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIGLAGETNIQGEEQK**
Found in **AT1G43670.1** in **TAIR_Arabidopsis**, Symbols: | fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative | chr1:16470624-16472787 FORWARD

Match to Query 7814: 1718.818244 from(860.416398,2+) index(4544)
Title: Elution from: 44.198 to 44.198 scan no 5789 cid35.00 polarity:+
Data file D12h-2_2.mgf

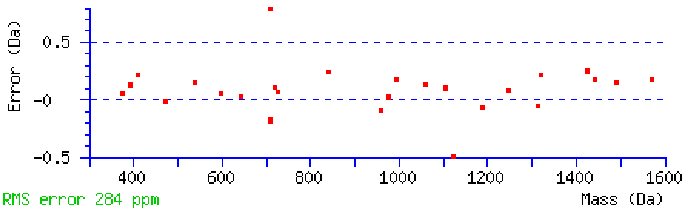
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

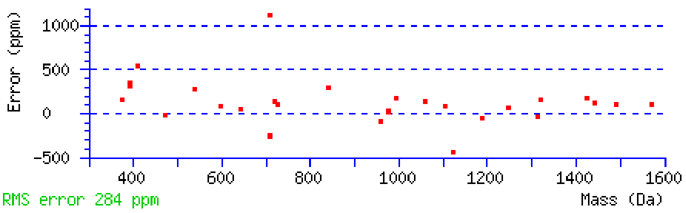


Monoisotopic mass of neutral peptide Mr(calc): 1718.8195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 1.3e-011
Matches : 31/148 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**16**
2	229.1695	115.0884					**I**	1605.7457	803.3765	1587.7221	794.3647	1587.7351	794.3712	**15**
3	287.1880	144.0976					**G**	***1491.6646***	746.3359	1473.6410	737.3241	1473.6540	737.3307	**14**
4	401.2691	201.1382					**L**	1433.6461	717.3267	1415.6225	708.3149	1415.6355	708.3214	**13**
5	**473.3032**	237.1552					**A**	***1319.5650***	660.2861	1301.5414	651.2744	1301.5544	651.2809	**12**
6	531.3217	266.1645					**G**	***1247.5309***	624.2691	1229.5073	615.2573	1229.5203	615.2638	**11**
7	661.3613	331.1843			643.3508	322.1790	**E**	***1189.5124***	595.2598	1171.4888	586.2480	1171.5018	586.2545	**10**
8	763.4061	382.2067			745.3955	373.2014	**T**	***1059.4727***	530.2400	1041.4491	521.2282	1041.4622	521.2347	**9**
9	879.4431	440.2252	861.4195	431.2134	861.4325	431.2199	**N**	***957.4280***	479.2176	939.4044	470.2059	939.4175	470.2124	**8**
10	**993.5242**	497.2657	975.5006	488.2539	975.5136	488.2604	**I**	***841.3910***	421.1991	823.3674	412.1874	823.3805	412.1939	**7**
11	**1123.5768**	562.2920	1105.5532	553.2802	1105.5662	553.2868	**Q**	***727.3099***	364.1586	709.2863	355.1468	709.2994	355.1533	**6**
12	1181.5953	591.3013	1163.5717	582.2895	1163.5847	582.2960	**G**	***597.2573***	299.1323	579.2337	290.1205	579.2467	290.1270	**5**
13	**1311.6349**	656.3211	1293.6113	647.3093	1293.6244	647.3158	**E**	***539.2388***	270.1230	521.2152	261.1112	521.2282	261.1177	**4**
14	**1441.6746**	721.3409	1423.6510	712.3291	1423.6640	712.3356	**E**	***409.1991***	205.1032	391.1756	196.0914	391.1886	196.0979	**3**
15	**1571.7272**	786.3672	1553.7036	777.3554	1553.7166	777.3620	**Q**	279.1595	140.0834	261.1359	131.0716			**2**
16							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT1G43670.1





NCBI **BLAST** search of LIGLAGETNIQGEEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
116.7	1718.8195	-0.0013	LIGLAGETNIQGEEQK
7.7	1718.8170	0.0012	SFRNESMVIDVFKK
3.2	1718.8192	-0.0010	FAMYWLLKTQEVR
0.8	1718.8148	0.0035	VSGFITGSMANSKAGKK

Mascot: http://www.matrixscience.com/

AT1G44575.1

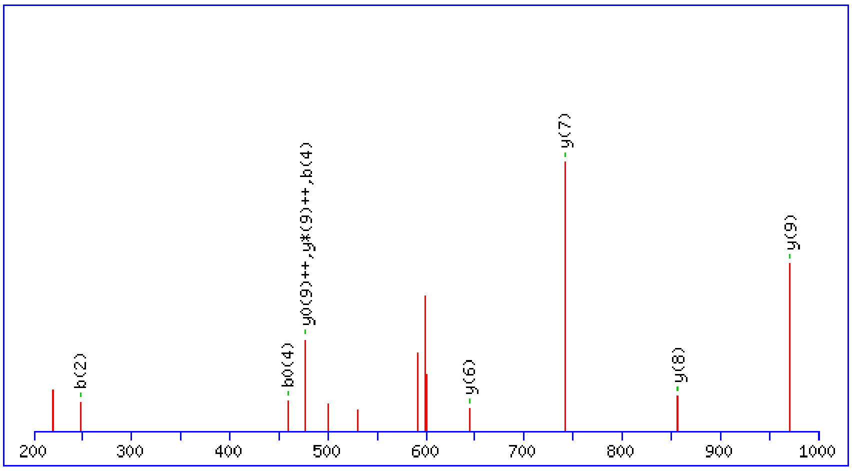
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVDDPPTGLEK**
Found in **AT1G44575.1** in **TAIR_Arabidopsis**, Symbols: PSBS, NPQ4 | NPQ4 (NONPHOTOCHEMICAL QUENCHING) | chr1:16874208-16875634 FORWARD

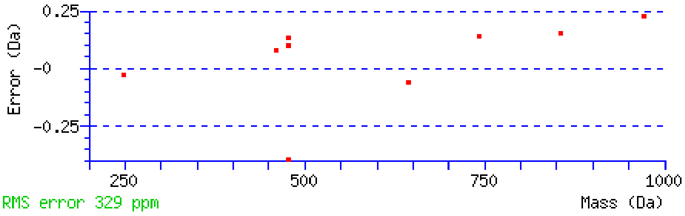
Match to Query 3717: 1216.598842 from(609.306697,2+) index(2962)
Title: Elution from: 32.644 to 32.644 scan no 3802 cid35.00 polarity:+
Data file D1d-2_2.mgf

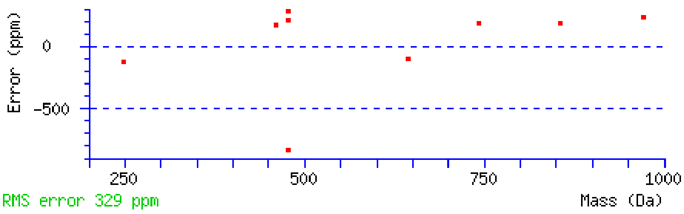
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1216.5976
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0012
Matches : 9/94 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							11
2	**247.1441**	124.0757			V	1070.5364	535.7719	1053.5099	527.2586	1052.5259	526.7666	10
3	362.1710	181.5892	344.1605	172.5839	D	***971.4680***	486.2376	954.4415	477.7244	953.4575	477.2324	9
4	**477.1980**	239.1026	459.1874	230.0974	D	***856.4411***	428.7242	839.4145	420.2109	838.4305	419.7189	8
5	574.2508	287.6290	556.2402	278.6237	P	***741.4141***	371.2107	724.3876	362.6974	723.4036	362.2054	7
6	671.3035	336.1554	653.2930	327.1501	P	***644.3614***	322.6843	627.3348	314.1710	626.3508	313.6790	6
7	772.3512	386.6792	754.3406	377.6740	T	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
8	829.3727	415.1900	811.3621	406.1847	G	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
9	942.4567	471.7320	924.4462	462.7267	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
10	1071.4993	536.2533	1053.4888	527.2480	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FVDDPPTGLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G44575.1

Score	Mr(calc)	Delta	Sequence
34.7	1216.5976	0.0013	FVDDPPTGLEK
3.3	1216.5982	0.0006	DKSQPMERAR

AT1G44810.1

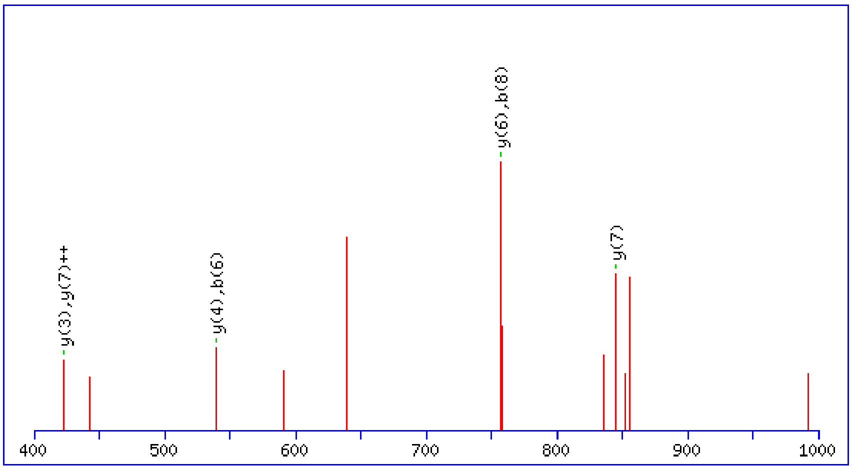
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASEGTSSKDIKR**
Found in **AT1G44810.1** in **TAIR_Arabidopsis**, Symbols: | transcription regulator | chr1:16926061-16926951 FORWARD

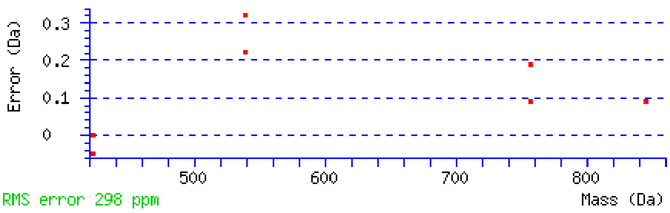
Match to Query 4674: 1294.604404 from(648.309478,2+) index(7117)
Title: Elution from: 63.760 to 63.760 scan no 9310 cid35.00 polarity:+
Data file 0-1_2.mgf

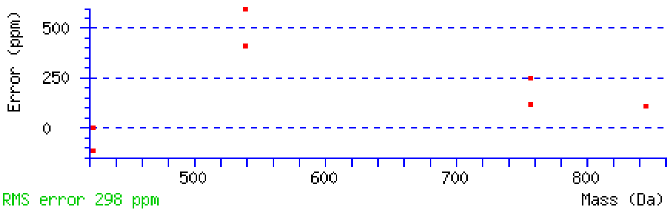
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1294.6071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0081
Matches : 7/110 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							12
2	161.0705	81.0389			143.0599	72.0336	S	1223.5803	612.2938	1205.5567	603.2820	1205.5697	603.2885	11
3	291.1101	146.0587			273.0996	137.0534	E	1135.5512	568.2792	1117.5276	559.2674	1117.5406	559.2740	10
4	349.1286	175.0679			331.1181	166.0627	G	1005.5116	503.2594	987.4880	494.2476	987.5010	494.2541	9
5	451.1733	226.0903			433.1628	217.0850	T	947.4931	474.2502	929.4695	465.2384	929.4825	465.2449	8
6	**539.2024**	270.1048			521.1918	261.0996	S	***845.4484***	423.2278	827.4248	414.2160	827.4378	414.2225	7
7	627.2315	314.1194			609.2209	305.1141	S	***757.4193***	379.2133	739.3957	370.2015	739.4087	370.2080	6
8	**757.3205**	379.1639	739.2969	370.1521	739.3099	370.1586	K	669.3902	335.1988	651.3667	326.1870	651.3797	326.1935	5
9	873.3445	437.1759	855.3209	428.1641	855.3339	428.1706	D	***539.3012***	270.1542	521.2776	261.1424	521.2906	261.1490	4
10	987.4256	494.2164	969.4020	485.2046	969.4150	485.2111	I	***423.2772***	212.1423	405.2536	203.1305			3
11	1117.5146	559.2609	1099.4910	550.2491	1099.5040	550.2557	K	309.1961	155.1017	291.1725	146.0899			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ASEGTSSKDIKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G44810.1

Score	Mr(calc)	Delta	Sequence
31.3	1294.6071	-0.0027	ASEGTSSKDIKR
6.7	1294.6020	0.0024	KYLEESCKPK
3.7	1294.6017	0.0027	RATSDIYHRR
2.8	1294.6017	0.0027	GRDGGLFGPSRR
2.8	1294.6033	0.0011	AMMICRVIAGR
0.8	1294.6071	-0.0027	EKPKTASTSSSR
0.5	1294.6046	-0.0002	CRQAILVANSF
0.2	1294.6024	0.0020	LTDMRERSAAK

AT1G45000.1

Mascot Search Results

Peptide View

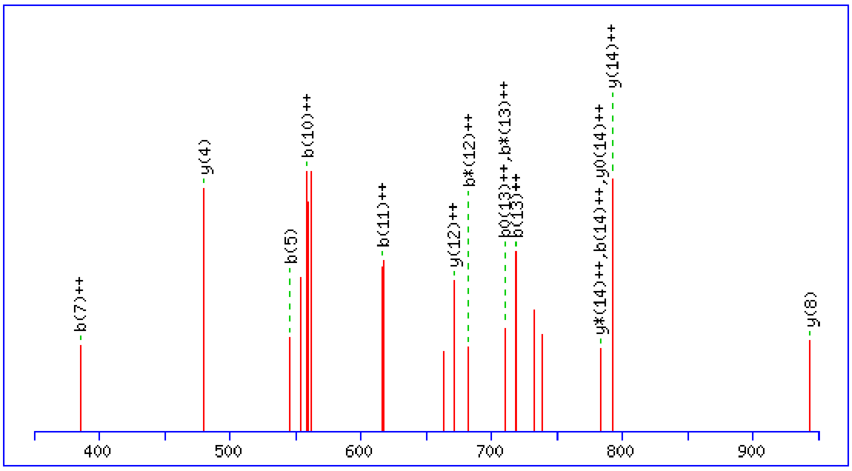
MS/MS Fragmentation of **KLESSSHYNADFGKE**
Found in **AT1G45000.1** in **TAIR_Arabidopsis**, Symbols: | 26S proteasome regulatory complex subunit p42D, putative | chr1:17011660-17014047 FORWARD

Match to Query 8123: 1710.785883 from(571.269237,3+) index(1177)
Title: Elution from: 19.968 to 19.968 scan no 1735 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

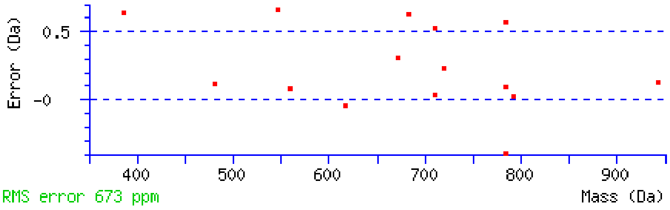
Or, Plot from 350 to 950 Da Full range

Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

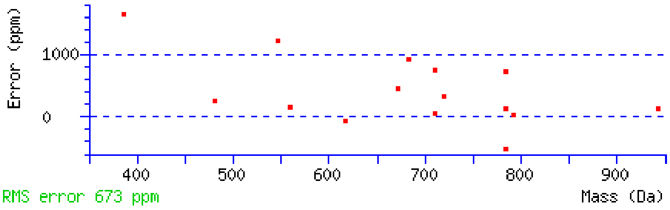


Monoisotopic mass of neutral peptide Mr(calc): 1710.7849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.018
Matches : 15/162 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							15
2	242.1863	121.5968	225.1598	113.0835			L	1583.6972	792.3523	1566.6707	783.8390	1565.6867	783.3470	14
3	371.2289	186.1181	354.2023	177.6048	353.2183	177.1128	E	1470.6132	735.8102	1453.5866	727.2970	1452.6026	726.8049	13
4	458.2609	229.6341	441.2344	221.1208	440.2504	220.6288	S	1341.5706	671.2889	1324.5440	662.7757	1323.5600	662.2836	12
5	545.2930	273.1501	528.2664	264.6368	527.2824	264.1448	S	1254.5386	627.7729	1237.5120	619.2596	1236.5280	618.7676	11
6	632.3250	316.6661	615.2984	308.1529	614.3144	307.6608	S	1167.5065	584.2569	1150.4800	575.7436	1149.4960	575.2516	10
7	769.3839	***385.1956***	752.3573	376.6823	751.3733	376.1903	H	1080.4745	540.7409	1063.4480	532.2276	1062.4639	531.7356	9
8	932.4472	466.7272	915.4207	458.2140	914.4367	457.7220	Y	**943.4156**	472.2114	926.3890	463.6982	925.4050	463.2061	8
9	1046.4901	523.7487	1029.4636	515.2354	1028.4796	514.7434	N	780.3523	390.6798	763.3257	382.1665	762.3417	381.6745	7
10	1117.5273	***559.2673***	1100.5007	550.7540	1099.5167	550.2620	A	666.3093	333.6583	649.2828	325.1450	648.2988	324.6530	6
11	1232.5542	***616.7807***	1215.5277	608.2675	1214.5436	607.7755	D	595.2722	298.1397	578.2457	289.6265	577.2617	289.1345	5
12	1379.6226	690.3149	1362.5961	681.8017	1361.6121	681.3097	F	**480.2453**	240.6263	463.2187	232.1130	462.2347	231.6210	4
13	1436.6441	***718.8257***	1419.6175	710.3124	1418.6335	709.8204	G	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
14	1564.7390	***782.8732***	1547.7125	774.3599	1546.7285	773.8679	K	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15							E	148.0604	74.5339			130.0499	65.5286	1



RMS error 673 ppm



RMS error 673 ppm

AT1G45000.1

NCBI **BLAST** search of KLESSSHYNADFGKE
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.4	1710.7849	0.0010	KLESSSHYNADFGKE
1.8	1710.7858	0.0001	DPYEGIPMSFPRMR
0.4	1710.7818	0.0041	MRSSNFIVSSMHGDK

AT1G47128.1

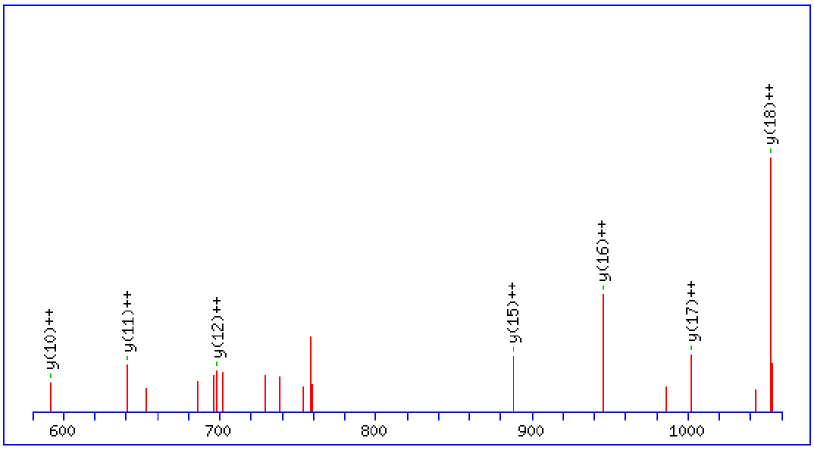
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVTIDSYEDVPTYSEESLKK**
Found in **AT1G47128.1** in **TAIR_Arabidopsis**, Symbols: RD21A, RD21 | RD21 (RESPONSIVE TO DEHYDRATION 21); cysteine-type peptidase | chr1:17285579-17288049 REVERSE

Match to Query 10189: 2301.124443 from(768.048757,3+) index(6362)
Title: Elution from: 56.105 to 56.105 scan no 8149 cid35.00 polarity:+
Data file C7-1_2.mgf

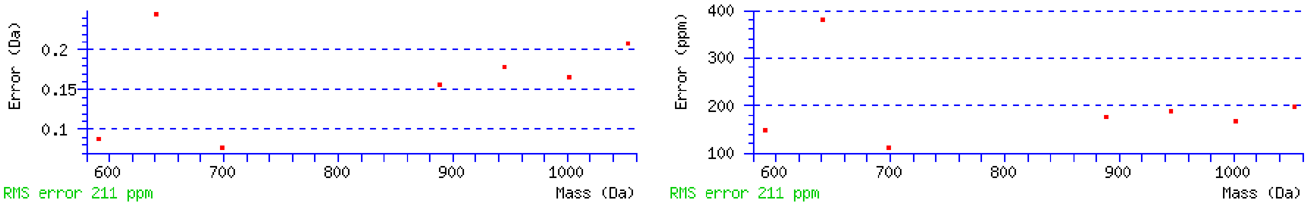
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 580 to 1060 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2301.1264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00023
Matches : 7/182 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							20
2	199.1441	100.0757					V	2203.0653	1102.0363	2186.0387	1093.5230	2185.0547	1093.0310	19
3	300.1918	150.5995			282.1812	141.5942	T	2103.9968	1052.5021	2086.9703	1043.9888	2085.9863	1043.4968	18
4	413.2758	207.1416			395.2653	198.1363	I	2002.9492	1001.9782	1985.9226	993.4649	1984.9386	992.9729	17
5	528.3028	264.6550			510.2922	255.6498	D	1889.8651	945.4362	1872.8385	936.9229	1871.8545	936.4309	16
6	615.3348	308.1710			597.3243	299.1658	S	1774.8382	887.9227	1757.8116	879.4094	1756.8276	878.9174	15
7	778.3981	389.7027			760.3876	380.6974	Y	1687.8061	844.4067	1670.7796	835.8934	1669.7956	835.4014	14
8	907.4407	454.2240			889.4302	445.2187	E	1524.7428	762.8750	1507.7162	754.3618	1506.7322	753.8698	13
9	1022.4677	511.7375			1004.4571	502.7322	D	1395.7002	698.3537	1378.6737	689.8405	1377.6896	689.3485	12
10	1121.5361	561.2717			1103.5255	552.2664	V	1280.6733	640.8403	1263.6467	632.3270	1262.6627	631.8350	11
11	1218.5889	609.7981			1200.5783	600.7928	P	1181.6048	591.3061	1164.5783	582.7928	1163.5943	582.3008	10
12	1319.6365	660.3219			1301.6260	651.3166	T	1084.5521	542.7797	1067.5255	534.2664	1066.5415	533.7744	9
13	1482.6999	741.8536			1464.6893	732.8483	Y	983.5044	492.2558	966.4779	483.7426	965.4938	483.2506	8
14	1569.7319	785.3696			1551.7213	776.3643	S	820.4411	410.7242	803.4145	402.2109	802.4305	401.7189	7
15	1698.7745	849.8909			1680.7639	840.8856	E	733.4090	367.2082	716.3825	358.6949	715.3985	358.2029	6
16	1827.8171	914.4122			1809.8065	905.4069	E	604.3665	302.6869	587.3399	294.1736	586.3559	293.6816	5
17	1914.8491	957.9282			1896.8385	948.9229	S	475.3239	238.1656	458.2973	229.6523	457.3133	229.1603	4
18	2027.9332	1014.4702			2009.9226	1005.4649	L	388.2918	194.6496	371.2653	186.1363			3
19	2156.0281	1078.5177	2139.0016	1070.0044	2138.0176	1069.5124	K	275.2078	138.1075	258.1812	129.5942			2
20							K	147.1128	74.0600	130.0863	65.5468			1

AT1G47128.1



NCBI **BLAST** search of VVTIDSYEDVPTYSEESLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.0	2301.1264	-0.0019	VVTIDSYEDVPTYSEESLKK
4.3	2301.1218	0.0026	SDKEGFYTAAFWLYKNHPK
0.6	2301.1271	-0.0026	TGLSPSSALTSQGGRDMIPPEGK
0.5	2301.1271	-0.0026	LTHVGIAGEAQMVDVSSKDNSK

Mascot: http://www.matrixscience.com/

AT1G47250.1

Mascot Search Results

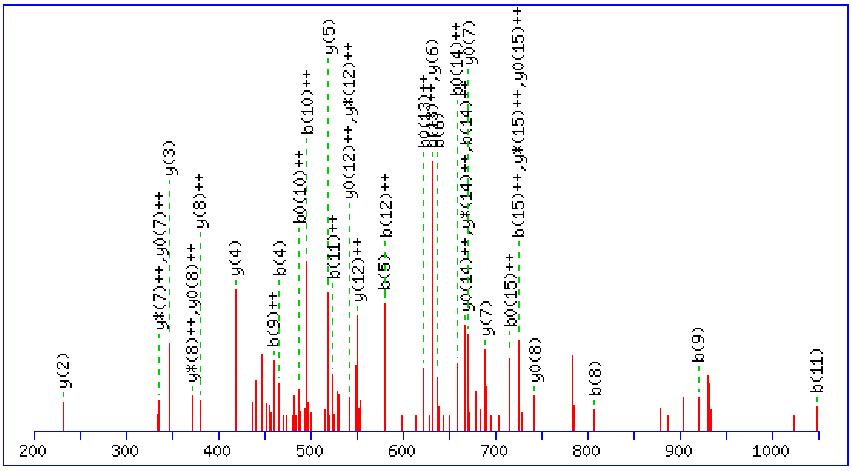
Peptide View

MS/MS Fragmentation of **VDDHIGVAIAGLTADGR**
Found in **AT1G47250.1** in **TAIR_Arabidopsis**, Symbols: PAF2 | PAF2 (20S proteasome alpha subunit F2); peptidase | chr1:17321660-17323340 FORWARD

Match to Query 8132: 1678.863900 from(560.628576,3+) index(7020)
Title: Elution from: 61.491 to 61.491 scan no 8960 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

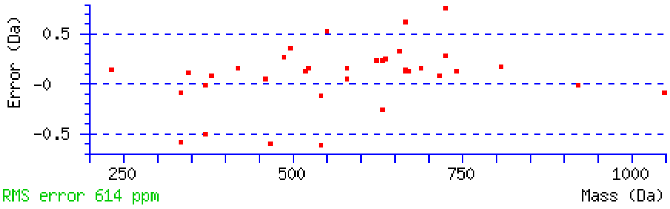
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

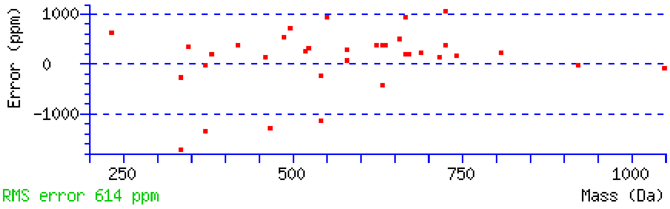


Monoisotopic mass of neutral peptide Mr(calc): 1678.8639
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00023
Matches : 37/154 fragment ions using 47 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415			V							17
2	215.1026	108.0550	197.0921	99.0497	D	1580.8027	790.9050	1563.7762	782.3917	1562.7921	781.8997	16
3	330.1296	165.5684	312.1190	156.5631	D	1465.7758	733.3915	1448.7492	724.8782	1447.7652	724.3862	15
4	***467.1885***	234.0979	449.1779	225.0926	H	1350.7488	675.8781	1333.7223	667.3648	1332.7383	666.8728	14
5	***580.2726***	290.6399	562.2620	281.6346	I	1213.6899	607.3486	1196.6634	598.8353	1195.6793	598.3433	13
6	***637.2940***	319.1506	619.2835	310.1454	G	1100.6058	550.8066	1083.5793	542.2933	1082.5953	541.8013	12
7	736.3624	368.6849	718.3519	359.6796	V	1043.5844	522.2958	1026.5578	513.7826	1025.5738	513.2905	11
8	***807.3995***	404.2034	789.3890	395.1981	A	944.5160	472.7616	927.4894	464.2483	926.5054	463.7563	10
9	***920.4836***	***460.7454***	902.4730	451.7402	I	873.4789	437.2431	856.4523	428.7298	855.4683	428.2378	9
10	991.5207	***496.2640***	973.5102	487.2587	A	760.3948	380.7010	743.3682	372.1878	742.3842	371.6958	8
11	***1048.5422***	***524.7747***	1030.5316	515.7694	G	**689.3577**	345.1825	672.3311	336.6692	671.3471	336.1772	7
12	1161.6262	***581.3168***	1143.6157	572.3115	L	**632.3362**	316.6717	615.3097	308.1585	614.3257	307.6665	6
13	1262.6739	***631.8406***	1244.6634	622.8353	T	**519.2522**	260.1297	502.2256	251.6164	501.2416	251.1244	5
14	1333.7110	***667.3592***	1315.7005	658.3539	A	**418.2045**	209.6059	401.1779	201.0926	400.1939	200.6006	4
15	1448.7380	***724.8726***	1430.7274	715.8673	D	**347.1674**	174.0873	330.1408	165.5740	329.1568	165.0820	3
16	1505.7594	753.3834	1487.7489	744.3781	G	**232.1404**	116.5738	215.1139	108.0606			2
17					R	175.1190	88.0631	158.0924	79.5498			1

AT1G47250.1





NCBI **BLAST** search of VDDHIGVAIAGLTADGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.3	1678.8639	0.0000	VDDHIGVAIAGLTADGR

Mascot: http://www.matrixscience.com/

AT1G47260.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFEQIEVER**
Found in **AT1G47260.1** in **TAIR_Arabidopsis**, Symbols: GAMMA CA2, APFI | APFI; carbonate dehydratase | chr1:17323824-17325787 REVERSE

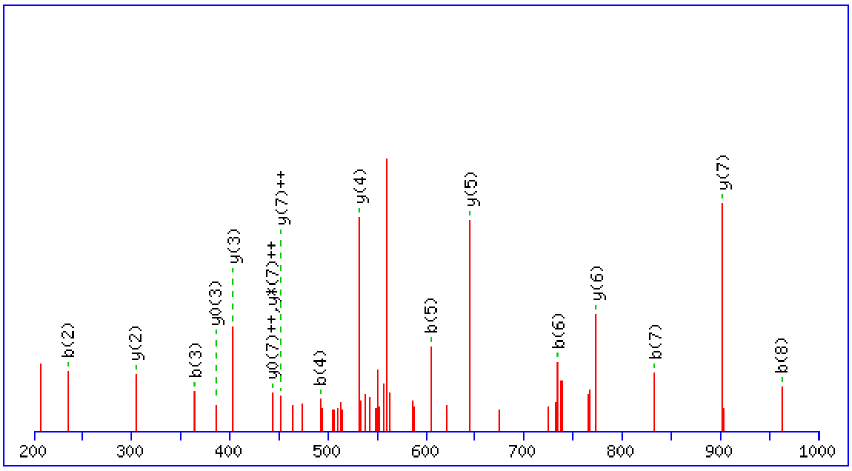
Match to Query 3210: 1135.550604 from(568.782578,2+) index(3219)
Title: Elution from: 34.568 to 34.568 scan no 4135 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1000 Da Full range

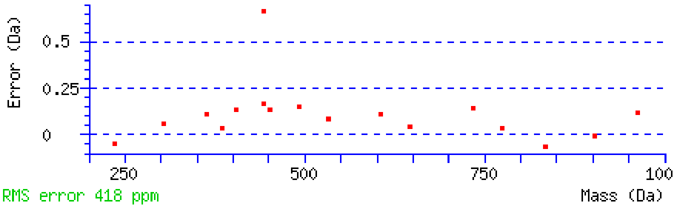
Label all possible matches ○ Label matches used for scoring ●

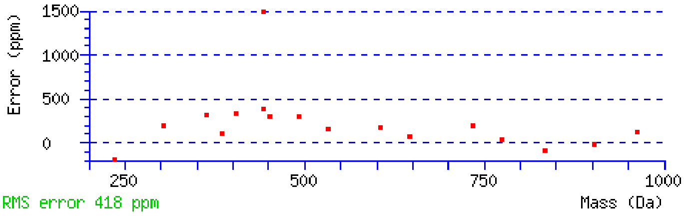
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1135.5509
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 8.6e-006
Matches : 17/88 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	***235.1077***	118.0575			217.0972	109.0522	F	1049.5262	525.2667	1032.4997	516.7535	1031.5156	516.2615	8
3	***364.1503***	182.5788			346.1397	173.5735	E	**902.4578**	451.7325	885.4312	443.2193	884.4472	442.7272	7
4	***492.2089***	246.6081	475.1823	238.0948	474.1983	237.6028	Q	**773.4152**	387.2112	756.3886	378.6980	755.4046	378.2060	6
5	***605.2930***	303.1501	588.2664	294.6368	587.2824	294.1448	I	**645.3566**	323.1819	628.3301	314.6687	627.3461	314.1767	5
6	***734.3355***	367.6714	717.3090	359.1581	716.3250	358.6661	E	**532.2726**	266.6399	515.2460	258.1266	514.2620	257.6346	4
7	***833.4040***	417.2056	816.3774	408.6923	815.3934	408.2003	V	**403.2300**	202.1186	386.2034	193.6053	385.2194	193.1133	3
8	***962.4466***	481.7269	945.4200	473.2136	944.4360	472.7216	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SFEQIEVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G47260.1

55.9	1135.5509	-0.0003	SFEQIEVER
5.0	1135.5509	-0.0003	VYDQLDVER
3.4	1135.5516	-0.0010	MTRGSQRER

AT1G47270.1

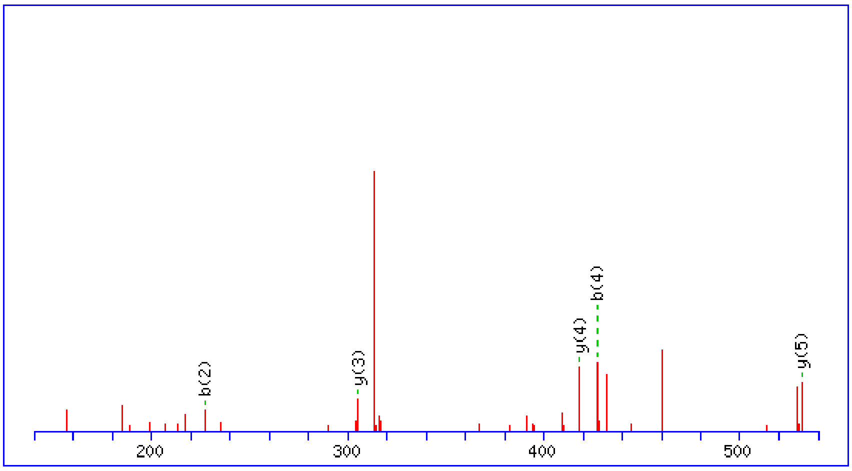
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLSAK**
Found in **AT1G47270.1** in **TAIR_Arabidopsis**, Symbols: AtTLP6 | AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcription factor | chr1:17329268-17331004 FORWARD

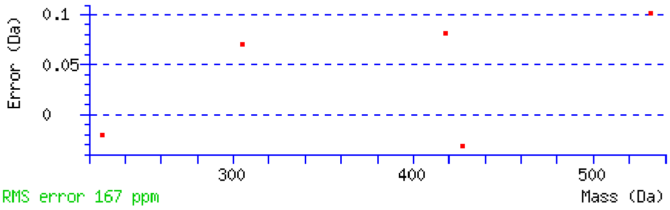
Match to Query 573: 643.427480 from(322.721016,2+) index(1045)
Title: Elution from: 16.152 to 16.152 scan no 1452 cid35.00 polarity:+
Data file 0-3_2.mgf

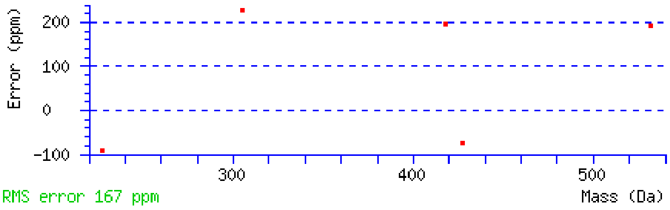
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 540 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 643.4268
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.017
Matches : 5/40 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							6
2	***227.1754***	114.0913			L	***531.3501***	266.1787	514.3235	257.6654	513.3395	257.1734	5
3	340.2595	170.6334			L	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	4
4	***427.2915***	214.1494	409.2809	205.1441	S	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	3
5	498.3286	249.6679	480.3180	240.6627	A	218.1499	109.5786	201.1234	101.0653			2
6					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LLLSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.9	643.4268	0.0006	LLLSAK
23.2	643.4268	0.0006	IISLAK
23.2	643.4268	0.0006	ILSLAK

AT1G47270.1

17.7	643.4268	0.0006	LLIGTK
17.2	643.4268	0.0006	LLTVAK
11.4	643.4268	0.0006	IISAIK
11.4	643.4268	0.0006	IISALK
11.4	643.4268	0.0006	LISALK
11.4	643.4268	0.0006	LLSAIK
9.1	643.4268	0.0006	LITAVK

AT1G47420.1

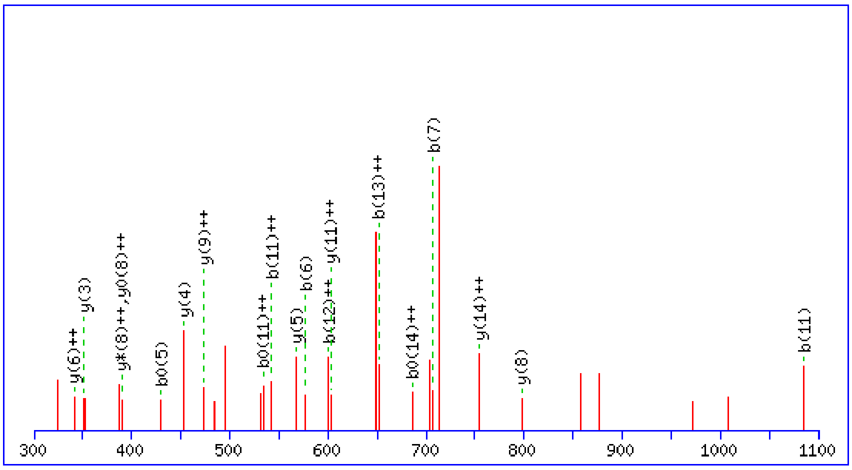
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAEAVEEFGGILTSIK**
Found in **AT1G47420.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Uncharacterized protein At1g47420, mitochondrial precursor [Arabidopsis Thaliana] (GB:Q9SX77); similar to APFI, carbonate dehydratase [Arabidopsis thaliana] (TAIR:AT1G47260.1); similar to unknown [Populus trichocarpa] (GB:A

Match to Query 7826: 1650.801753 from(551.274527,3+) index(9856)
Title: Elution from: 89.641 to 89.641 scan no 13457 cid35.00 polarity:+
Data file C7-3_1.mgf

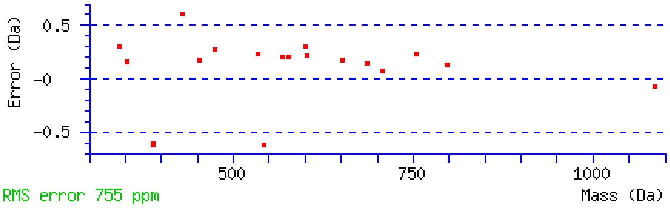
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

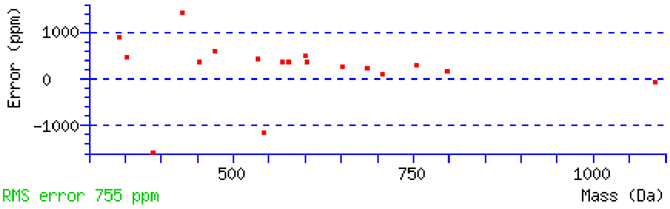


Monoisotopic mass of neutral peptide Mr(calc): 1650.8059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.027
Matches : 19/142 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							16
2	145.0756	73.0414			A	1579.7790	790.3932	1561.7554	781.3814	1561.7685	781.3879	15
3	275.1152	138.0612	257.1046	129.0560	E	1507.7449	754.3761	1489.7213	745.3643	1489.7343	745.3708	14
4	347.1494	174.0783	329.1388	165.0730	A	1377.7052	689.3563	1359.6817	680.3445	1359.6947	680.3510	13
5	447.2148	224.1110	429.2042	215.1058	V	1305.6711	653.3392	1287.6475	644.3274	1287.6605	644.3339	12
6	**577.2544**	289.1309	559.2439	280.1256	E	1205.6057	603.3065	1187.5821	594.2947	1187.5951	594.3012	11
7	**707.2941**	354.1507	689.2835	345.1454	E	1075.5660	538.2866	1057.5424	529.2749	1057.5555	529.2814	10
8	855.3595	428.1834	837.3489	419.1781	F	945.5264	473.2668	927.5028	464.2550	927.5158	464.2616	9
9	913.3780	457.1926	895.3674	448.1874	G	***797.4609***	399.2341	779.4374	390.2223	779.4504	390.2288	8
10	971.3965	486.2019	953.3859	477.1966	G	739.4424	370.2249	721.4189	361.2131	721.4319	361.2196	7
11	**1085.4776**	**543.2424**	1067.4670	534.2372	I	681.4239	341.2156	663.4004	332.2038	663.4134	332.2103	6
12	1199.5587	**600.2830**	1181.5481	591.2777	L	***567.3428***	284.1751	549.3193	275.1633	549.3323	275.1698	5
13	1301.6034	**651.3053**	1283.5928	642.3001	T	***453.2617***	227.1345	435.2382	218.1227	435.2512	218.1292	4
14	1389.6325	695.3199	1371.6219	686.3146	S	***351.2170***	176.1122	333.1935	167.1004	333.2065	167.1069	3
15	1503.7136	752.3604	1485.7030	743.3551	I	263.1880	132.0976	245.1644	123.0858			2
16					K	149.1069	75.0571	131.0833	66.0453			1

AT1G47420.1





NCBI **BLAST** search of AAEAVEEFGGILTSIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.8	1650.8059	-0.0041	AAEAVEEFGGILTSIK
3.0	1650.8038	-0.0021	LHQMLYERIQTAK
1.3	1650.8063	-0.0046	ELAVERERSATLEK

Mascot: http://www.matrixscience.com/

AT1G48030.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVEVDLPAMLAQK**
Found in **AT1G48030.1** in **TAIR_Arabidopsis**, Symbols: MTLPD1 | dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1) | chr1:17721101-17722810 REVERSE

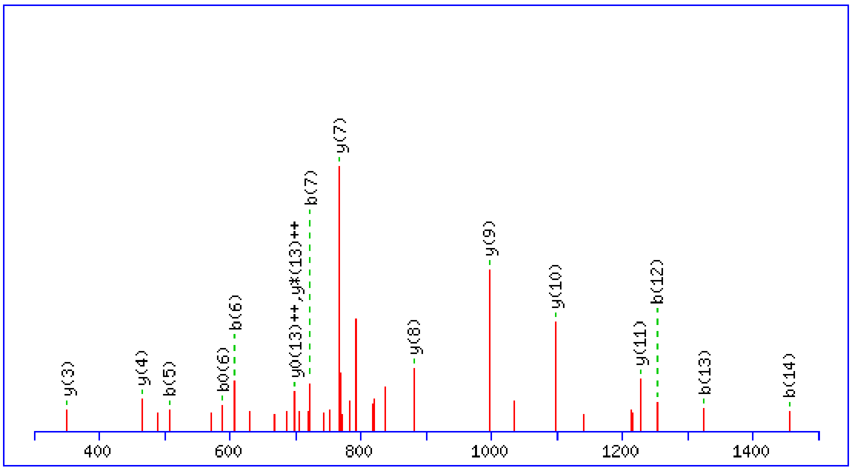
Match to Query 6934: 1602.784732 from(802.399642,2+) index(8030)
Title: Elution from: 72.013 to 72.013 scan no 10765 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

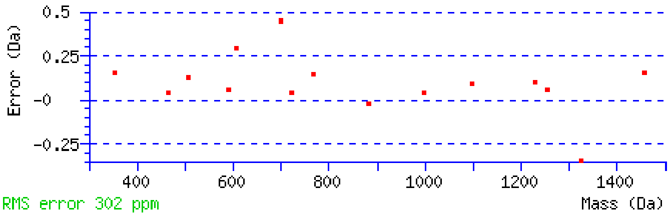
Label all possible matches ○ Label matches used for scoring ●

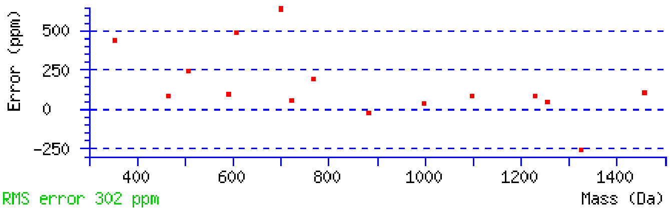
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1602.7881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 4e-006
Matches : 16/124 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							15
2	189.1018	95.0545			171.0912	86.0492	S	1503.7300	752.3686	1485.7064	743.3568	1485.7194	743.3633	14
3	277.1309	139.0691			259.1203	130.0638	S	1415.7009	708.3541	1397.6773	699.3423	1397.6903	699.3488	13
4	377.1963	189.1018			359.1857	180.0965	V	1327.6718	664.3396	1309.6483	655.3278	1309.6613	655.3343	12
5	***507.2359***	254.1216			489.2254	245.1163	E	***1227.6064***	614.3068	1209.5828	605.2950	1209.5958	605.3016	11
6	***607.3014***	304.1543			589.2908	295.1490	V	***1097.5668***	549.2870	1079.5432	540.2752	1079.5562	540.2817	10
7	***723.3254***	362.1663			705.3148	353.1610	D	***997.5013***	499.2543	979.4777	490.2425	979.4907	490.2490	9
8	837.4065	419.2069			819.3959	410.2016	L	***881.4773***	441.2423	863.4538	432.2305			8
9	935.4563	468.2318			917.4457	459.2265	P	***767.3962***	384.2018	749.3727	375.1900			7
10	1007.4904	504.2488			989.4798	495.2436	A	669.3464	335.1769	651.3229	326.1651			6
11	1139.5279	570.2676			1121.5174	561.2623	M	597.3123	299.1598	579.2887	290.1480			5
12	***1253.6090***	627.3081			1235.5985	618.3029	L	***465.2748***	233.1410	447.2512	224.1292			4
13	***1325.6432***	663.3252			1307.6326	654.3199	A	***351.1937***	176.1005	333.1701	167.0887			3
14	***1455.6958***	728.3515	1437.6722	719.3398	1437.6853	719.3463	Q	279.1595	140.0834	261.1359	131.0716			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT1G48030.1

NCBI **BLAST** search of VSSVEVDLPAMLAQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.7	1602.7881	-0.0034	VSSVEVDLPAMLAQK
10.0	1602.7874	-0.0027	NKVLASTLASHEWK
6.8	1602.7852	-0.0005	DSEIGNLVKKNHTK
3.6	1602.7800	0.0047	MFTYDPKARISIK
0.6	1602.7800	0.0047	STPEMWPGLIQKAK
0.4	1602.7834	0.0013	YTGGARMLLMLSLK

AT1G48040.1

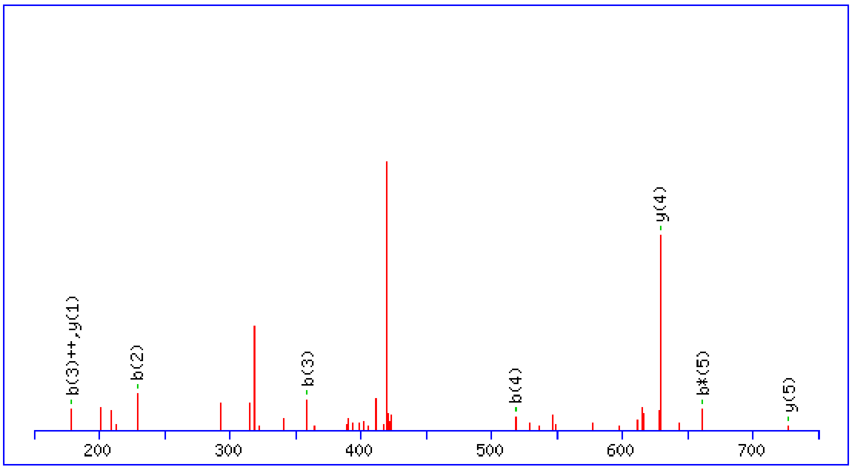
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPQRRR**
Found in **AT1G48040.1** in **TAIR_Arabidopsis**, Symbols: | protein serine/threonine phosphatase | chr1:17723733-17725367 REVERSE

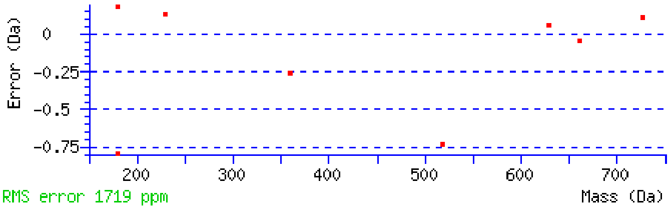
Match to Query 1436: 856.435494 from(429.225023,2+) index(2109)
Title: Elution from: 24.726 to 24.726 scan no 2722 cid35.00 polarity:+
Data file C7-2_1.mgf

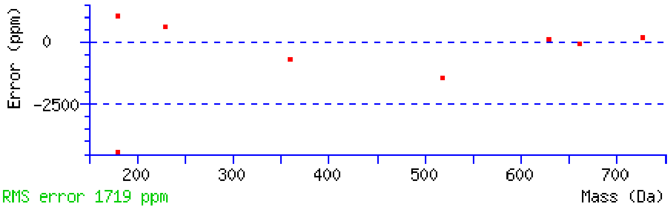
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 856.4334
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.03
Matches : 8/40 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	131.0599	66.0336	113.0363	57.0218	Q					6
2	***229.1097***	115.0585	211.0861	106.0467	P	***727.3880***	364.1977	709.3645	355.1859	5
3	***359.1624***	180.0848	341.1388	171.0730	Q	***629.3382***	315.1728	611.3147	306.1610	4
4	***519.2516***	260.1294	501.2280	251.1177	R	499.2856	250.1464	481.2620	241.1346	3
5	679.3409	340.1741	661.3173	331.1623	R	339.1963	170.1018	321.1728	161.0900	2
6					R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of QPQRRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.2	856.4334	0.0021	QPQRRR
11.0	856.4334	0.0021	QGAPRRR
10.0	856.4337	0.0018	LLADMLR
9.9	856.4330	0.0025	SHKAFVR

AT1G48040.1

5.3	856.4337	0.0018	SMVEILR
1.6	856.4337	0.0018	LLDLMSR
1.5	856.4337	0.0018	LLVSCAGK
1.2	856.4337	0.0018	KILDACK
0.8	856.4337	0.0018	VESMLLR
0.6	856.4330	0.0025	QWQKVR

AT1G48350.1

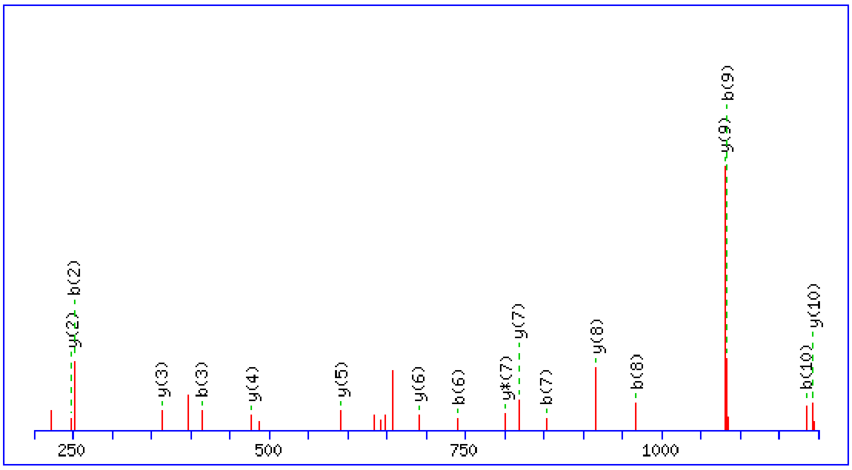
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLYVQVIDDTK**
Found in **AT1G48350.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L18 family protein | chr1:17870937-17871883 FORWARD

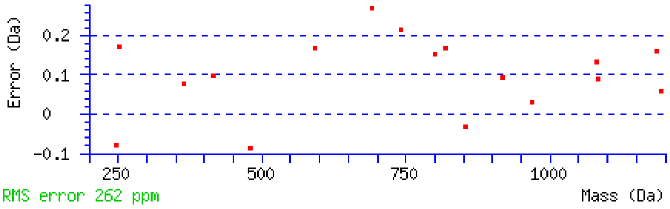
Match to Query 5293: 1329.691126 from(665.852839,2+) index(3942)
Title: Elution from: 37.435 to 37.435 scan no 4882 cid35.00 polarity:+
Data file 0-1_1.mgf

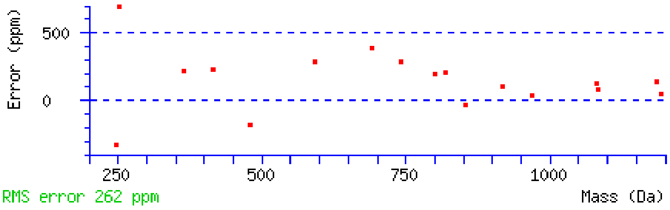
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1329.6929
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 2.3e-008
Matches : 17/96 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							11
2	**251.1503**	126.0788					L	*1193.6412*	597.3243	1176.6147	588.8110	1175.6307	588.3190	10
3	**414.2136**	207.6104					Y	*1080.5572*	540.7822	1063.5306	532.2689	1062.5466	531.7769	9
4	513.2820	257.1446					V	*917.4938*	459.2506	900.4673	450.7373	899.4833	450.2453	8
5	641.3406	321.1739	624.3140	312.6607			Q	*818.4254*	409.7164	801.3989	401.2031	800.4149	400.7111	7
6	**740.4090**	370.7081	723.3824	362.1949			V	*690.3668*	345.6871	673.3403	337.1738	672.3563	336.6818	6
7	**853.4931**	427.2502	836.4665	418.7369			I	*591.2984*	296.1529	574.2719	287.6396	573.2879	287.1476	5
8	**968.5200**	484.7636	951.4934	476.2504	950.5094	475.7584	D	*478.2144*	239.6108	461.1878	231.0975	460.2038	230.6055	4
9	**1083.5469**	542.2771	1066.5204	533.7638	1065.5364	533.2718	D	*363.1874*	182.0974	346.1609	173.5841	345.1769	173.0921	3
10	**1184.5946**	592.8009	1167.5681	584.2877	1166.5841	583.7957	T	*248.1605*	124.5839	231.1339	116.0706	230.1499	115.5786	2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HLYVQVIDDTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G48350.1

Score	Mr(calc)	Delta	Sequence
83.0	1329.6929	-0.0017	HLYVQVIDDTK

Mascot: http://www.matrixscience.com/

AT1G48420.1

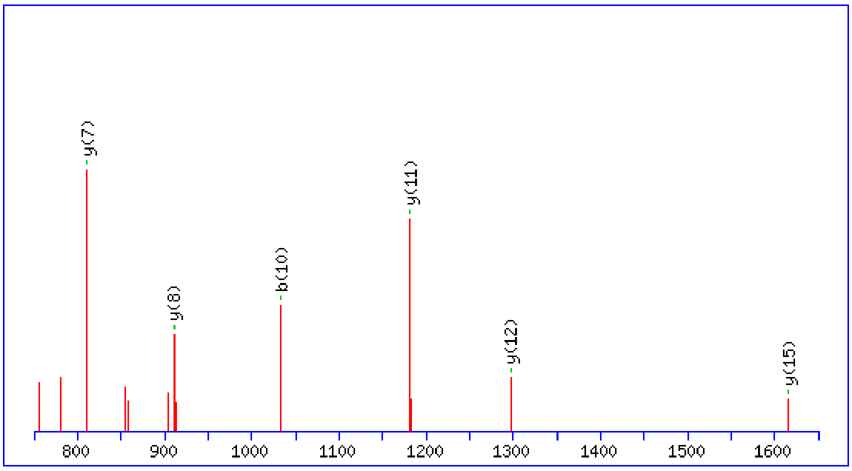
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLADEDPGLVGNLLVER**
Found in **AT1G48420.1** in **TAIR_Arabidopsis**, Symbols: D-CDES | D-CDES (D-CYSTEINE DESULFHYDRASE); 1-aminocyclopropane-1-carboxylate deaminase/ D-cysteine desulfhydrase/ catalytic | chr1:17900435-17902471 REVERSE

Match to Query 8600: 1842.920000 from(922.467276,2+) index(9205)
Title: Elution from: 83.623 to 83.623 scan no 12643 cid35.00 polarity:+
Data file D12h-1_3.mgf

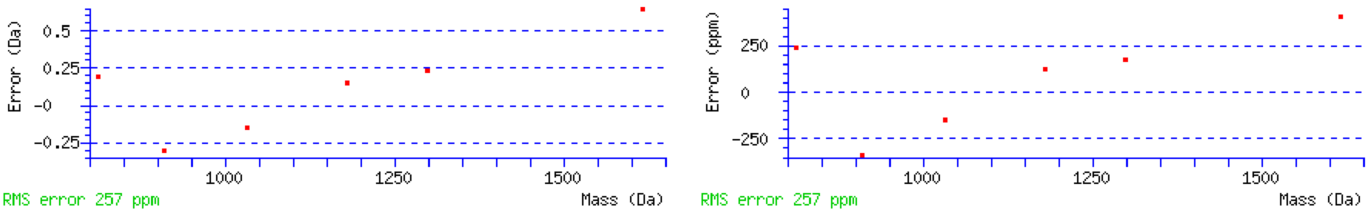
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 750 to 1650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1842.9213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00059
Matches : 6/162 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**17**
2	229.1695	115.0884					**L**	1729.8475	865.4274	1711.8240	856.4156	1711.8370	856.4221	**16**
3	301.2036	151.1054					**A**	***1615.7664***	808.3869	1597.7429	799.3751	1597.7559	799.3816	**15**
4	417.2276	209.1174			399.2170	200.1122	**D**	1543.7323	772.3698	1525.7087	763.3580	1525.7217	763.3645	**14**
5	547.2672	274.1373			529.2567	265.1320	**E**	1427.7083	714.3578	1409.6847	705.3460	1409.6977	705.3525	**13**
6	663.2912	332.1492			645.2806	323.1440	**D**	***1297.6687***	649.3380	1279.6451	640.3262	1279.6581	640.3327	**12**
7	761.3410	381.1741			743.3304	372.1689	**P**	***1181.6447***	591.3260	1163.6211	582.3142	1163.6341	582.3207	**11**
8	819.3595	410.1834			801.3489	401.1781	**G**	1083.5949	542.3011	1065.5713	533.2893	1065.5843	533.2958	**10**
9	933.4406	467.2239			915.4300	458.2187	**L**	1025.5764	513.2918	1007.5528	504.2801	1007.5658	504.2866	**9**
10	1033.5061	517.2567			1015.4955	508.2514	**V**	***911.4953***	456.2513	893.4717	447.2395	893.4847	447.2460	**8**
11	1091.5246	546.2659			1073.5140	537.2606	**G**	***811.4299***	406.2186	793.4063	397.2068	793.4193	397.2133	**7**
12	1207.5615	604.2844	1189.5380	595.2726	1189.5510	595.2791	**N**	753.4114	377.2093	735.3878	368.1975	735.4008	368.2040	**6**
13	1321.6426	661.3250	1303.6191	652.3132	1303.6321	652.3197	**L**	637.3744	319.1908	619.3508	310.1790	619.3638	310.1855	**5**
14	1435.7237	718.3655	1417.7002	709.3537	1417.7132	709.3602	**L**	523.2933	262.1503	505.2697	253.1385	505.2827	253.1450	**4**
15	1535.7892	768.3982	1517.7656	759.3864	1517.7786	759.3930	**V**	409.2122	205.1097	391.1886	196.0979	391.2016	196.1044	**3**
16	1665.8288	833.4180	1647.8052	824.4063	1647.8183	824.4128	**E**	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	**2**
17							**R**	179.1071	90.0572	161.0835	81.0454			**1**

AT1G48420.1



NCBI **BLAST** search of LLADEDPGLVGNLLVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.7	1842.9213	-0.0013	LLADEDPGLVGNLLVER
9.2	1842.9166	0.0034	YGKEALDMLLKLQQR
1.3	1842.9166	0.0034	MPETARYTALVAKNIK

Mascot: http://www.matrixscience.com/

AT1G48470.1

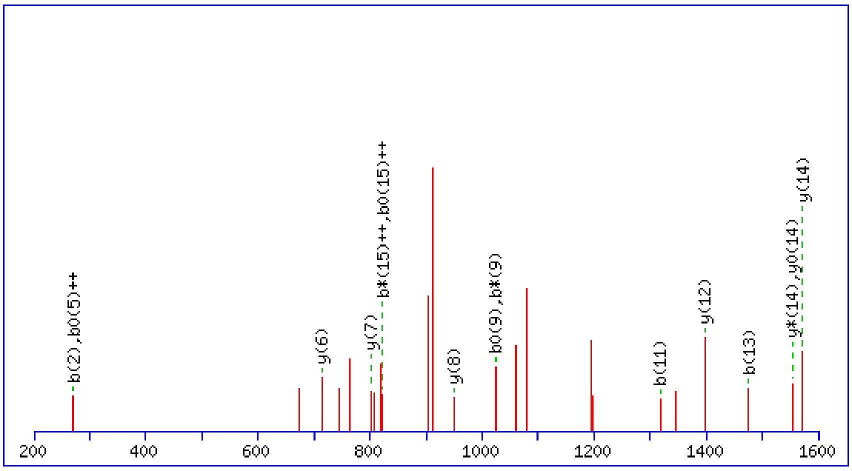
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HETADINTFSWGVADR**
Found in **AT1G48470.1** in **TAIR_Arabidopsis**, Symbols: GLN1;5 | GLN1;5 (GLUTAMINE SYNTHETASE 1;5); glutamate-ammonia ligase | chr1:17917452-17919594 FORWARD

Match to Query 9187: 1840.767532 from(921.391042,2+) index(6497)
Title: Elution from: 56.568 to 56.568 scan no 8166 cid35.00 polarity:+
Data file D12h-1_1.mgf

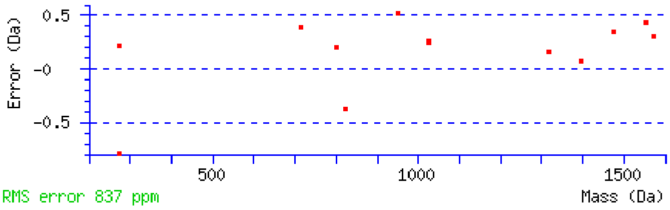
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

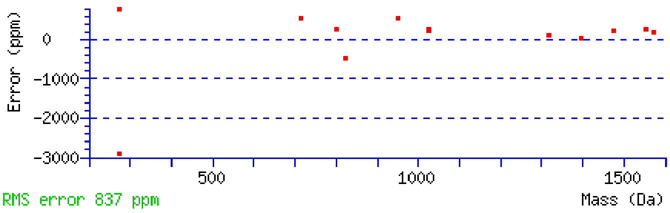


Monoisotopic mass of neutral peptide Mr(calc): 1840.7650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.0088
Matches : 15/164 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	141.0573	71.0323					**H**							**16**
2	***271.0969***	136.0521			253.0864	127.0468	**E**	1701.7223	851.3648	1683.6988	842.3530	1683.7118	842.3595	**15**
3	373.1416	187.0745			355.1311	178.0692	**T**	***1571.6827***	786.3450	1553.6591	777.3332	1553.6721	777.3397	**14**
4	445.1758	223.0915			427.1652	214.0862	**A**	1469.6380	735.3226	1451.6144	726.3108	1451.6274	726.3174	**13**
5	561.1998	281.1035			543.1892	272.0982	**D**	***1397.6038***	699.3056	1379.5803	690.2938	1379.5933	690.3003	**12**
6	675.2809	338.1441			657.2703	329.1388	**I**	1281.5799	641.2936	1263.5563	632.2818	1263.5693	632.2883	**11**
7	791.3179	396.1626	773.2943	387.1508	773.3073	387.1573	**N**	1167.4988	584.2530	1149.4752	575.2412	1149.4882	575.2477	**10**
8	893.3626	447.1849	875.3390	438.1731	875.3520	438.1796	**T**	1051.4618	526.2345	1033.4382	517.2227	1033.4512	517.2292	**9**
9	1041.4280	521.2176	1023.4044	512.2059	1023.4175	512.2124	**F**	***949.4171***	475.2122	931.3935	466.2004	931.4065	466.2069	**8**
10	1129.4571	565.2322	1111.4335	556.2204	1111.4465	556.2269	**S**	***801.3516***	401.1794	783.3280	392.1677	783.3410	392.1742	**7**
11	***1317.5305***	659.2689	1299.5069	650.2571	1299.5199	650.2636	**W**	***713.3226***	357.1649	695.2990	348.1531	695.3120	348.1596	**6**
12	1375.5490	688.2781	1357.5254	679.2663	1357.5384	679.2728	**G**	525.2492	263.1282	507.2256	254.1164	507.2386	254.1229	**5**
13	***1475.6144***	738.3108	1457.5908	729.2991	1457.6038	729.3056	**V**	467.2307	234.1190	449.2071	225.1072	449.2201	225.1137	**4**
14	1547.6486	774.3279	1529.6250	765.3161	1529.6380	765.3226	**A**	367.1652	184.0862	349.1416	175.0745	349.1547	175.0810	**3**
15	1663.6725	832.3399	1645.6490	823.3281	1645.6620	823.3346	**D**	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	**2**
16							**R**	179.1071	90.0572	161.0835	81.0454			**1**

AT1G48470.1





NCBI **BLAST** search of HETADINTFSWGVADR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.8	1840.7650	0.0025	HETADINTFSWGVADR
4.4	1840.7637	0.0038	MRGQFDGSCFLTNIR
1.2	1840.7713	-0.0038	AVMHVIGTEMDFVDDK

Mascot: http://www.matrixscience.com/

AT1G48630.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGVILLWDLAEGK**
Found in **AT1G48630.1** in **TAIR_Arabidopsis**, Symbols: | guanine nucleotide-binding family protein / activated protein kinase C receptor, putative / RACK, putative | chr1:17985645-17986936 REVERSE

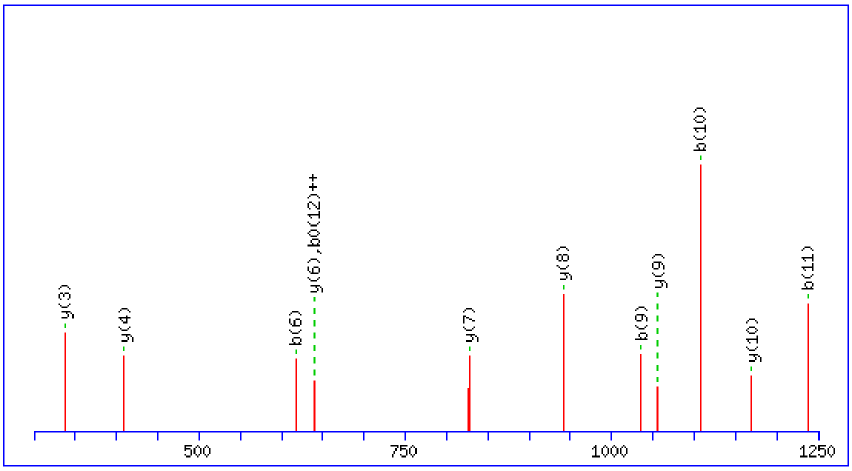
Match to Query 5648: 1442.720406 from(722.367479,2+) index(11037)
Title: Elution from: 110.556 to 110.556 scan no 16185 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1250 Da Full range

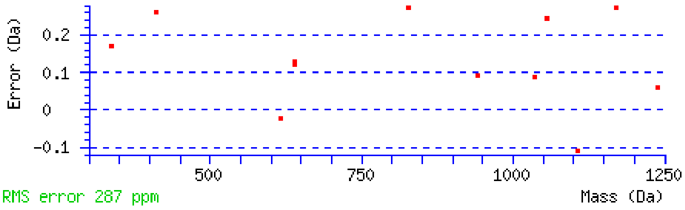
Label all possible matches ○ Label matches used for scoring ●

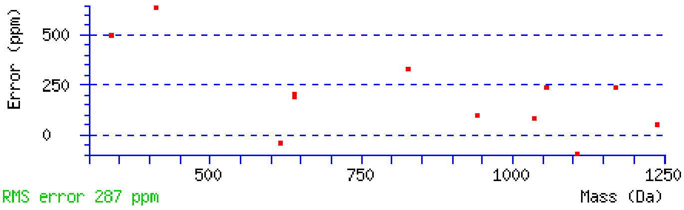
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1442.7215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.5e-007
Matches : 12/116 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							13
2	175.0498	88.0285	157.0392	79.0232	G	1327.7049	664.3561	1309.6813	655.3443	1309.6943	655.3508	12
3	275.1152	138.0612	257.1046	129.0560	V	1269.6864	635.3468	1251.6628	626.3350	1251.6758	626.3415	11
4	389.1963	195.1018	371.1857	186.0965	I	***1169.6209***	585.3141	1151.5973	576.3023	1151.6103	576.3088	10
5	503.2774	252.1423	485.2668	243.1371	L	***1055.5398***	528.2735	1037.5162	519.2618	1037.5292	519.2683	9
6	**617.3585**	309.1829	599.3479	300.1776	L	***941.4587***	471.2330	923.4351	462.2212	923.4481	462.2277	8
7	805.4319	403.2196	787.4213	394.2143	W	***827.3776***	414.1924	809.3540	405.1807	809.3670	405.1872	7
8	921.4559	461.2316	903.4453	452.2263	D	***639.3042***	320.1558	621.2806	311.1440	621.2937	311.1505	6
9	**1035.5370**	518.2721	1017.5264	509.2668	L	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	5
10	**1107.5711**	554.2892	1089.5605	545.2839	A	***409.1992***	205.1032	391.1756	196.0914	391.1886	196.0979	4
11	**1237.6107**	619.3090	1219.6002	610.3037	E	***337.1650***	169.0861	319.1414	160.0743	319.1544	160.0809	3
12	1295.6292	648.3183	1277.6187	639.3130	G	207.1254	104.0663	189.1018	95.0545			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DGVILLWDLAEGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G48630.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.4	1442.7215	-0.0011	DGVILLWDLAEGK
16.4	1442.7193	0.0011	LPESEVAALDAKGK
7.9	1442.7168	0.0036	AYVGALNKMLGFK
3.7	1442.7215	-0.0011	FTTTVTGFLEKGK

Mascot: http://www.matrixscience.com/

AT1G48660.1

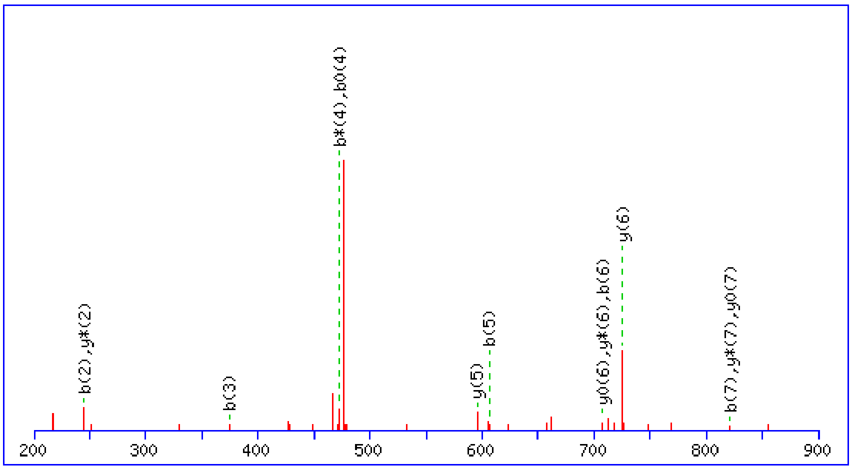
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIQDDVLK**
Found in **AT1G48660.1** in **TAIR_Arabidopsis**, Symbols: | auxin-responsive GH3 family protein | chr1:17999616-18001640 REVERSE

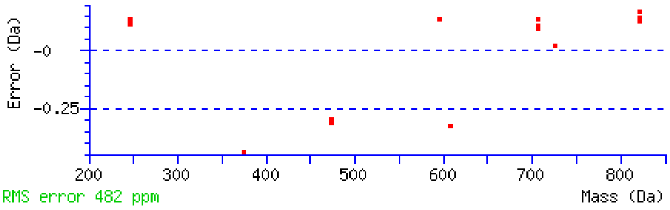
Match to Query 2183: 968.482288 from(485.248420,2+) index(2353)
Title: Elution from: 26.924 to 26.924 scan no 3034 cid35.00 polarity:+
Data file 0-3_1.mgf

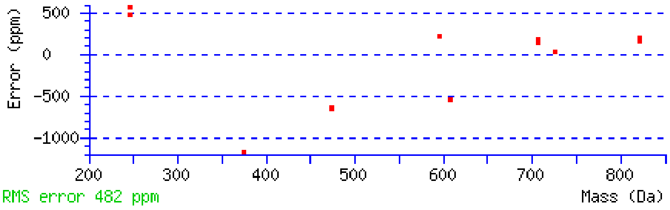
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.4805
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.011
Matches : 14/72 fragment ions using 23 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0599	66.0336	113.0363	57.0218			Q							8
2	***245.1410***	123.0741	227.1174	114.0624			I	839.4351	420.2212	821.4115	411.2094	821.4246	411.2159	7
3	***375.1937***	188.1005	357.1701	179.0887			Q	**725.3540**	363.1807	707.3304	354.1689	707.3435	354.1754	6
4	491.2176	246.1125	473.1941	237.1007	473.2071	237.1072	D	**595.3014**	298.1543	577.2778	289.1425	577.2908	289.1490	5
5	***607.2416***	304.1245	589.2180	295.1127	589.2311	295.1192	D	479.2774	240.1423	461.2538	231.1305	461.2668	231.1371	4
6	***707.3071***	354.1572	689.2835	345.1454	689.2965	345.1519	V	363.2534	182.1303	345.2298	173.1186			3
7	***821.3882***	411.1977	803.3646	402.1859	803.3776	402.1924	L	263.1880	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QIQDDVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.8	968.4805	0.0018	QIQDDVLK
14.6	968.4805	0.0018	AIGEVDLNK

AT1G48660.1

14.6	968.4805	0.0018	ELQALQEK
14.6	968.4805	0.0018	ELQENVVK
10.6	968.4805	0.0018	ISAVQTDPK
7.1	968.4805	0.0018	EDQINVLK
5.1	968.4805	0.0018	LEAEVELR
2.9	968.4827	-0.0004	QPPDYVLK
2.8	968.4805	0.0018	ELAQQIEK
2.0	968.4832	-0.0009	VSPSGAPRGK

AT1G48830.1

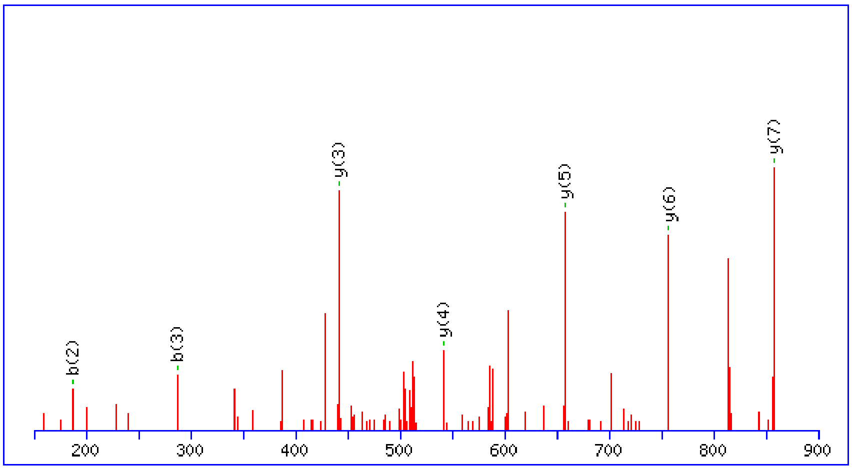
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIVVNVPYR**
Found in **AT1G48830.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S7 (RPS7A) | chr1:18063522-18064603 REVERSE

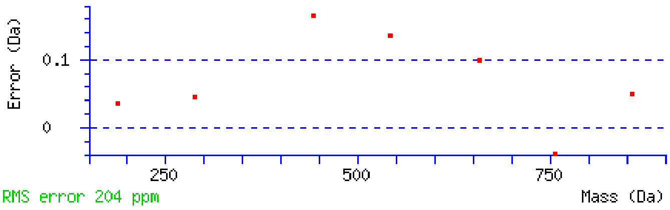
Match to Query 2754: 1042.556310 from(522.285431,2+) index(4552)
Title: Elution from: 41.628 to 41.628 scan no 5715 cid35.00 polarity:+
Data file 0-3_2.mgf

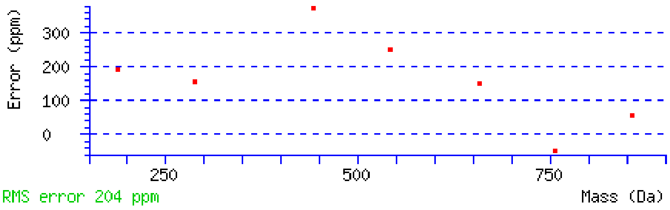
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1042.5586
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00016
Matches : 7/56 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	73.0414	37.0244			A					9
2	**187.1225**	94.0649			I	971.5317	486.2695	953.5081	477.2577	8
3	**287.1880**	144.0976			V	***857.4506***	429.2289	839.4270	420.2171	7
4	387.2534	194.1303			V	***757.3852***	379.1962	739.3616	370.1844	6
5	503.2904	252.1488	485.2668	243.1371	N	***657.3197***	329.1635	639.2961	320.1517	5
6	603.3559	302.1816	585.3323	293.1698	V	***541.2827***	271.1450	523.2591	262.1332	4
7	701.4057	351.2065	683.3821	342.1947	P	***441.2173***	221.1123	423.1937	212.1005	3
8	865.4660	433.2367	847.4424	424.2249	Y	343.1675	172.0874	325.1439	163.0756	2
9					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of AIVVNVPYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.6	1042.5586	-0.0023	AIVVNVPYR

AT1G48830.1

6.4	1042.5563	-0.0000	ALVKAGDLSR
6.4	1042.5563	-0.0000	LAVESLNRK
1.3	1042.5590	-0.0027	GKPIAQTRR

AT1G48920.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGHVEFASSEEAQK**
Found in **AT1G48920.1** in **TAIR_Arabidopsis**, Symbols: ATNUC-L1, PARL1 | ATNUC-L1/PARL1 (PARALLEL 1); nucleic acid binding | chr1:18101854-18105090 FORWARD

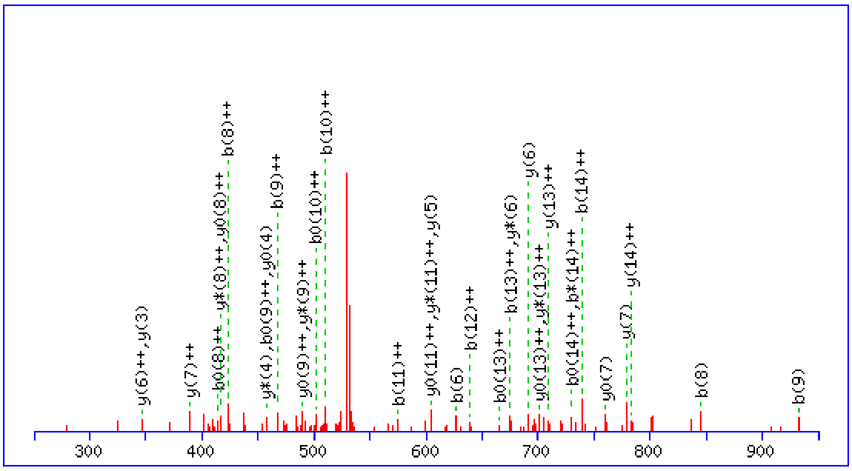
Match to Query 7660: 1621.734783 from(541.585537,3+) index(3344)
Title: Elution from: 32.226 to 32.226 scan no 4130 cid35.00 polarity:+
Data file C7-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 950 Da Full range

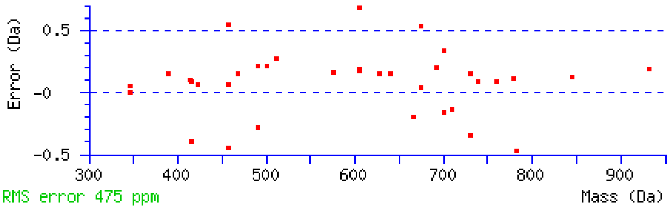
Label all possible matches ○ Label matches used for scoring ●

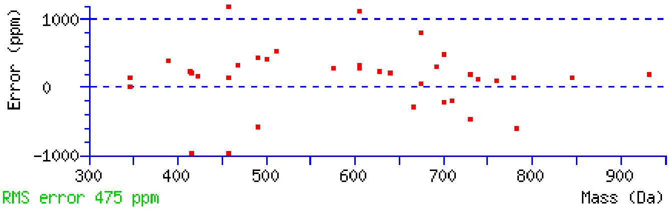
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1621.7372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0015
Matches : 36/126 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							15
2	205.0972	103.0522					F	1565.7231	783.3652	1548.6965	774.8519	1547.7125	774.3599	14
3	262.1186	131.5629					G	1418.6546	709.8310	1401.6281	701.3177	1400.6441	700.8257	13
4	399.1775	200.0924					H	1361.6332	681.3202	1344.6066	672.8070	1343.6226	672.3149	12
5	498.2459	249.6266					V	1224.5743	612.7908	1207.5477	604.2775	1206.5637	603.7855	11
6	**627.2885**	314.1479			609.2780	305.1426	E	1125.5059	563.2566	1108.4793	554.7433	1107.4953	554.2513	10
7	774.3570	387.6821			756.3464	378.6768	F	996.4633	498.7353	979.4367	490.2220	978.4527	489.7300	9
8	**845.3941**	***423.2007***			827.3835	414.1954	A	849.3949	425.2011	832.3683	416.6878	831.3843	416.1958	8
9	**932.4261**	***466.7167***			914.4155	457.7114	S	**778.3577**	389.6825	761.3312	381.1692	760.3472	380.6772	7
10	1019.4581	***510.2327***			1001.4476	501.2274	S	**691.3257**	346.1665	674.2992	337.6532	673.3151	337.1612	6
11	1148.5007	***574.7540***			1130.4901	565.7487	E	**604.2937**	302.6505	587.2671	294.1372	586.2831	293.6452	5
12	1277.5433	***639.2753***			1259.5327	630.2700	E	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
13	1348.5804	***674.7938***			1330.5699	665.7886	A	**346.2085**	173.6079	329.1819	165.0946			3
14	1476.6390	***738.8231***	1459.6125	730.3099	1458.6284	729.8179	Q	275.1714	138.0893	258.1448	129.5761			2
15							K	147.1128	74.0600	130.0863	65.5468			1





AT1G48920.1

NCBI **BLAST** search of GFGHVEFASSEEAQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.9	1621.7372	-0.0025	GFGHVEFASSEEAQK

Mascot: http://www.matrixscience.com/

AT1G49240.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YPIEHGVVSNWDDMEK**
Found in **AT1G49240.1** in **TAIR_Arabidopsis**, Symbols: ACT8 | ACT8 (ACTIN 8); structural constituent of cytoskeleton | chr1:18220207-18221615 FORWARD

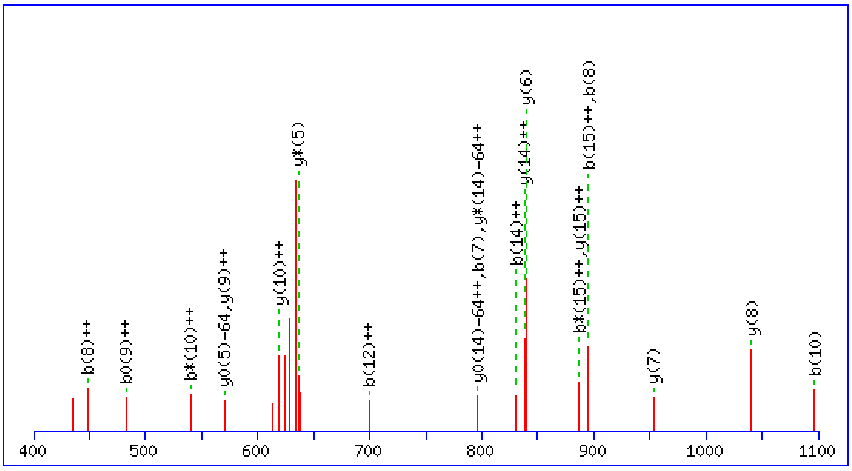
Match to Query 9076: 1933.847886 from(645.623238,3+) index(4628)
Title: Elution from: 41.210 to 41.210 scan no 5767 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●

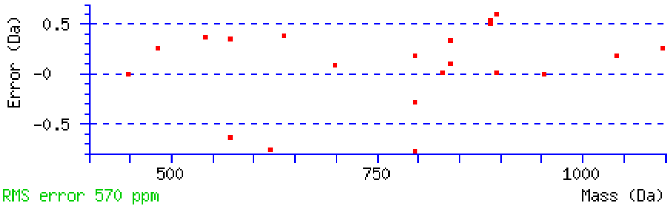
Show Y-axis ☐

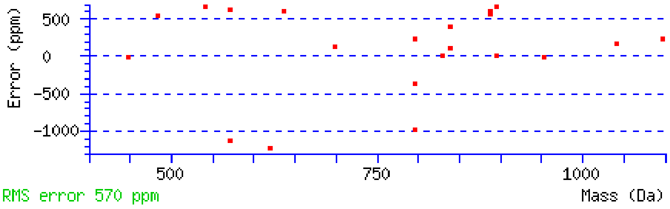


Monoisotopic mass of neutral peptide Mr(calc): 1933.8516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0003
Matches : 21/244 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.0706	82.5389					**Y**							**16**
2	261.1234	131.0653					**P**	1771.7956	886.4014	1754.7690	877.8882	1753.7850	877.3961	**15**
3	374.2074	187.6074					**I**	1674.7428	837.8750	1657.7163	829.3618	1656.7322	828.8698	**14**
4	503.2500	252.1287			485.2395	243.1234	**E**	1561.6587	781.3330	1544.6322	772.8197	1543.6482	772.3277	**13**
5	640.3089	320.6581			622.2984	311.6528	**H**	1432.6162	716.8117	1415.5896	708.2984	1414.6056	707.8064	**12**
6	697.3304	349.1688			679.3198	340.1636	**G**	1295.5572	648.2823	1278.5307	639.7690	1277.5467	639.2770	**11**
7	**796.3988**	398.7030			778.3883	389.6978	**V**	1238.5358	619.7715	1221.5092	611.2583	1220.5252	610.7662	**10**
8	**895.4672**	***448.2373***			877.4567	439.2320	**V**	1139.4674	570.2373	1122.4408	561.7240	1121.4568	561.2320	**9**
9	982.4993	491.7533			964.4887	482.7480	**S**	**1040.3990**	520.7031	1023.3724	512.1898	1022.3884	511.6978	**8**
10	**1096.5422**	548.7747	1079.5156	540.2615	1078.5316	539.7694	**N**	**953.3669**	477.1871	936.3404	468.6738	935.3564	468.1818	**7**
11	1282.6215	641.8144	1265.5949	633.3011	1264.6109	632.8091	**W**	**839.3240**	420.1656	822.2974	411.6524	821.3134	411.1604	**6**
12	1397.6484	***699.3279***	1380.6219	690.8146	1379.6379	690.3226	**D**	653.2447	327.1260	636.2181	318.6127	635.2341	318.1207	**5**
13	1512.6754	756.8413	1495.6488	748.3281	1494.6648	747.8360	**D**	538.2177	269.6125	521.1912	261.0992	520.2072	260.6072	**4**
14	1659.7108	***830.3590***	1642.6842	821.8458	1641.7002	821.3537	**M**	423.1908	212.0990	406.1642	203.5858	405.1802	203.0938	**3**
15	1788.7534	***894.8803***	1771.7268	886.3671	1770.7428	885.8750	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT1G49240.1





NCBI **BLAST** search of YPIEHGVVSNWDDMEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.5	1933.8516	-0.0037	YPIEHGVVSNWDDMEK

Mascot: http://www.matrixscience.com/

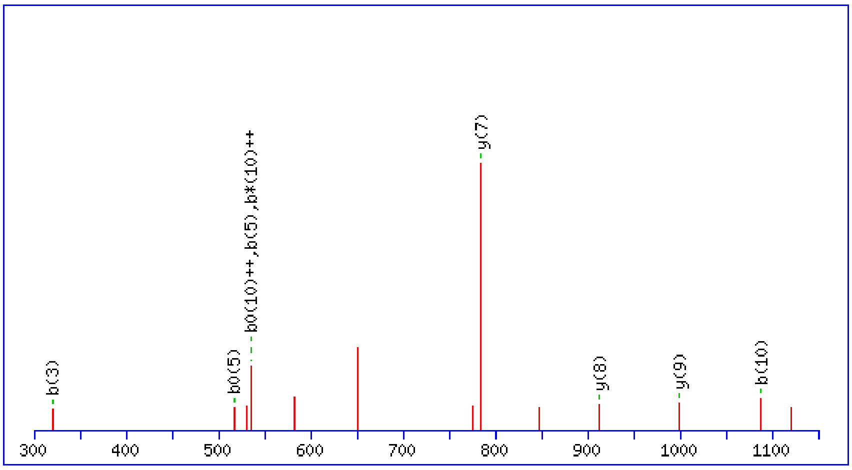
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVYSQPDNILGR**
Found in **AT1G49630.1** in **TAIR_Arabidopsis**, Symbols: ATPREP2 | ATPREP2; metalloendopeptidase | chr1:18372073-18379004 REVERSE

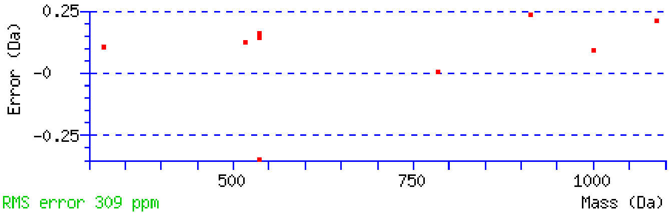
Match to Query 4969: 1317.667008 from(659.840780,2+) index(4555)
Title: Elution from: 41.386 to 41.386 scan no 5689 cid35.00 polarity:+
Data file C7-2_2.mgf

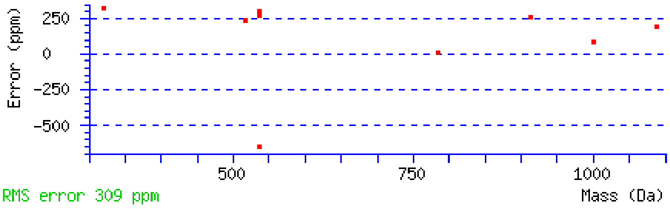
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1317.6677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0045
Matches : 9/108 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							12
2	157.0972	79.0522					V	1261.6535	631.3304	1244.6270	622.8171	1243.6430	622.3251	11
3	***320.1605***	160.5839					Y	1162.5851	581.7962	1145.5586	573.2829	1144.5745	572.7909	10
4	407.1925	204.0999			389.1819	195.0946	S	***999.5218***	500.2645	982.4952	491.7513	981.5112	491.2592	9
5	***535.2511***	268.1292	518.2245	259.6159	517.2405	259.1239	Q	***912.4898***	456.7485	895.4632	448.2352	894.4792	447.7432	8
6	632.3039	316.6556	615.2773	308.1423	614.2933	307.6503	P	***784.4312***	392.7192	767.4046	384.2060	766.4206	383.7139	7
7	747.3308	374.1690	730.3042	365.6558	729.3202	365.1638	D	687.3784	344.1928	670.3519	335.6796	669.3678	335.1876	6
8	861.3737	431.1905	844.3472	422.6772	843.3632	422.1852	N	572.3515	286.6794	555.3249	278.1661			5
9	974.4578	487.7325	957.4312	479.2193	956.4472	478.7272	I	458.3085	229.6579	441.2820	221.1446			4
10	***1087.5419***	544.2746	1070.5153	535.7613	1069.5313	535.2693	L	345.2245	173.1159	328.1979	164.6026			3
11	1144.5633	572.7853	1127.5368	564.2720	1126.5527	563.7800	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GVYSQPDNILGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G49630.1

Score	Mr(calc)	Delta	Sequence
29.1	1317.6677	-0.0007	GVYSQPDNILGR

Mascot: http://www.matrixscience.com/

AT1G49760.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGVGNIFIK**
Found in **AT1G49760.1** in **TAIR_Arabidopsis**, Symbols: PAB8 | PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor | chr1:18420408-18423421 FORWARD

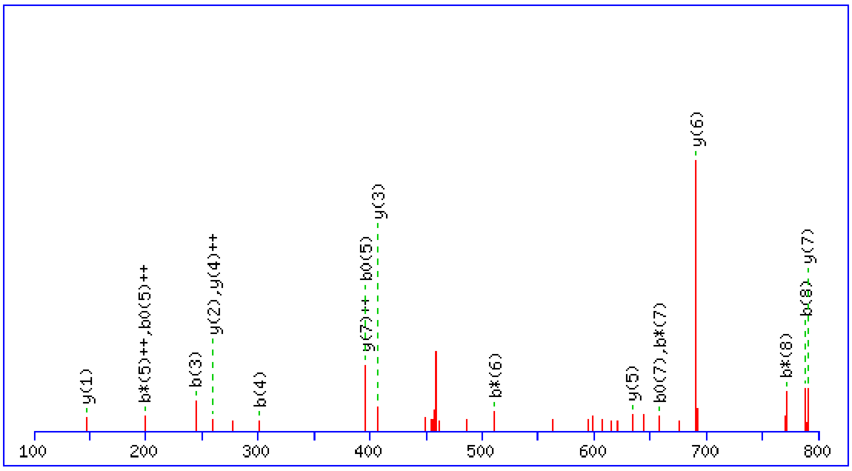
Match to Query 1608: 933.529394 from(467.771973,2+) index(4370)
Title: Elution from: 41.409 to 41.409 scan no 5601 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

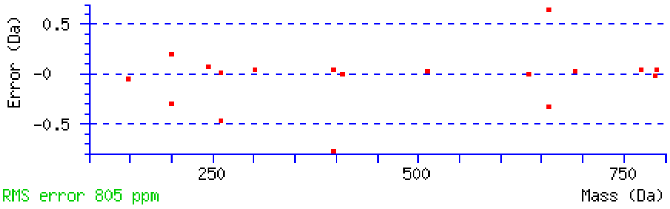
Label all possible matches ○ Label matches used for scoring ●

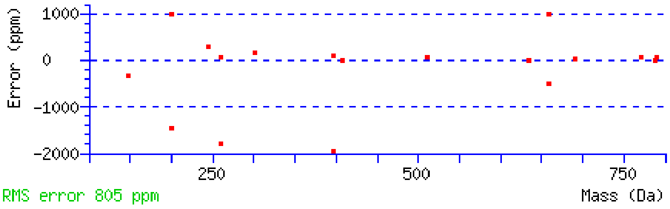
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 933.5284
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 3.6e-005
Matches : 18/72 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	88.0393	44.5233			70.0287	35.5180	S					9
2	145.0608	73.0340			127.0502	64.0287	G	847.5036	424.2554	830.4771	415.7422	8
3	**244.1292**	122.5682			226.1186	113.5629	V	***790.4822***	395.7447	773.4556	387.2314	7
4	**301.1506**	151.0790			283.1401	142.0737	G	***691.4137***	346.2105	674.3872	337.6972	6
5	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	N	***634.3923***	317.6998	617.3657	309.1865	5
6	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	I	520.3493	260.6783	503.3228	252.1650	4
7	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	F	***407.2653***	204.1363	390.2387	195.6230	3
8	**788.4301**	394.7187	771.4036	386.2054	770.4195	385.7134	I	***260.1969***	130.6021	243.1703	122.0888	2
9							K	***147.1128***	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of SGVGNIFIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G49760.1

52.8	933.5284	0.0010	SGVGNIFIK
21.6	933.5283	0.0011	YKNLTAPK
14.5	933.5284	0.0010	YGKKDVPK
10.8	933.5317	-0.0023	SGVLVGMKK
8.6	933.5317	-0.0023	KMKETGLK
7.8	933.5283	0.0011	ELERLFK
6.9	933.5284	0.0010	VVSYNPKK
6.5	933.5284	0.0010	KKGVYDPK
6.5	933.5284	0.0010	KVVSYNPK
6.4	933.5317	-0.0023	MKKETGLK

AT1G50200.1

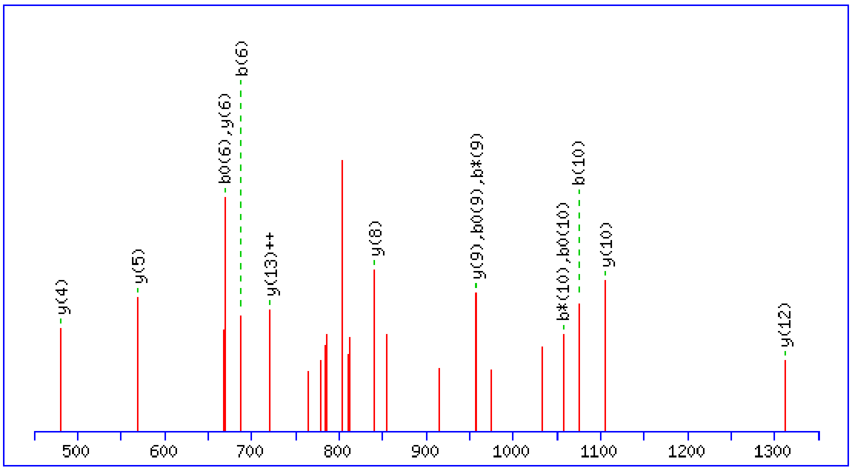
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEEGFFNGLVSSVIR**
Found in **AT1G50200.1** in **TAIR_Arabidopsis**, Symbols: ACD, ALATS | ALATS (ALANYL-TRNA SYNTHETASE); ATP binding / alanine-tRNA ligase/ ligase, forming aminoacyl-tRNA and related compounds / nucleic acid binding | chr1:18595097-18601979 REVERSE

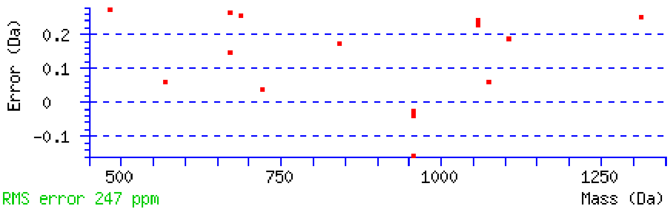
Match to Query 7987: 1642.770342 from(822.392447,2+) index(10739)
Title: Elution from: 99.186 to 99.186 scan no 15032 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

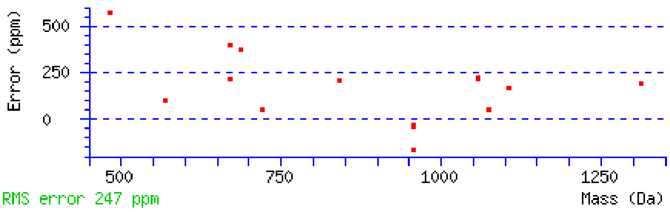


Monoisotopic mass of neutral peptide Mr(calc): 1642.7693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 3.3e-006
Matches : 15/148 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							15
2	203.0811	102.0442			185.0705	93.0389	E	1571.7425	786.3749	1553.7189	777.3631	1553.7319	777.3696	14
3	333.1207	167.0640			315.1101	158.0587	E	1441.7028	721.3551	1423.6793	712.3433	1423.6923	712.3498	13
4	391.1392	196.0732			373.1286	187.0679	G	***1311.6632***	656.3352	1293.6396	647.3234	1293.6526	647.3300	12
5	539.2046	270.1060			521.1941	261.1007	F	1253.6447	627.3260	1235.6211	618.3142	1235.6341	618.3207	11
6	687.2701	344.1387			669.2595	335.1334	F	***1105.5793***	553.2933	1087.5557	544.2815	1087.5687	544.2880	10
7	803.3071	402.1572	785.2835	393.1454	785.2965	393.1519	N	***957.5138***	479.2605	939.4902	470.2488	939.5032	470.2553	9
8	861.3256	431.1664	843.3020	422.1546	843.3150	422.1611	G	***841.4768***	421.2420	823.4532	412.2303	823.4662	412.2368	8
9	975.4067	488.2070	957.3831	479.1952	957.3961	479.2017	L	783.4583	392.2328	765.4347	383.2210	765.4477	383.2275	7
10	**1075.4721**	538.2397	1057.4485	529.2279	1057.4616	529.2344	V	***669.3772***	335.1922	651.3536	326.1805	651.3666	326.1870	6
11	1163.5012	582.2542	1145.4776	573.2424	1145.4906	573.2489	S	***569.3118***	285.1595	551.2882	276.1477	551.3012	276.1542	5
12	1251.5302	626.2688	1233.5067	617.2570	1233.5197	617.2635	S	***481.2827***	241.1450	463.2591	232.1332	463.2721	232.1397	4
13	1351.5957	676.3015	1333.5721	667.2897	1333.5851	667.2962	V	393.2536	197.1305	375.2301	188.1187			3
14	1465.6768	733.3420	1447.6532	724.3302	1447.6662	724.3368	I	293.1882	147.0977	275.1646	138.0859			2
15							R	179.1071	90.0572	161.0835	81.0454			1



RMS error 247 ppm



RMS error 247 ppm

AT1G50200.1

NCBI **BLAST** search of AEEGFFNGLVSSVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.6	1642.7693	0.0010	AEEGFFNGLVSSVIR
8.3	1642.7713	-0.0010	LKIRAMTNVGDMMK
4.3	1642.7727	-0.0024	SLNFVSGLEVMEKR
2.0	1642.7697	0.0006	LRLYDSQADRQQK
1.8	1642.7747	-0.0043	SFLGRFRGHIESGR
1.2	1642.7697	0.0006	TPSRVAGRFSGTQEK
0.5	1642.7702	0.0001	FKICIDKLCNWK

AT1G50260.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQRKESVEWVNMVLGK**
Found in **AT1G50260.1** in **TAIR_Arabidopsis**, Symbols: NTMC2TYPE5.1, NTMC2T5.1 | NTMC2T5.1/NTMC2TYPE5.1 | chr1:18621923-18625311 REVERSE

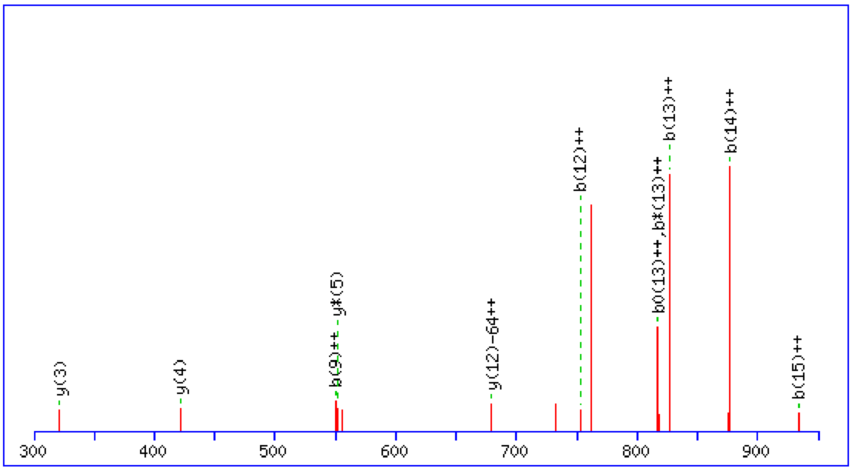
Match to Query 9491: 2070.986700 from(691.336176,3+) index(9133)
Title: Elution from: 81.171 to 81.171 scan no 12271 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 950 Da Full range

Label all possible matches ○ Label matches used for scoring ●

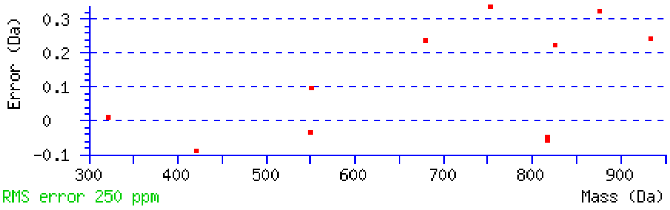
Show Y-axis ☐

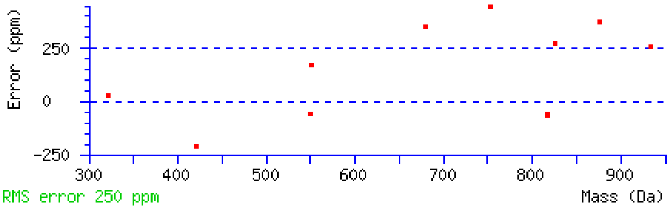


Monoisotopic mass of neutral peptide Mr(calc): 2070.9827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 0.011
Matches : 11/260 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							17
2	231.1124	116.0598			213.1018	107.0545	L	1955.9660	978.4866	1937.9424	969.4748	1937.9554	969.4813	16
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	Q	1841.8849	921.4461	1823.8613	912.4343	1823.8743	912.4408	15
4	521.2543	261.1308	503.2307	252.1190	503.2437	252.1255	R	1711.8322	856.4198	1693.8087	847.4080	1693.8217	847.4145	14
5	651.3433	326.1753	633.3197	317.1635	633.3327	317.1700	K	1551.7430	776.3751	1533.7194	767.3633	1533.7324	767.3698	13
6	781.3829	391.1951	763.3593	382.1833	763.3723	382.1898	E	1421.6540	711.3306	1403.6304	702.3188	1403.6434	702.3253	12
7	869.4120	435.2096	851.3884	426.1978	851.4014	426.2043	S	1291.6143	646.3108	1273.5907	637.2990	1273.6038	637.3055	11
8	969.4774	485.2423	951.4538	476.2306	951.4669	476.2371	V	1203.5853	602.2963	1185.5617	593.2845	1185.5747	593.2910	10
9	1099.5171	***550.2622***	1081.4935	541.2504	1081.5065	541.2569	E	1103.5198	552.2635	1085.4962	543.2518	1085.5092	543.2583	9
10	1287.5904	644.2989	1269.5669	635.2871	1269.5799	635.2936	W	973.4802	487.2437	955.4566	478.2319			8
11	1387.6559	694.3316	1369.6323	685.3198	1369.6453	685.3263	V	785.4068	393.2070	767.3832	384.1952			7
12	1503.6929	***752.3501***	1485.6693	743.3383	1485.6823	743.3448	N	685.3414	343.1743	667.3178	334.1625			6
13	1651.7253	***826.3663***	1633.7017	817.3545	1633.7148	817.3610	M	569.3044	285.1558	551.2808	276.1440			5
14	1751.7908	***876.3990***	1733.7672	867.3872	1733.7802	867.3937	V	**421.2719**	211.1396	403.2483	202.1278			4
15	1865.8719	***933.4396***	1847.8483	924.4278	1847.8613	924.4343	L	**321.2065**	161.1069	303.1829	152.0951			3
16	1923.8904	962.4488	1905.8668	953.4370	1905.8798	953.4435	G	207.1254	104.0663	189.1018	95.0545			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT1G50260.1





NCBI **BLAST** search of DLQRKESVEWVNMVLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.3	2070.9827	0.0040	DLQRKESVEWVNMVLGK
11.0	2070.9849	0.0018	DFVHYTKGNPLALQMLGK
7.4	2070.9897	-0.0030	SVENLIYIGFPGDPSTAIR
7.2	2070.9820	0.0047	NGGTVFRFGRSNSLSFLGK
6.8	2070.9908	-0.0041	SNNIMITGDGIGKTIITGDK
2.5	2070.9878	-0.0011	IRERTDALDAAGNTTAAIGK
1.3	2070.9854	0.0013	FENGRIEMHSLLRQLGK

Mascot: http://www.matrixscience.com/

AT1G50320.1

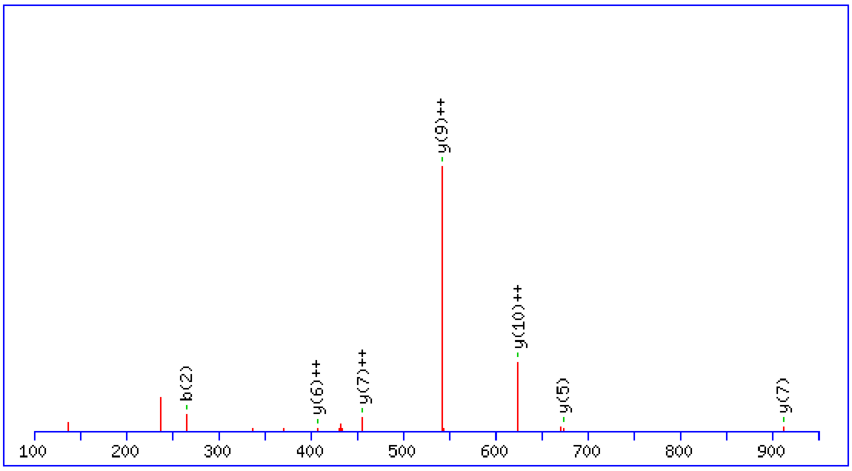
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYGLPHFILFK**
Found in **AT1G50320.1** in **TAIR_Arabidopsis**, Symbols: ATX, ATHX | ATHX (THIOREDOXIN X); thiol-disulfide exchange intermediate | chr1:18642274-18643132 REVERSE

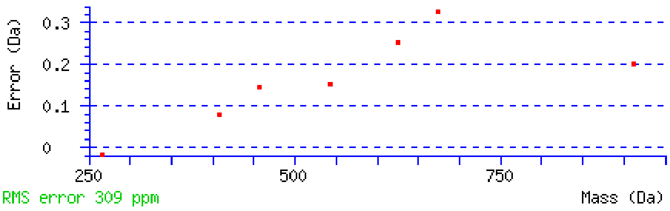
Match to Query 5054: 1346.717985 from(449.913271,3+) index(9084)
Title: Elution from: 80.592 to 80.592 scan no 12179 cid35.00 polarity:+
Data file D6h-3_2.mgf

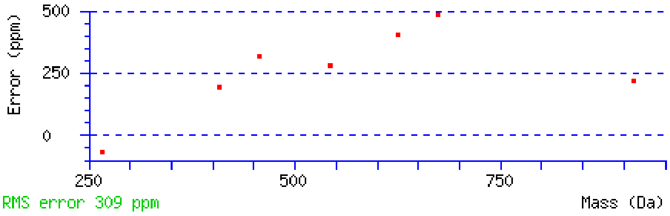
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1346.7179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.021
Matches : 7/60 fragment ions using 11 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	101.0727	51.0400	V					11
2	265.1331	133.0702	Y	1247.6597	624.3335	1229.6362	615.3217	10
3	323.1516	162.0794	G	1083.5994	542.3033	1065.5758	533.2915	9
4	437.2327	219.1200	L	1025.5809	513.2941	1007.5573	504.2823	8
5	535.2825	268.1449	P	**911.4998**	456.2535	893.4762	447.2417	7
6	675.3325	338.1699	H	813.4500	407.2286	795.4264	398.2168	6
7	823.3980	412.2026	F	**673.4000**	337.2036	655.3764	328.1918	5
8	937.4791	469.2432	I	525.3345	263.1709	507.3109	254.1591	4
9	1051.5602	526.2837	L	411.2534	206.1303	393.2298	197.1186	3
10	1199.6256	600.3164	F	297.1723	149.0898	279.1487	140.0780	2
11			K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of VYGLPHFILFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G50320.1

Score	Mr(calc)	Delta	Sequence
23.1	1346.7179	0.0001	VYGLPHFILFK
2.0	1346.7195	-0.0015	TCITPRLLKAR

Mascot: http://www.matrixscience.com/

AT1G50360.1

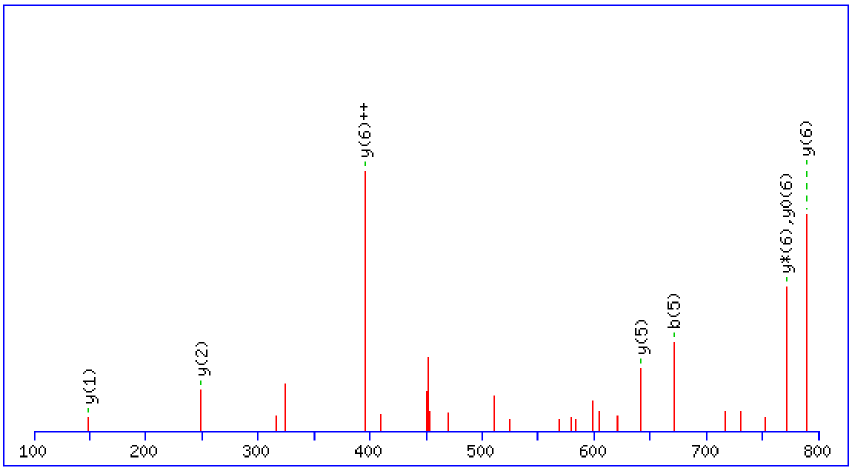
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFLMEVK**
Found in **AT1G50360.1** in **TAIR_Arabidopsis**, Symbols: ATVIIIA, VIIIA | VIIIA (Myosin-like protein VIIA); motor | chr1:18654356-18660774 FORWARD

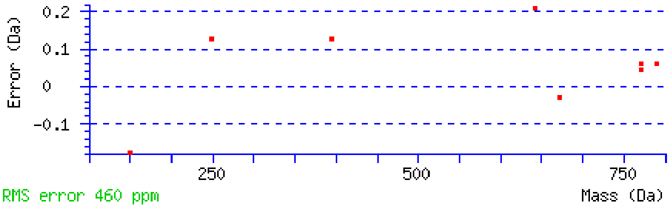
Match to Query 1860: 918.473046 from(460.243799,2+) index(7422)
Title: Elution from: 65.408 to 65.408 scan no 9612 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

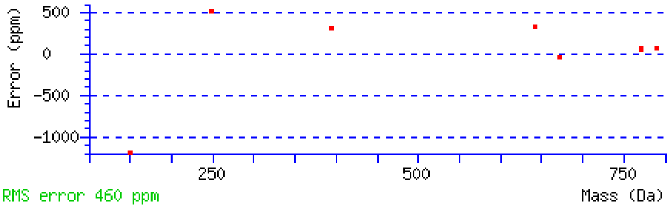


Monoisotopic mass of neutral peptide Mr(calc): 918.4727
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.01
Matches : 9/94 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							7
2	279.1618	140.0845	261.1382	131.0727			F	***789.3909***	395.1991	771.3673	386.1873	771.3804	386.1938	6
3	393.2429	197.1251	375.2193	188.1133			L	***641.3255***	321.1664	623.3019	312.1546	623.3149	312.1611	5
4	541.2753	271.1413	523.2517	262.1295			M	527.2444	264.1258	509.2208	255.1140	509.2338	255.1205	4
5	**671.3149**	336.1611	653.2913	327.1493	653.3044	327.1558	E	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
6	**771.3804**	386.1938	753.3568	377.1820	753.3698	377.1885	V	***249.1723***	125.0898	231.1487	116.0780			2
7							K	***149.1069***	75.0571	131.0833	66.0453			1



RMS error 460 ppm



RMS error 460 ppm

NCBI **BLAST** search of KFLMEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.4	918.4727	0.0004	KFLMEVK

AT1G50360.1

22.9	918.4754	-0.0023	FIMRNVK
21.0	918.4753	-0.0023	FVGRMVAK
20.2	918.4731	-0.0001	RSMKSVAK
16.3	918.4727	0.0004	MKELVFK
16.3	918.4731	-0.0001	MKQLSRK
15.4	918.4727	0.0004	KYVIMEK
12.1	918.4731	-0.0001	MTRQKVK
12.1	918.4705	0.0026	MVSSTKLK
12.1	918.4705	0.0026	MVSTSKIK

AT1G50840.1

Mascot Search Results

Peptide View

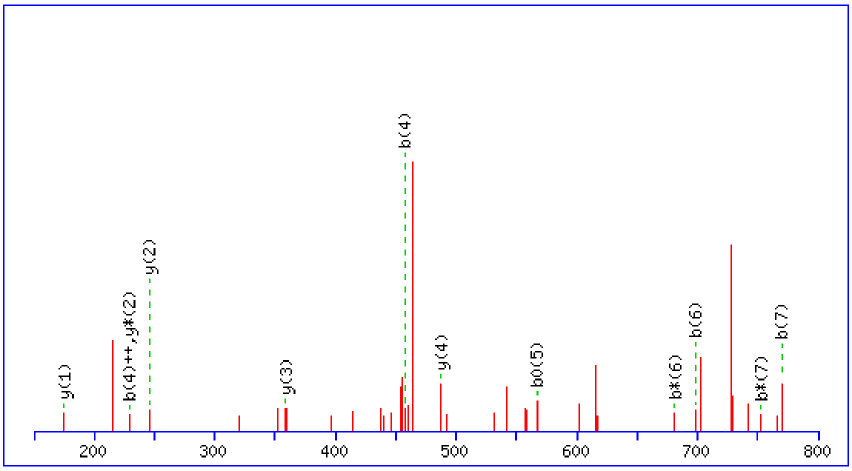
MS/MS Fragmentation of **ERNGQIAR**
Found in **AT1G50840.1** in **TAIR_Arabidopsis**, Symbols: POLGAMMA2 | POLGAMMA2 (polymerase gamma 2); DNA binding / DNA-directed DNA polymerase | chr1:18842945-18847981 FORWARD

Match to Query 1671: 942.498956 from(472.256754,2+) index(1265)
Title: Elution from: 18.883 to 18.883 scan no 1768 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

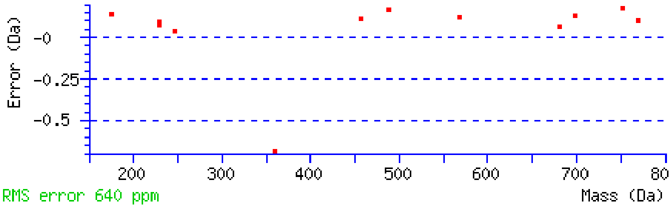
Or, Plot from 150 to 800 Da Full range

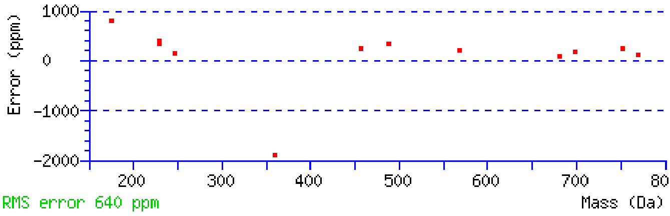
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 942.4995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 0.039
Matches : 12/68 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.0499	65.5286			112.0393	56.5233	E					8
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	R	814.4642	407.7357	797.4377	399.2225	7
3	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	N	658.3631	329.6852	641.3366	321.1719	6
4	**457.2154**	229.1113	440.1888	220.5980	439.2048	220.1060	G	544.3202	272.6637	527.2936	264.1504	5
5	585.2739	293.1406	568.2474	284.6273	567.2634	284.1353	Q	***487.2987***	244.1530	470.2722	235.6397	4
6	**698.3580**	349.6826	681.3315	341.1694	680.3474	340.6774	I	***359.2401***	180.1237	342.2136	171.6104	3
7	**769.3951**	385.2012	752.3686	376.6879	751.3846	376.1959	A	***246.1561***	123.5817	229.1295	115.0684	2
8							R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of ERNGQIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.0	942.4995	-0.0005	ERNGQIAR

AT1G50840.1

3.0	942.4995	-0.0006	QSGAARTPR
1.6	942.4995	-0.0005	QLDNRAAR

Mascot: http://www.matrixscience.com/

AT1G51400.1

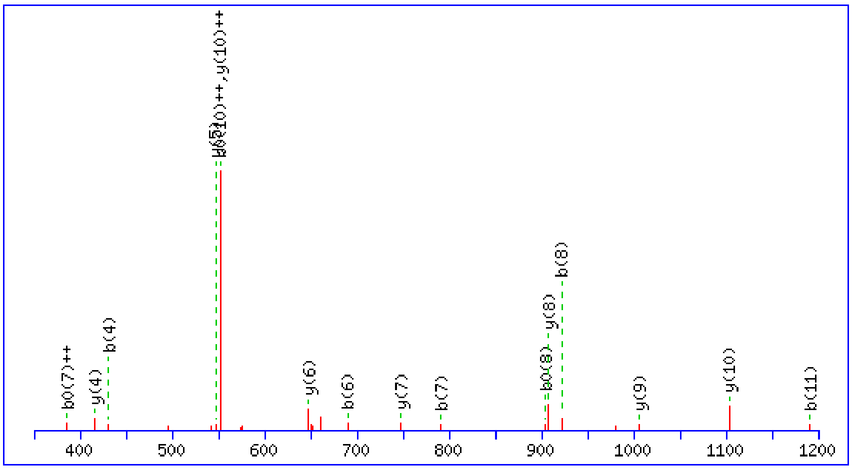
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAPVCVTMPTAK**
Found in **AT1G51400.1** in **TAIR_Arabidopsis**, Symbols: | photosystem II 5 kD protein | chr1:19055840-19056160 REVERSE

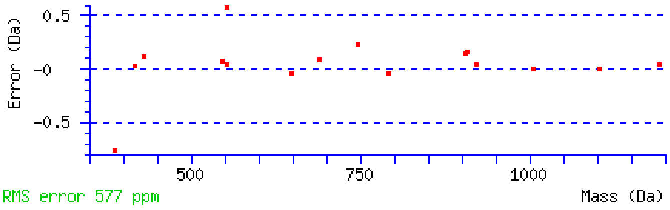
Match to Query 5010: 1336.649332 from(669.331942,2+) index(4608)
Title: Elution from: 42.000 to 42.000 scan no 5757 cid35.00 polarity:+
Data file D12h-1_2.mgf

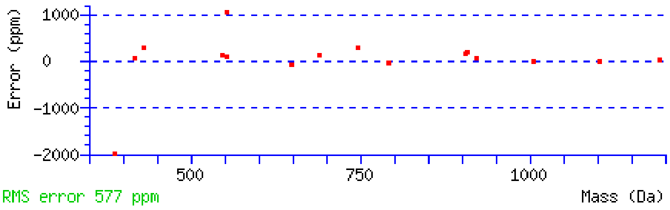
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1336.6519
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 5.2e-007
Matches : 16/94 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389			Y							12
2	235.1077	118.0575			A	1174.5959	587.8016	1157.5693	579.2883	1156.5853	578.7963	11
3	332.1605	166.5839			P	***1103.5588***	552.2830	1086.5322	543.7697	1085.5482	543.2777	10
4	***431.2289***	216.1181			V	***1006.5060***	503.7566	989.4795	495.2434	988.4954	494.7514	9
5	591.2595	296.1334			C	***907.4376***	454.2224	890.4110	445.7092	889.4270	445.2171	8
6	***690.3280***	345.6676			V	***747.4069***	374.2071	730.3804	365.6938	729.3964	365.2018	7
7	***791.3756***	396.1915	773.3651	387.1862	T	***648.3385***	324.6729	631.3120	316.1596	630.3280	315.6676	6
8	***922.4161***	461.7117	904.4056	452.7064	M	***547.2908***	274.1491	530.2643	265.6358	529.2803	265.1438	5
9	1019.4689	510.2381	1001.4583	501.2328	P	***416.2504***	208.6288	399.2238	200.1155	398.2398	199.6235	4
10	1120.5166	560.7619	1102.5060	551.7566	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
11	***1191.5537***	596.2805	1173.5431	587.2752	A	218.1499	109.5786	201.1234	101.0653			2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YAPVCVTMPTAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G51400.1

Score	Mr(calc)	Delta	Sequence
69.3	1336.6519	-0.0026	YAPVCVTMPTAK
8.3	1336.6486	0.0008	FSNIVWTMDPK
2.1	1336.6517	-0.0024	VQRNESMSRSK

Mascot: http://www.matrixscience.com/

AT1G51440.1

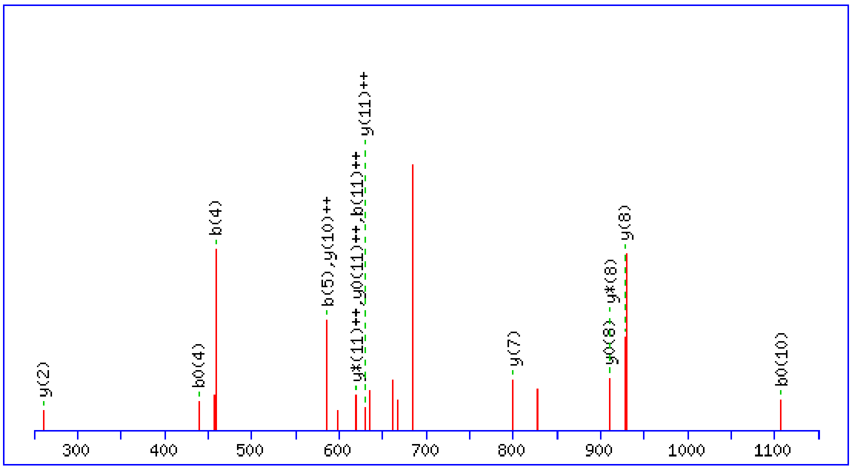
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSNKQTHVSDNK**
Found in **AT1G51440.1** in **TAIR_Arabidopsis**, Symbols: | lipase class 3 family protein | chr1:19074639-19076222 FORWARD

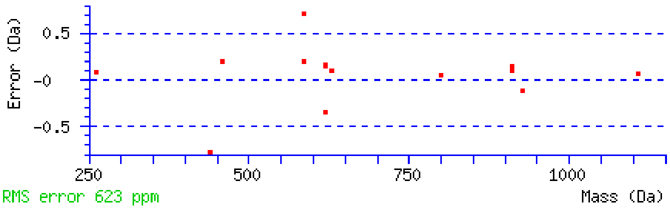
Match to Query 4790: 1384.668330 from(693.341441,2+) index(4689)
Title: Elution from: 44.941 to 44.941 scan no 6039 cid35.00 polarity:+
Data file D1d-1_3.mgf

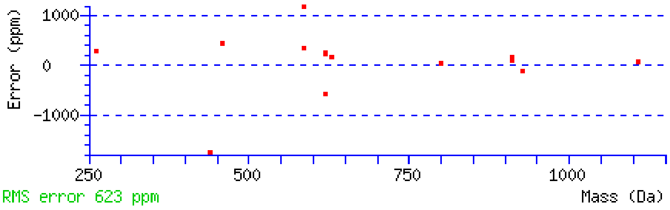
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1384.6695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.031
Matches : 14/126 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							12
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	S	1257.6182	629.3127	1240.5917	620.7995	1239.6076	620.3075	11
3	330.1408	165.5740	313.1143	157.0608	312.1302	156.5688	N	1170.5862	585.7967	1153.5596	577.2835	1152.5756	576.7914	10
4	**458.2358**	229.6215	441.2092	221.1082	440.2252	220.6162	K	1056.5432	528.7753	1039.5167	520.2620	1038.5327	519.7700	9
5	**586.2944**	293.6508	569.2678	285.1375	568.2838	284.6455	Q	***928.4483***	464.7278	911.4217	456.2145	910.4377	455.7225	8
6	687.3420	344.1747	670.3155	335.6614	669.3315	335.1694	T	***800.3897***	400.6985	783.3632	392.1852	782.3791	391.6932	7
7	824.4009	412.7041	807.3744	404.1908	806.3904	403.6988	H	699.3420	350.1747	682.3155	341.6614	681.3315	341.1694	6
8	923.4694	462.2383	906.4428	453.7250	905.4588	453.2330	V	562.2831	281.6452	545.2566	273.1319	544.2726	272.6399	5
9	1010.5014	505.7543	993.4748	497.2411	992.4908	496.7490	S	463.2147	232.1110	446.1882	223.5977	445.2041	223.1057	4
10	1125.5283	563.2678	1108.5018	554.7545	1107.5178	554.2625	D	376.1827	188.5950	359.1561	180.0817	358.1721	179.5897	3
11	1239.5713	620.2893	1222.5447	611.7760	1221.5607	611.2840	N	***261.1557***	131.0815	244.1292	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of QSNKQTHVSDNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G51440.1

Score	Mr(calc)	Delta	Sequence
19.0	1384.6695	-0.0012	QSNKQTHVSDNK
7.7	1384.6656	0.0027	VNDELKTYMTR
5.0	1384.6722	-0.0038	ETLEQTSSYSIK
2.9	1384.6697	-0.0013	LPYVYDDNMKK
1.5	1384.6657	0.0027	TLDCSSVTLFSR

Mascot: http://www.matrixscience.com/

AT1G51540.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTPGLEHWSIAVK**
Found in **AT1G51540.1** in **TAIR_Arabidopsis**, Symbols: | similar to kelch repeat-containing protein [Arabidopsis thaliana] (TAIR:AT3G27220.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41666.1); contains InterPro domain Kelch repeat type 1 (InterPro:IPR006652); contains Inter

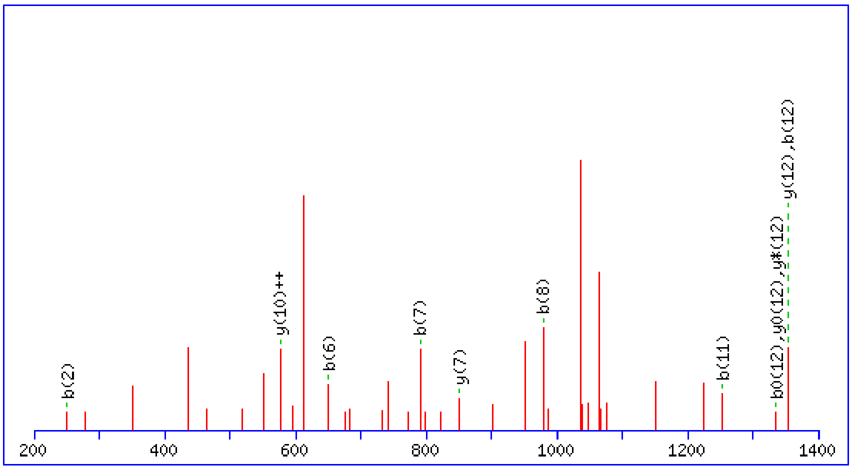
Match to Query 6528: 1500.730988 from(751.372770,2+) index(9384)
Title: Elution from: 84.687 to 84.687 scan no 12691 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

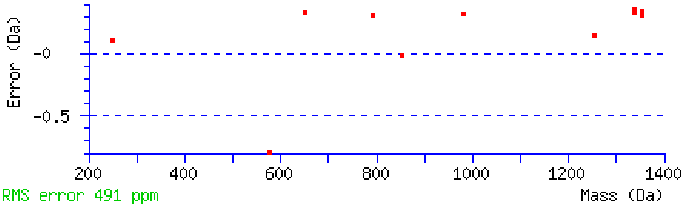
Label all possible matches ○ Label matches used for scoring ●

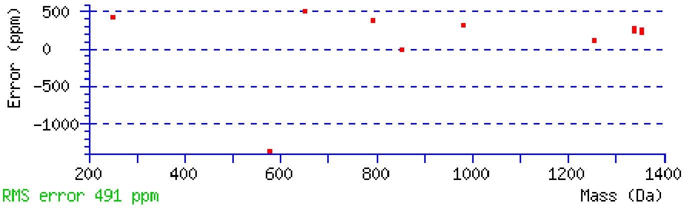
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1500.7319
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.031
Matches : 12/110 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400			**F**							**13**
2	***251.1174***	126.0624	233.1069	117.0571	**T**	**1353.6738**	677.3405	1335.6502	668.3287	1335.6632	668.3352	**12**
3	349.1672	175.0873	331.1567	166.0820	**P**	1251.6291	626.3182	1233.6055	617.3064	1233.6185	617.3129	**11**
4	407.1857	204.0965	389.1752	195.0912	**G**	1153.5793	577.2933	1135.5557	568.2815	1135.5687	568.2880	**10**
5	521.2668	261.1371	503.2563	252.1318	**L**	1095.5608	548.2840	1077.5372	539.2722	1077.5502	539.2787	**9**
6	***651.3065***	326.1569	633.2959	317.1516	**E**	981.4797	491.2435	963.4561	482.2317	963.4691	482.2382	**8**
7	***791.3565***	396.1819	773.3459	387.1766	**H**	**851.4400**	426.2237	833.4165	417.2119	833.4295	417.2184	**7**
8	***979.4299***	490.2186	961.4193	481.2133	**W**	711.3900	356.1986	693.3664	347.1869	693.3795	347.1934	**6**
9	1067.4589	534.2331	1049.4484	525.2278	**S**	523.3166	262.1620	505.2931	253.1502	505.3061	253.1567	**5**
10	1181.5400	591.2737	1163.5295	582.2684	**I**	435.2876	218.1474	417.2640	209.1356			**4**
11	***1253.5742***	627.2907	1235.5636	618.2854	**A**	321.2065	161.1069	303.1829	152.0951			**3**
12	***1353.6396***	677.3234	1335.6291	668.3182	**V**	249.1723	125.0898	231.1487	116.0780			**2**
13					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of FTPGLEHWSIAVK

AT1G51540.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.0	1500.7319	-0.0009	FTPGLEHWSIAVK
14.3	1500.7331	-0.0021	MESIPDPSVPRKK
12.5	1500.7297	0.0013	FEGVRKQYSLEK
11.3	1500.7270	0.0040	EFVKSSYEIGLSK
6.7	1500.7274	0.0035	GEVEVAKEAPAGVAR
6.7	1500.7281	0.0029	LRCLVRTHHGAR
6.2	1500.7274	0.0035	EKAHDVKETVAQK
2.7	1500.7319	-0.0009	QFKYALVWGSSAK
1.8	1500.7270	0.0040	TKYSVYIAEEGVK
1.0	1500.7275	0.0035	IPKENQQQLQEK

AT1G51980.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVLAASGVEHEELLK**
Found in **AT1G51980.1** in **TAIR_Arabidopsis**, Symbols: | mitochondrial processing peptidase alpha subunit, putative | chr1:19327361-19330440 REVERSE

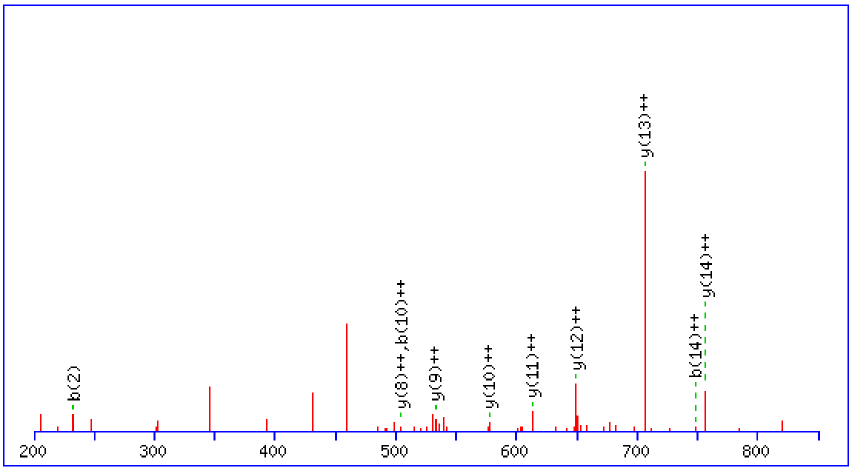
Match to Query 7462: 1642.797552 from(548.606460,3+) index(5248)
Title: Elution from: 46.833 to 46.833 scan no 6597 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 850 Da Full range

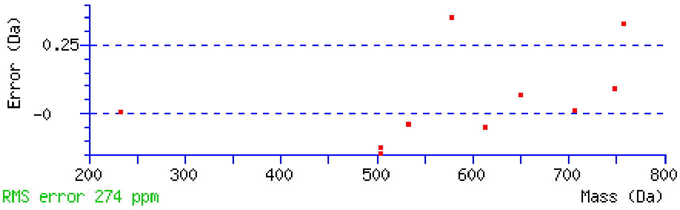
Label all possible matches ○ Label matches used for scoring ●

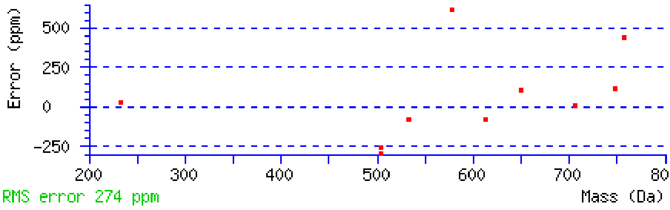
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1642.7961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0069
Matches : 10/124 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260			M							15
2	233.1102	117.0588			V	1511.7658	756.3866	1493.7422	747.3748	1493.7553	747.3813	14
3	347.1913	174.0993			L	1411.7004	706.3538	1393.6768	697.3420	1393.6898	697.3485	13
4	419.2255	210.1164			A	1297.6193	649.3133	1279.5957	640.3015	1279.6087	640.3080	12
5	491.2596	246.1335			A	1225.5851	613.2962	1207.5615	604.2844	1207.5746	604.2909	11
6	579.2887	290.1480	561.2781	281.1427	S	1153.5510	577.2791	1135.5274	568.2673	1135.5404	568.2738	10
7	637.3072	319.1572	619.2966	310.1520	G	1065.5219	533.2646	1047.4983	524.2528	1047.5114	524.2593	9
8	737.3727	369.1900	719.3621	360.1847	V	1007.5034	504.2553	989.4798	495.2436	989.4929	495.2501	8
9	867.4123	434.2098	849.4017	425.2045	E	907.4380	454.2226	889.4144	445.2108	889.4274	445.2173	7
10	1007.4623	504.2348	989.4517	495.2295	H	777.3983	389.2028	759.3748	380.1910	759.3878	380.1975	6
11	1137.5019	569.2546	1119.4914	560.2493	E	637.3483	319.1778	619.3247	310.1660	619.3378	310.1725	5
12	1267.5416	634.2744	1249.5310	625.2691	E	507.3087	254.1580	489.2851	245.1462	489.2981	245.1527	4
13	1381.6227	691.3150	1363.6121	682.3097	L	377.2691	189.1382	359.2455	180.1264			3
14	1495.7038	748.3555	1477.6932	739.3502	L	263.1880	132.0976	245.1644	123.0858			2
15					K	149.1069	75.0571	131.0833	66.0453			1





AT1G51980.1

NCBI **BLAST** search of MVLAASGVEHEELLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.9	1642.7961	0.0015	MVLAASGVEHEELLK
4.4	1642.8012	-0.0037	KSTTTSASSKGLAQQK
2.0	1642.7961	0.0015	ETKELVAMKYIER

AT1G52230.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFETFAAPFTK**
Found in **AT1G52230.1** in **TAIR_Arabidopsis**, Symbols: PSAH2, PSAH-2, PSI-H | PSAH-2/PSAH2/PSI-H (PHOTOSYSTEM I SUBUNIT H-2) | chr1:19458571-19459177 FORWARD

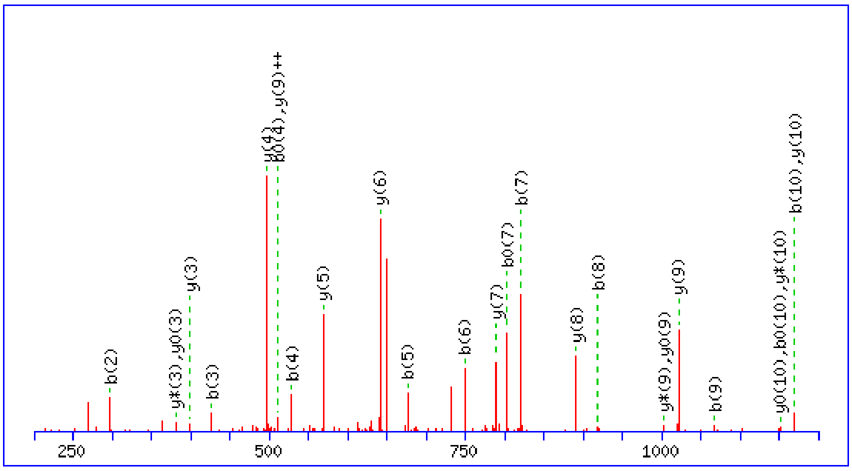
Match to Query 4673: 1316.608638 from(659.311595,2+) index(8793)
Title: Elution from: 80.762 to 80.762 scan no 11824 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1200 Da Full range

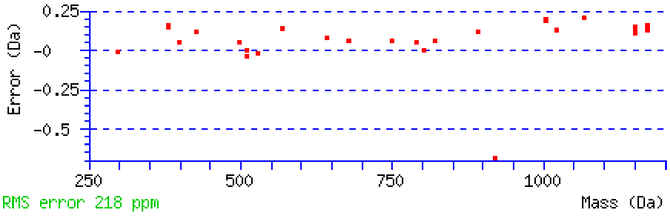
Label all possible matches ○ Label matches used for scoring ●

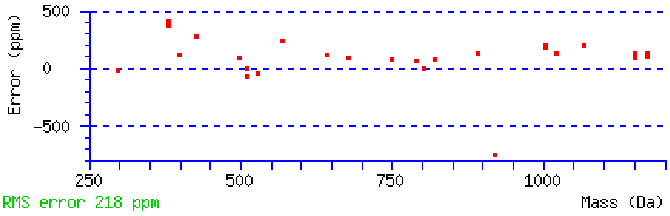
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1316.6085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 1.6e-008
Matches : 27/94 fragment ions using 30 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	149.0727	75.0400			F							11
2	***297.1382***	149.0727			F	***1169.5504***	585.2788	1151.5268	576.2670	1151.5398	576.2735	10
3	***427.1778***	214.0925	409.1672	205.0873	E	***1021.4849***	511.2461	1003.4613	502.2343	1003.4744	502.2408	9
4	***529.2225***	265.1149	511.2120	256.1096	T	***891.4453***	446.2263	873.4217	437.2145	873.4347	437.2210	8
5	***677.2880***	339.1476	659.2774	330.1423	F	***789.4006***	395.2039	771.3770	386.1921	771.3900	386.1986	7
6	***749.3221***	375.1647	731.3115	366.1594	A	***641.3351***	321.1712	623.3115	312.1594	623.3246	312.1659	6
7	***821.3563***	411.1818	803.3457	402.1765	A	***569.3010***	285.1541	551.2774	276.1423	551.2904	276.1488	5
8	***919.4061***	460.2067	901.3955	451.2014	P	***497.2668***	249.1371	479.2433	240.1253	479.2563	240.1318	4
9	***1067.4715***	534.2394	1049.4609	525.2341	F	***399.2170***	200.1122	381.1935	191.1004	381.2065	191.1069	3
10	***1169.5162***	585.2617	1151.5057	576.2565	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FFETFAAPFTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G52230.1

Score	Mr(calc)	Delta	Sequence
85.7	1316.6085	0.0001	FFETFAAPFTK
21.8	1316.6074	0.0012	HVETITLSEMK
21.7	1316.6074	0.0012	TKTMESSFKTK
15.7	1316.6063	0.0023	DITYNFEFKK
11.9	1316.6067	0.0019	FKDTYDRTVR
9.3	1316.6049	0.0037	MNCLFLFKSK
8.2	1316.6067	0.0019	GYGVDKRNYTK
7.2	1316.6101	-0.0014	TGVHGMVKQDTK
6.9	1316.6097	-0.0011	YLKTSSAPYMK
6.2	1316.6124	-0.0037	KSEKCYLFAR

AT1G52300.1

Mascot Search Results

Peptide View

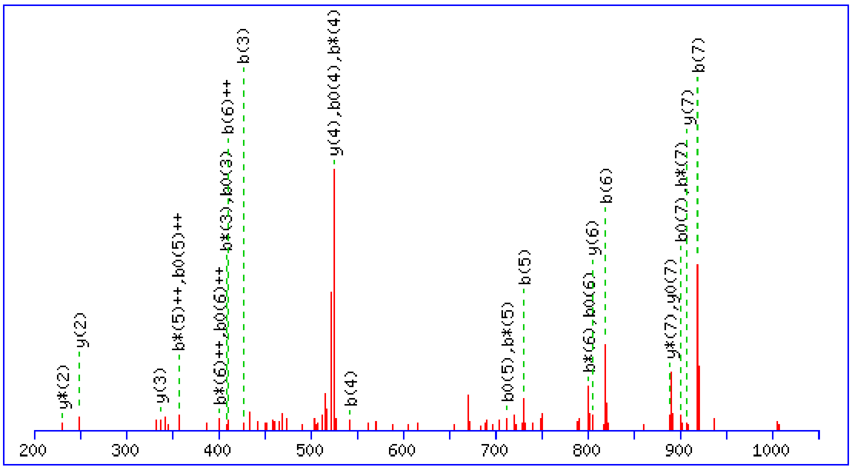
MS/MS Fragmentation of **RTYNWSVK**
Found in **AT1G52300.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L37 (RPL37B) | chr1:19478882-19479821 REVERSE

Match to Query 3239: 1066.500674 from(534.257613,2+) index(1544)
Title: Elution from: 20.917 to 20.917 scan no 2091 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

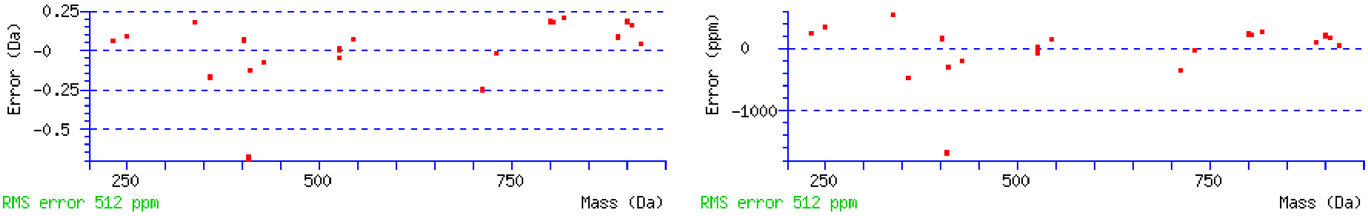
Or, Plot from 200 to 1050 Da Full range

Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1066.4988
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.037
Matches : 28/78 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							8
2	263.1412	132.0743	245.1177	123.0625	245.1307	123.0690	T	***907.4168***	454.2121	889.3933	445.2003	889.4063	445.2068	7
3	***427.2016***	214.1044	409.1780	205.0926	409.1910	205.0992	Y	***805.3721***	403.1897	787.3485	394.1779	787.3616	394.1844	6
4	***543.2386***	272.1229	525.2150	263.1111	525.2280	263.1177	N	641.3118	321.1595	623.2882	312.1477	623.3012	312.1542	5
5	***731.3120***	366.1596	713.2884	357.1478	713.3014	357.1543	W	***525.2748***	263.1410	507.2512	254.1292	507.2642	254.1357	4
6	***819.3410***	410.1742	801.3175	401.1624	801.3305	401.1689	S	***337.2014***	169.1043	319.1778	160.0925	319.1908	160.0990	3
7	***919.4065***	460.2069	901.3829	451.1951	901.3959	451.2016	V	***249.1723***	125.0898	231.1487	116.0780			2
8							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of RTYNWSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.4	1066.4988	0.0019	RTYNWSVK
18.1	1066.5000	0.0007	RSSSVNMKK

AT1G52300.1

11.4	1066.4984	0.0023	TWVDYFVK
7.3	1066.5000	0.0007	SRAMTKNTK
5.2	1066.5017	-0.0011	GYMFALEVK
4.9	1066.5018	-0.0011	LYFNEMLK
4.6	1066.4984	0.0023	WFSYDVLK
3.6	1066.5018	-0.0011	FYNIEMLK
2.1	1066.5022	-0.0015	KLNYCSLR
1.5	1066.5022	-0.0015	CEIYRKGK

AT1G52400.1

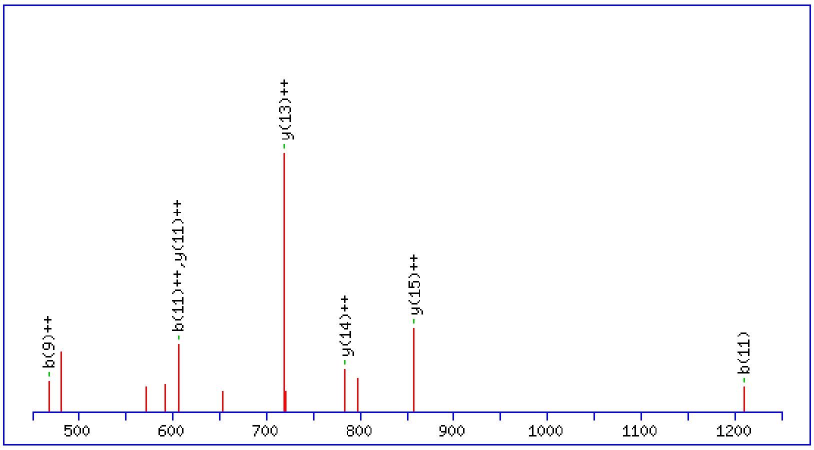
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGIAHSPAWFEPQDLEHVGGSIER**
Found in **AT1G52400.1** in **TAIR_Arabidopsis**, Symbols: BGL1 | BGL1 (BETA-GLUCOSIDASE HOMOLOG 1); hydrolase, hydrolyzing O-glycosyl compounds | chr1:19518919-19521599 FORWARD

Match to Query 10238: 2644.304836 from(662.083485,4+) index(7889)
Title: Elution from: 70.697 to 70.697 scan no 10457 cid35.00 polarity:+
Data file D1d-2_3.mgf

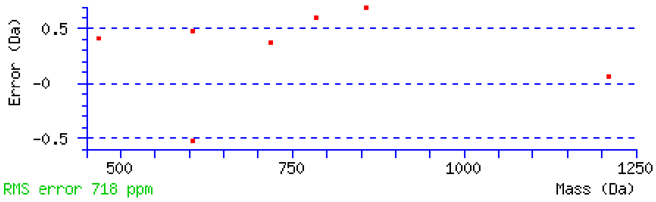
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

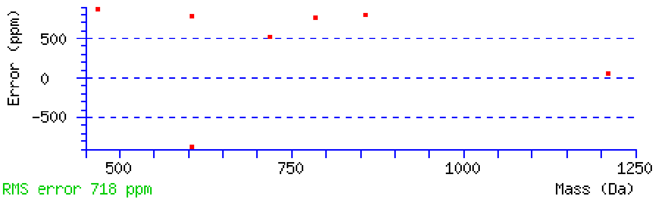


Monoisotopic mass of neutral peptide Mr(calc): 2644.3034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.035
Matches : 7/240 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							24
2	171.1128	86.0600					G	2532.2266	1266.6169	2515.2001	1258.1037	2514.2160	1257.6117	23
3	284.1969	142.6021					I	2475.2051	1238.1062	2458.1786	1229.5929	2457.1946	1229.1009	22
4	355.2340	178.1206					A	2362.1211	1181.5642	2345.0945	1173.0509	2344.1105	1172.5589	21
5	492.2929	246.6501					H	2291.0840	1146.0456	2274.0574	1137.5323	2273.0734	1137.0403	20
6	579.3249	290.1661			561.3144	281.1608	S	2154.0251	1077.5162	2136.9985	1069.0029	2136.0145	1068.5109	19
7	676.3777	338.6925			658.3671	329.6872	P	2066.9930	1034.0002	2049.9665	1025.4869	2048.9825	1024.9949	18
8	747.4148	374.2110			729.4042	365.2058	A	1969.9403	985.4738	1952.9137	976.9605	1951.9297	976.4685	17
9	933.4941	**467.2507**			915.4835	458.2454	W	1898.9032	949.9552	1881.8766	941.4419	1880.8926	940.9499	16
10	1080.5625	540.7849			1062.5520	531.7796	F	1712.8238	856.9156	1695.7973	848.4023	1694.8133	847.9103	15
11	1209.6051	**605.3062**			1191.5946	596.3009	E	1565.7554	783.3814	1548.7289	774.8681	1547.7449	774.3761	14
12	1306.6579	653.8326			1288.6473	644.8273	P	1436.7128	718.8601	1419.6863	710.3468	1418.7023	709.8548	13
13	1434.7165	717.8619	1417.6899	709.3486	1416.7059	708.8566	Q	1339.6601	670.3337	1322.6335	661.8204	1321.6495	661.3284	12
14	1549.7434	775.3753	1532.7169	766.8621	1531.7328	766.3701	D	1211.6015	606.3044	1194.5749	597.7911	1193.5909	597.2991	11
15	1662.8275	831.9174	1645.8009	823.4041	1644.8169	822.9121	L	1096.5745	548.7909	1079.5480	540.2776	1078.5640	539.7856	10
16	1791.8701	896.4387	1774.8435	887.9254	1773.8595	887.4334	E	983.4905	492.2489	966.4639	483.7356	965.4799	483.2436	9
17	1928.9290	964.9681	1911.9024	956.4549	1910.9184	955.9628	H	854.4479	427.7276	837.4213	419.2143	836.4373	418.7223	8
18	2027.9974	1014.5023	2010.9708	1005.9891	2009.9868	1005.4970	V	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
19	2085.0189	1043.0131	2067.9923	1034.4998	2067.0083	1034.0078	G	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
20	2142.0403	1071.5238	2125.0138	1063.0105	2124.0298	1062.5185	G	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
21	2229.0723	1115.0398	2212.0458	1106.5265	2211.0618	1106.0345	S	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
22	2342.1564	1171.5818	2325.1299	1163.0686	2324.1458	1162.5766	I	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
23	2471.1990	1236.1031	2454.1725	1227.5899	2453.1884	1227.0979	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
24							R	175.1190	88.0631	158.0924	79.5498			1

AT1G52400.1





NCBI **BLAST** search of IGIAHSPAWFEPQDLEHVGGSIER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	2644.3034	0.0014	IGIAHSPAWFEPQDLEHVGGSIER
3.4	2644.3080	-0.0031	DGLLPGDVILAVDGTELSNSGSDSVSK
2.8	2644.2989	0.0060	SNLGSNAYVLNALLDMYAKCGNLK

AT1G52450.1

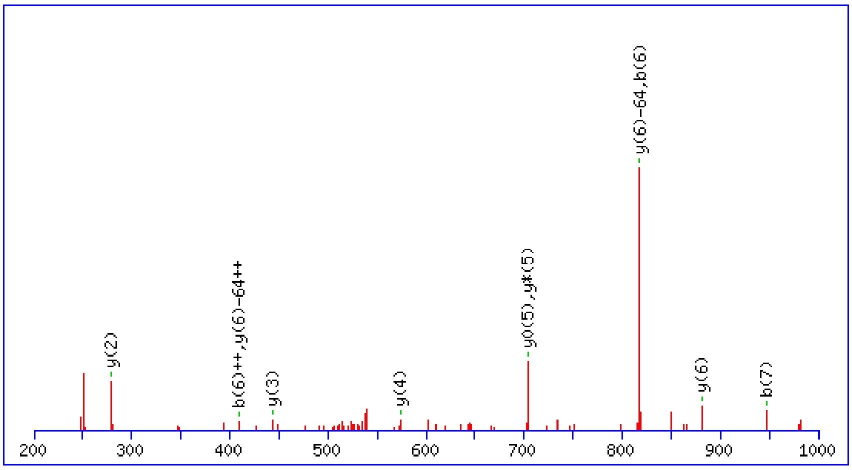
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIRMEYQK**
Found in **AT1G52450.1** in **TAIR_Arabidopsis**, Symbols: | ubiquitin carboxyl-terminal hydrolase-related | chr1:19545353-19549935 REVERSE

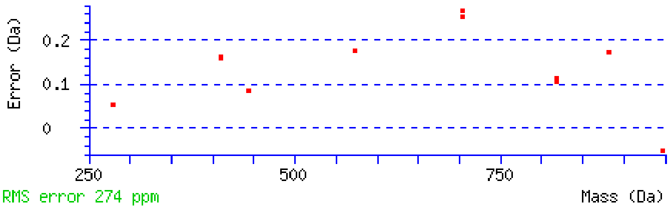
Match to Query 3311: 1094.521772 from(548.268162,2+) index(3571)
Title: Elution from: 35.495 to 35.495 scan no 4505 cid35.00 polarity:+
Data file 0-3_1.mgf

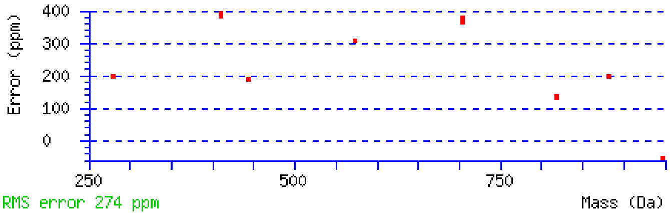
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1094.5205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.022
Matches : 11/106 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							8
2	215.1538	108.0805					I	995.4623	498.2348	977.4387	489.2230	977.4517	489.2295	7
3	375.2431	188.1252	357.2195	179.1134			R	***881.3812***	441.1942	863.3576	432.1824	863.3706	432.1890	6
4	523.2755	262.1414	505.2519	253.1296			M	721.2919	361.1496	703.2684	352.1378	703.2814	352.1443	5
5	653.3151	327.1612	635.2916	318.1494	635.3046	318.1559	E	***573.2595***	287.1334	555.2359	278.1216	555.2489	278.1281	4
6	**817.3755**	409.1914	799.3519	400.1796	799.3649	400.1861	Y	***443.2199***	222.1136	425.1963	213.1018			3
7	**947.4281**	474.2177	929.4046	465.2059	929.4176	465.2124	Q	***279.1595***	140.0834	261.1359	131.0716			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VIRMEYQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.5	1094.5205	0.0013	VIRMEYQK

AT1G52450.1

18.4	1094.5205	0.0013	SDCFGKIKK
17.9	1094.5205	0.0013	MVASFEKVR
14.1	1094.5231	-0.0014	MKYNPRVR
13.1	1094.5205	0.0013	DMLRIYQK
10.1	1094.5205	0.0013	LMESGYRVK
8.8	1094.5205	0.0013	QFSAMNKLK
8.3	1094.5205	0.0013	IQRYVMEK
7.5	1094.5204	0.0013	FKVATGQGMK
4.8	1094.5205	0.0013	LMKDAVYAR

AT1G52510.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEVLEVK**
Found in **AT1G52510.1** in **TAIR_Arabidopsis**, Symbols: | hydrolase, alpha/beta fold family protein | chr1:19566708-19568929 REVERSE

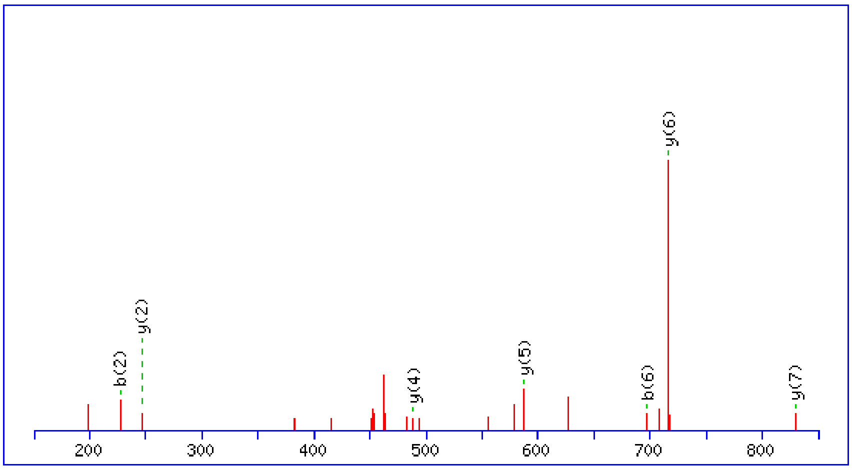
Match to Query 1924: 941.580102 from(471.797327,2+) index(6296)
Title: Elution from: 55.744 to 55.744 scan no 8082 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

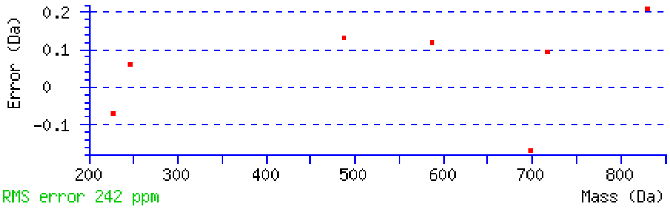
Label all possible matches ○ Label matches used for scoring ●

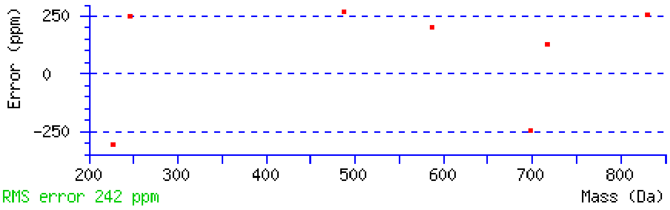
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 941.5797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.00067
Matches : 7/62 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							8
2	**227.1754**	114.0913			L	***829.5029***	415.2551	812.4764	406.7418	811.4924	406.2498	7
3	356.2180	178.6126	338.2074	169.6074	E	***716.4189***	358.7131	699.3923	350.1998	698.4083	349.7078	6
4	455.2864	228.1468	437.2758	219.1416	V	***587.3763***	294.1918	570.3497	285.6785	569.3657	285.1865	5
5	568.3705	284.6889	550.3599	275.6836	L	***488.3079***	244.6576	471.2813	236.1443	470.2973	235.6523	4
6	**697.4131**	349.2102	679.4025	340.2049	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
7	796.4815	398.7444	778.4709	389.7391	V	***246.1812***	123.5942	229.1547	115.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LLEVLEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.5	941.5797	0.0004	LLEVLEVK
21.4	941.5797	0.0004	ILLDEIVK

AT1G52510.1

14.1	941.5797	0.0004	LLDEIIVK
8.1	941.5797	0.0004	LLDLVELK
7.1	941.5811	-0.0010	LIVQKWR
4.7	941.5797	0.0004	LLVVEIEK

AT1G52570.1

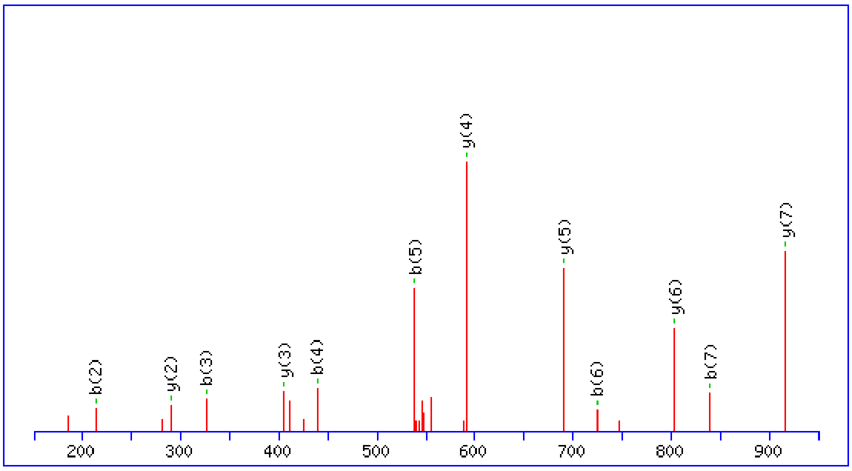
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILLVWDDR**
Found in **AT1G52570.1** in **TAIR_Arabidopsis**, Symbols: PLDALPHA2 | PLDALPHA2 (PHOSPHLIPASE D ALPHA 2); phospholipase D | chr1:19587609-19590220 REVERSE

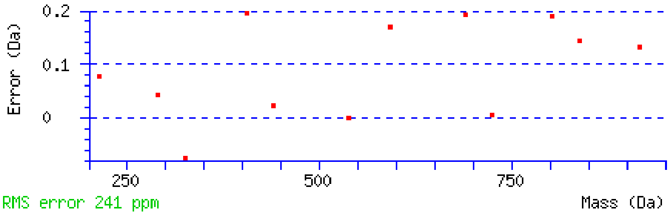
Match to Query 3763: 1127.635204 from(564.824878,2+) index(9196)
Title: Elution from: 81.871 to 81.871 scan no 12286 cid35.00 polarity:+
Data file 0-2_1.mgf

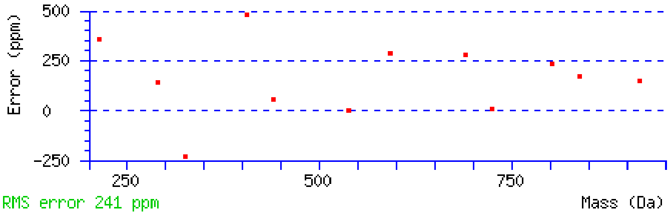
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1127.6339
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 3.6e-006
Matches : 12/66 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							9
2	*213.1598*	107.0835			I	1029.5728	515.2900	1012.5462	506.7767	1011.5622	506.2847	8
3	*326.2438*	163.6255			L	*916.4887*	458.7480	899.4621	450.2347	898.4781	449.7427	7
4	*439.3279*	220.1676			L	*803.4046*	402.2060	786.3781	393.6927	785.3941	393.2007	6
5	*538.3963*	269.7018			V	*690.3206*	345.6639	673.2940	337.1506	672.3100	336.6586	5
6	*724.4756*	362.7414			W	*591.2522*	296.1297	574.2256	287.6164	573.2416	287.1244	4
7	*839.5026*	420.2549	821.4920	411.2496	D	*405.1728*	203.0901	388.1463	194.5768	387.1623	194.0848	3
8	954.5295	477.7684	936.5189	468.7631	D	*290.1459*	145.5766	273.1193	137.0633	272.1353	136.5713	2
9					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VILLVWDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G52570.1

57.4	1127.6339	0.0013	VILLVWDDR
57.4	1127.6339	0.0013	VLLLVWDDR

Mascot: http://www.matrixscience.com/

AT1G52740.1

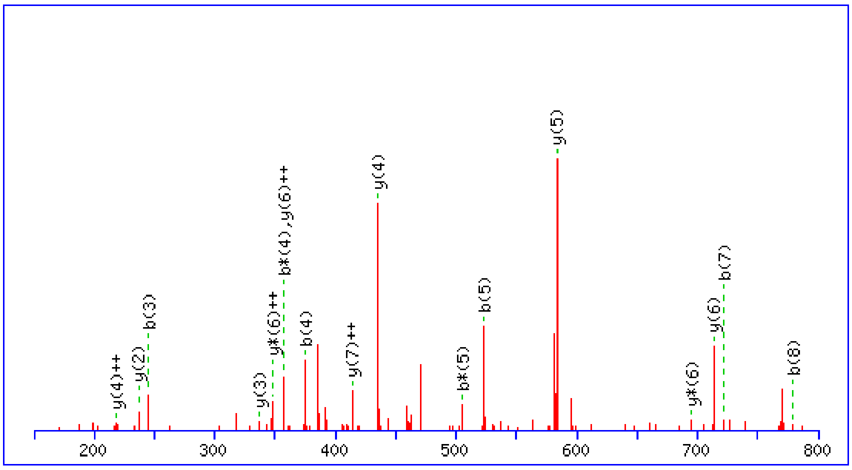
Mascot Search Results

Peptide View

MS/MS Fragmentation of AGLQFPVGR
Found in AT1G52740.1 in TAIR_Arabidopsis, Symbols: HTA9 | HTA9; DNA binding | chr1:19649077-19649889 FORWARD

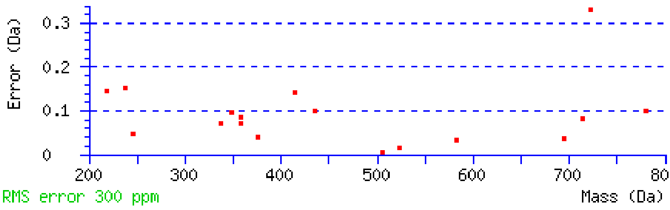
Match to Query 2083: 956.484898 from(479.249725,2+) index(4550)
Title: Elution from: 41.934 to 41.934 scan no 5721 cid35.00 polarity:+
Data file D6h-1_3.mgf

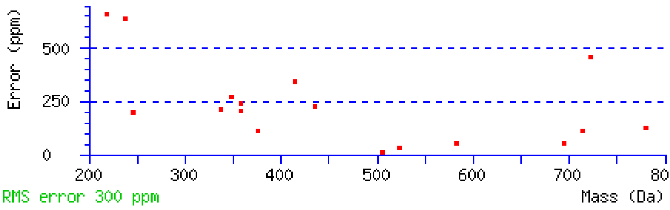
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 956.4854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.015
Matches : 17/58 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	73.0414	37.0244			A					9
2	131.0599	66.0336			G	885.4585	443.2329	867.4349	434.2211	8
3	***245.1410***	123.0741			L	827.4400	414.2237	809.4165	405.2119	7
4	***375.1937***	188.1005	357.1701	179.0887	Q	***713.3589***	357.1831	695.3354	348.1713	6
5	***523.2591***	262.1332	505.2355	253.1214	F	***583.3063***	292.1568	565.2827	283.1450	5
6	621.3089	311.1581	603.2853	302.1463	P	***435.2408***	218.1241	417.2173	209.1123	4
7	***721.3744***	361.1908	703.3508	352.1790	V	***337.1910***	169.0992	319.1675	160.0874	3
8	***779.3929***	390.2001	761.3693	381.1883	G	***237.1256***	119.0664	219.1020	110.0546	2
9					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of AGLQFPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.5	956.4854	-0.0005	AGIQFPVGR

AT1G52740.1

29.5	956.4854	-0.0005	AGLQFPVGR
17.9	956.4832	0.0017	KIQQEAAR
17.9	956.4832	0.0017	LQEELRR
6.3	956.4832	0.0017	LEERLQR
1.4	956.4861	-0.0012	KLEMEGIK
0.8	956.4861	-0.0012	ELKIEGMK
0.8	956.4827	0.0022	IEEPKGFK

AT1G53050.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGCVCGKPSAIEDSK**
Found in **AT1G53050.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:19776242-19779199 FORWARD

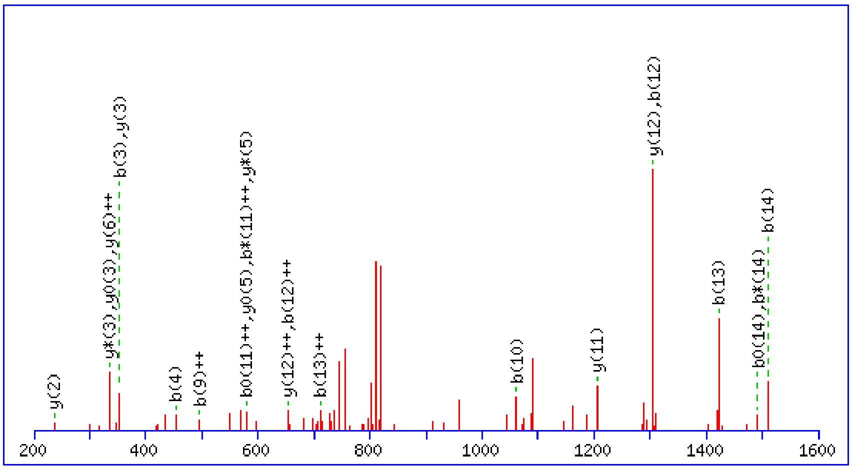
Match to Query 7617: 1656.660694 from(829.337623,2+) index(3819)
Title: Elution from: 35.975 to 35.975 scan no 4757 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1600 Da Full range

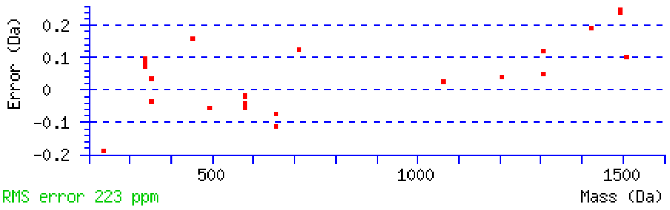
Label all possible matches ○ Label matches used for scoring ●

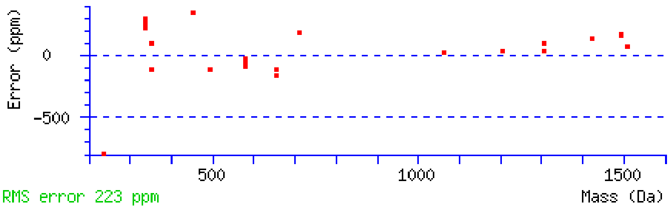
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1656.6648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00069
Matches : 23/138 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							15
2	191.0633	96.0353					G	1525.6346	763.3209	1507.6110	754.3091	1507.6240	754.3156	14
3	***353.0880***	177.0476					C	1467.6161	734.3117	1449.5925	725.2999	1449.6055	725.3064	13
4	***453.1535***	227.0804					V	**1305.5914**	653.2993	1287.5678	644.2875	1287.5808	644.2940	12
5	615.1782	308.0927					C	**1205.5259**	603.2666	1187.5023	594.2548	1187.5153	594.2613	11
6	673.1967	337.1020					G	1043.5012	522.2542	1025.4776	513.2424	1025.4906	513.2489	10
7	803.2857	402.1465	785.2621	393.1347			K	985.4827	493.2450	967.4591	484.2332	967.4721	484.2397	9
8	901.3355	451.1714	883.3119	442.1596			P	855.3937	428.2005	837.3701	419.1887	837.3831	419.1952	8
9	989.3646	**495.1859**	971.3410	486.1741	971.3540	486.1806	S	757.3439	379.1756	739.3203	370.1638	739.3333	370.1703	7
10	***1061.3987***	531.2030	1043.3751	522.1912	1043.3882	522.1977	A	669.3148	335.1610	651.2912	326.1492	651.3042	326.1558	6
11	1175.4798	588.2435	1157.4562	579.2318	1157.4693	579.2383	I	597.2806	299.1440	579.2571	290.1322	579.2701	290.1387	5
12	***1305.5195***	**653.2634**	1287.4959	644.2516	1287.5089	644.2581	E	483.1995	242.1034	465.1760	233.0916	465.1890	233.0981	4
13	***1421.5434***	**711.2754**	1403.5198	702.2636	1403.5329	702.2701	D	**353.1599**	177.0836	335.1363	168.0718	335.1493	168.0783	3
14	***1509.5725***	755.2899	1491.5489	746.2781	1491.5619	746.2846	S	**237.1359**	119.0716	219.1124	110.0598	219.1254	110.0663	2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MGCVCGKPSAIEDSK

AT1G53050.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.3	1656.6648	-0.0041	MGCVCGKPSAIEDSK
9.4	1656.6579	0.0028	LDFSEEKDDEETGK
0.8	1656.6639	-0.0032	VGTMETISNEGDVDR

AT1G53090.1

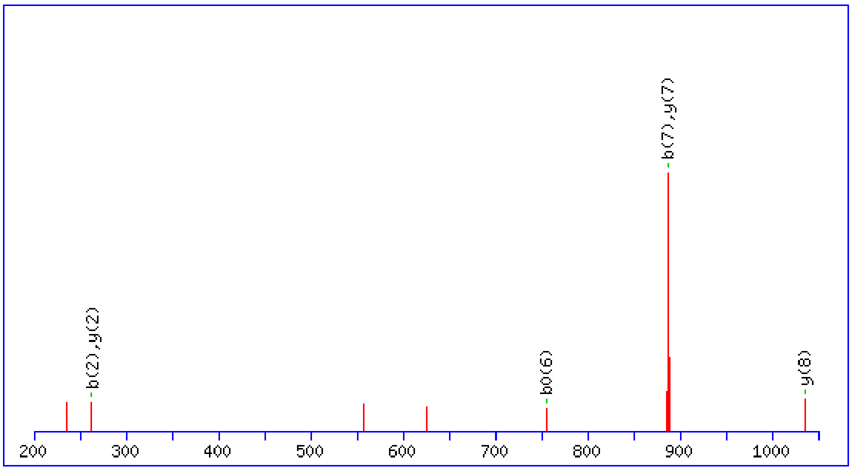
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFECESIIK**
Found in **AT1G53090.1** in **TAIR_Arabidopsis**, Symbols: SPA4 | SPA4 (SPA1-RELATED 4); signal transducer | chr1:19787416-19790358 FORWARD

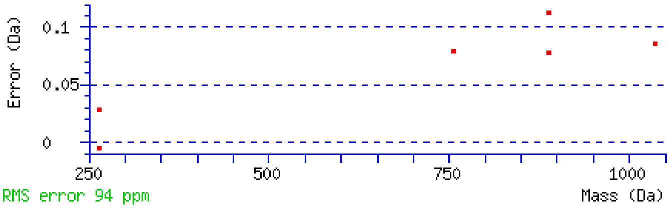
Match to Query 3748: 1148.540396 from(575.277474,2+) index(8546)
Title: Elution from: 77.117 to 77.117 scan no 11362 cid35.00 polarity:+
Data file D6h-2_2.mgf

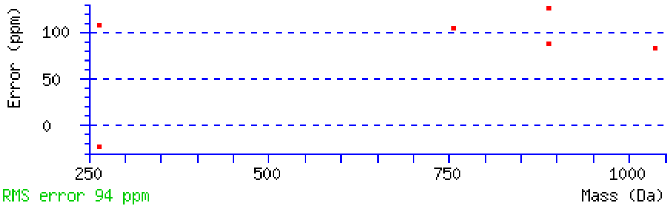
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1148.5414
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.023
Matches : 6/70 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							9
2	**263.1538**	132.0805			F	***1035.4676***	518.2374	1017.4440	509.2256	1017.4570	509.2321	8
3	393.1935	197.1004	375.1829	188.0951	E	***887.4021***	444.2047	869.3785	435.1929	869.3915	435.1994	7
4	555.2182	278.1127	537.2076	269.1074	C	757.3625	379.1849	739.3389	370.1731	739.3519	370.1796	6
5	685.2578	343.1325	667.2472	334.1273	E	595.3378	298.1725	577.3142	289.1607	577.3272	289.1672	5
6	773.2869	387.1471	755.2763	378.1418	S	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
7	**887.3680**	444.1876	869.3574	435.1823	I	377.2691	189.1382	359.2455	180.1264			3
8	1001.4491	501.2282	983.4385	492.2229	I	***263.1880***	132.0976	245.1644	123.0858			2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IFECESIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G53090.1

26.5	1148.5414	-0.0010	IFECESIIK
24.9	1148.5418	-0.0014	TRDMLKENK
21.3	1148.5418	-0.0014	IMKRQAEDK
5.7	1148.5418	-0.0014	IMQADKSLGR
5.7	1148.5392	0.0012	ISSGSGIMELK
5.7	1148.5414	-0.0010	LYEACLEIK
5.6	1148.5414	-0.0010	YLDLCVDLK
4.6	1148.5418	-0.0014	MTDGGKRELK

AT1G53210.1

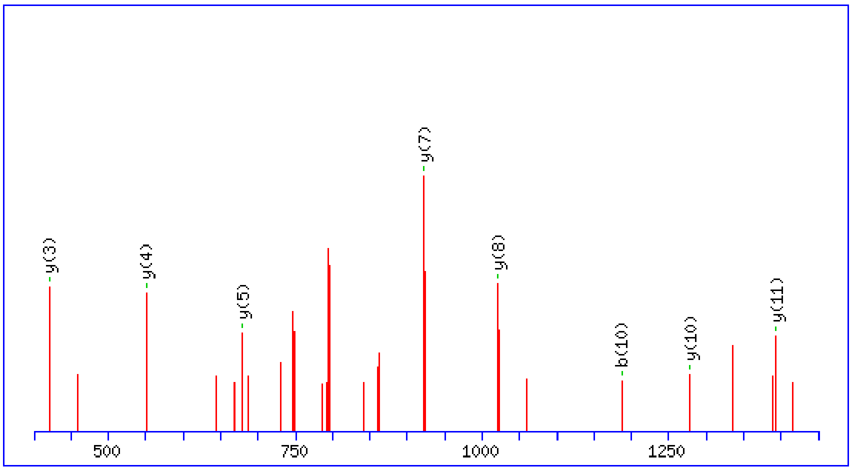
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLDEQVDQEEFVR**
Found in **AT1G53210.1** in **TAIR_Arabidopsis**, Symbols: | sodium/calcium exchanger family protein / calcium-binding EF hand family protein | chr1:19848458-19851201 FORWARD

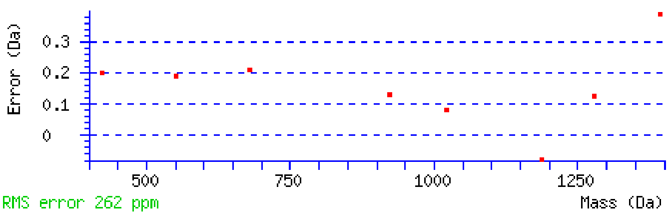
Match to Query 7064: 1606.747366 from(804.380959,2+) index(4941)
Title: Elution from: 43.286 to 43.286 scan no 6187 cid35.00 polarity:+
Data file D1d-3_3.mgf

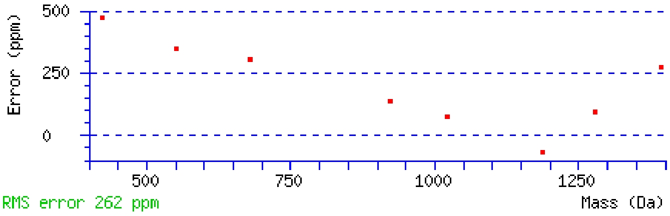
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1606.7475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 4.7e-006
Matches : 8/130 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**13**
2	215.1390	108.0731			197.1285	99.0679	**L**	1506.7071	753.8572	1489.6805	745.3439	1488.6965	744.8519	**12**
3	330.1660	165.5866			312.1554	156.5813	**D**	***1393.6230***	697.3151	1376.5965	688.8019	1375.6125	688.3099	**11**
4	459.2086	230.1079			441.1980	221.1026	**E**	***1278.5961***	639.8017	1261.5695	631.2884	1260.5855	630.7964	**10**
5	587.2671	294.1372	570.2406	285.6239	569.2566	285.1319	**Q**	1149.5535	575.2804	1132.5269	566.7671	1131.5429	566.2751	**9**
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	**V**	***1021.4949***	511.2511	1004.4684	502.7378	1003.4843	502.2458	**8**
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	**D**	***922.4265***	461.7169	905.3999	453.2036	904.4159	452.7116	**7**
8	929.4211	465.2142	912.3945	456.7009	911.4105	456.2089	**Q**	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	**6**
9	1058.4637	529.7355	1041.4371	521.2222	1040.4531	520.7302	**E**	***679.3410***	340.1741	662.3144	331.6608	661.3304	331.1688	**5**
10	1187.5063	594.2568	1170.4797	585.7435	1169.4957	585.2515	**E**	***550.2984***	275.6528	533.2718	267.1396	532.2878	266.6475	**4**
11	1334.5747	667.7910	1317.5481	659.2777	1316.5641	658.7857	**F**	***421.2558***	211.1315	404.2292	202.6183			**3**
12	1433.6431	717.3252	1416.6165	708.8119	1415.6325	708.3199	**V**	274.1874	137.5973	257.1608	129.0840			**2**
13							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TLDEQVDQEEFVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G53210.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.4	1606.7475	-0.0001	TLDEQVDQEEFVR
1.3	1606.7488	-0.0014	SNAFHGSINQNGFSK

AT1G53240.1

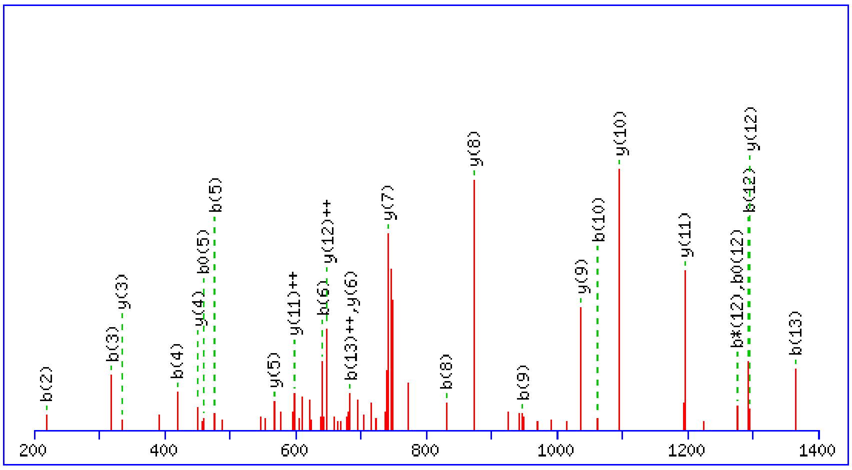
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEVVGYMGDDNLAK**
Found in **AT1G53240.1** in **TAIR_Arabidopsis**, Symbols: | malate dehydrogenase (NAD), mitochondrial | chr1:19858634-19860470 REVERSE

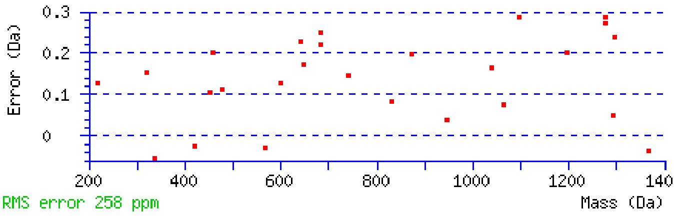
Match to Query 6503: 1512.632962 from(757.323757,2+) index(4418)
Title: Elution from: 42.228 to 42.228 scan no 5588 cid35.00 polarity:+
Data file D6h-2_1.mgf

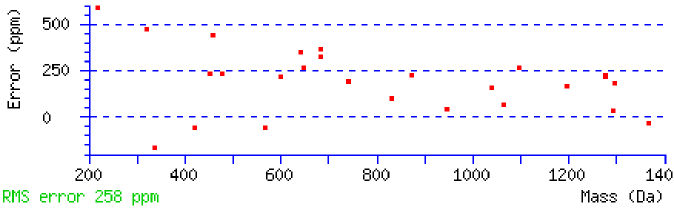
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1512.6342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 1.5e-008
Matches : 26/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	**S**							**14**
2	***219.0760***	110.0416			201.0654	101.0363	**E**	1425.6125	713.3099	1407.5889	704.2981	1407.6019	704.3046	**13**
3	***319.1414***	160.0743			301.1309	151.0691	**V**	***1295.5729***	648.2901	1277.5493	639.2783	1277.5623	639.2848	**12**
4	***419.2069***	210.1071			401.1963	201.1018	**V**	***1195.5074***	598.2573	1177.4838	589.2455	1177.4968	589.2521	**11**
5	***477.2254***	239.1163			459.2148	230.1110	**G**	***1095.4420***	548.2246	1077.4184	539.2128	1077.4314	539.2193	**10**
6	***641.2857***	321.1465			623.2752	312.1412	**Y**	***1037.4235***	519.2154	1019.3999	510.2036	1019.4129	510.2101	**9**
7	773.3232	387.1653			755.3127	378.1600	**M**	***873.3631***	437.1852	855.3395	428.1734	855.3525	428.1799	**8**
8	***831.3417***	416.1745			813.3312	407.1692	**G**	***741.3256***	371.1664	723.3020	362.1546	723.3150	362.1611	**7**
9	***947.3657***	474.1865			929.3552	465.1812	**D**	***683.3071***	342.1572	665.2835	333.1454	665.2965	333.1519	**6**
10	***1063.3897***	532.1985			1045.3791	523.1932	**D**	***567.2831***	284.1452	549.2595	275.1334	549.2725	275.1399	**5**
11	1179.4267	590.2170	1161.4031	581.2052	1161.4161	581.2117	**N**	***451.2591***	226.1332	433.2355	217.1214			**4**
12	***1293.5078***	647.2575	1275.4842	638.2457	1275.4972	638.2523	**L**	***335.2221***	168.1147	317.1985	159.1029			**3**
13	***1365.5419***	683.2746	1347.5184	674.2628	1347.5314	674.2693	**A**	221.1410	111.0741	203.1174	102.0624			**2**
14							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of SEVVGYMGDDNLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G53240.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.0	1512.6342	-0.0013	SEVVGYMGDDNLAK
11.8	1512.6347	-0.0017	GRVCNSSGEEASLK
10.8	1512.6286	0.0043	FADLDSESQQQTK
0.7	1512.6369	-0.0040	TDPTFREMENVR
0.2	1512.6349	-0.0019	AFQECRKQMHR

AT1G53310.1

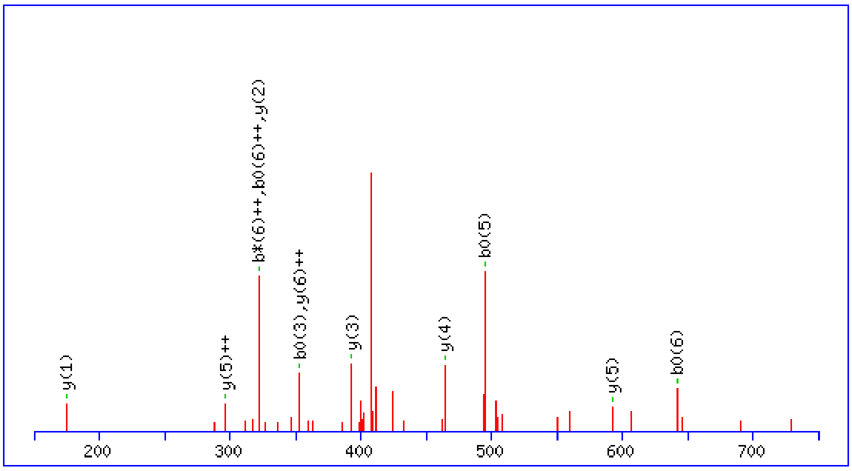
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIQAAFR**
Found in **AT1G53310.1** in **TAIR_Arabidopsis**, Symbols: ATPPC1 | ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); phosphoenolpyruvate carboxylase | chr1:19887929-19891738 REVERSE

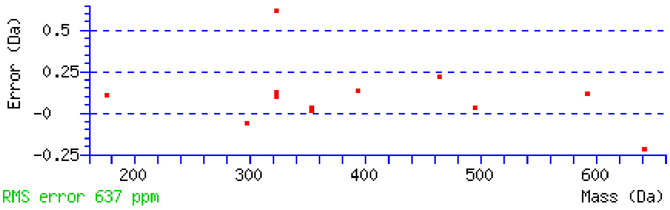
Match to Query 1187: 833.439070 from(417.726811,2+) index(1778)
Title: Elution from: 23.332 to 23.332 scan no 2369 cid35.00 polarity:+
Data file D6h-2_2.mgf

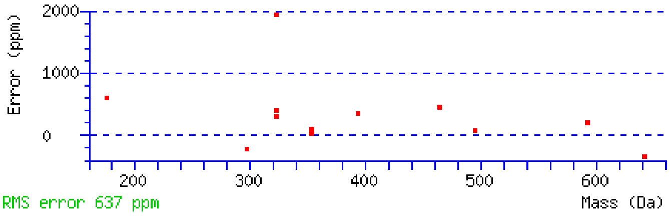
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 833.4395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0021
Matches : 12/56 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.0499	65.5286			112.0393	56.5233	E					7
2	243.1339	122.0706			225.1234	113.0653	I	705.4042	353.2058	688.3777	344.6925	6
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	Q	***592.3202***	296.6637	575.2936	288.1504	5
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	A	***464.2616***	232.6344	447.2350	224.1212	4
5	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	A	***393.2245***	197.1159	376.1979	188.6026	3
6	660.3352	330.6712	643.3086	322.1579	642.3246	321.6659	F	***322.1874***	161.5973	305.1608	153.0840	2
7							R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of EIQAAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.7	833.4395	-0.0005	EIQAAFR
7.4	833.4395	-0.0005	EVGNLFR

AT1G53310.1

7.4	833.4395	-0.0005	QSSPLFR
0.7	833.4395	-0.0005	QSIPYAR

AT1G53500.1

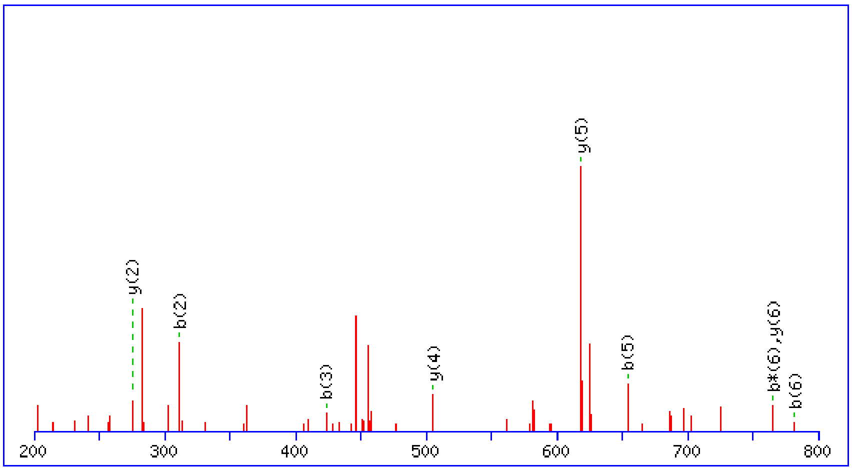
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFLDDQK**
Found in **AT1G53500.1** in **TAIR_Arabidopsis**, Symbols: RHM2, MUM4 | MUM4 (MUCILAGE-MODIFIED 4); catalytic | chr1:19970825-19972907 REVERSE

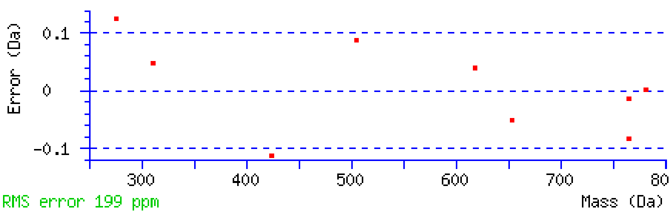
Match to Query 1810: 927.433742 from(464.724147,2+) index(2773)
Title: Elution from: 28.440 to 28.440 scan no 3484 cid35.00 polarity:+
Data file C7-3_3.mgf

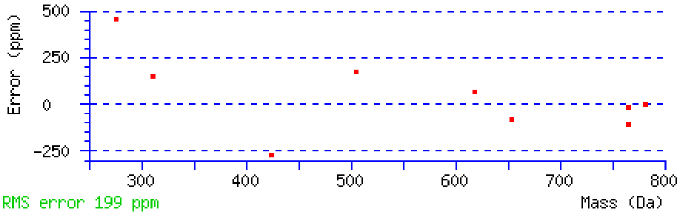
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 927.4338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.012
Matches : 9/52 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							7
2	***311.1390***	156.0731					F	***765.3777***	383.1925	748.3512	374.6792	747.3672	374.1872	6
3	***424.2231***	212.6152					L	***618.3093***	309.6583	601.2828	301.1450	600.2988	300.6530	5
4	539.2500	270.1287			521.2395	261.1234	D	***505.2253***	253.1163	488.1987	244.6030	487.2147	244.1110	4
5	***654.2770***	327.6421			636.2664	318.6368	D	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
6	***782.3355***	391.6714	765.3090	383.1581	764.3250	382.6661	Q	***275.1714***	138.0893	258.1448	129.5761			2
7							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YFLDDQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.8	927.4338	-0.0001	YFLDDQK
7.8	927.4338	-0.0000	FYIENDK

AT1G53500.1

7.3	927.4338	-0.0001	YFPGSTEK
2.9	927.4340	-0.0003	MVMRTMK

Mascot: http://www.matrixscience.com/

AT1G53850.1

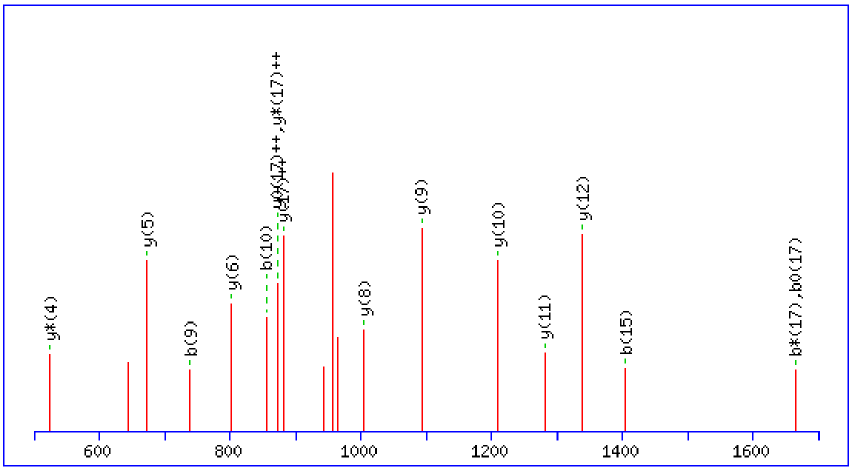
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIGSGSEGADSSLQEQFNK**
Found in **AT1G53850.1** in **TAIR_Arabidopsis**, Symbols: PAE1 | PAE1 (20S proteasome alpha subunit E1); peptidase | chr1:20107799-20109460 REVERSE

Match to Query 8810: 1946.811672 from(974.413112,2+) index(3662)
Title: Elution from: 37.643 to 37.643 scan no 4672 cid35.00 polarity:+
Data file D12h-2_2.mgf

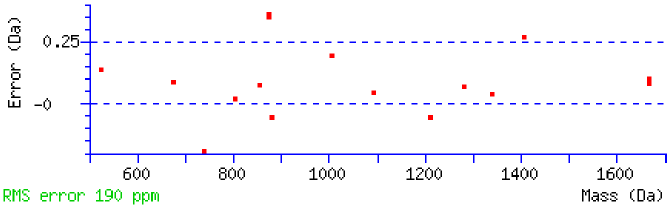
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

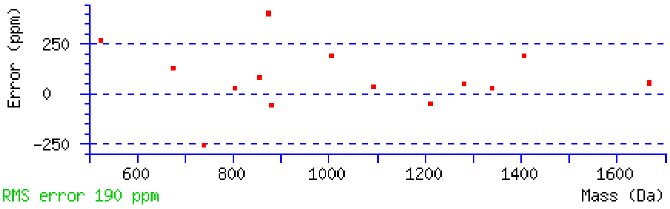


Monoisotopic mass of neutral peptide Mr(calc): 1946.8128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.6e-005
Matches : 16/176 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							19
2	187.1225	94.0649					I	1875.7859	938.3966	1857.7624	929.3848	1857.7754	929.3913	18
3	245.1410	123.0741					G	1761.7048	881.3561	1743.6813	872.3443	1743.6943	872.3508	17
4	333.1701	167.0887			315.1595	158.0834	S	1703.6863	852.3468	1685.6628	843.3350	1685.6758	843.3415	16
5	391.1886	196.0979			373.1780	187.0926	G	1615.6573	808.3323	1597.6337	799.3205	1597.6467	799.3270	15
6	479.2176	240.1125			461.2071	231.1072	S	1557.6388	779.3230	1539.6152	770.3112	1539.6282	770.3177	14
7	609.2573	305.1323			591.2467	296.1270	E	1469.6097	735.3085	1451.5861	726.2967	1451.5992	726.3032	13
8	667.2758	334.1415			649.2652	325.1362	G	***1339.5701***	670.2887	1321.5465	661.2769	1321.5595	661.2834	12
9	**739.3099**	370.1586			721.2994	361.1533	A	***1281.5516***	641.2794	1263.5280	632.2676	1263.5410	632.2742	11
10	**855.3339**	428.1706			837.3233	419.1653	D	***1209.5174***	605.2624	1191.4939	596.2506	1191.5069	596.2571	10
11	943.3630	472.1851			925.3524	463.1798	S	***1093.4935***	547.2504	1075.4699	538.2386	1075.4829	538.2451	9
12	1031.3920	516.1997			1013.3815	507.1944	S	***1005.4644***	503.2358	987.4408	494.2240	987.4538	494.2306	8
13	1145.4731	573.2402			1127.4626	564.2349	L	917.4353	459.2213	899.4118	450.2095	899.4248	450.2160	7
14	1275.5258	638.2665	1257.5022	629.2547	1257.5152	629.2612	Q	***803.3542***	402.1808	785.3307	393.1690	785.3437	393.1755	6
15	**1405.5654**	703.2863	1387.5418	694.2745	1387.5548	694.2811	E	***673.3016***	337.1544	655.2780	328.1426	655.2910	328.1492	5
16	1535.6180	768.3127	1517.5945	759.3009	1517.6075	759.3074	Q	543.2620	272.1346	525.2384	263.1228			4
17	1683.6835	842.3454	1665.6599	833.3336	1665.6729	833.3401	F	413.2093	207.1083	395.1857	198.0965			3
18	1799.7205	900.3639	1781.6969	891.3521	1781.7099	891.3586	N	265.1439	133.0756	247.1203	124.0638			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT1G53850.1





NCBI **BLAST** search of AIGSGSEGADSSLQEQFNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.6	1946.8128	-0.0011	AIGSGSEGADSSLQEQFNK
2.3	1946.8069	0.0047	YPPPPSQSEDVEHWTR
1.8	1946.8137	-0.0020	DRVPKMTSHFESMAEK
0.4	1946.8099	0.0018	GYPGYMYTDLATIYER

Mascot: http://www.matrixscience.com/

AT1G54010.1

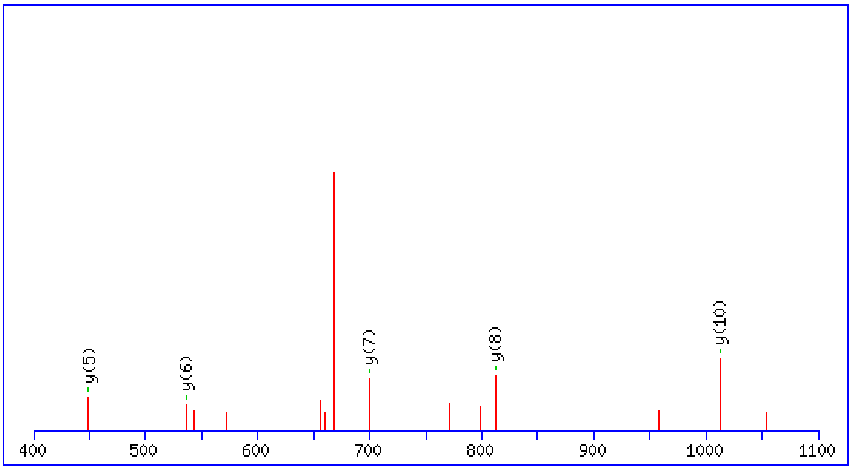
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDISLLYSSGASK**
Found in **AT1G54010.1** in **TAIR_Arabidopsis**, Symbols: | myrosinase-associated protein, putative | chr1:20162522-20164415 REVERSE

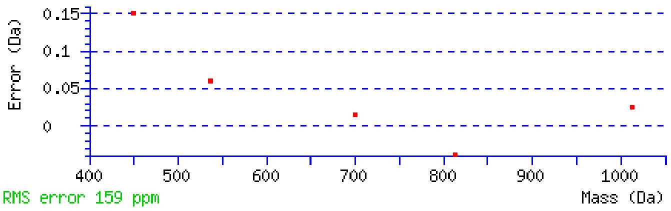
Match to Query 5054: 1353.677460 from(677.846006,2+) index(5026)
Title: Elution from: 45.049 to 45.049 scan no 6298 cid35.00 polarity:+
Data file 0-1_3.mgf

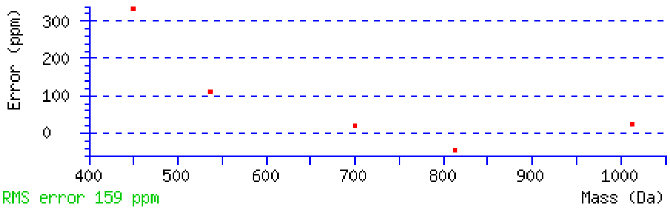
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1353.6776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0014
Matches : 5/140 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	D	1240.6420	620.8246	1223.6154	612.3113	1222.6314	611.8193	12
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	I	1125.6150	563.3111	1108.5885	554.7979	1107.6045	554.3059	11
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	S	***1012.5310***	506.7691	995.5044	498.2558	994.5204	497.7638	10
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	L	925.4989	463.2531	908.4724	454.7398	907.4884	454.2478	9
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	L	***812.4149***	406.7111	795.3883	398.1978	794.4043	397.7058	8
7	819.4247	410.2160	802.3981	401.7027	801.4141	401.2107	Y	***699.3308***	350.1690	682.3042	341.6558	681.3202	341.1638	7
8	906.4567	453.7320	889.4302	445.2187	888.4462	444.7267	S	***536.2675***	268.6374	519.2409	260.1241	518.2569	259.6321	6
9	993.4888	497.2480	976.4622	488.7347	975.4782	488.2427	S	***449.2354***	225.1214	432.2089	216.6081	431.2249	216.1161	5
10	1050.5102	525.7587	1033.4837	517.2455	1032.4997	516.7535	G	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	4
11	1121.5473	561.2773	1104.5208	552.7640	1103.5368	552.2720	A	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
12	1208.5794	604.7933	1191.5528	596.2800	1190.5688	595.7880	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NDISLLYSSGASK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G54010.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.3	1353.6776	-0.0001	NDISLLYSSGASK
21.8	1353.6776	-0.0001	SDINLLYSSGASK
2.0	1353.6785	-0.0010	NLVILNMCYSK

AT1G54270.1

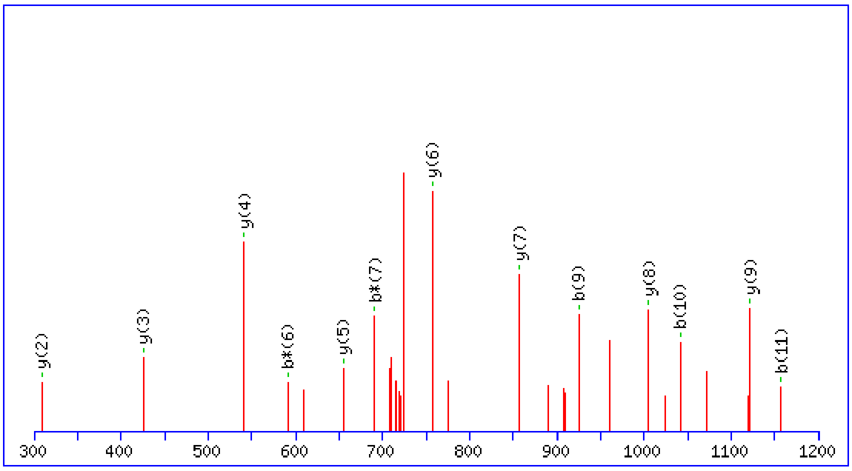
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVAINFVTLDDQR**
Found in **AT1G54270.1** in **TAIR_Arabidopsis**, Symbols: EIF4A-2 | EIF4A-2 (eukaryotic translation initiation factor 4A-2); ATP-dependent helicase | chr1:20264162-20265685 FORWARD

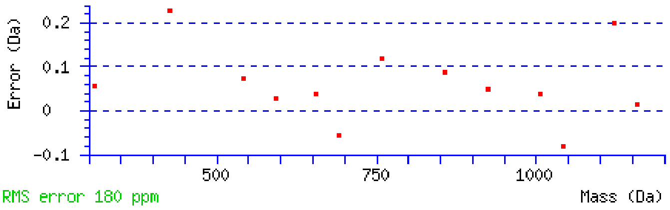
Match to Query 5693: 1464.697440 from(733.355996,2+) index(7180)
Title: Elution from: 63.956 to 63.956 scan no 9360 cid35.00 polarity:+
Data file C7-1_3.mgf

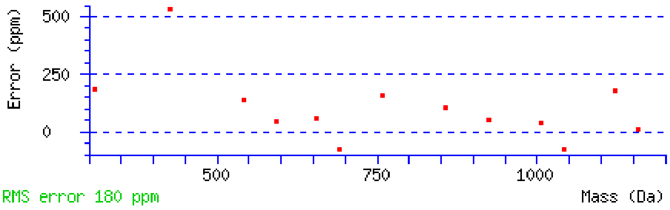
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1464.6933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 4.1e-007
Matches : 13/118 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							13
2	159.0912	80.0492					V	1407.6821	704.3447	1389.6585	695.3329	1389.6715	695.3394	12
3	231.1254	116.0663					A	1307.6166	654.3120	1289.5931	645.3002	1289.6061	645.3067	11
4	345.2065	173.1069					I	1235.5825	618.2949	1217.5589	609.2831	1217.5719	609.2896	10
5	461.2435	231.1254	443.2199	222.1136			N	***1121.5014***	561.2543	1103.4778	552.2425	1103.4908	552.2491	9
6	609.3089	305.1581	591.2853	296.1463			F	***1005.4644***	503.2358	987.4408	494.2240	987.4538	494.2306	8
7	709.3744	355.1908	691.3508	346.1790			V	***857.3990***	429.2031	839.3754	420.1913	839.3884	420.1978	7
8	811.4191	406.2132	793.3955	397.2014	793.4085	397.2079	T	***757.3335***	379.1704	739.3099	370.1586	739.3229	370.1651	6
9	**925.5002**	463.2537	907.4766	454.2419	907.4896	454.2484	L	***655.2888***	328.1480	637.2652	319.1362	637.2782	319.1428	5
10	**1041.5242**	521.2657	1023.5006	512.2539	1023.5136	512.2604	D	***541.2077***	271.1075	523.1841	262.0957	523.1971	262.1022	4
11	**1157.5481**	579.2777	1139.5246	570.2659	1139.5376	570.2724	D	***425.1837***	213.0955	407.1601	204.0837	407.1732	204.0902	3
12	1287.6008	644.3040	1269.5772	635.2922	1269.5902	635.2987	Q	***309.1597***	155.0835	291.1362	146.0717			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GVAINFVTLDDQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G54270.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.3	1464.6933	0.0042	GVAINFVTLDDQR
11.4	1464.6933	0.0041	YAANVIDQPGGSKK
11.0	1464.6989	-0.0015	ALPVMLLYNNER
4.4	1464.6940	0.0034	VEEVTETKMQLK
4.2	1464.6989	-0.0015	VLHSMDYSKLQK
1.4	1464.6989	-0.0015	SASMAKIPLPFDR
0.8	1464.6937	0.0037	RKNDAAVALSDQR

AT1G54350.1

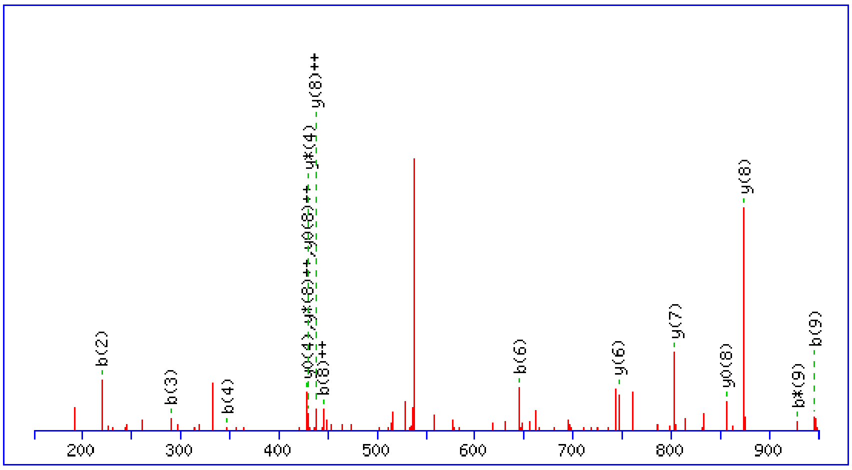
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMAGLWRSGK**
Found in **AT1G54350.1** in **TAIR_Arabidopsis**, Symbols: | ABC transporter family protein | chr1:20290584-20293912 FORWARD

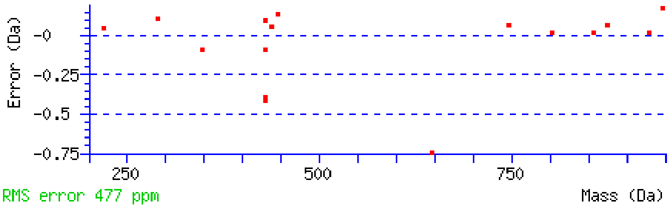
Match to Query 3556: 1091.556438 from(546.785495,2+) index(1904)
Title: Elution from: 22.542 to 22.542 scan no 2480 cid35.00 polarity:+
Data file D1d-3_1.mgf

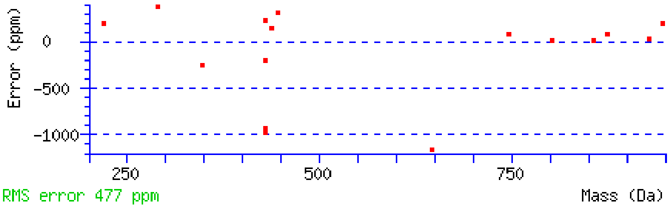
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1091.5546
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24  Expect: 0.016
Matches : 16/110 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							10
2	***219.0798***	110.0435					M	1021.5248	511.2660	1004.4982	502.7527	1003.5142	502.2607	9
3	***290.1169***	145.5621					A	**874.4894**	437.7483	857.4628	429.2350	856.4788	428.7430	8
4	***347.1384***	174.0728					G	**803.4522**	402.2298	786.4257	393.7165	785.4417	393.2245	7
5	460.2224	230.6149					L	**746.4308**	373.7190	729.4042	365.2058	728.4202	364.7137	6
6	***646.3017***	323.6545					W	633.3467	317.1770	616.3202	308.6637	615.3362	308.1717	5
7	802.4029	401.7051	785.3763	393.1918			R	447.2674	224.1373	430.2409	215.6241	429.2568	215.1321	4
8	889.4349	445.2211	872.4083	436.7078	871.4243	436.2158	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
9	***946.4563***	473.7318	929.4298	465.2185	928.4458	464.7265	G	204.1343	102.5708	187.1077	94.0575			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AMAGLWRSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G54350.1

Score	Mr(calc)	Delta	Sequence
24.4	1091.5546	0.0019	AMAGLWRSGK
11.5	1091.5532	0.0032	MAADSLDLLK
8.7	1091.5532	0.0032	LSLDEVMASK
4.5	1091.5546	0.0018	KWKGTCAGGK
3.1	1091.5532	0.0032	MAVEKELEK
2.7	1091.5579	-0.0015	AMRIMAIDR
0.0	1091.5546	0.0019	CKKTQYHK

AT1G54410.1

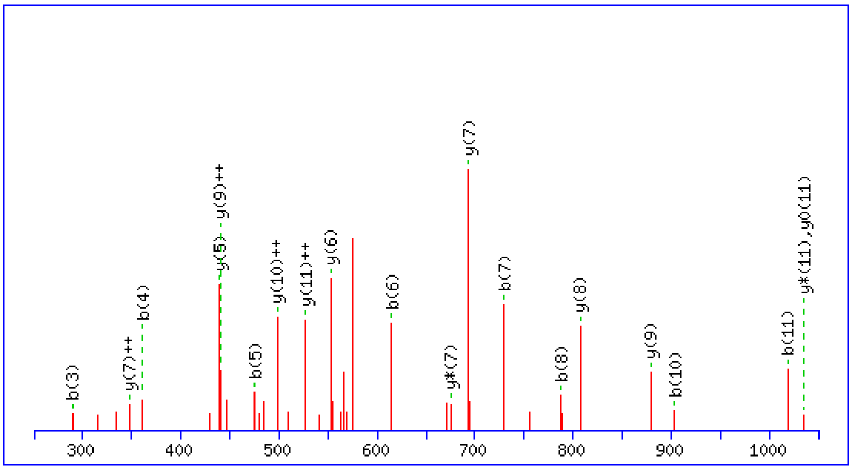
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGDALHIGGGNK**
Found in **AT1G54410.1** in **TAIR_Arabidopsis**, Symbols: | dehydrin family protein | chr1:20313972-20314268 REVERSE

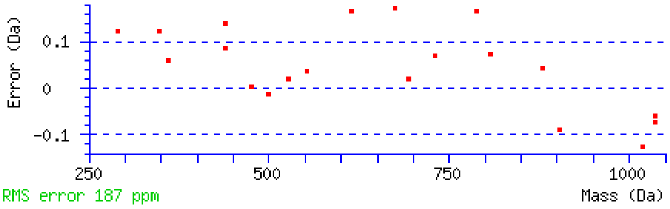
Match to Query 3410: 1166.561266 from(584.287909,2+) index(1829)
Title: Elution from: 23.084 to 23.084 scan no 2421 cid35.00 polarity:+
Data file D12h-2_3.mgf

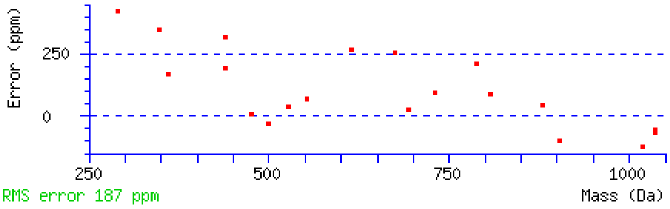
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1166.5620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.8e-007
Matches : 20/90 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					I							12
2	173.1069	87.0571					G	1053.4882	527.2477	1035.4646	518.2360	1035.4776	518.2425	11
3	***289.1309***	145.0691			271.1203	136.0638	D	995.4697	498.2385	977.4461	489.2267	977.4591	489.2332	10
4	***361.1650***	181.0861			343.1544	172.0809	A	**879.4457**	440.2265	861.4221	431.2147			9
5	***475.2461***	238.1267			457.2355	229.1214	L	**807.4116**	404.2094	789.3880	395.1976			8
6	***615.2961***	308.1517			597.2856	299.1464	H	**693.3305**	347.1689	675.3069	338.1571			7
7	***729.3772***	365.1922			711.3667	356.1870	I	**553.2805**	277.1439	535.2569	268.1321			6
8	***787.3957***	394.2015			769.3851	385.1962	G	**439.1994**	220.1033	421.1758	211.0915			5
9	845.4142	423.2107			827.4036	414.2055	G	381.1809	191.0941	363.1573	182.0823			4
10	***903.4327***	452.2200			885.4221	443.2147	G	323.1624	162.0848	305.1388	153.0730			3
11	***1019.4697***	510.2385	1001.4461	501.2267	1001.4591	501.2332	N	265.1439	133.0756	247.1203	124.0638			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IGDALHIGGGNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G54410.1

Score	Mr(calc)	Delta	Sequence
75.8	1166.5620	-0.0007	IGDALHIGGGNK
19.0	1166.5595	0.0017	FKRLHCYK
8.9	1166.5616	-0.0003	YAEAIEKGFK
3.3	1166.5580	0.0033	MSQSKVAMKK
2.9	1166.5620	-0.0008	RLYREAESK
2.5	1166.5595	0.0017	FAHRKYMAK
0.1	1166.5593	0.0019	IETEIGDLHK

AT1G54580.1

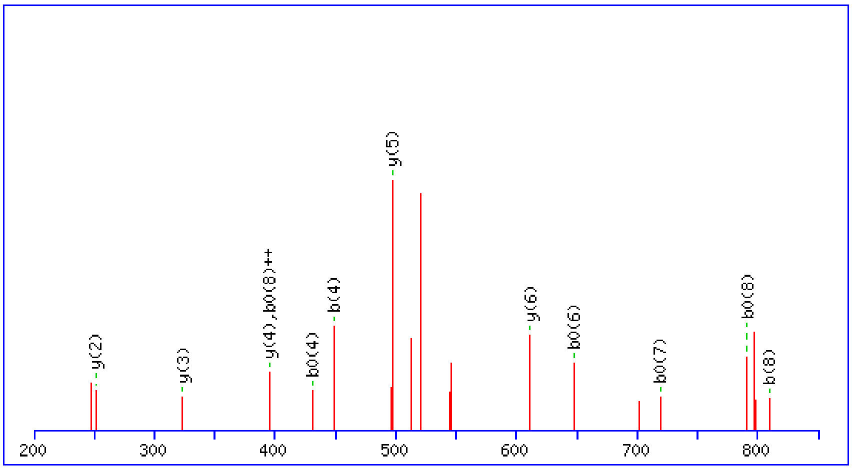
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EADEITAATK**
Found in **AT1G54580.1** in **TAIR_Arabidopsis**, Symbols: ACP2 | ACP2 (ACYL CARRIER PROTEIN 2) | chr1:20393239-20394437 FORWARD

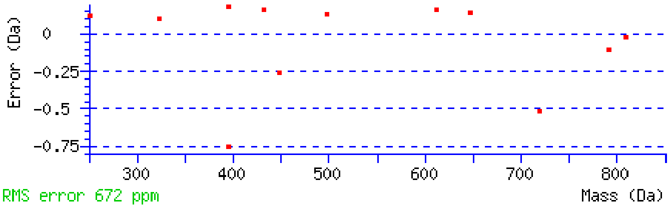
Match to Query 2934: 1058.474488 from(530.244520,2+) index(723)
Title: Elution from: 13.255 to 13.255 scan no 1078 cid35.00 polarity:+
Data file C7-1_2.mgf

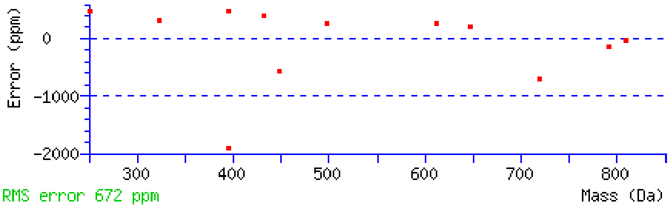
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1058.4758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00034
Matches : 12/88 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							10
2	203.0811	102.0442	185.0705	93.0389	A	929.4435	465.2254	911.4199	456.2136	911.4329	456.2201	9
3	319.1050	160.0562	301.0945	151.0509	D	857.4093	429.2083	839.3857	420.1965	839.3987	420.2030	8
4	**449.1447**	225.0760	431.1341	216.0707	E	741.3853	371.1963	723.3617	362.1845	723.3748	362.1910	7
5	563.2258	282.1165	545.2152	273.1112	I	***611.3457***	306.1765	593.3221	297.1647	593.3351	297.1712	6
6	665.2705	333.1389	647.2599	324.1336	T	***497.2646***	249.1359	479.2410	240.1241	479.2540	240.1307	5
7	737.3046	369.1559	719.2941	360.1507	A	***395.2199***	198.1136	377.1963	189.1018	377.2093	189.1083	4
8	**809.3388**	405.1730	791.3282	396.1677	A	***323.1857***	162.0965	305.1622	153.0847	305.1752	153.0912	3
9	911.3835	456.1954	893.3729	447.1901	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EADEITAATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G54580.1

40.6	1058.4758	-0.0013	EADEITAATK
2.9	1058.4758	-0.0013	QLDSIEESK
1.4	1058.4758	-0.0013	VEESLQSEK

AT1G54610.1

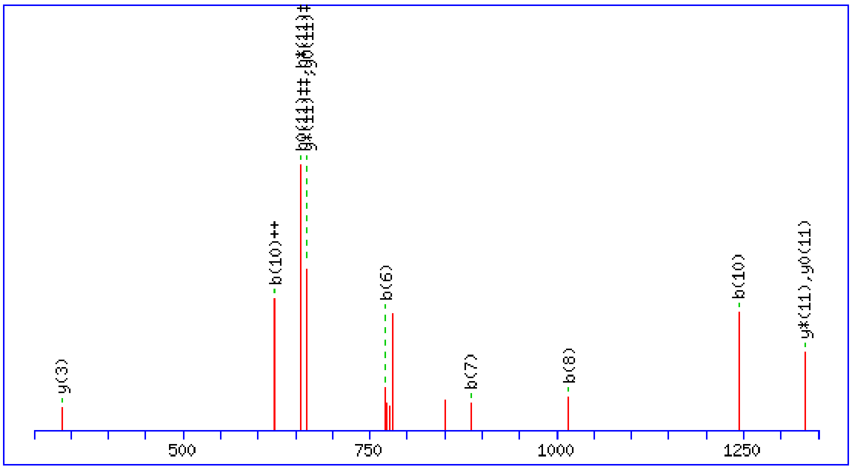
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVRFDNLEPESVK**
Found in **AT1G54610.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:20397629-20400569 REVERSE

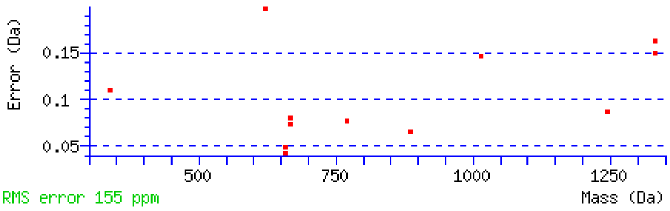
Match to Query 6701: 1578.778024 from(790.396288,2+) index(9886)
Title: Elution from: 93.648 to 93.648 scan no 14219 cid35.00 polarity:+
Data file D12h-3_3.mgf

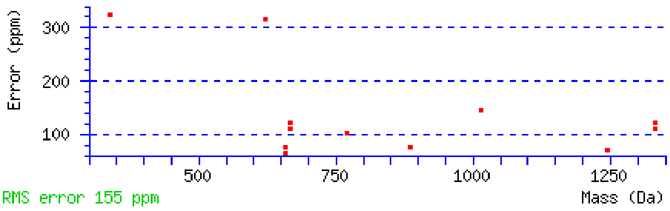
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1578.7744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0011
Matches : 14/132 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0963	66.0518	113.0727	57.0400			K							13
2	231.1618	116.0845	213.1382	107.0727			V	1449.6927	725.3500	1431.6691	716.3382	1431.6821	716.3447	12
3	391.2510	196.1291	373.2274	187.1174			R	1349.6272	675.3172	1331.6036	666.3055	1331.6166	666.3120	11
4	539.3165	270.1619	521.2929	261.1501			F	1189.5380	595.2726	1171.5144	586.2608	1171.5274	586.2673	10
5	655.3404	328.1739	637.3169	319.1621	637.3299	319.1686	D	1041.4725	521.2399	1023.4489	512.2281	1023.4619	512.2346	9
6	***771.3774***	386.1924	753.3538	377.1806	753.3669	377.1871	N	925.4485	463.2279	907.4250	454.2161	907.4380	454.2226	8
7	***885.4585***	443.2329	867.4349	434.2211	867.4480	434.2276	L	809.4115	405.2094	791.3880	396.1976	791.4010	396.2041	7
8	***1015.4982***	508.2527	997.4746	499.2409	997.4876	499.2474	E	695.3304	348.1689	677.3069	339.1571	677.3199	339.1636	6
9	1113.5480	557.2776	1095.5244	548.2658	1095.5374	548.2723	P	565.2908	283.1490	547.2672	274.1373	547.2802	274.1438	5
10	***1243.5876***	**622.2974**	1225.5640	613.2856	1225.5770	613.2921	E	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
11	***1331.6166***	**666.3120**	1313.5931	657.3002	1313.6061	657.3067	S	337.2014	169.1043	319.1778	160.0925	319.1908	160.0990	3
12	1431.6821	716.3447	1413.6585	707.3329	1413.6715	707.3394	V	249.1723	125.0898	231.1487	116.0780			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KVRFDNLEPESVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G54610.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.9	1578.7744	0.0036	KVRFDNLEPESVK
39.4	1578.7774	0.0007	VFSPEEISAMILTK
19.7	1578.7778	0.0002	AQAMVDAAIKAASSVK
8.4	1578.7827	-0.0047	ARQKCVPAAPFSVK
3.8	1578.7825	-0.0045	DLTKTVESIKDANK

Mascot: http://www.matrixscience.com/

AT1G54780.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETYVVDDAGVLSR**
Found in **AT1G54780.1** in **TAIR_Arabidopsis**, Symbols: | thylakoid lumen 18.3 kDa protein | chr1:20443200-20444620 FORWARD

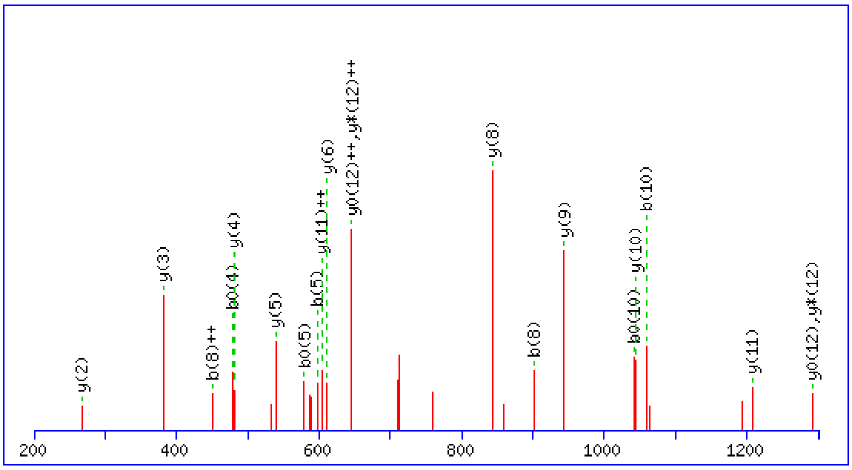
Match to Query 5950: 1438.650488 from(720.332520,2+) index(5294)
Title: Elution from: 47.273 to 47.273 scan no 6606 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

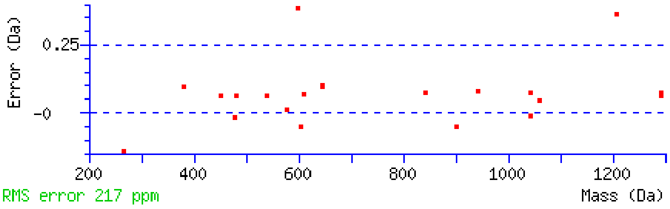
Label all possible matches ○ Label matches used for scoring ●

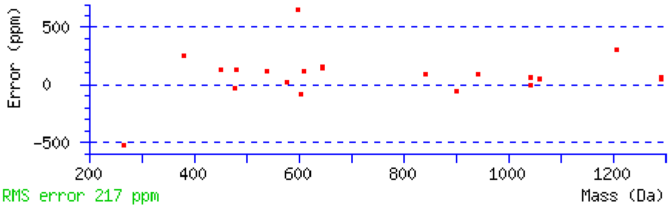
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1438.6516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 8.8e-007
Matches : 21/118 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	**E**							**13**
2	233.0916	117.0494	215.0811	108.0442	**T**	1309.6193	655.3133	1291.5957	646.3015	1291.6087	646.3080	**12**
3	397.1520	199.0796	379.1414	190.0743	**Y**	***1207.5746***	604.2909	1189.5510	595.2791	1189.5640	595.2856	**11**
4	497.2174	249.1124	479.2069	240.1071	**V**	***1043.5142***	522.2607	1025.4906	513.2489	1025.5036	513.2555	**10**
5	**597.2829**	299.1451	579.2723	290.1398	**V**	***943.4488***	472.2280	925.4252	463.2162	925.4382	463.2227	**9**
6	713.3069	357.1571	695.2963	348.1518	**D**	***843.3833***	422.1953	825.3597	413.1835	825.3727	413.1900	**8**
7	829.3308	415.1691	811.3203	406.1638	**D**	727.3593	364.1833	709.3357	355.1715	709.3488	355.1780	**7**
8	**901.3650**	451.1861	883.3544	442.1808	**A**	***611.3354***	306.1713	593.3118	297.1595	593.3248	297.1660	**6**
9	959.3835	480.1954	941.3729	471.1901	**G**	***539.3012***	270.1542	521.2776	261.1424	521.2906	261.1490	**5**
10	**1059.4489**	530.2281	1041.4384	521.2228	**V**	***481.2827***	241.1450	463.2591	232.1332	463.2721	232.1397	**4**
11	1173.5300	587.2687	1155.5195	578.2634	**L**	***381.2173***	191.1123	363.1937	182.1005	363.2067	182.1070	**3**
12	1261.5591	631.2832	1243.5485	622.2779	**S**	***267.1362***	134.0717	249.1126	125.0599	249.1256	125.0664	**2**
13					**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of ETYVVDDAGVLSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G54780.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.9	1438.6516	-0.0011	ETYVVDDAGVLSR
12.9	1438.6469	0.0036	MLPGSSYTPVAQR
11.4	1438.6494	0.0011	TTSSASSQTPEAKK
8.4	1438.6529	-0.0024	RGCMLNAAVAGATK
3.6	1438.6516	-0.0011	VEKSSGNDDFVVK
2.2	1438.6494	0.0011	GSVETASSTLLSDR
1.8	1438.6538	-0.0033	LADFGLAVDFGGDK
1.6	1438.6521	-0.0016	KSRESSPSTPTSR
1.5	1438.6473	0.0032	RGLDMAREAVER
1.3	1438.6543	-0.0038	TSWNTRSPSEKK

AT1G54820.1

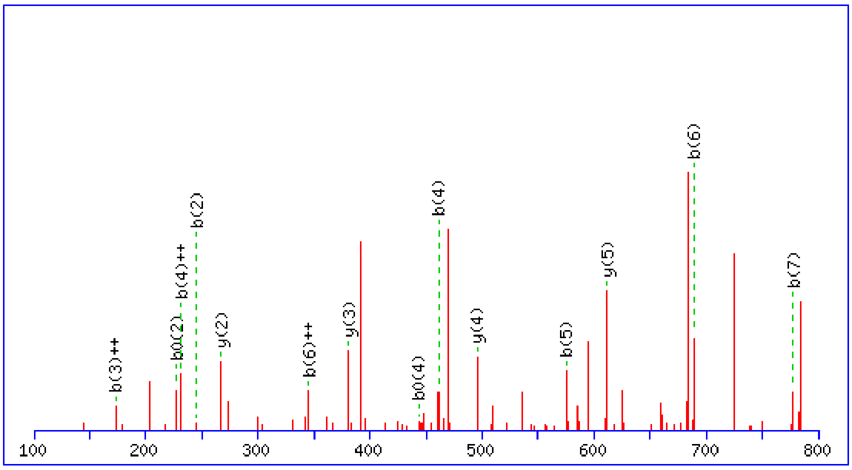
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEVDLLSR**
Found in **AT1G54820.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:20451037-20454428 FORWARD

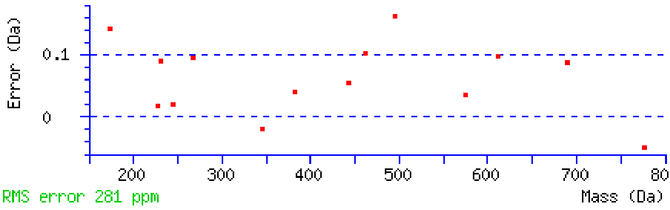
Match to Query 2000: 954.499008 from(478.256780,2+) index(5025)
Title: Elution from: 45.149 to 45.149 scan no 6338 cid35.00 polarity:+
Data file D6h-2_3.mgf

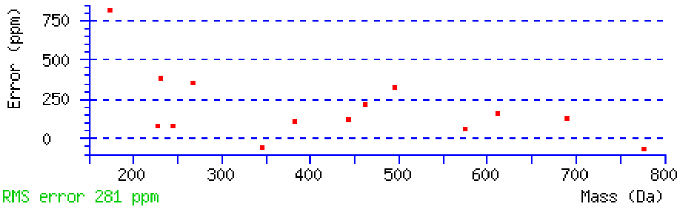
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 954.5012
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0067
Matches : 15/66 fragment ions using 35 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478			L							8
2	***245.1280***	123.0676	227.1174	114.0624	E	841.4274	421.2173	823.4038	412.2056	823.4168	412.2121	7
3	***345.1935***	**173.1004**	327.1829	164.0951	V	711.3878	356.1975	693.3642	347.1857	693.3772	347.1922	6
4	***461.2174***	**231.1124**	443.2069	222.1071	D	**611.3223**	306.1648	593.2987	297.1530	593.3118	297.1595	5
5	***575.2985***	288.1529	557.2880	279.1476	L	**495.2984**	248.1528	477.2748	239.1410	477.2878	239.1475	4
6	***689.3796***	**345.1935**	671.3691	336.1882	L	**381.2173**	191.1123	363.1937	182.1005	363.2067	182.1070	3
7	***777.4087***	389.2080	759.3981	380.2027	S	**267.1362**	134.0717	249.1126	125.0599	249.1256	125.0664	2
8					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LEVDLLSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.1	954.5012	-0.0022	LEVDLLSR
25.6	954.5012	-0.0022	LDILDISR

AT1G54820.1

16.6	954.5012	-0.0022	ELVDLSLR
13.4	954.5012	-0.0022	VLELDLSR
9.3	954.5012	-0.0022	DIVENVKK
9.2	954.4965	0.0025	MPLLISNR
6.2	954.5012	-0.0022	LTIIEEAR
5.5	954.5012	-0.0022	IEIVDLSR
5.3	954.5012	-0.0022	LGLGTDLQK
1.7	954.5012	-0.0022	INLEKEAK

AT1G55090.1

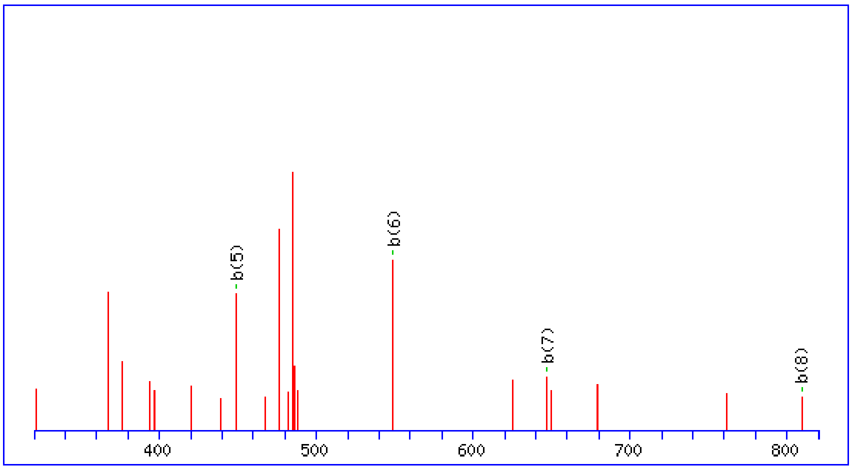
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVAVPCR**
Found in **AT1G55090.1** in **TAIR_Arabidopsis**, Symbols: | carbon-nitrogen hydrolase family protein | chr1:20558524-20561855 FORWARD

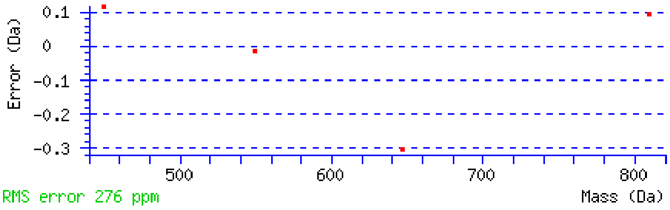
Match to Query 2533: 986.463584 from(494.239068,2+) index(665)
Title: Elution from: 11.519 to 11.519 scan no 950 cid35.00 polarity:+
Data file D1d-3_2.mgf

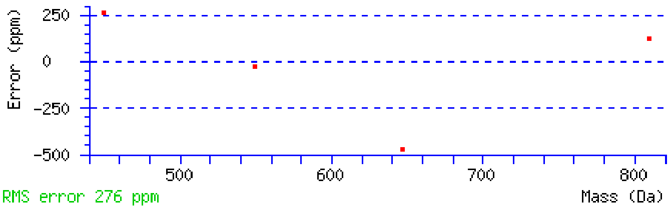
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 320 to 820 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 986.4630
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.047
Matches : 4/66 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							9
2	189.1018	95.0545	171.0912	86.0492	S	887.4048	444.2060	869.3812	435.1942	869.3942	435.2007	8
3	277.1309	139.0691	259.1203	130.0638	S	799.3757	400.1915	781.3521	391.1797	781.3652	391.1862	7
4	377.1963	189.1018	359.1857	180.0965	V	711.3467	356.1770	693.3231	347.1652			6
5	***449.2304***	225.1189	431.2199	216.1136	A	611.2812	306.1442	593.2576	297.1324			5
6	***549.2959***	275.1516	531.2853	266.1463	V	539.2471	270.1272	521.2235	261.1154			4
7	***647.3457***	324.1765	629.3351	315.1712	P	439.1816	220.0944	421.1580	211.0827			3
8	***809.3704***	405.1888	791.3599	396.1836	C	341.1318	171.0695	323.1082	162.0578			2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VSSVAVPCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.1	986.4630	0.0006	VSSVAVPCR

AT1G55090.1

15.1	986.4622	0.0014	GRTYYRR
9.4	986.4629	0.0006	MQELGLQR
8.5	986.4630	0.0006	MSQPNLLR
1.8	986.4652	-0.0016	LMPWERK
1.6	986.4623	0.0013	GFNPPARGR
1.6	986.4656	-0.0020	AARLPGACR
1.4	986.4623	0.0013	NRLFHER
1.2	986.4622	0.0014	LHEFGGRR
1.1	986.4630	0.0006	LQSNMPLR

AT1G55480.1

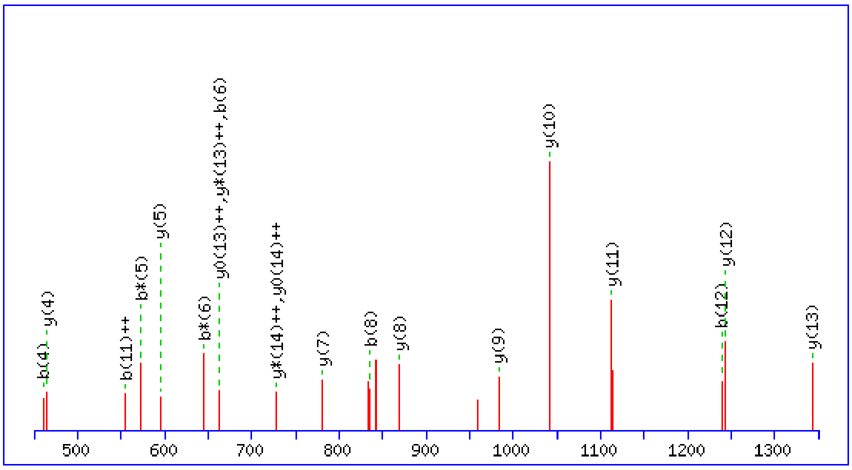
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNQVQAGLSALEEALK**
Found in **AT1G55480.1** in **TAIR_Arabidopsis**, Symbols: | binding / protein binding | chr1:20717488-20719017 FORWARD

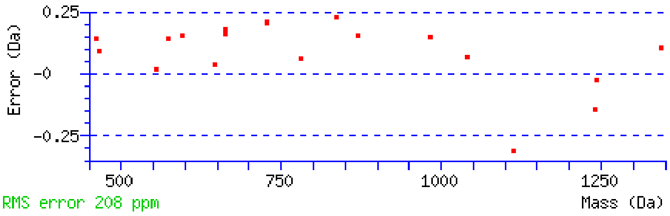
Match to Query 7614: 1702.859596 from(852.437074,2+) index(10118)
Title: Elution from: 101.475 to 101.475 scan no 14783 cid35.00 polarity:+
Data file D1d-1-2.mgf

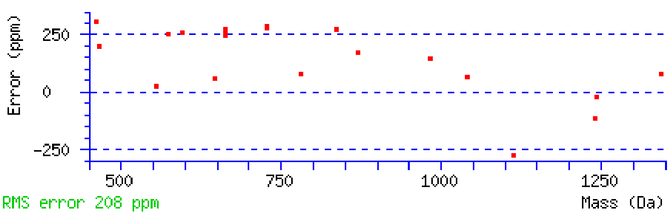
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1702.8610
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 1.4e-008
Matches : 20/156 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							16
2	231.1254	116.0663	213.1018	107.0545			N	1589.7872	795.3972	1571.7636	786.3854	1571.7766	786.3919	15
3	361.1780	181.0926	343.1544	172.0809			Q	1473.7502	737.3787	1455.7266	728.3669	1455.7396	728.3734	14
4	**461.2435**	231.1254	443.2199	222.1136			V	***1343.6975***	672.3524	1325.6739	663.3406	1325.6870	663.3471	13
5	591.2961	296.1517	573.2725	287.1399			Q	***1243.6321***	622.3197	1225.6085	613.3079	1225.6215	613.3144	12
6	**663.3303**	332.1688	645.3067	323.1570			A	***1113.5794***	557.2934	1095.5559	548.2816	1095.5689	548.2881	11
7	721.3488	361.1780	703.3252	352.1662			G	***1041.5453***	521.2763	1023.5217	512.2645	1023.5347	512.2710	10
8	**835.4299**	418.2186	817.4063	409.2068			L	***983.5268***	492.2670	965.5032	483.2552	965.5162	483.2617	9
9	923.4589	462.2331	905.4353	453.2213	905.4484	453.2278	S	***869.4457***	435.2265	851.4221	426.2147	851.4351	426.2212	8
10	995.4931	498.2502	977.4695	489.2384	977.4825	489.2449	A	***781.4166***	391.2120	763.3930	382.2002	763.4061	382.2067	7
11	1109.5742	555.2907	1091.5506	546.2789	1091.5636	546.2854	L	709.3825	355.1949	691.3589	346.1831	691.3719	346.1896	6
12	**1239.6138**	620.3105	1221.5902	611.2987	1221.6032	611.3053	E	***595.3014***	298.1543	577.2778	289.1425	577.2908	289.1490	5
13	1369.6534	685.3304	1351.6298	676.3186	1351.6429	676.3251	E	***465.2618***	233.1345	447.2382	224.1227	447.2512	224.1292	4
14	1441.6876	721.3474	1423.6640	712.3356	1423.6770	712.3421	A	335.2221	168.1147	317.1985	159.1029			3
15	1555.7687	778.3880	1537.7451	769.3762	1537.7581	769.3827	L	263.1880	132.0976	245.1644	123.0858			2
16							K	149.1069	75.0571	131.0833	66.0453			1





AT1G55480.1

NCBI **BLAST** search of LNQVQAGLSALEEALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
85.6	1702.8610	-0.0014	LNQVQAGLSALEEALK
10.1	1702.8551	0.0045	SLPYELRLLHWEK
5.2	1702.8563	0.0033	MTKLRYLAVSLSER
2.7	1702.8610	-0.0014	NLVELSQPLLVSESR

AT1G55490.1

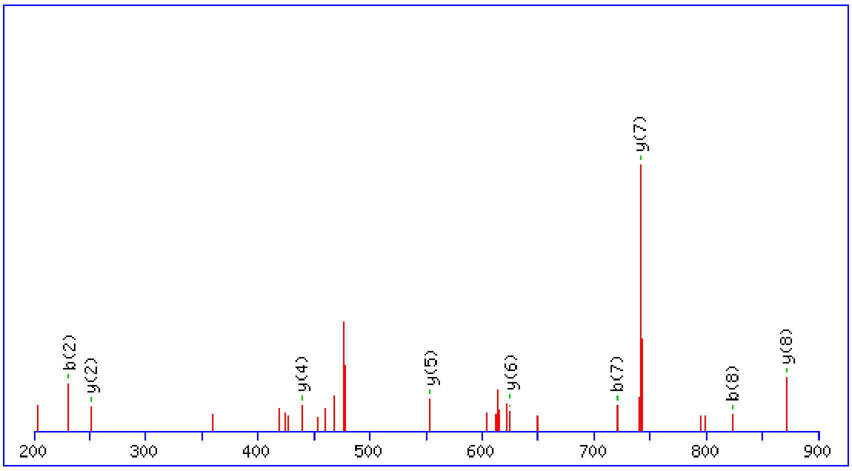
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEDALNATK**
Found in **AT1G55490.1** in **TAIR_Arabidopsis**, Symbols: LEN1, CPN60B | CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding | chr1:20719383-20722339 REVERSE

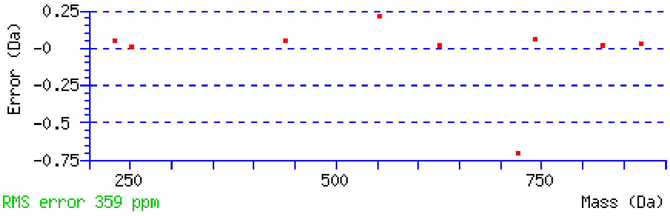
Match to Query 2265: 970.459096 from(486.236824,2+) index(676)
Title: Elution from: 11.218 to 11.218 scan no 932 cid35.00 polarity:+
Data file D1d-3_3.mgf

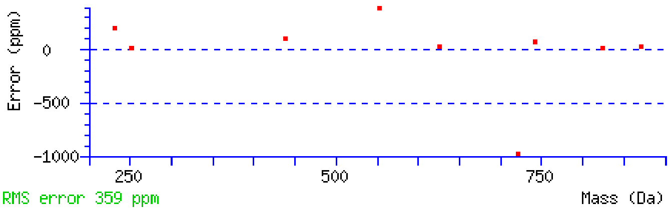
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 970.4597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00031
Matches : 9/82 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400					V							9
2	**231.1124**	116.0598			213.1018	107.0545	E	***871.4016***	436.2044	853.3780	427.1926	853.3910	427.1991	8
3	347.1363	174.0718			329.1258	165.0665	D	***741.3620***	371.1846	723.3384	362.1728	723.3514	362.1793	7
4	419.1705	210.0889			401.1599	201.0836	A	***625.3380***	313.1726	607.3144	304.1608	607.3274	304.1673	6
5	533.2516	267.1294			515.2410	258.1241	L	***553.3038***	277.1556	535.2802	268.1438	535.2933	268.1503	5
6	649.2886	325.1479	631.2650	316.1361	631.2780	316.1426	N	***439.2227***	220.1150	421.1991	211.1032	421.2122	211.1097	4
7	**721.3227**	361.1650	703.2991	352.1532	703.3122	352.1597	A	323.1857	162.0965	305.1622	153.0847	305.1752	153.0912	3
8	**823.3674**	412.1874	805.3439	403.1756	805.3569	403.1821	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VEDALNATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G55490.1

44.5	970.4597	-0.0007	VEDALNATK
10.8	970.4620	-0.0029	LDWETIGK
10.5	970.4597	-0.0007	EVLQENTK
10.2	970.4598	-0.0007	NLNETLEK
9.4	970.4598	-0.0007	INVSPSTDK
8.4	970.4606	-0.0015	GGLQPMKVM
6.8	970.4597	-0.0007	EVSVELER
6.1	970.4597	-0.0007	DLDDINKK
6.1	970.4597	-0.0007	GAVNTEIEK
3.9	970.4597	-0.0007	IETAIEER

AT1G55670.1

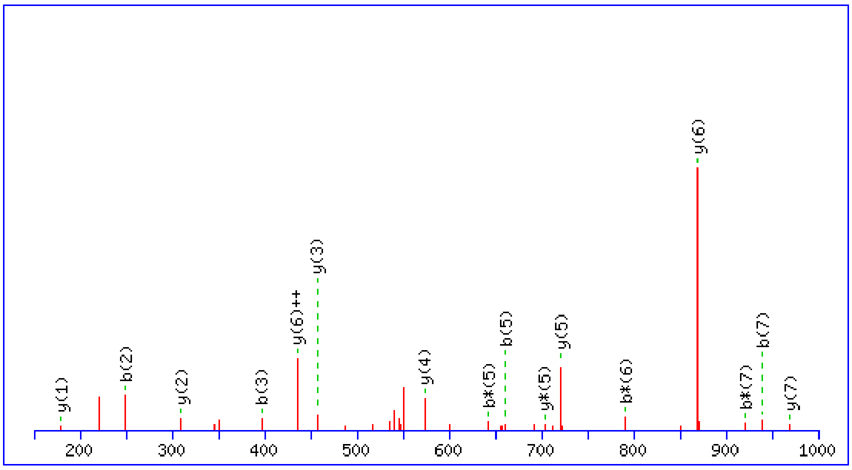
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVFFNFQR**
Found in **AT1G55670.1** in **TAIR_Arabidopsis**, Symbols: PSAG | PSAG | chr1:20806540-20807022 REVERSE

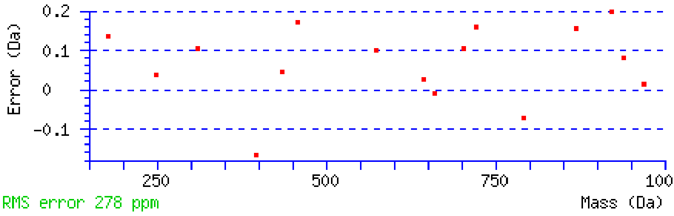
Match to Query 3411: 1116.517438 from(559.265995,2+) index(8844)
Title: Elution from: 78.019 to 78.019 scan no 11763 cid35.00 polarity:+
Data file D6h-3_2.mgf

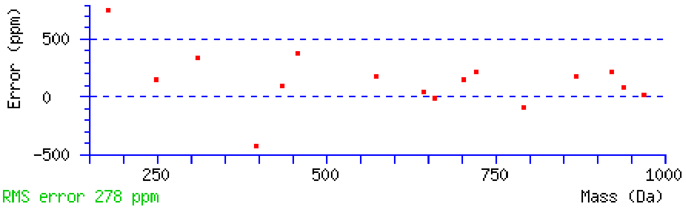
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5167
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.8e-005
Matches : 16/48 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	149.0727	75.0400			F					8
2	**249.1382**	125.0727			V	***969.4585***	485.2329	951.4349	476.2211	7
3	**397.2036**	199.1054			F	***869.3931***	435.2002	851.3695	426.1884	6
4	545.2691	273.1382			F	***721.3276***	361.1675	703.3040	352.1557	5
5	**661.3061**	331.1567	643.2825	322.1449	N	***573.2622***	287.1347	555.2386	278.1229	4
6	809.3715	405.1894	791.3479	396.1776	F	***457.2252***	229.1162	439.2016	220.1044	3
7	**939.4242**	470.2157	921.4006	461.2039	Q	***309.1597***	155.0835	291.1362	146.0717	2
8					R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of FVFFNFQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.2	1116.5167	0.0008	FVFFNFQR
11.7	1116.5149	0.0025	RSRYGYAAR

6.6	1116.5203	-0.0029	VVVDDGKSER
6.6	1116.5203	-0.0029	QDEKIVSER
5.8	1116.5203	-0.0029	EAAAEKISER
5.8	1116.5203	-0.0029	EIEAAKASER
5.6	1116.5177	-0.0002	EAITEESTVK
5.0	1116.5153	0.0021	RAGGARHSQR
4.2	1116.5156	0.0018	LIIANAGDCR
4.1	1116.5156	0.0018	DIPKKACDR

AT1G55860.1

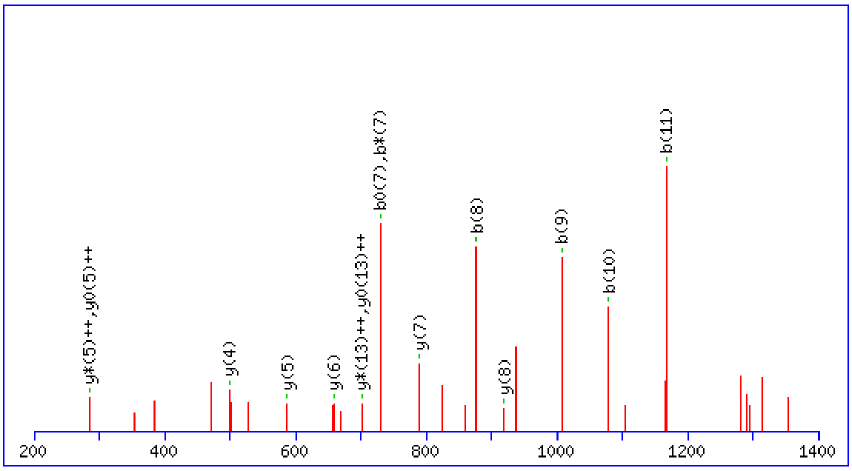
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LENKPVGEEASSETR**
Found in **AT1G55860.1** in **TAIR_Arabidopsis**, Symbols: UPL1 | UPL1 (UBIQUITIN-PROTEIN LIGASE 1); ubiquitin-protein ligase | chr1:20883566-20899059 REVERSE

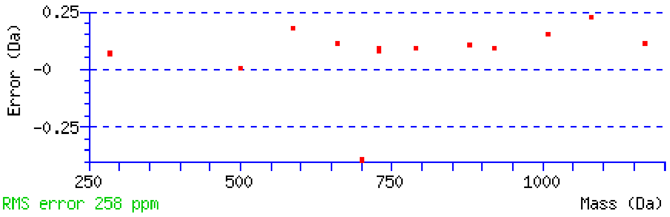
Match to Query 8164: 1664.735180 from(833.374866,2+) index(9175)
Title: Elution from: 81.049 to 81.049 scan no 12246 cid35.00 polarity:+
Data file D1d-3_1.mgf

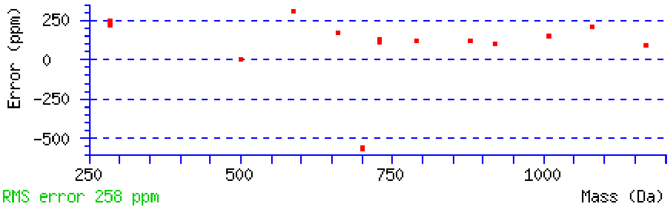
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1664.7362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.021
Matches : 15/160 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							15
2	245.1280	123.0676			227.1174	114.0624	E	1551.6624	776.3348	1533.6388	767.3230	1533.6518	767.3295	14
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	N	1421.6227	711.3150	1403.5992	702.3032	1403.6122	702.3097	13
4	491.2540	246.1307	473.2304	237.1189	473.2435	237.1254	K	1305.5857	653.2965	1287.5622	644.2847	1287.5752	644.2912	12
5	589.3038	295.1556	571.2802	286.1438	571.2933	286.1503	P	1175.4967	588.2520	1157.4731	579.2402	1157.4861	579.2467	11
6	689.3693	345.1883	671.3457	336.1765	671.3587	336.1830	V	1077.4469	539.2271	1059.4233	530.2153	1059.4363	530.2218	10
7	747.3878	374.1975	729.3642	365.1857	729.3772	365.1922	G	977.3815	489.1944	959.3579	480.1826	959.3709	480.1891	9
8	**877.4274**	439.2173	859.4038	430.2056	859.4168	430.2121	E	***919.3630***	460.1851	901.3394	451.1733	901.3524	451.1798	8
9	**1007.4670**	504.2372	989.4435	495.2254	989.4565	495.2319	E	***789.3233***	395.1653	771.2998	386.1535	771.3128	386.1600	7
10	**1079.5012**	540.2542	1061.4776	531.2424	1061.4906	531.2489	A	***659.2837***	330.1455	641.2601	321.1337	641.2731	321.1402	6
11	**1167.5302**	584.2688	1149.5067	575.2570	1149.5197	575.2635	S	***587.2496***	294.1284	569.2260	285.1166	569.2390	285.1231	5
12	1255.5593	628.2833	1237.5357	619.2715	1237.5487	619.2780	S	***499.2205***	250.1139	481.1969	241.1021	481.2099	241.1086	4
13	1385.5989	693.3031	1367.5754	684.2913	1367.5884	684.2978	E	411.1914	206.0994	393.1678	197.0876	393.1809	197.0941	3
14	1487.6437	744.3255	1469.6201	735.3137	1469.6331	735.3202	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
15							R	179.1071	90.0572	161.0835	81.0454			1





AT1G55860.1

NCBI **BLAST** search of LENKPVGEEASSETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.4	1664.7362	-0.0010	LENKPVGEEASSETR
9.6	1664.7357	-0.0006	ETTYVETSTNITYK

Mascot: http://www.matrixscience.com/

AT1G56070.1

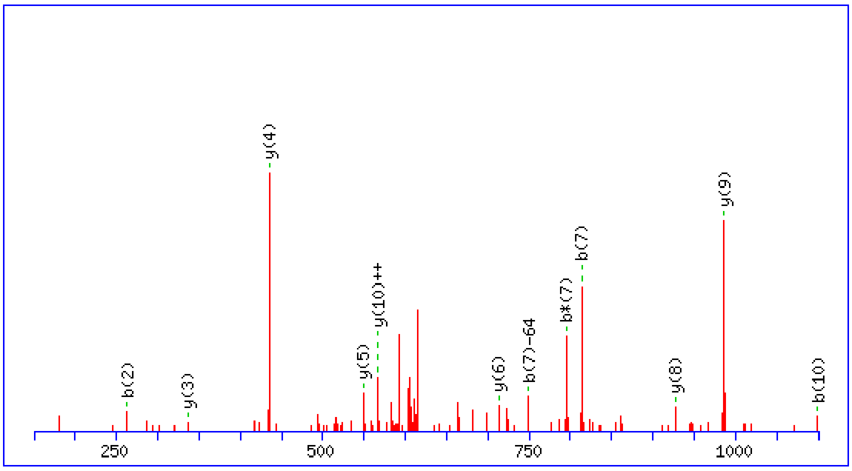
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMGPNYIPGEK**
Found in **AT1G56070.1** in **TAIR_Arabidopsis**, Symbols: AT1G56075.1, LOS1 | LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation factor, nucleic acid binding | chr1:20971910-20974742 REVERSE

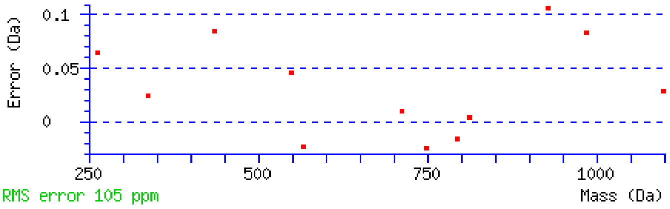
Match to Query 3944: 1246.566092 from(624.290322,2+) index(2893)
Title: Elution from: 30.032 to 30.032 scan no 3662 cid35.00 polarity:+
Data file D1d-2_3.mgf

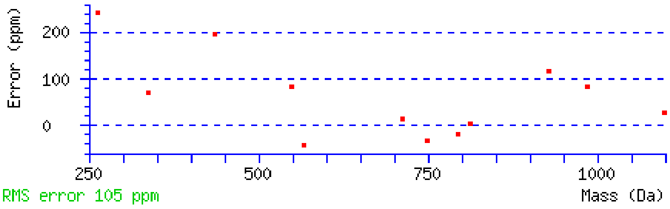
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.5678
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 44 **Expect:** 0.00029
Matches : 12/130 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							11
2	**263.1208**	132.0640					M	1133.4940	567.2506	1115.4704	558.2388	1115.4834	558.2454	10
3	321.1393	161.0733					G	***985.4616***	493.2344	967.4380	484.2226	967.4510	484.2291	9
4	419.1891	210.0982					P	***927.4431***	464.2252	909.4195	455.2134	909.4325	455.2199	8
5	535.2261	268.1167	517.2025	259.1049			N	829.3933	415.2003	811.3697	406.1885	811.3827	406.1950	7
6	699.2865	350.1469	681.2629	341.1351			Y	***713.3563***	357.1818	695.3327	348.1700	695.3457	348.1765	6
7	**813.3676**	407.1874	795.3440	398.1756			I	***549.2959***	275.1516	531.2723	266.1398	531.2853	266.1463	5
8	911.4174	456.2123	893.3938	447.2005			P	***435.2148***	218.1110	417.1912	209.0992	417.2042	209.1058	4
9	969.4359	485.2216	951.4123	476.2098			G	***337.1650***	169.0861	319.1414	160.0743	319.1544	160.0809	3
10	**1099.4755**	550.2414	1081.4519	541.2296	1081.4649	541.2361	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IMGPNYIPGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G56070.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.2	1246.5678	-0.0017	IMGPNYIPGEK
19.0	1246.5656	0.0005	MKNDAIDGELK
7.4	1246.5678	-0.0017	ELFTAEMHLK
7.1	1246.5626	0.0035	GRVNNLEDANK
6.9	1246.5626	0.0035	RRLDPEGSGDK
5.9	1246.5656	0.0005	LTENQQMELK
4.0	1246.5656	0.0005	LMPQDKDKDK
2.5	1246.5656	0.0005	SMVDQGILGDAK
2.3	1246.5649	0.0012	FSAITNLHGDR
2.2	1246.5678	-0.0017	LMEETAHYIK

AT1G56110.1

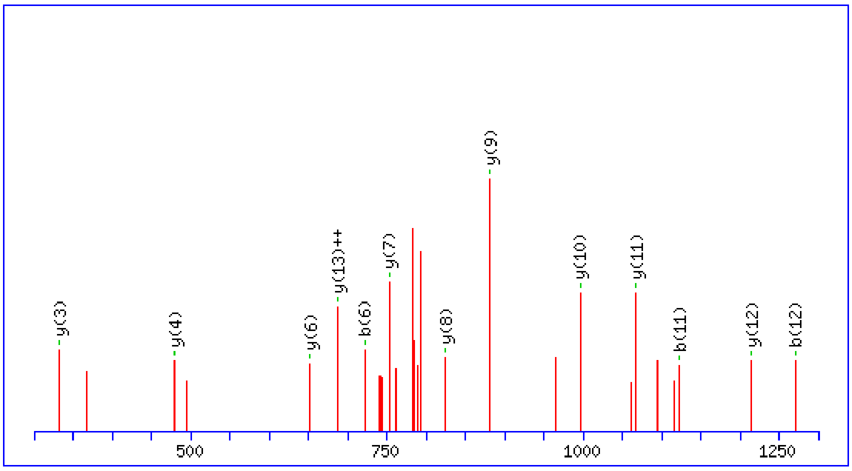
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDCFADGATTAFGEK**
Found in **AT1G56110.1** in **TAIR_Arabidopsis**, Symbols: NOP56 | NOP56 (ARABIDOPSIS HOMOLOG OF NUCLEOLAR PROTEIN NOP56) | chr1:20988209-20990558 REVERSE

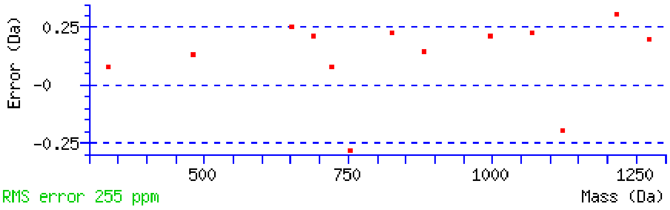
Match to Query 7456: 1601.702640 from(801.858596,2+) index(5797)
Title: Elution from: 51.789 to 51.789 scan no 7310 cid35.00 polarity:+
Data file D12h-3_1.mgf

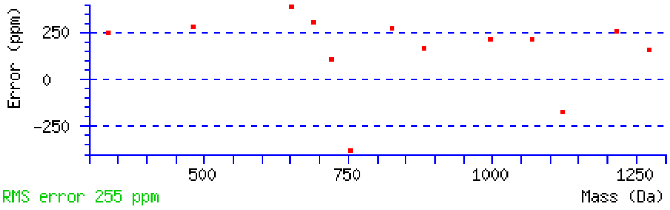
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1601.7032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.9e-007
Matches : 13/136 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							15
2	229.1183	115.0628	211.1077	106.0575	D	1489.6264	745.3168	1472.5998	736.8036	1471.6158	736.3115	14
3	389.1489	195.0781	371.1384	186.0728	C	1374.5994	687.8034	1357.5729	679.2901	1356.5889	678.7981	13
4	536.2173	268.6123	518.2068	259.6070	F	***1214.5688***	607.7880	1197.5422	599.2748	1196.5582	598.7828	12
5	607.2545	304.1309	589.2439	295.1256	A	***1067.5004***	534.2538	1050.4738	525.7406	1049.4898	525.2485	11
6	**722.2814**	361.6443	704.2708	352.6391	D	***996.4633***	498.7353	979.4367	490.2220	978.4527	489.7300	10
7	779.3029	390.1551	761.2923	381.1498	G	***881.4363***	441.2218	864.4098	432.7085	863.4258	432.2165	9
8	850.3400	425.6736	832.3294	416.6683	A	***824.4149***	412.7111	807.3883	404.1978	806.4043	403.7058	8
9	951.3877	476.1975	933.3771	467.1922	T	***753.3777***	377.1925	736.3512	368.6792	735.3672	368.1872	7
10	1052.4353	526.7213	1034.4248	517.7160	T	***652.3301***	326.6687	635.3035	318.1554	634.3195	317.6634	6
11	**1123.4725**	562.2399	1105.4619	553.2346	A	551.2824	276.1448	534.2558	267.6316	533.2718	267.1396	5
12	**1270.5409**	635.7741	1252.5303	626.7688	F	***480.2453***	240.6263	463.2187	232.1130	462.2347	231.6210	4
13	1327.5623	664.2848	1309.5518	655.2795	G	***333.1769***	167.0921	316.1503	158.5788	315.1663	158.0868	3
14	1456.6049	728.8061	1438.5944	719.8008	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15					K	147.1128	74.0600	130.0863	65.5468			1





AT1G56110.1

NCBI **BLAST** search of IDCFADGATTAFGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.2	1601.7032	-0.0005	IDCFADGATTAFGEK

Mascot: http://www.matrixscience.com/

AT1G56190.1

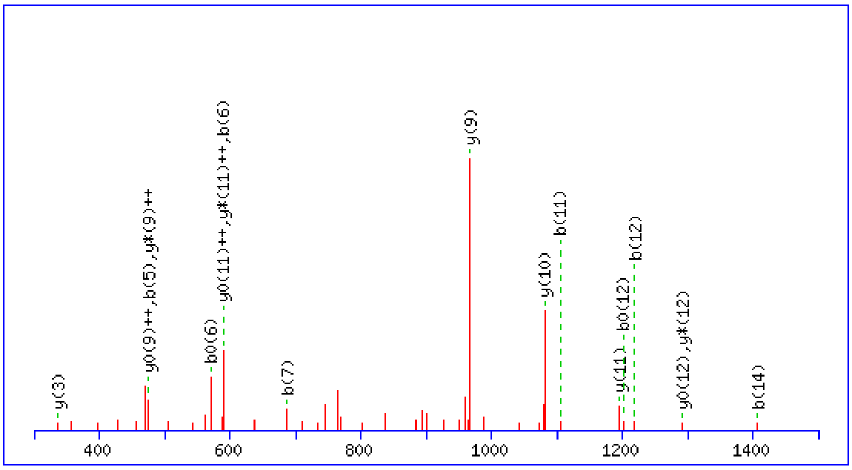
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVSLLLPTDVVIADK**
Found in **AT1G56190.1** in **TAIR_Arabidopsis**, Symbols: | phosphoglycerate kinase, putative | chr1:21032068-21034119 FORWARD

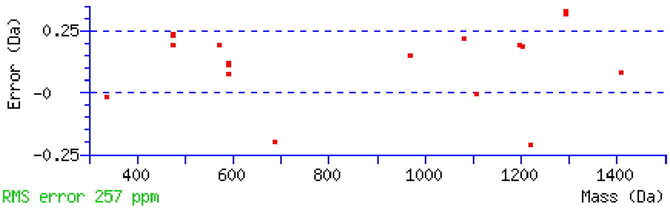
Match to Query 7198: 1554.844218 from(778.429385,2+) index(9680)
Title: Elution from: 86.060 to 86.060 scan no 12973 cid35.00 polarity:+
Data file D12h-1_1.mgf

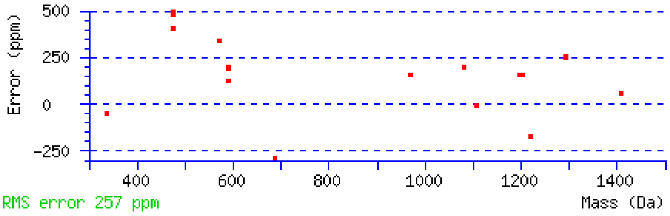
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1554.8445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.00066
Matches : 19/134 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			G							15
2	159.0912	80.0492			V	1497.8333	749.4203	1479.8097	740.4085	1479.8227	740.4150	14
3	247.1203	124.0638	229.1097	115.0585	S	1397.7678	699.3876	1379.7443	690.3758	1379.7573	690.3823	13
4	361.2014	181.1043	343.1908	172.0990	L	1309.7388	655.3730	1291.7152	646.3612	1291.7282	646.3677	12
5	***475.2825***	238.1449	457.2719	229.1396	L	**1195.6577**	598.3325	1177.6341	589.3207	1177.6471	589.3272	11
6	***589.3636***	295.1854	571.3530	286.1801	L	**1081.5766**	541.2919	1063.5530	532.2801	1063.5660	532.2866	10
7	***687.4134***	344.2103	669.4028	335.2050	P	**967.4955**	484.2514	949.4719	475.2396	949.4849	475.2461	9
8	789.4581	395.2327	771.4475	386.2274	T	869.4457	435.2265	851.4221	426.2147	851.4351	426.2212	8
9	905.4821	453.2447	887.4715	444.2394	D	767.4010	384.2041	749.3774	375.1923	749.3904	375.1988	7
10	1005.5475	503.2774	987.5370	494.2721	V	651.3770	326.1921	633.3534	317.1803	633.3664	317.1869	6
11	***1105.6130***	553.3101	1087.6024	544.3048	V	551.3115	276.1594	533.2880	267.1476	533.3010	267.1541	5
12	***1219.6941***	610.3507	1201.6835	601.3454	I	451.2461	226.1267	433.2225	217.1149	433.2355	217.1214	4
13	***1291.7282***	646.3677	1273.7177	637.3625	A	**337.1650**	169.0861	319.1414	160.0743	319.1544	160.0809	3
14	***1407.7522***	704.3797	1389.7416	695.3745	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
15					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GVSLLLPTDVVIADK

AT1G56190.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.0	1554.8445	-0.0003	GVSLLLPTDVVIADK
12.8	1554.8398	0.0044	MPLEEILSRLPLK
4.2	1554.8445	-0.0003	EVLLKLPSSESPLK
0.4	1554.8445	-0.0003	VAALLDVSPITDVVK

AT1G56290.1

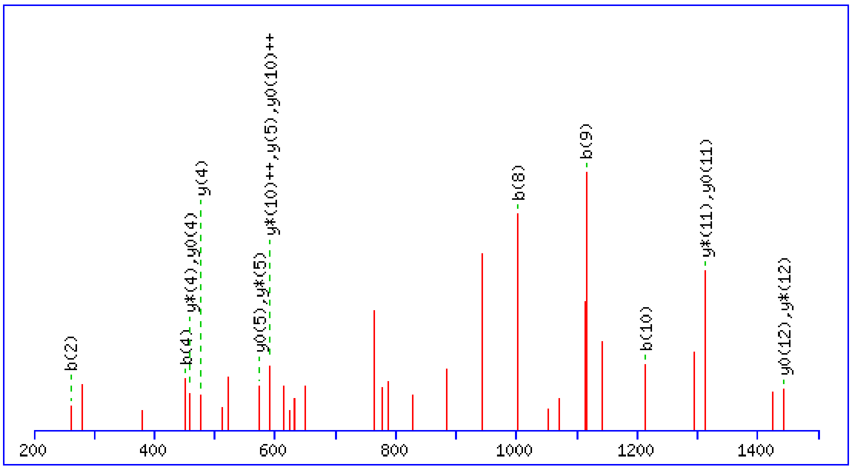
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KKMGLDWMLPPTR**
Found in **AT1G56290.1** in **TAIR_Arabidopsis**, Symbols: | CwfJ-like family protein | chr1:21079604-21082273 FORWARD

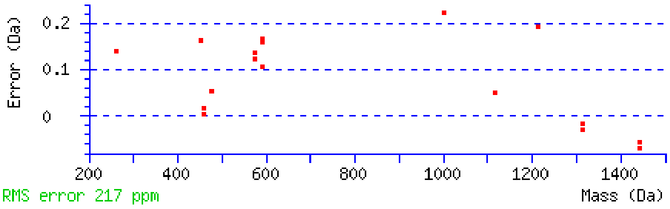
Match to Query 6704: 1590.771816 from(796.393184,2+) index(4939)
Title: Elution from: 47.617 to 47.617 scan no 6349 cid35.00 polarity:+
Data file D1d-2_2.mgf

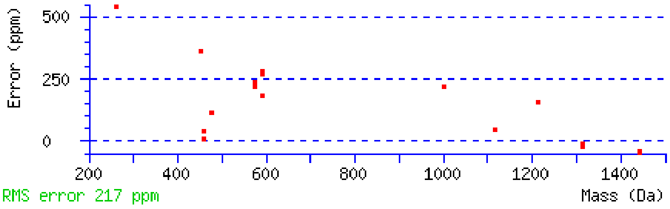
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1590.7753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.014
Matches : 17/132 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0963	66.0518	113.0727	57.0400			K							13
2	***261.1853***	131.0963	243.1618	122.0845			K	1461.6935	731.3504	1443.6700	722.3386	1443.6830	722.3451	12
3	393.2229	197.1151	375.1993	188.1033			M	1331.6045	666.3059	1313.5809	657.2941	1313.5939	657.3006	11
4	***451.2414***	226.1243	433.2178	217.1125			G	1199.5670	600.2871	1181.5434	591.2753	1181.5564	591.2818	10
5	565.3225	283.1649	547.2989	274.1531			L	1141.5485	571.2779	1123.5249	562.2661	1123.5379	562.2726	9
6	681.3464	341.1769	663.3229	332.1651	663.3359	332.1716	D	1027.4674	514.2373	1009.4438	505.2255	1009.4568	505.2320	8
7	869.4198	435.2135	851.3962	426.2018	851.4093	426.2083	W	911.4434	456.2253	893.4198	447.2135	893.4328	447.2201	7
8	***1001.4573***	501.2323	983.4338	492.2205	983.4468	492.2270	M	723.3700	362.1886	705.3464	353.1769	705.3595	353.1834	6
9	***1115.5384***	558.2729	1097.5149	549.2611	1097.5279	549.2676	L	**591.3325**	296.1699	573.3089	287.1581	573.3219	287.1646	5
10	***1213.5882***	607.2978	1195.5647	598.2860	1195.5777	598.2925	P	**477.2514**	239.1293	459.2278	230.1175	459.2408	230.1241	4
11	1311.6380	656.3227	1293.6145	647.3109	1293.6275	647.3174	P	379.2016	190.1044	361.1780	181.0926	361.1910	181.0992	3
12	1413.6828	707.3450	1395.6592	698.3332	1395.6722	698.3397	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KKMGLDWMLPPTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G56290.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.8	1590.7753	-0.0035	KKMGLDWMLPPTR
11.4	1590.7760	-0.0042	IPMDLVMCNILLK
9.6	1590.7722	-0.0004	LTKGATSSDDHALKK
8.5	1590.7722	-0.0004	LEQTNQIDLQNKK
8.5	1590.7674	0.0044	LSPGRVSAVMGPSGAGK
6.8	1590.7695	0.0023	EIISSIDNSLQLDK
6.2	1590.7693	0.0026	ISMAYIEWYKKK
6.0	1590.7740	-0.0022	YPPYPLNTIELEK
1.0	1590.7751	-0.0033	CIEDDLTKEVLLK
0.4	1590.7690	0.0028	HSRYHLTHYVKK

AT1G56340.1

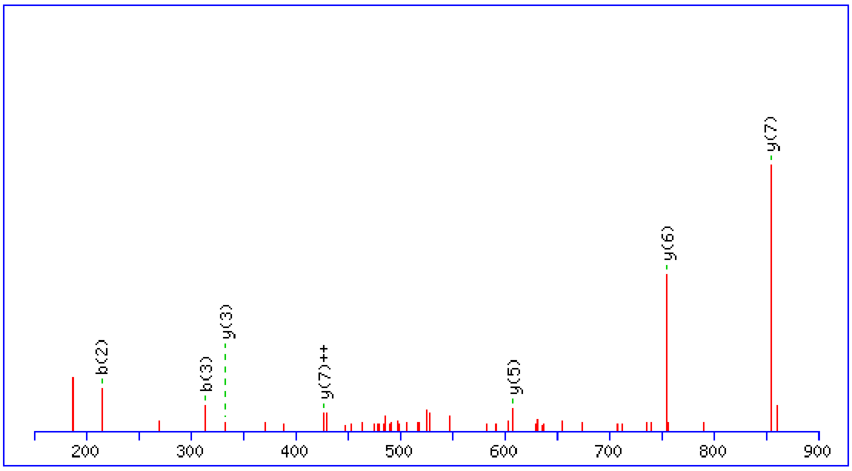
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLVFQFSVK**
Found in **AT1G56340.1** in **TAIR_Arabidopsis**, Symbols: CRT1 | CRT1 (CALRETICULIN 1); calcium ion binding | chr1:21093724-21096295 REVERSE

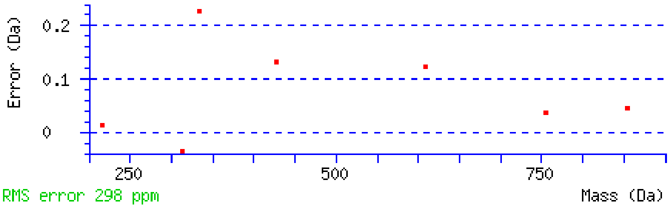
Match to Query 3046: 1067.601940 from(534.808246,2+) index(7221)
Title: Elution from: 64.513 to 64.513 scan no 9480 cid35.00 polarity:+
Data file D6h-1_3.mgf

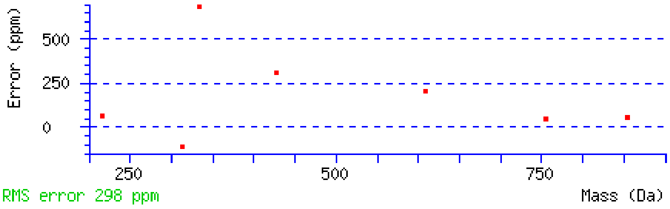
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1067.6015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.022
Matches : 7/84 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							9
2	**215.1390**	108.0731			197.1285	99.0679	L	967.5611	484.2842	950.5346	475.7709	949.5506	475.2789	8
3	**314.2074**	157.6074			296.1969	148.6021	V	***854.4771***	427.7422	837.4505	419.2289	836.4665	418.7369	7
4	461.2758	231.1416			443.2653	222.1363	F	***755.4087***	378.2080	738.3821	369.6947	737.3981	369.2027	6
5	589.3344	295.1709	572.3079	286.6576	571.3239	286.1656	Q	***608.3402***	304.6738	591.3137	296.1605	590.3297	295.6685	5
6	736.4028	368.7051	719.3763	360.1918	718.3923	359.6998	F	480.2817	240.6445	463.2551	232.1312	462.2711	231.6392	4
7	823.4349	412.2211	806.4083	403.7078	805.4243	403.2158	S	***333.2132***	167.1103	316.1867	158.5970	315.2027	158.1050	3
8	922.5033	461.7553	905.4767	453.2420	904.4927	452.7500	V	246.1812	123.5942	229.1547	115.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TLVFQFSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G56340.1

21.0	1067.6015	0.0004	TLVFQFSVK

Mascot: http://www.matrixscience.com/

AT1G56340.2

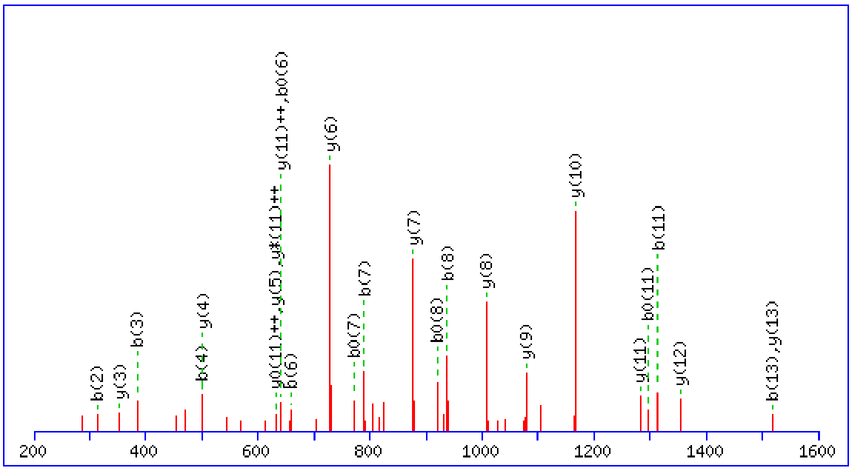
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FYAISAEFPEFSNK**
Found in **AT1G56340.2** in **TAIR_Arabidopsis**, Symbols: CRT1 | CRT1 (CALRETICULIN 1); calcium ion binding | chr1:21093687-21096295 REVERSE

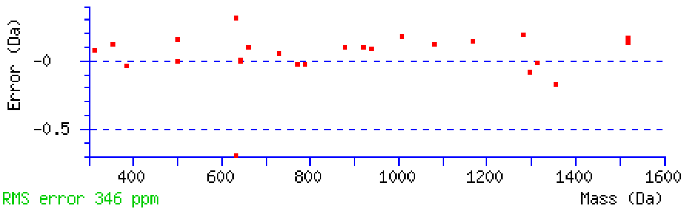
Match to Query 7911: 1664.734308 from(833.374430,2+) index(9050)
Title: Elution from: 80.975 to 80.975 scan no 12171 cid35.00 polarity:+
Data file D6h-3_1.mgf

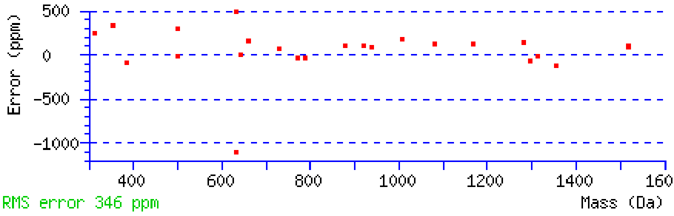
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1664.7299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 2.8e-009
Matches : 26/120 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							14
2	**313.1331**	157.0702					Y	***1517.6717***	759.3395	1499.6481	750.3277	1499.6611	750.3342	13
3	**385.1672**	193.0873					A	***1353.6113***	677.3093	1335.5878	668.2975	1335.6008	668.3040	12
4	**499.2483**	250.1278					I	***1281.5772***	641.2922	1263.5536	632.2804	1263.5666	632.2870	11
5	587.2774	294.1423			569.2668	285.1371	S	***1167.4961***	584.2517	1149.4725	575.2399	1149.4855	575.2464	10
6	**659.3115**	330.1594			641.3010	321.1541	A	***1079.4670***	540.2372	1061.4435	531.2254	1061.4565	531.2319	9
7	**789.3512**	395.1792			771.3406	386.1739	E	***1007.4329***	504.2201	989.4093	495.2083	989.4223	495.2148	8
8	**937.4166**	469.2120			919.4061	460.2067	F	***877.3933***	439.2003	859.3697	430.1885	859.3827	430.1950	7
9	1035.4664	518.2369			1017.4559	509.2316	P	***729.3278***	365.1675	711.3042	356.1558	711.3172	356.1623	6
10	1165.5061	583.2567			1147.4955	574.2514	E	***631.2780***	316.1426	613.2544	307.1309	613.2674	307.1374	5
11	**1313.5715**	657.2894			1295.5609	648.2841	F	***501.2384***	251.1228	483.2148	242.1110	483.2278	242.1175	4
12	1401.6006	701.3039			1383.5900	692.2986	S	***353.1729***	177.0901	335.1493	168.0783	335.1624	168.0848	3
13	**1517.6376**	759.3224	1499.6140	750.3106	1499.6270	750.3171	N	265.1439	133.0756	247.1203	124.0638			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FYAISAEFPEFSNK

AT1G56340.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.1	1664.7299	0.0044	FYAISAEFPEFSNK
17.4	1664.7362	-0.0019	LENKPVGEEASSETR
16.1	1664.7357	-0.0014	ETTYVETSTNITYK
7.7	1664.7393	-0.0050	MCGGAIISDFIPPPR
4.8	1664.7366	-0.0023	DFSTTVIMKSFMDK

AT1G56450.1

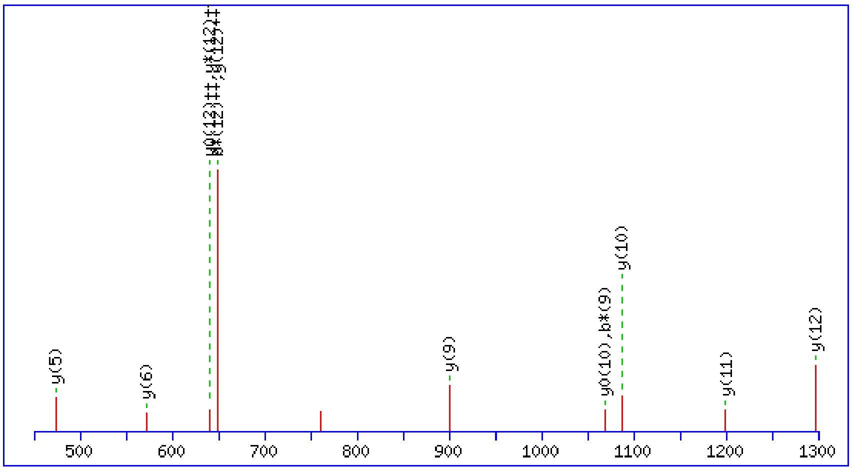
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNPLWNTLVLGGVK**
Found in **AT1G56450.1** in **TAIR_Arabidopsis**, Symbols: PBG1 | PBG1 (20S proteasome beta subunit G1); peptidase | chr1:21145635-21147851 FORWARD

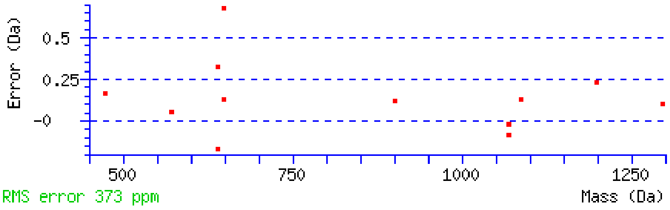
Match to Query 6608: 1556.871218 from(779.442885,2+) index(9935)
Title: Elution from: 92.899 to 92.899 scan no 14056 cid35.00 polarity:+
Data file D12h-1_3.mgf

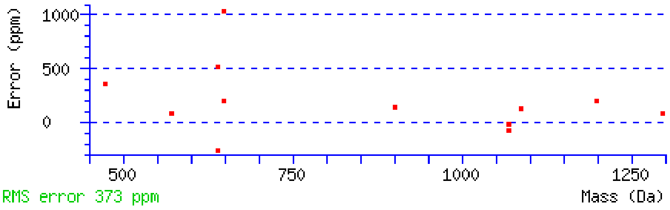
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1556.8715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 3.3e-005
Matches : 12/128 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					**F**							**14**
2	262.1186	131.5629	245.0921	123.0497			**N**	1410.8104	705.9088	1393.7838	697.3955	1392.7998	696.9035	**13**
3	359.1714	180.0893	342.1448	171.5761			**P**	***1296.7674***	648.8874	1279.7409	640.3741	1278.7569	639.8821	**12**
4	472.2554	236.6314	455.2289	228.1181			**L**	***1199.7147***	600.3610	1182.6881	591.8477	1181.7041	591.3557	**11**
5	658.3348	329.6710	641.3082	321.1577			**W**	***1086.6306***	543.8189	1069.6041	535.3057	1068.6200	534.8137	**10**
6	772.3777	386.6925	755.3511	378.1792			**N**	***900.5513***	450.7793	883.5247	442.2660	882.5407	441.7740	**9**
7	873.4254	437.2163	856.3988	428.7030	855.4148	428.2110	**T**	786.5084	393.7578	769.4818	385.2445	768.4978	384.7525	**8**
8	986.5094	493.7584	969.4829	485.2451	968.4989	484.7531	**L**	685.4607	343.2340	668.4341	334.7207			**7**
9	1085.5778	543.2926	1068.5513	534.7793	1067.5673	534.2873	**V**	***572.3766***	286.6919	555.3501	278.1787			**6**
10	1198.6619	599.8346	1181.6354	591.3213	1180.6513	590.8293	**L**	***473.3082***	237.1577	456.2817	228.6445			**5**
11	1255.6834	628.3453	1238.6568	619.8320	1237.6728	619.3400	**G**	360.2241	180.6157	343.1976	172.1024			**4**
12	1312.7048	656.8561	1295.6783	648.3428	1294.6943	647.8508	**G**	303.2027	152.1050	286.1761	143.5917			**3**
13	1411.7732	706.3903	1394.7467	697.8770	1393.7627	697.3850	**V**	246.1812	123.5942	229.1547	115.0810			**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of FNPLWNTLVLGGVK

AT1G56450.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.6	1556.8715	-0.0003	FNPLWNTLVLGGVK
6.7	1556.8755	-0.0043	MMNLVRANRIIAR

Mascot: http://www.matrixscience.com/

AT1G57720.1

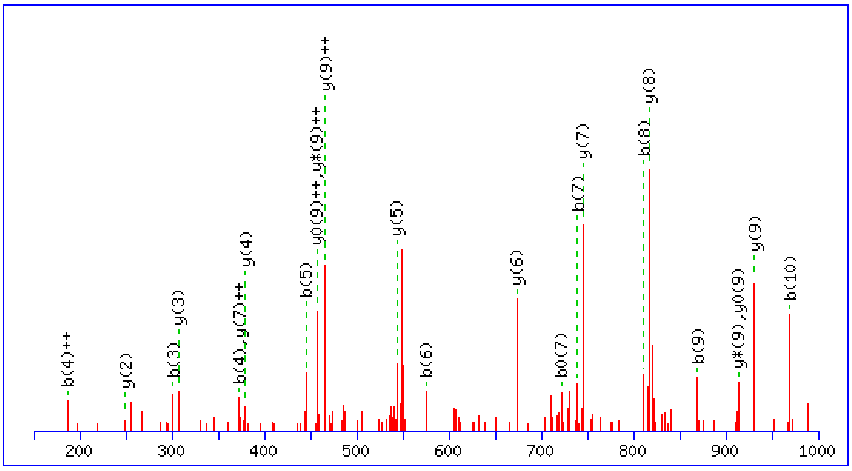
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALIAAEYAGVK**
Found in **AT1G57720.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1B-gamma, putative / eEF-1B gamma, putative | chr1:21381538-21383779 FORWARD

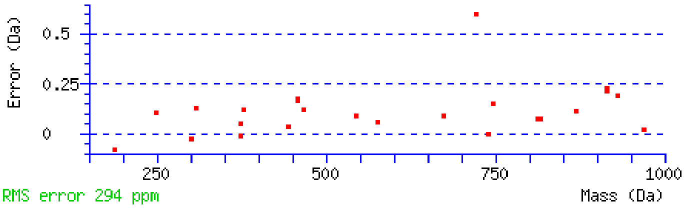
Match to Query 3490: 1116.584428 from(559.299490,2+) index(4291)
Title: Elution from: 39.800 to 39.800 scan no 5390 cid35.00 polarity:+
Data file D12h-3_2.mgf

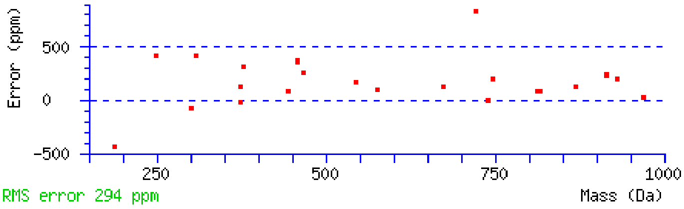
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 6e-007
Matches : 25/80 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							11
2	187.1225	94.0649			L	1045.5555	523.2814	1027.5319	514.2696	1027.5449	514.2761	10
3	301.2036	151.1054			I	931.4744	466.2408	913.4508	457.2290	913.4638	457.2355	9
4	373.2378	187.1225			A	817.3933	409.2003	799.3697	400.1885	799.3827	400.1950	8
5	445.2719	223.1396			A	745.3591	373.1832	727.3355	364.1714	727.3485	364.1779	7
6	575.3115	288.1594	557.3010	279.1541	E	673.3250	337.1661	655.3014	328.1543	655.3144	328.1608	6
7	739.3719	370.1896	721.3613	361.1843	Y	543.2853	272.1463	525.2618	263.1345			5
8	811.4061	406.2067	793.3955	397.2014	A	379.2250	190.1161	361.2014	181.1043			4
9	869.4246	435.2159	851.4140	426.2106	G	307.1908	154.0990	289.1672	145.0873			3
10	969.4900	485.2486	951.4794	476.2434	V	249.1723	125.0898	231.1487	116.0780			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ALIAAEYAGVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G57720.1

Score	Mr(calc)	Delta	Sequence
72.6	1116.5823	0.0021	ALIAAEYAGVK
8.3	1116.5823	0.0021	ALIEGQFLSK
4.6	1116.5823	0.0021	FVQEVKDLK
3.1	1116.5828	0.0017	ALAREIVSSR
0.5	1116.5824	0.0021	SPSSLLNIFK
0.4	1116.5823	0.0021	IASQELAFVK

AT1G58080.1

MATRIX SCIENCE Mascot Search Results

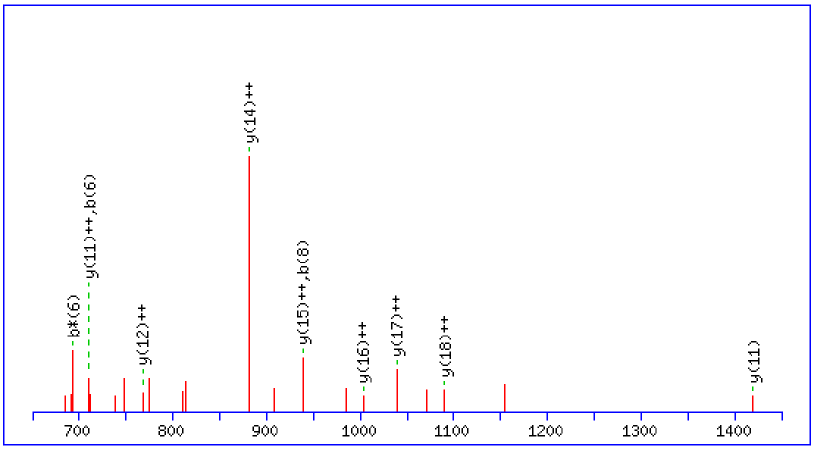
Peptide View

MS/MS Fragmentation of **QYVAQIPQLPNTEVWFQRPK**
Found in **AT1G58080.1** in **TAIR_Arabidopsis**, Symbols: HISN1A, ATATP-PRT1 | ATATP-PRT1 (ATP PHOSPHORIBOSYL TRANSFERASE) | chr1:21508227-21511094 REVERSE

Match to Query 10571: 2471.193519 from(824.738449,3+) index(9351)
Title: Elution from: 84.352 to 84.352 scan no 12637 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

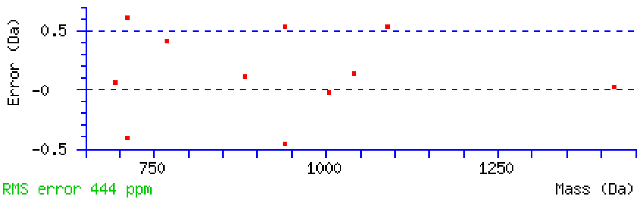
Or, Plot from 650 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

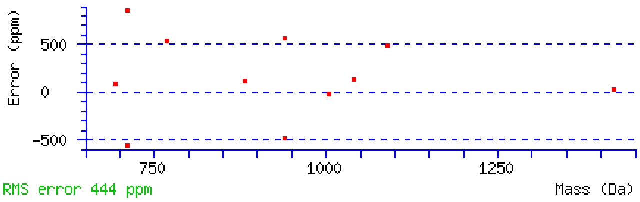


Monoisotopic mass of neutral peptide Mr(calc): 2471.1966
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0015
Matches : 11/192 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							20
2	295.1203	148.0638	277.0967	139.0520			Y	2342.1512	1171.5793	2324.1277	1162.5675	2324.1407	1162.5740	19
3	395.1857	198.0965	377.1622	189.0847			V	2178.0909	1089.5491	2160.0673	1080.5373	2160.0803	1080.5438	18
4	467.2199	234.1136	449.1963	225.1018			A	2078.0254	1039.5164	2060.0018	1030.5046	2060.0149	1030.5111	17
5	597.2725	299.1399	579.2489	290.1281			Q	2005.9913	1003.4993	1987.9677	994.4875	1987.9807	994.4940	16
6	**711.3536**	356.1805	693.3300	347.1687			I	1875.9386	938.4730	1857.9150	929.4612	1857.9281	929.4677	15
7	809.4034	405.2054	791.3798	396.1936			P	1761.8575	881.4324	1743.8339	872.4206	1743.8470	872.4271	14
8	**939.4561**	470.2317	921.4325	461.2199			Q	1663.8077	832.4075	1645.7842	823.3957	1645.7972	823.4022	13
9	1053.5372	527.2722	1035.5136	518.2604			L	1533.7551	767.3812	1515.7315	758.3694	1515.7445	758.3759	12
10	1151.5870	576.2971	1133.5634	567.2853			P	1419.6740	710.3406	1401.6504	701.3288	1401.6634	701.3353	11
11	1267.6240	634.3156	1249.6004	625.3038			N	1321.6242	661.3157	1303.6006	652.3039	1303.6136	652.3105	10
12	1369.6687	685.3380	1351.6451	676.3262	1351.6581	676.3327	T	1205.5872	603.2972	1187.5636	594.2854	1187.5766	594.2920	9
13	1499.7083	750.3578	1481.6847	741.3460	1481.6977	741.3525	E	1103.5425	552.2749	1085.5189	543.2631	1085.5319	543.2696	8
14	1599.7738	800.3905	1581.7502	791.3787	1581.7632	791.3852	V	973.5029	487.2551	955.4793	478.2433			7
15	1787.8471	894.4272	1769.8236	885.4154	1769.8366	885.4219	W	873.4374	437.2223	855.4138	428.2105			6
16	1935.9126	968.4599	1917.8890	959.4481	1917.9020	959.4547	F	685.3640	343.1856	667.3404	334.1739			5
17	2065.9652	1033.4863	2047.9417	1024.4745	2047.9547	1024.4810	Q	537.2986	269.1529	519.2750	260.1411			4
18	2226.0545	1113.5309	2208.0309	1104.5191	2208.0439	1104.5256	R	407.2459	204.1266	389.2223	195.1148			3
19	2324.1043	1162.5558	2306.0807	1153.5440	2306.0937	1153.5505	P	247.1567	124.0820	229.1331	115.0702			2
20							K	149.1069	75.0571	131.0833	66.0453			1

AT1G58080.1





NCBI **BLAST** search of QYVAQIPQLPNTEVWFQRPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.0	2471.1966	-0.0031	QYVAQIPQLPNTEVWFQRPK
11.6	2471.1944	-0.0008	FDHTSPDNILRYNLALTVPVR
8.5	2471.1944	-0.0008	YSDPLVYTGFIRARTGNEILR
6.3	2471.2000	-0.0065	SENLYLNPAMNGVIPKYLIHR
4.4	2471.1908	0.0028	YLIGSAVMMIGVVLPVGYMMFR
4.3	2471.1976	-0.0041	SDVTGEKSIVPKTEPSSSNVIAAK
3.6	2471.1944	-0.0009	QPFSQIPQLVAQPGPSSVNPPPR
2.7	2471.1923	0.0012	CVILGCLVRFWLGLMWFKF
2.6	2471.1903	0.0032	MELHGALVASPGMGHAVPILELGK
2.6	2471.1870	0.0066	AYPVGPLLHLKNVNCDYVDKK

Mascot: http://www.matrixscience.com/

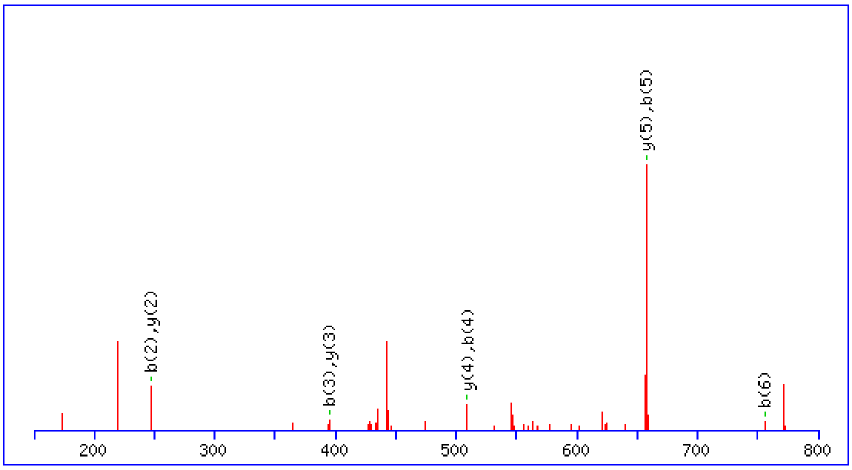
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NEFLFPK**
Found in **AT1G58230.1** in **TAIR_Arabidopsis**, Symbols: | WD-40 repeat family protein / beige-related | chr1:21577371-21582530 FORWARD

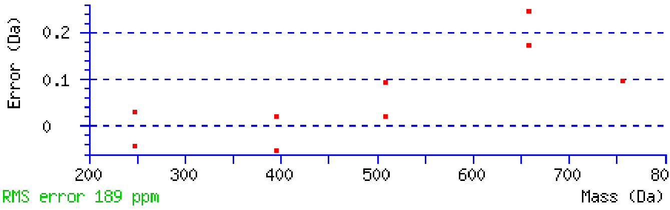
Match to Query 1724: 902.440676 from(452.227614,2+) index(5961)
Title: Elution from: 52.187 to 52.187 scan no 7513 cid35.00 polarity:+
Data file D6h-1_1.mgf

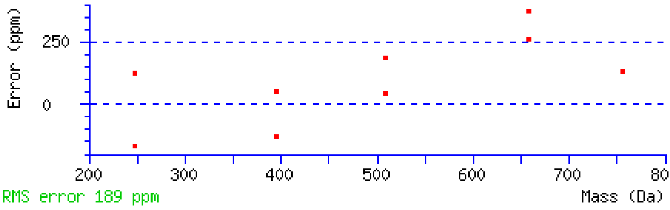
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 902.4380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.048
Matches : 9/60 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							7
2	***247.0839***	124.0456	229.0603	115.0338	229.0733	115.0403	E	787.4083	394.2078	769.3847	385.1960	769.3977	385.2025	6
3	***395.1493***	198.0783	377.1258	189.0665	377.1388	189.0730	F	**657.3687**	329.1880	639.3451	320.1762			5
4	***509.2304***	255.1189	491.2069	246.1071	491.2199	246.1136	L	**509.3032**	255.1552	491.2796	246.1435			4
5	***657.2959***	329.1516	639.2723	320.1398	639.2853	320.1463	F	**395.2221**	198.1147	377.1985	189.1029			3
6	***755.3457***	378.1765	737.3221	369.1647	737.3351	369.1712	P	**247.1567**	124.0820	229.1331	115.0702			2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NEFLFPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	902.4380	0.0027	NEFLFPK
20.3	902.4414	-0.0007	MLKYDPK
17.4	902.4414	-0.0007	MLFDIQK

AT1G58230.1

10.3	902.4414	-0.0007	MLDQFLK
8.5	902.4414	-0.0007	DFVAAMIK
7.2	902.4414	-0.0007	KIMFDPK
7.0	902.4391	0.0015	MTASIGSVK
6.1	902.4414	-0.0007	QMLVYPK
5.6	902.4418	-0.0011	GRSGLCIK
5.0	902.4418	-0.0012	KMQNKNK

AT1G58270.1

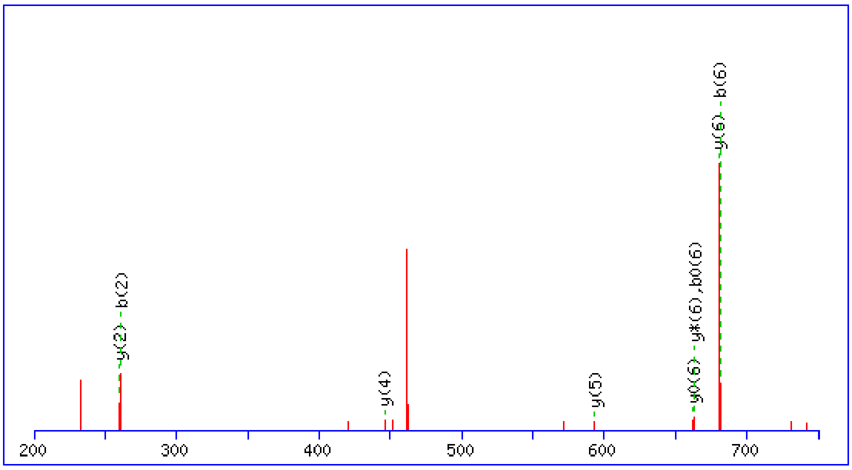
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLSFADIK**
Found in **AT1G58270.1** in **TAIR_Arabidopsis**, Symbols: ZW9 | ZW9 | chr1:21616059-21617754 REVERSE

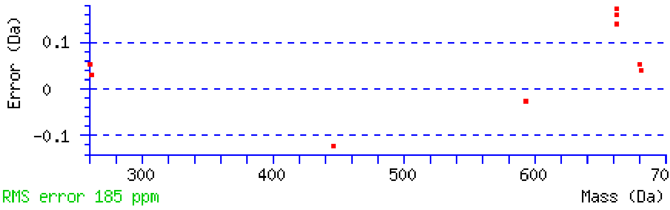
Match to Query 1928: 939.507188 from(470.760870,2+) index(7162)
Title: Elution from: 63.522 to 63.522 scan no 9351 cid35.00 polarity:+
Data file D12h-3_2.mgf

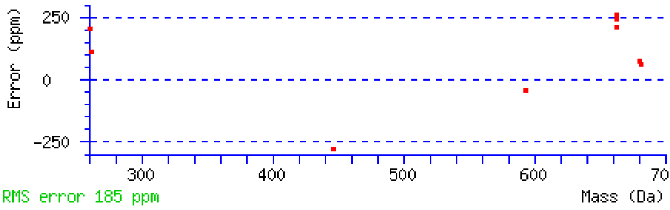
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 939.5066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0032
Matches : 9/62 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							8
2	**261.1598**	131.0835			L	793.4454	397.2264	776.4189	388.7131	775.4349	388.2211	7
3	348.1918	174.5995	330.1812	165.5942	S	***680.3614***	340.6843	663.3348	332.1710	662.3508	331.6790	6
4	495.2602	248.1337	477.2496	239.1285	F	***593.3293***	297.1683	576.3028	288.6550	575.3188	288.1630	5
5	566.2973	283.6523	548.2867	274.6470	A	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
6	**681.3243**	341.1658	663.3137	332.1605	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
7	794.4083	397.7078	776.3978	388.7025	I	***260.1969***	130.6021	243.1703	122.0888			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FLSFADIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.7	939.5066	0.0006	FLSFADIK
0.2	939.5066	0.0006	TVFFLGEK

AT1G58270.1

Mascot: http://www.matrixscience.com/

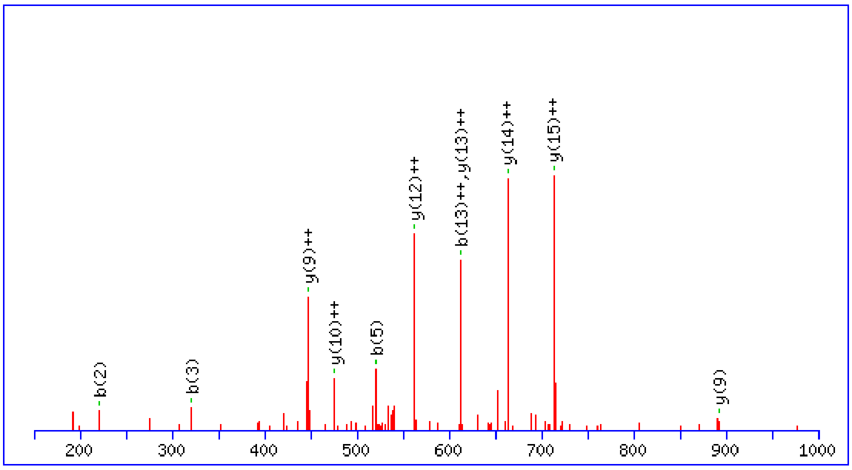
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFVVVGDGNGHVGLGVK**
Found in **AT1G58380.1** in **TAIR_Arabidopsis**, Symbols: XW6 | XW6; structural constituent of ribosome | chr1:21692780-21693750 FORWARD

Match to Query 7767: 1644.815019 from(549.278949,3+) index(5769)
Title: Elution from: 51.018 to 51.018 scan no 7236 cid35.00 polarity:+
Data file C7-3_1.mgf

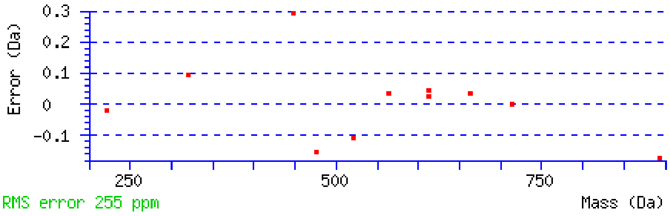
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

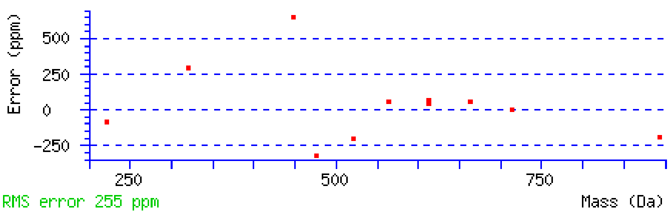


Monoisotopic mass of neutral peptide Mr(calc): 1644.8110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0013
Matches : 11/144 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							17
2	**221.1069**	111.0571					F	1573.7842	787.3957	1555.7606	778.3839	1555.7736	778.3904	16
3	**321.1723**	161.0898					V	1425.7187	713.3630	1407.6951	704.3512	1407.7081	704.3577	15
4	421.2378	211.1225					V	1325.6533	663.3303	1307.6297	654.3185	1307.6427	654.3250	14
5	**521.3032**	261.1552					V	1225.5878	613.2975	1207.5642	604.2857	1207.5772	604.2923	13
6	579.3217	290.1645					G	1125.5224	563.2648	1107.4988	554.2530	1107.5118	554.2595	12
7	695.3457	348.1765			677.3351	339.1712	D	1067.5039	534.2556	1049.4803	525.2438	1049.4933	525.2503	11
8	753.3642	377.1857			735.3536	368.1805	G	951.4799	476.2436	933.4563	467.2318			10
9	869.4012	435.2042	851.3776	426.1924	851.3906	426.1990	N	893.4614	447.2343	875.4378	438.2225			9
10	927.4197	464.2135	909.3961	455.2017	909.4091	455.2082	G	777.4244	389.2158	759.4008	380.2040			8
11	1067.4697	534.2385	1049.4461	525.2267	1049.4591	525.2332	H	719.4059	360.2066	701.3823	351.1948			7
12	1167.5352	584.2712	1149.5116	575.2594	1149.5246	575.2659	V	579.3559	290.1816	561.3323	281.1698			6
13	1225.5537	613.2805	1207.5301	604.2687	1207.5431	604.2752	G	479.2904	240.1488	461.2668	231.1371			5
14	1339.6348	670.3210	1321.6112	661.3092	1321.6242	661.3157	L	421.2719	211.1396	403.2483	202.1278			4
15	1397.6533	699.3303	1379.6297	690.3185	1379.6427	690.3250	G	307.1908	154.0990	289.1672	145.0873			3
16	1497.7187	749.3630	1479.6951	740.3512	1479.7081	740.3577	V	249.1723	125.0898	231.1487	116.0780			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT1G58380.1





NCBI **BLAST** search of AFVVVGDGNGHVGLGVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.6	1644.8110	0.0040	AFVVVGDGNGHVGLGVK
7.0	1644.8191	-0.0041	TVQEVVAAGEKLPER
0.5	1644.8191	-0.0041	RQEEVVQVTDVVPK
0.3	1644.8170	-0.0020	CVIAIVRHGDRTPK

Mascot: http://www.matrixscience.com/

AT1G59171.1

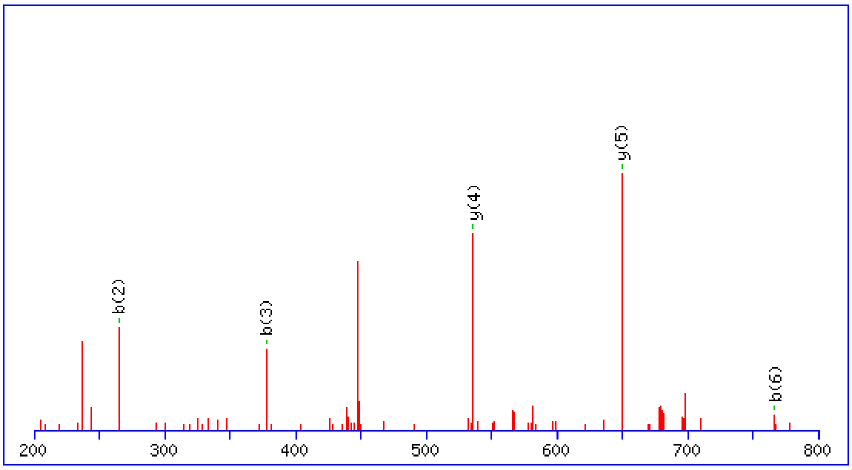
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYLEMLK**
Found in **AT1G59171.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G58936.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G58643.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G59312.1); contains InterPro domain P

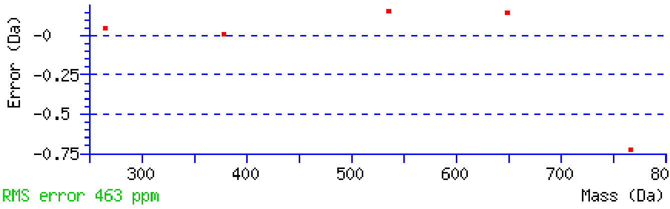
Match to Query 1698: 912.462384 from(457.238468,2+) index(2871)
Title: Elution from: 29.604 to 29.604 scan no 3627 cid35.00 polarity:+
Data file 0-2_2.mgf

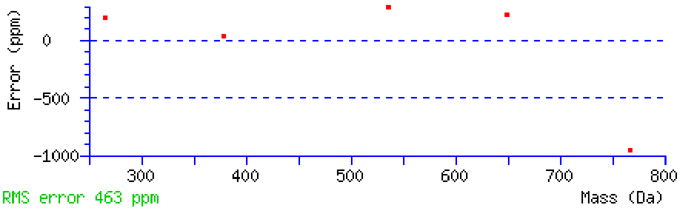
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 912.4626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.0029
Matches : 5/84 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							7
2	***265.1183***	133.0628	247.1077	124.0575	Y	812.4223	406.7148	795.3957	398.2015	794.4117	397.7095	6
3	***378.2023***	189.6048	360.1918	180.5995	L	**649.3589**	325.1831	632.3324	316.6698	631.3484	316.1778	5
4	507.2449	254.1261	489.2344	245.1208	E	**536.2749**	268.6411	519.2483	260.1278	518.2643	259.6358	4
5	654.2803	327.6438	636.2698	318.6385	M	407.2323	204.1198	390.2057	195.6065			3
6	***767.3644***	384.1858	749.3538	375.1806	L	260.1969	130.6021	243.1703	122.0888			2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TYLEMLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G59171.1

27.1	912.4626	-0.0002	TYLEMLK
2.4	912.4626	-0.0002	LYTLEMK
0.2	912.4599	0.0024	RMSYRGK

Mascot: http://www.matrixscience.com/

AT1G59870.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALVFDK**
Found in **AT1G59870.1** in **TAIR_Arabidopsis**, Symbols: PEN3, PDR8 | PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter | chr1:22038326-22043509 FORWARD

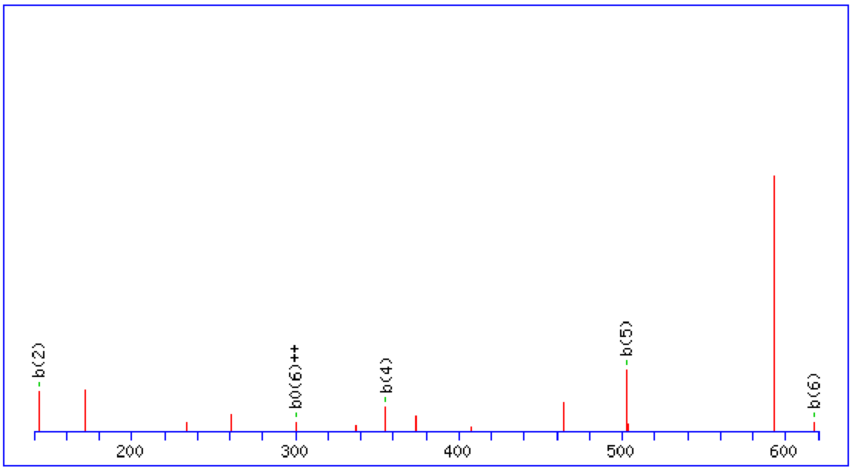
Match to Query 788: 762.426996 from(382.220774,2+) index(5338)
Title: Elution from: 48.530 to 48.530 scan no 6784 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 140 to 620 Da Full range

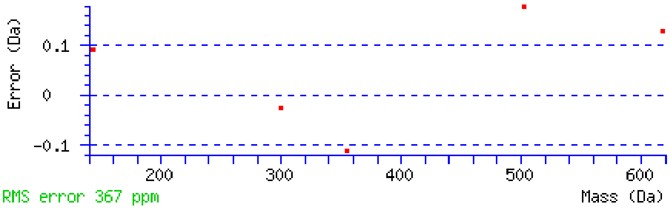
Label all possible matches ○ Label matches used for scoring ●

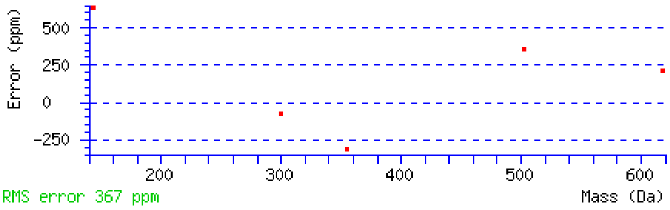
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 762.4276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.025
Matches : 5/48 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			A							7
2	***143.0815***	72.0444			A	692.3978	346.7025	675.3712	338.1892	674.3872	337.6972	6
3	256.1656	128.5864			L	621.3606	311.1840	604.3341	302.6707	603.3501	302.1787	5
4	***355.2340***	178.1206			V	508.2766	254.6419	491.2500	246.1287	490.2660	245.6366	4
5	***502.3024***	251.6548			F	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
6	***617.3293***	309.1683	599.3188	300.1630	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AALVFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	762.4276	-0.0006	AALVFDK
19.8	762.4276	-0.0006	GIEGLFK

19.3	762.4276	-0.0006	GLEIFGK
12.7	762.4276	-0.0006	IFLENK
10.3	762.4276	-0.0006	FLGALDK
6.7	762.4276	-0.0006	LVSGYPK
5.3	762.4276	-0.0006	LTGTFPK
4.0	762.4276	-0.0006	GLAEFVK
3.8	762.4276	-0.0006	GLFLEGK
3.8	762.4276	-0.0006	IGFGIEK

Mascot: http://www.matrixscience.com/

AT1G60690.1

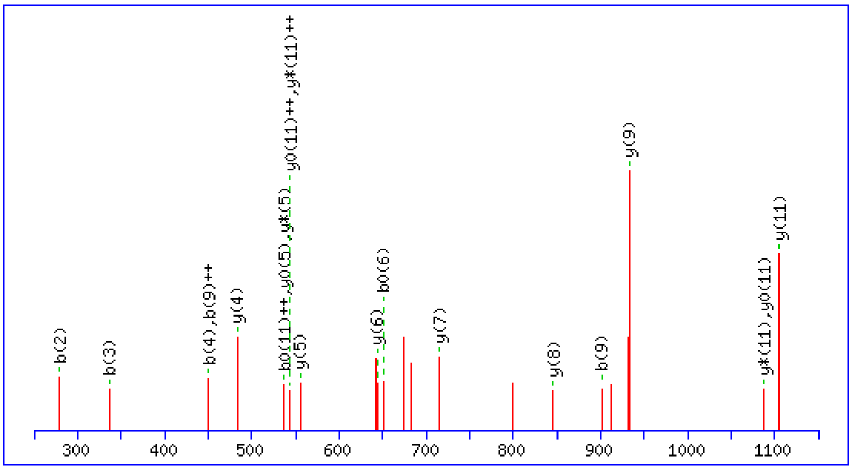
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YIGLSEASASTIR**
Found in **AT1G60690.1** in **TAIR_Arabidopsis**, Symbols: | aldo/keto reductase family protein | chr1:22353557-22355333 REVERSE

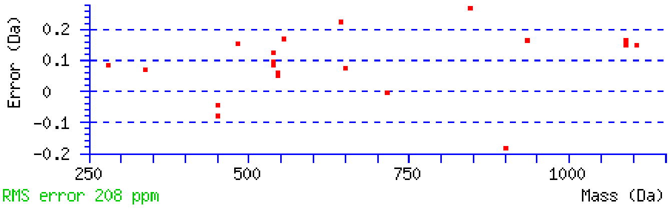
Match to Query 5366: 1382.665240 from(692.339896,2+) index(4796)
Title: Elution from: 43.909 to 43.909 scan no 6057 cid35.00 polarity:+
Data file D6h-3_1.mgf

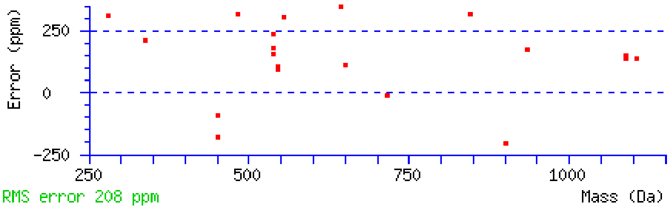
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.6618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 5.5e-006
Matches : 20/108 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375			Y							13
2	**279.1487**	140.0780			I	1219.6087	610.3080	1201.5851	601.2962	1201.5982	601.3027	12
3	**337.1672**	169.0873			G	***1105.5276***	553.2674	1087.5040	544.2557	1087.5171	544.2622	11
4	**451.2483**	226.1278			L	1047.5091	524.2582	1029.4855	515.2464	1029.4986	515.2529	10
5	539.2774	270.1423	521.2668	261.1371	S	***933.4280***	467.2176	915.4044	458.2059	915.4175	458.2124	9
6	669.3170	335.1622	651.3065	326.1569	E	***845.3990***	423.2031	827.3754	414.1913	827.3884	414.1978	8
7	741.3512	371.1792	723.3406	362.1739	A	***715.3593***	358.1833	697.3357	349.1715	697.3488	349.1780	7
8	829.3802	415.1938	811.3697	406.1885	S	***643.3252***	322.1662	625.3016	313.1544	625.3146	313.1609	6
9	**901.4144**	451.2108	883.4038	442.2055	A	***555.2961***	278.1517	537.2725	269.1399	537.2856	269.1464	5
10	989.4435	495.2254	971.4329	486.2201	S	***483.2620***	242.1346	465.2384	233.1228	465.2514	233.1293	4
11	1091.4882	546.2477	1073.4776	537.2424	T	395.2329	198.1201	377.2093	189.1083	377.2223	189.1148	3
12	1205.5693	603.2883	1187.5587	594.2830	I	293.1882	147.0977	275.1646	138.0859			2
13					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of YIGLSEASASTIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G60690.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.9	1382.6618	0.0034	YIGLSEASASTIR
20.9	1382.6674	-0.0022	MKETAEAFLGKK
13.7	1382.6645	0.0008	QFDSTNQLRKK
13.3	1382.6674	-0.0022	MKETAEAYLGKK
9.3	1382.6640	0.0012	DFQSVLKEFQK
7.1	1382.6640	0.0012	KFAELSGNDIFK
2.9	1382.6678	-0.0026	QMKAAASGKSLTR
2.0	1382.6645	0.0008	FQSIDSAVSRVR
2.0	1382.6644	0.0008	FQSVDTAVSRVR
2.0	1382.6674	-0.0022	LYAAESMLNTKK

AT1G60950.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVSGSVDQSDQSFLDDEQIGEGFVLTCAAYPTSDVTIETHKEEDIV**
Found in **AT1G60950.1** in **TAIR_Arabidopsis**, Symbols: ATFD2, FED A | FED A (FERREDOXIN 2); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding | chr1:22448230-22448676 FORWARD

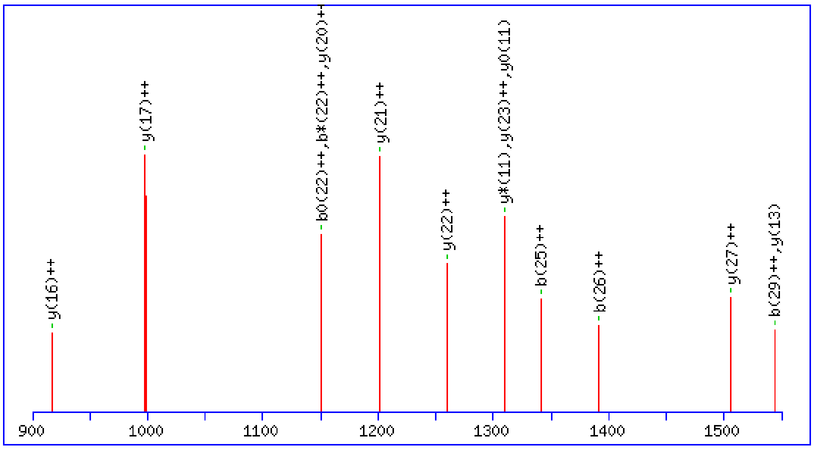
Match to Query 10799: 5082.166588 from(1271.548923,4+) index(10348)
Title: Elution from: 99.977 to 99.977 scan no 14936 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 900 to 1550 Da Full range

Label all possible matches ○ Label matches used for scoring ●

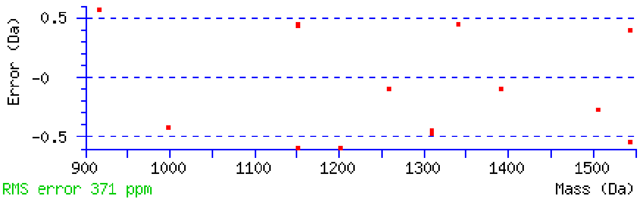
Show Y-axis ☐

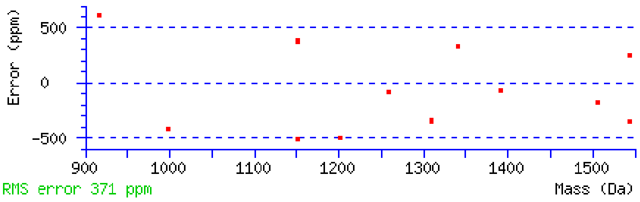


Monoisotopic mass of neutral peptide Mr(calc): 5082.1614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 4.5e-006
Matches : 15/508 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							46
2	201.1382	101.0727					V	4983.1033	2492.0553	4965.0797	2483.0435	4965.0928	2483.0500	45
3	289.1672	145.0873			271.1567	136.0820	S	4883.0379	2442.0226	4865.0143	2433.0108	4865.0273	2433.0173	44
4	347.1857	174.0965			329.1752	165.0912	G	4795.0088	2398.0080	4776.9852	2388.9963	4776.9982	2389.0028	43
5	435.2148	218.1110			417.2042	209.1058	S	4736.9903	2368.9988	4718.9667	2359.9870	4718.9797	2359.9935	42
6	535.2802	268.1438			517.2697	259.1385	V	4648.9612	2324.9843	4630.9377	2315.9725	4630.9507	2315.9790	41
7	651.3042	326.1558			633.2937	317.1505	D	4548.8958	2274.9515	4530.8722	2265.9397	4530.8852	2265.9463	40
8	781.3569	391.1821	763.3333	382.1703	763.3463	382.1768	Q	4432.8718	2216.9395	4414.8482	2207.9278	4414.8613	2207.9343	39
9	869.3859	435.1966	851.3624	426.1848	851.3754	426.1913	S	4302.8192	2151.9132	4284.7956	2142.9014	4284.8086	2142.9079	38
10	985.4099	493.2086	967.3863	484.1968	967.3993	484.2033	D	4214.7901	2107.8987	4196.7665	2098.8869	4196.7795	2098.8934	37
11	1115.4626	558.2349	1097.4390	549.2231	1097.4520	549.2296	Q	4098.7661	2049.8867	4080.7425	2040.8749	4080.7556	2040.8814	36
12	1203.4916	602.2494	1185.4680	593.2377	1185.4811	593.2442	S	3968.7135	1984.8604	3950.6899	1975.8486	3950.7029	1975.8551	35
13	1351.5571	676.2822	1333.5335	667.2704	1333.5465	667.2769	F	3880.6844	1940.8458	3862.6608	1931.8341	3862.6739	1931.8406	34
14	1465.6382	733.3227	1447.6146	724.3109	1447.6276	724.3174	L	3732.6190	1866.8131	3714.5954	1857.8013	3714.6084	1857.8078	33
15	1581.6621	791.3347	1563.6386	782.3229	1563.6516	782.3294	D	3618.5379	1809.7726	3600.5143	1800.7608	3600.5273	1800.7673	32
16	1697.6861	849.3467	1679.6625	840.3349	1679.6756	840.3414	D	3502.5139	1751.7606	3484.4903	1742.7488	3484.5033	1742.7553	31
17	1827.7258	914.3665	1809.7022	905.3547	1809.7152	905.3612	E	3386.4899	1693.7486	3368.4663	1684.7368	3368.4794	1684.7433	30
18	1957.7784	979.3928	1939.7548	970.3810	1939.7678	970.3876	Q	3256.4503	1628.7288	3238.4267	1619.7170	3238.4397	1619.7235	29
19	2071.8595	1036.4334	2053.8359	1027.4216	2053.8489	1027.4281	I	3126.3976	1563.7025	3108.3741	1554.6907	3108.3871	1554.6972	28
20	2129.8780	1065.4426	2111.8544	1056.4308	2111.8674	1056.4374	G	3012.3165	1506.6619	2994.2930	1497.6501	2994.3060	1497.6566	27
21	2259.9176	1130.4625	2241.8940	1121.4507	2241.9071	1121.4572	E	2954.2980	1477.6527	2936.2745	1468.6409	2936.2875	1468.6474	26
22	2317.9361	1159.4717	2299.9125	1150.4599	2299.9256	1150.4664	G	2824.2584	1412.6328	2806.2348	1403.6211	2806.2479	1403.6276	25
23	2466.0016	1233.5044	2447.9780	1224.4926	2447.9910	1224.4991	F	2766.2399	1383.6236	2748.2163	1374.6118	2748.2294	1374.6183	24
24	2566.0670	1283.5372	2548.0434	1274.5254	2548.0565	1274.5319	V	2618.1745	1309.5909	2600.1509	1300.5791	2600.1639	1300.5856	23

25	2680.1481	**1340.5777**	2662.1245	1331.5659	2662.1376	1331.5724	L	2518.1090	1259.5581	2500.0854	1250.5464	2500.0985	1250.5529	22
26	2782.1928	**1391.6001**	2764.1693	1382.5883	2764.1823	1382.5948	T	2404.0279	1202.5176	2386.0043	1193.5058	2386.0174	1193.5123	21
27	2944.2176	1472.6124	2926.1940	1463.6006	2926.2070	1463.6071	C	2301.9832	1151.4952	2283.9596	1142.4834	2283.9726	1142.4900	20
28	3016.2517	1508.6295	2998.2281	1499.6177	2998.2411	1499.6242	A	2139.9585	1070.4829	2121.9349	1061.4711	2121.9479	1061.4776	19
29	3088.2859	**1544.6466**	3070.2623	1535.6348	3070.2753	1535.6413	A	2067.9243	1034.4658	2049.9008	1025.4540	2049.9138	1025.4605	18
30	3252.3462	1626.6767	3234.3226	1617.6650	3234.3357	1617.6715	Y	1995.8902	998.4487	1977.8666	989.4369	1977.8796	989.4435	17
31	3350.3960	1675.7016	3332.3724	1666.6899	3332.3855	1666.6964	P	1831.8298	916.4186	1813.8062	907.4068	1813.8193	907.4133	16
32	3452.4407	1726.7240	3434.4171	1717.7122	3434.4302	1717.7187	T	1733.7800	867.3937	1715.7564	858.3819	1715.7695	858.3884	15
33	3540.4698	1770.7385	3522.4462	1761.7267	3522.4592	1761.7333	S	1631.7353	816.3713	1613.7117	807.3595	1613.7248	807.3660	14
34	3656.4938	1828.7505	3638.4702	1819.7387	3638.4832	1819.7452	D	1543.7063	772.3568	1525.6827	763.3450	1525.6957	763.3515	13
35	3756.5592	1878.7832	3738.5356	1869.7715	3738.5487	1869.7780	V	1427.6823	714.3448	1409.6587	705.3330	1409.6717	705.3395	12
36	3858.6039	1929.8056	3840.5803	1920.7938	3840.5934	1920.8003	T	1327.6168	664.3121	1309.5932	655.3003	1309.6063	655.3068	11
37	3972.6850	1986.8462	3954.6614	1977.8344	3954.6745	1977.8409	I	1225.5721	613.2897	1207.5485	604.2779	1207.5615	604.2844	10
38	4102.7247	2051.8660	4084.7011	2042.8542	4084.7141	2042.8607	E	1111.4910	556.2491	1093.4674	547.2374	1093.4804	547.2439	9
39	4204.7694	2102.8883	4186.7458	2093.8765	4186.7588	2093.8830	T	981.4514	491.2293	963.4278	482.2175	963.4408	482.2240	8
40	4344.8194	2172.9133	4326.7958	2163.9015	4326.8088	2163.9081	H	879.4067	440.2070	861.3831	431.1952	861.3961	431.2017	7
41	4474.9084	2237.9578	4456.8848	2228.9461	4456.8979	2228.9526	K	739.3567	370.1820	721.3331	361.1702	721.3461	361.1767	6
42	4604.9481	2302.9777	4586.9245	2293.9659	4586.9375	2293.9724	E	609.2676	305.1374			591.2571	296.1322	5
43	4734.9877	2367.9975	4716.9641	2358.9857	4716.9771	2358.9922	E	479.2280	240.1176			461.2174	231.1124	4
44	4851.0117	2426.0095	4832.9881	2416.9977	4833.0011	2417.0042	D	349.1884	175.0978			331.1778	166.0925	3
45	4965.0928	2483.0500	4947.0692	2474.0382	4947.0822	2474.0447	I	233.1644	117.0858					2
46							V	119.0833	60.0453					1





NCBI **BLAST** search of VVSGSVDQSDQSFLDDEQIGEGFVLTCAAYPTSDVTIETHKEEDIV
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.7	5082.1614	0.0052	VVSGSVDQSDQSFLDDEQIGEGFVLTCAAYPTSDVTIETHKEEDIV
5.4	5082.1549	0.0117	EDDCEELQVPVGTLTSIGFSISNNNDRDKMSVLEVEAPNQVTDSR

Mascot: http://www.matrixscience.com/

AT1G61520.1

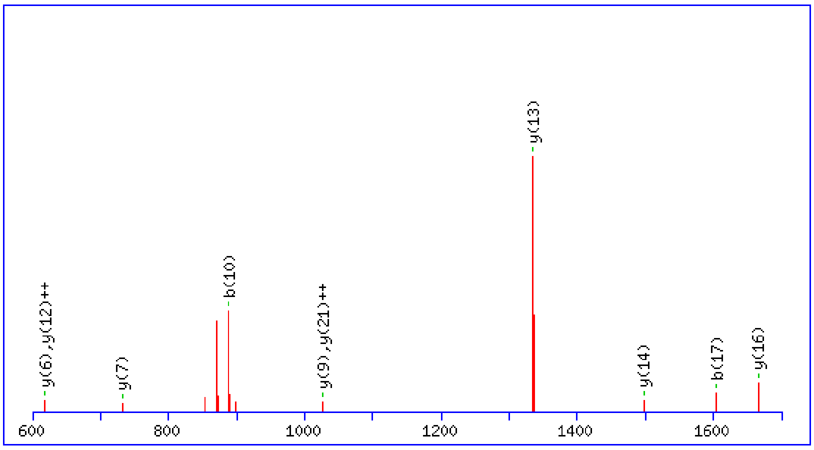
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLAGSGNPAYPGGPFFNPLGFGK**
Found in **AT1G61520.1** in **TAIR_Arabidopsis**, Symbols: LHCA3 | LHCA3 (Photosystem I light harvesting complex gene 3); chlorophyll binding | chr1:22703817-22704814 FORWARD

Match to Query 10439: 2221.090512 from(1111.552532,2+) index(10492)
Title: Elution from: 95.621 to 95.621 scan no 14522 cid35.00 polarity:+
Data file D6h-1_1.mgf

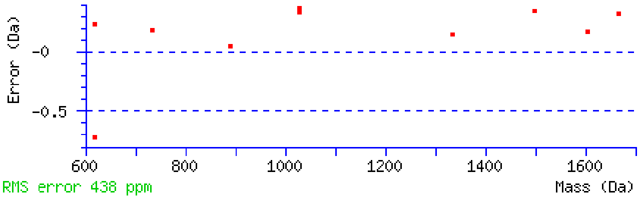
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

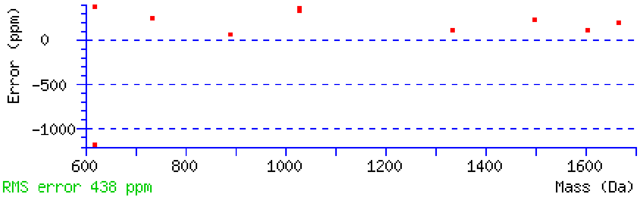


Monoisotopic mass of neutral peptide Mr(calc): 2221.0957
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.7e-005
Matches : 10/208 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							23
2	171.1128	86.0600					L	2165.0815	1083.0444	2148.0549	1074.5311	2147.0709	1074.0391	22
3	242.1499	121.5786					A	2051.9974	1026.5023	2034.9708	1017.9891	2033.9868	1017.4970	21
4	299.1714	150.0893					G	1980.9603	990.9838	1963.9337	982.4705	1962.9497	981.9785	20
5	386.2034	193.6053			368.1928	184.6001	S	1923.9388	962.4730	1906.9123	953.9598	1905.9282	953.4678	19
6	443.2249	222.1161			425.2143	213.1108	G	1836.9068	918.9570	1819.8802	910.4438			18
7	557.2678	279.1375	540.2413	270.6243	539.2572	270.1323	N	1779.8853	890.4463	1762.8588	881.9330			17
8	654.3206	327.6639	637.2940	319.1506	636.3100	318.6586	P	***1665.8424***	833.4248	1648.8158	824.9116			16
9	725.3577	363.1825	708.3311	354.6692	707.3471	354.1772	A	1568.7896	784.8985	1551.7631	776.3852			15
10	**888.4210**	444.7141	871.3945	436.2009	870.4104	435.7089	Y	***1497.7525***	749.3799	1480.7260	740.8666			14
11	985.4738	493.2405	968.4472	484.7272	967.4632	484.2352	P	***1334.6892***	667.8482	1317.6626	659.3350			13
12	1042.4952	521.7513	1025.4687	513.2380	1024.4847	512.7460	G	1237.6364	619.3218	1220.6099	610.8086			12
13	1099.5167	550.2620	1082.4902	541.7487	1081.5061	541.2567	G	1180.6150	590.8111	1163.5884	582.2978			11
14	1196.5695	598.7884	1179.5429	590.2751	1178.5589	589.7831	P	1123.5935	562.3004	1106.5669	553.7871			10
15	1343.6379	672.3226	1326.6113	663.8093	1325.6273	663.3173	F	***1026.5407***	513.7740	1009.5142	505.2607			9
16	1490.7063	745.8568	1473.6797	737.3435	1472.6957	736.8515	F	879.4723	440.2398	862.4458	431.7265			8
17	**1604.7492**	802.8782	1587.7227	794.3650	1586.7387	793.8730	N	***732.4039***	366.7056	715.3774	358.1923			7
18	1701.8020	851.4046	1684.7754	842.8914	1683.7914	842.3993	P	***618.3610***	309.6841	601.3344	301.1709			6
19	1814.8860	907.9467	1797.8595	899.4334	1796.8755	898.9414	L	521.3082	261.1577	504.2817	252.6445			5
20	1871.9075	936.4574	1854.8810	927.9441	1853.8969	927.4521	G	408.2241	204.6157	391.1976	196.1024			4
21	2018.9759	1009.9916	2001.9494	1001.4783	2000.9654	1000.9863	F	351.2027	176.1050	334.1761	167.5917			3
22	2075.9974	1038.5023	2058.9708	1029.9891	2057.9868	1029.4970	G	204.1343	102.5708	187.1077	94.0575			2
23							K	147.1128	74.0600	130.0863	65.5468			1

AT1G61520.1





NCBI **BLAST** search of GLAGSGNPAYPGGPFFNPLGFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.6	2221.0957	-0.0051	GLAGSGNPAYPGGPFFNPLGFGK

Mascot: http://www.matrixscience.com/

AT1G61600.1

MATRIX SCIENCE Mascot Search Results

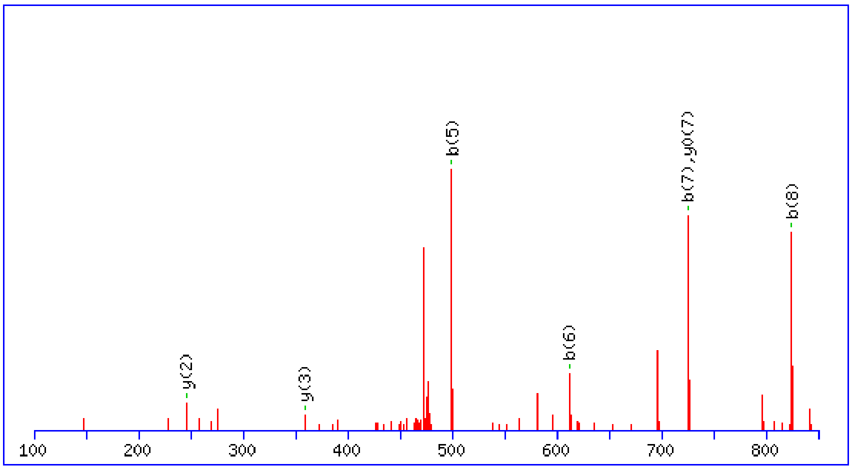
Peptide View

MS/MS Fragmentation of **RADGVLLVK**
Found in **AT1G61600.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13520.1); similar to unknown [Populus trichocarpa] (GB:ABK94028.1); contains InterPro domain Protein of unknown function DUF1262 (InterPro:IPR010683) | chr1:22733481-22734847 F

Match to Query 1778: 969.597306 from(485.805929,2+) index(2417)
Title: Elution from: 27.800 to 27.800 scan no 3123 cid35.00 polarity:+
Data file D1d-1_3.mgf

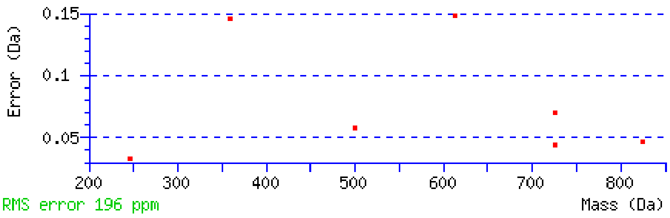
Click mouse within plot area to zoom in by factor of two about that point

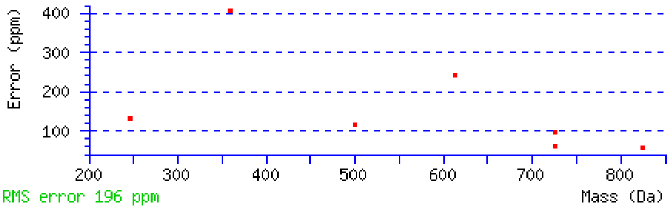
Or, [Plot from] [100] to [850] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 969.5971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0021
Matches : 7/80 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							9
2	228.1455	114.5764	211.1190	106.0631			A	814.5033	407.7553	797.4767	399.2420	796.4927	398.7500	8
3	343.1724	172.0899	326.1459	163.5766	325.1619	163.0846	D	743.4662	372.2367	726.4396	363.7234	725.4556	363.2314	7
4	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	G	628.4392	314.7233	611.4127	306.2100			6
5	***499.2623***	250.1348	482.2358	241.6215	481.2518	241.1295	V	571.4178	286.2125	554.3912	277.6992			5
6	***612.3464***	306.6768	595.3198	298.1636	594.3358	297.6715	L	472.3493	236.6783	455.3228	228.1650			4
7	***725.4305***	363.2189	708.4039	354.7056	707.4199	354.2136	L	**359.2653**	180.1363	342.2387	171.6230			3
8	***824.4989***	412.7531	807.4723	404.2398	806.4883	403.7478	V	**246.1812**	123.5942	229.1547	115.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RADGVLLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G61600.1

Score	Mr(calc)	Delta	Sequence
33.4	969.5971	0.0002	RADGVLLVK
33.4	969.5971	0.0002	RLNDLLVK
18.1	969.5971	0.0002	RINDLVLK
12.8	969.5984	-0.0011	RLWRLAR
11.5	969.5971	0.0002	VISKAISPR
7.3	969.5971	0.0002	RIKLSPEK
6.3	969.5971	0.0002	LQLKEIAR
2.9	969.5971	0.0002	LNVVVISAR
2.4	969.5971	0.0002	NKKKPLDK
0.8	969.5971	0.0002	ALRAGLLEK

AT1G62020.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RGTGGSAVFIAR**
Found in **AT1G62020.1** in **TAIR_Arabidopsis**, Symbols: | coatomer protein complex, subunit alpha, putative | chr1:22923479-22927393 FORWARD

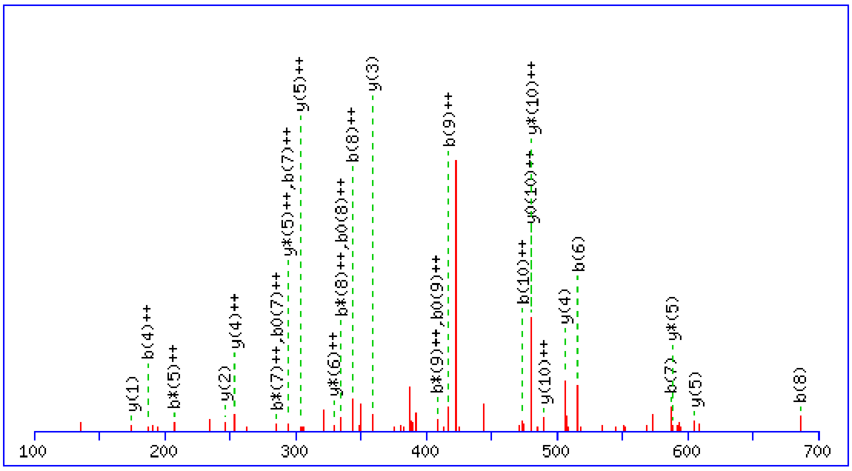
Match to Query 3771: 1190.652045 from(397.891291,3+) index(1290)
Title: Elution from: 20.827 to 20.827 scan no 1866 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

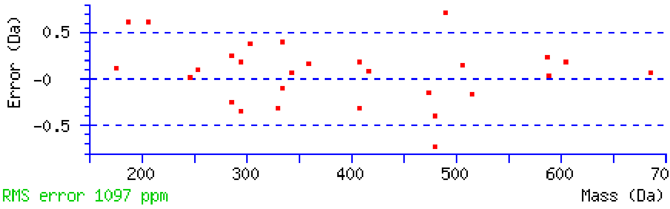
Label all possible matches ○ Label matches used for scoring ●

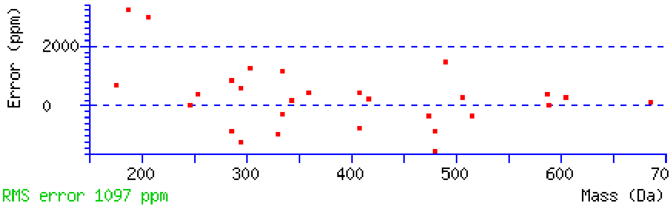
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1190.6520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.011
Matches : 28/116 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	214.1299	107.5686	197.1033	99.0553			G	1035.5582	518.2827	1018.5316	509.7694	1017.5476	509.2774	11
3	315.1775	158.0924	298.1510	149.5791	297.1670	149.0871	T	978.5367	489.7720	961.5102	481.2587	960.5261	480.7667	10
4	372.1990	***186.6031***	355.1724	178.0899	354.1884	177.5979	G	877.4890	439.2482	860.4625	430.7349	859.4785	430.2429	9
5	429.2205	215.1139	412.1939	206.6006	411.2099	206.1086	G	820.4676	410.7374	803.4410	402.2241	802.4570	401.7321	8
6	**516.2525**	258.6299	499.2259	250.1166	498.2419	249.6246	S	763.4461	382.2267	746.4196	373.7134	745.4355	373.2214	7
7	**587.2896**	***294.1484***	570.2631	285.6352	569.2790	285.1432	A	676.4141	338.7107	659.3875	330.1974			6
8	**686.3580**	***343.6826***	669.3315	335.1694	668.3474	334.6774	V	***605.3770***	303.1921	588.3504	294.6788			5
9	833.4264	***417.2169***	816.3999	408.7036	815.4159	408.2116	F	***506.3085***	253.6579	489.2820	245.1446			4
10	946.5105	***473.7589***	929.4839	465.2456	928.4999	464.7536	I	***359.2401***	180.1237	342.2136	171.6104			3
11	1017.5476	509.2774	1000.5211	500.7642	999.5370	500.2722	A	***246.1561***	123.5817	229.1295	115.0684			2
12							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of RGTGGSAVFIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G62020.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.3	1190.6520	0.0000	RGTGGSAVFIAR
10.7	1190.6547	-0.0026	YLTEALGPLSK
4.3	1190.6520	0.0001	VPLPAPRNDGR
3.1	1190.6554	-0.0033	CSVAKTRLTR
1.2	1190.6520	0.0001	YDKLRNVGAR

Mascot: http://www.matrixscience.com/

AT1G62380.1

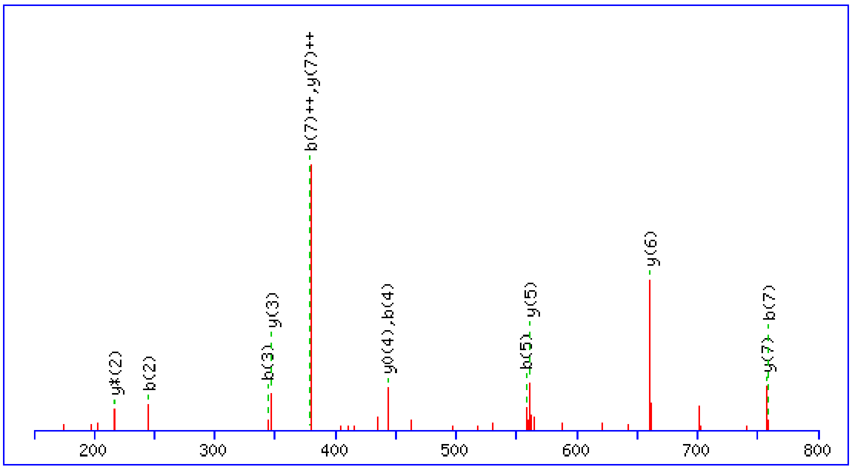
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPVVDLSK**
Found in **AT1G62380.1** in **TAIR_Arabidopsis**, Symbols: ATACO2, ACO2 | ACO2 (ACC OXIDASE 2) | chr1:23086005-23087733 FORWARD

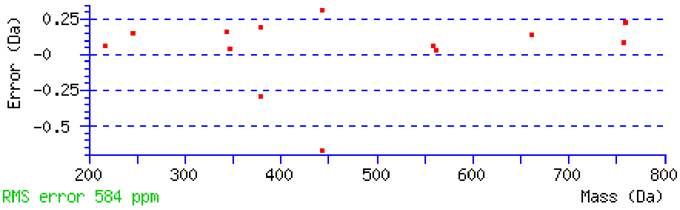
Match to Query 1716: 903.506846 from(452.760699,2+) index(5543)
Title: Elution from: 49.568 to 49.568 scan no 6975 cid35.00 polarity:+
Data file 0-2_1.mgf

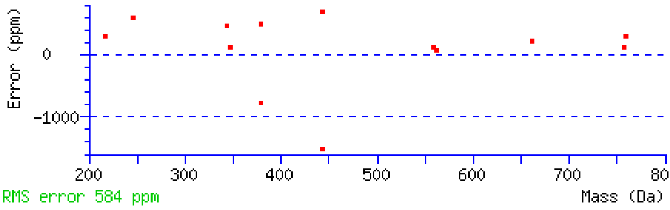
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 903.5066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.00032
Matches : 13/60 fragment ions using 17 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415			F							8
2	***245.1285***	123.0679			P	***757.4454***	379.2264	740.4189	370.7131	739.4349	370.2211	7
3	***344.1969***	172.6021			V	***660.3927***	330.7000	643.3661	322.1867	642.3821	321.6947	6
4	***443.2653***	222.1363			V	***561.3243***	281.1658	544.2977	272.6525	543.3137	272.1605	5
5	***558.2922***	279.6498	540.2817	270.6445	D	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
6	671.3763	336.1918	653.3657	327.1865	L	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
7	***758.4083***	379.7078	740.3978	370.7025	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FPVVDLSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.6	903.5066	0.0003	FPVVDLSK
7.2	903.5072	-0.0004	RSVKQMR

AT1G62380.1

6.9	903.5072	-0.0004	MARINRK
2.6	903.5072	-0.0004	MGRGSLRK
1.6	903.5072	-0.0004	KVSRCVR
1.2	903.5072	-0.0004	MISRNKR
1.0	903.5072	-0.0004	RAKGLGMR
0.4	903.5066	0.0003	VLVAYDPK
0.4	903.5066	0.0003	LPEVYVGK
0.2	903.5066	0.0003	TDPFLALK

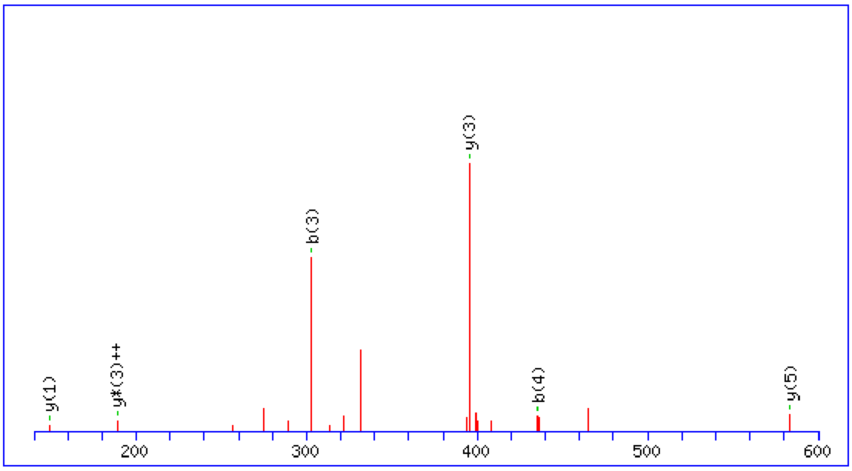
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGQMLK**
Found in **AT1G62430.1** in **TAIR_Arabidopsis**, Symbols: ATCDS1 | ATCDS1 (CDP-diacylglycerol synthase 1); phosphatidate cytidylyltransferase | chr1:23109939-23112588 REVERSE

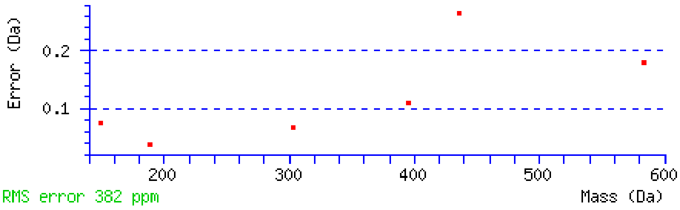
Match to Query 638: 696.369250 from(349.191901,2+) index(7126)
Title: Elution from: 63.208 to 63.208 scan no 9204 cid35.00 polarity:+
Data file D12h-3_1.mgf

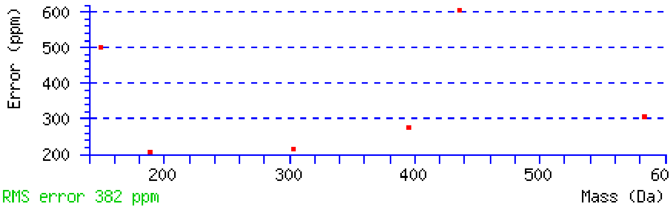
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 696.3705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.037
Matches : 6/36 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	115.0884	58.0478			L					6
2	173.1069	87.0571			G	***583.2966***	292.1520	565.2731	283.1402	5
3	***303.1595***	152.0834	285.1359	143.0716	Q	525.2781	263.1427	507.2546	254.1309	4
4	***435.1970***	218.1022	417.1735	209.0904	M	***395.2255***	198.1164	377.2019	189.1046	3
5	549.2781	275.1427	531.2546	266.1309	L	263.1880	132.0976	245.1644	123.0858	2
6					K	***149.1069***	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LGQMLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.9	696.3705	-0.0012	LGQMLK
18.0	696.3705	-0.0012	LQGLMK
18.0	696.3693	-0.0001	LWPFK

AT1G62430.1

9.8	696.3693	-0.0001	WLPFK
7.3	696.3705	-0.0012	IAMGIGK
7.3	696.3705	-0.0012	ICVAVK
5.0	696.3705	-0.0012	ANMIIK
2.0	696.3693	-0.0001	LFPWK

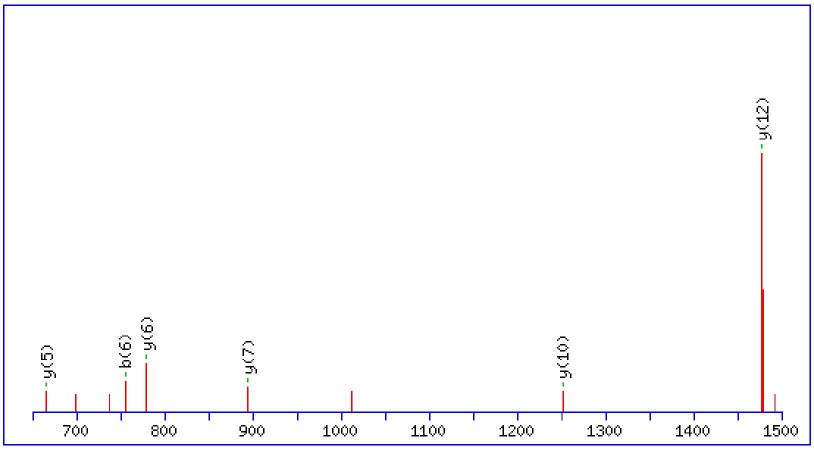
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSYEDIPEDLEDLAQEYR**
Found in **AT1G62750.1** in **TAIR_Arabidopsis**, Symbols: ATSCO1, ATSCO1/CPEF-G, SCO1 | ATSCO1/ATSCO1/CPEF-G/SCO1 (SNOWY COTYLEDON1); translation elongation factor/ translation factor, nucleic acid binding | chr1:23237287-23239986 REVERSE

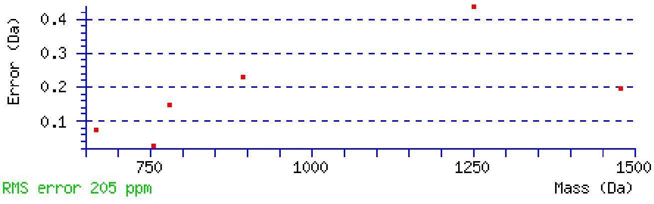
Match to Query 10194: 2230.991654 from(1116.503103,2+) index(11238)
Title: Elution from: 120.086 to 120.086 scan no 16770 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

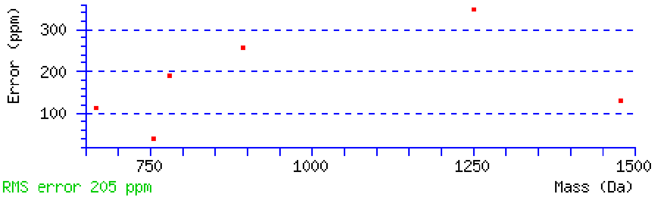


Monoisotopic mass of neutral peptide Mr(calc): 2230.9906
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0013
Matches : 6/170 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							18
2	235.1077	118.0575			217.0972	109.0522	S	2084.9295	1042.9684	2067.9029	1034.4551	2066.9189	1033.9631	17
3	398.1710	199.5892			380.1605	190.5839	Y	1997.8975	999.4524	1980.8709	990.9391	1979.8869	990.4471	16
4	527.2136	264.1105			509.2031	255.1052	E	1834.8341	917.9207	1817.8076	909.4074	1816.8236	908.9154	15
5	642.2406	321.6239			624.2300	312.6186	D	1705.7915	853.3994	1688.7650	844.8861	1687.7810	844.3941	14
6	755.3246	378.1660			737.3141	369.1607	I	1590.7646	795.8859	1573.7380	787.3727	1572.7540	786.8807	13
7	852.3774	426.6923			834.3668	417.6871	P	***1477.6805***	739.3439	1460.6540	730.8306	1459.6700	730.3386	12
8	981.4200	491.2136			963.4094	482.2084	E	1380.6278	690.8175	1363.6012	682.3042	1362.6172	681.8122	11
9	1096.4469	548.7271			1078.4364	539.7218	D	***1251.5852***	626.2962	1234.5586	617.7830	1233.5746	617.2909	10
10	1209.5310	605.2691			1191.5204	596.2639	L	1136.5582	568.7828	1119.5317	560.2695	1118.5477	559.7775	9
11	1338.5736	669.7904			1320.5630	660.7852	E	1023.4742	512.2407	1006.4476	503.7274	1005.4636	503.2354	8
12	1453.6005	727.3039			1435.5900	718.2986	D	***894.4316***	447.7194	877.4050	439.2062	876.4210	438.7141	7
13	1566.6846	783.8459			1548.6740	774.8407	L	***779.4046***	390.2060	762.3781	381.6927	761.3941	381.2007	6
14	1637.7217	819.3645			1619.7112	810.3592	A	***666.3206***	333.6639	649.2940	325.1506	648.3100	324.6586	5
15	1765.7803	883.3938	1748.7538	874.8805	1747.7697	874.3885	Q	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	4
16	1894.8229	947.9151	1877.7963	939.4018	1876.8123	938.9098	E	467.2249	234.1161	450.1983	225.6028	449.2143	225.1108	3
17	2057.8862	1029.4468	2040.8597	1020.9335	2039.8757	1020.4415	Y	338.1823	169.5948	321.1557	161.0815			2
18							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 205 ppm



RMS error 205 ppm

AT1G62750.1

NCBI **BLAST** search of FSYEDIPEDLEDLAQEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.5	2230.9906	0.0011	FSYEDIPEDLEDLAQEYR
14.5	2230.9908	0.0008	NMEIQSACAMLETQIDSFK
14.5	2230.9908	0.0008	NMEIQSACAMLETQIDSFK

AT1G62760.1

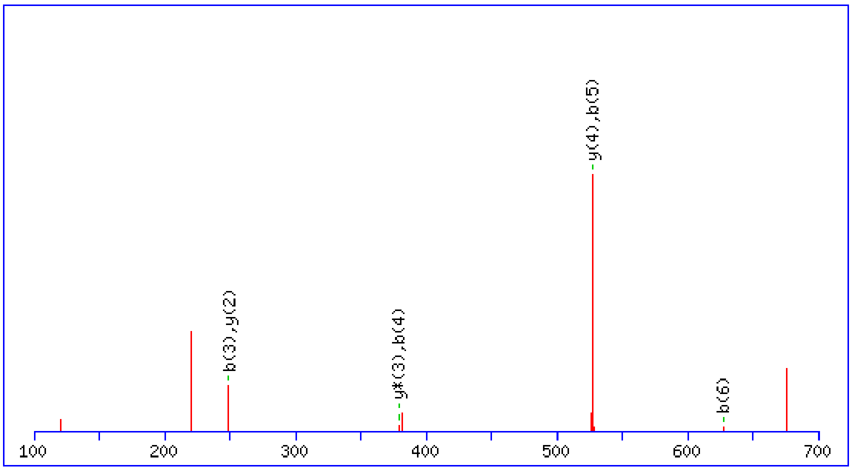
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SASKFVK**
Found in **AT1G62760.1** in **TAIR_Arabidopsis**, Symbols: | invertase/pectin methylesterase inhibitor family protein | chr1:23241239-23242177 REVERSE

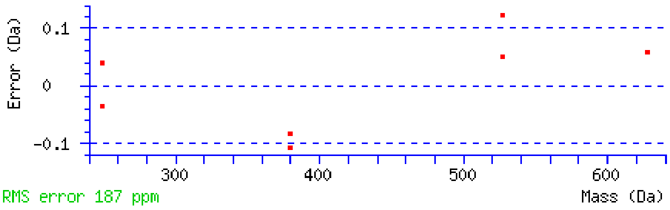
Match to Query 880: 774.413562 from(388.214057,2+) index(5718)
Title: Elution from: 51.135 to 51.135 scan no 7292 cid35.00 polarity:+
Data file 0-2_2.mgf

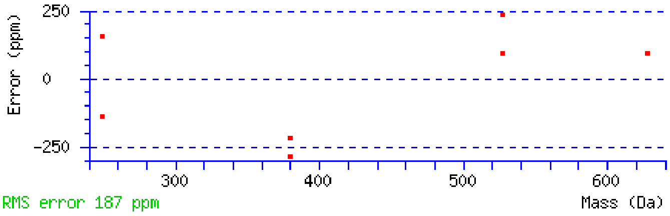
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 774.4118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.019
Matches : 7/58 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							7
2	161.0705	81.0389			143.0599	72.0336	A	687.3900	344.1986	669.3664	335.1869	669.3795	335.1934	6
3	***249.0996***	125.0534			231.0890	116.0481	S	615.3559	308.1816	597.3323	299.1698	597.3453	299.1763	5
4	***379.1886***	190.0979	361.1650	181.0861	361.1780	181.0926	K	**527.3268**	264.1670	509.3032	255.1552			4
5	***527.2540***	264.1307	509.2304	255.1189	509.2435	255.1254	F	397.2378	199.1225	379.2142	190.1107			3
6	***627.3195***	314.1634	609.2959	305.1516	609.3089	305.1581	V	**249.1723**	125.0898	231.1487	116.0780			2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SASKFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.2	774.4118	0.0018	SASKFVK
14.1	774.4140	-0.0005	VFGGLFK

14.1	774.4140	-0.0005	VFLFNK
10.4	774.4140	-0.0005	VFNFKI
3.6	774.4140	-0.0005	NFFLVK
3.6	774.4145	-0.0009	RSFVVR

AT1G62780.1

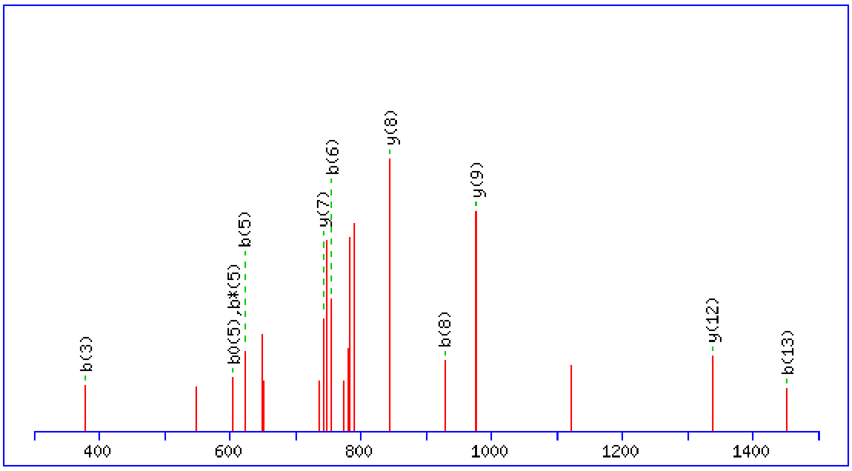
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQNELMTATNSLTK**
Found in **AT1G62780.1** in **TAIR_Arabidopsis**, Symbols: | similar to hypothetical protein [Vitis vinifera] (GB:CAN83165.1) | chr1:23253014-23254731 REVERSE

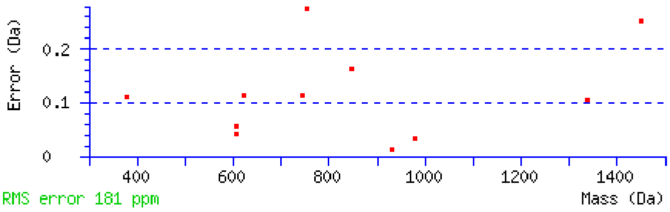
Match to Query 7085: 1598.704658 from(800.359605,2+) index(5615)
Title: Elution from: 49.893 to 49.893 scan no 7110 cid35.00 polarity:+
Data file 0-3_2.mgf

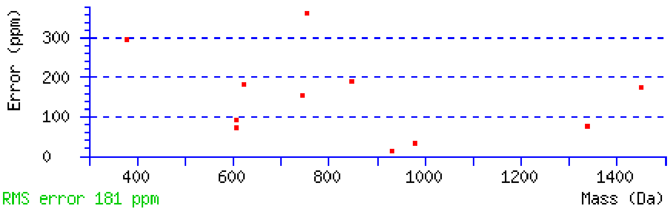
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1598.7005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00087
Matches : 11/146 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	133.0448	67.0260					M							14
2	263.0974	132.0524	245.0739	123.0406			Q	1467.6702	734.3387	1449.6466	725.3270	1449.6596	725.3335	13
3	*379.1344*	190.0709	361.1109	181.0591			N	*1337.6176*	669.3124	1319.5940	660.3006	1319.6070	660.3071	12
4	509.1741	255.0907	491.1505	246.0789	491.1635	246.0854	E	1221.5806	611.2939	1203.5570	602.2821	1203.5700	602.2886	11
5	*623.2552*	312.1312	605.2316	303.1194	605.2446	303.1259	L	1091.5409	546.2741	1073.5174	537.2623	1073.5304	537.2688	10
6	*755.2927*	378.1500	737.2691	369.1382	737.2821	369.1447	M	*977.4598*	489.2336	959.4363	480.2218	959.4493	480.2283	9
7	857.3374	429.1723	839.3138	420.1605	839.3268	420.1671	T	*845.4223*	423.2148	827.3987	414.2030	827.4118	414.2095	8
8	*929.3715*	465.1894	911.3480	456.1776	911.3610	456.1841	A	*743.3776*	372.1924	725.3540	363.1806	725.3670	363.1872	7
9	1031.4163	516.2118	1013.3927	507.2000	1013.4057	507.2065	T	671.3435	336.1754	653.3199	327.1636	653.3329	327.1701	6
10	1147.4533	574.2303	1129.4297	565.2185	1129.4427	565.2250	N	569.2987	285.1530	551.2752	276.1412	551.2882	276.1477	5
11	1235.4823	618.2448	1217.4587	609.2330	1217.4718	609.2395	S	453.2617	227.1345	435.2382	218.1227	435.2512	218.1292	4
12	1349.5634	675.2853	1331.5398	666.2736	1331.5529	666.2801	L	365.2327	183.1200	347.2091	174.1082	347.2221	174.1147	3
13	*1451.6081*	726.3077	1433.5845	717.2959	1433.5976	717.3024	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MQNELMTATNSLTK

AT1G62780.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.3	1598.7005	0.0042	MQNELMTATNSLTK
22.9	1598.7074	-0.0028	QFLMETSNELDIK
11.2	1598.7074	-0.0028	YAQEMQSIDELLK
8.4	1598.7094	-0.0047	WLSGVGFARGGGGGGDK
6.3	1598.7005	0.0042	IMVEEEGAEMRKK
4.2	1598.7054	-0.0007	DPFQQMIMLERR
3.6	1598.7027	0.0020	SKLVDMCQEFTPK
3.4	1598.7052	-0.0005	MDKTSSPESATISTK
3.0	1598.7005	0.0042	MLQSSGSCLINDIK
2.1	1598.7042	0.0004	MPEWTPDVRFFR

AT1G62820.1

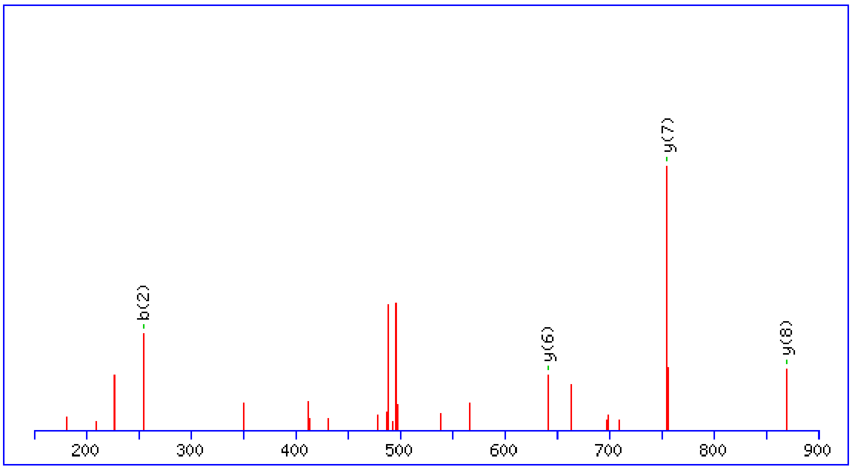
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HILTSIGEK**
Found in **AT1G62820.1** in **TAIR_Arabidopsis**, Symbols: | calmodulin, putative | chr1:23267487-23267933 REVERSE

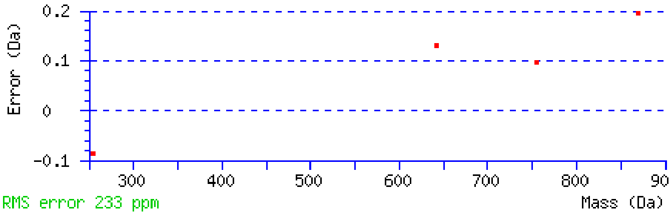
Match to Query 2553: 1008.523946 from(505.269249,2+) index(1435)
Title: Elution from: 19.526 to 19.526 scan no 1934 cid35.00 polarity:+
Data file 0-1_3.mgf

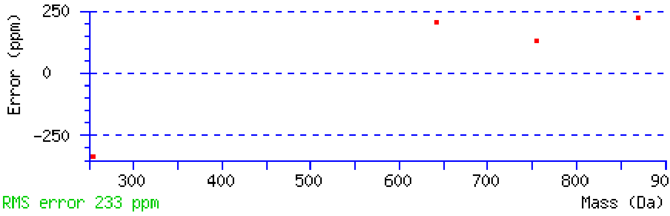
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1008.5248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.024
Matches : 4/72 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	141.0573	71.0323			H							9
2	255.1384	128.0728			I	***869.4821***	435.2447	851.4585	426.2329	851.4715	426.2394	8
3	369.2195	185.1134			L	***755.4010***	378.2041	737.3774	369.1923	737.3904	369.1988	7
4	471.2642	236.1357	453.2536	227.1305	T	***641.3199***	321.1636	623.2963	312.1518	623.3093	312.1583	6
5	559.2933	280.1503	541.2827	271.1450	S	539.2752	270.1412	521.2516	261.1294	521.2646	261.1359	5
6	673.3744	337.1908	655.3638	328.1855	I	451.2461	226.1267	433.2225	217.1149	433.2355	217.1214	4
7	731.3929	366.2001	713.3823	357.1948	G	337.1650	169.0861	319.1414	160.0743	319.1544	160.0809	3
8	861.4325	431.2199	843.4219	422.2146	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of HILTSIGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.6	1008.5248	-0.0009	HILTSIGEK

AT1G62820.1

Mascot: http://www.matrixscience.com/

AT1G62950.1

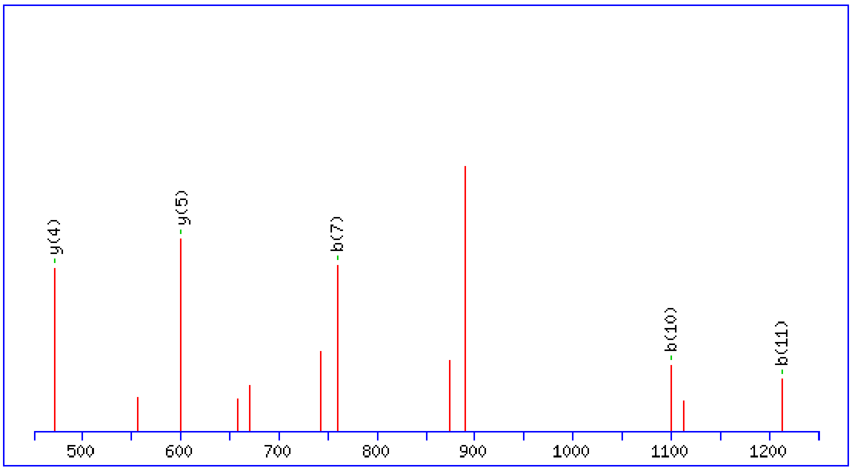
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGLICTTENPLK**
Found in **AT1G62950.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:23318959-23321726 FORWARD

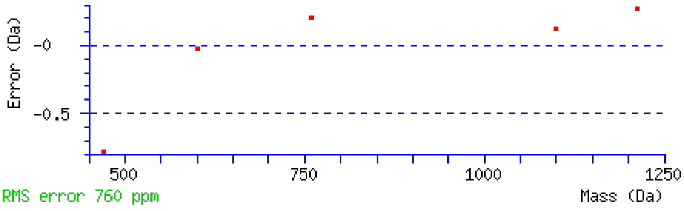
Match to Query 5043: 1357.724622 from(679.869587,2+) index(9799)
Title: Elution from: 91.818 to 91.818 scan no 13787 cid35.00 polarity:+
Data file D6h-1_3.mgf

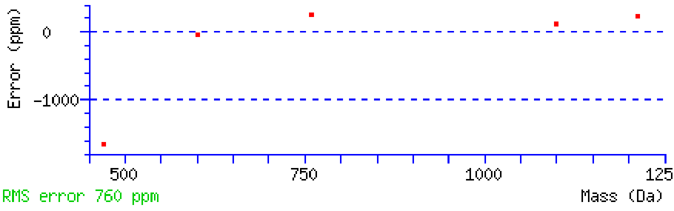
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1357.7275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22  Expect: 0.019
Matches : 5/98 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							12
2	171.1128	86.0600					G	1245.6508	623.3290	1228.6242	614.8157	1227.6402	614.3237	11
3	284.1969	142.6021					L	1188.6293	594.8183	1171.6027	586.3050	1170.6187	585.8130	10
4	397.2809	199.1441					I	1075.5452	538.2762	1058.5187	529.7630	1057.5347	529.2710	9
5	557.3116	279.1594					C	962.4612	481.7342	945.4346	473.2209	944.4506	472.7289	8
6	658.3593	329.6833			640.3487	320.6780	T	802.4305	401.7189	785.4040	393.2056	784.4199	392.7136	7
7	***759.4069***	380.2071			741.3964	371.2018	T	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	6
8	888.4495	444.7284			870.4390	435.7231	E	***600.3352***	300.6712	583.3086	292.1579	582.3246	291.6659	5
9	1002.4925	501.7499	985.4659	493.2366	984.4819	492.7446	N	***471.2926***	236.1499	454.2660	227.6366			4
10	***1099.5452***	550.2762	1082.5187	541.7630	1081.5347	541.2710	P	357.2496	179.1285	340.2231	170.6152			3
11	***1212.6293***	606.8183	1195.6027	598.3050	1194.6187	597.8130	L	260.1969	130.6021	243.1703	122.0888			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LGLICTTENPLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G62950.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.4	1357.7275	-0.0029	LGLICTTENPLK
13.8	1357.7275	-0.0029	LMSLAKDNPELK
2.3	1357.7275	-0.0029	EIVEKQSPGLMK
1.4	1357.7275	-0.0029	CILGGEVIGEALK

Mascot: http://www.matrixscience.com/

AT1G62960.1

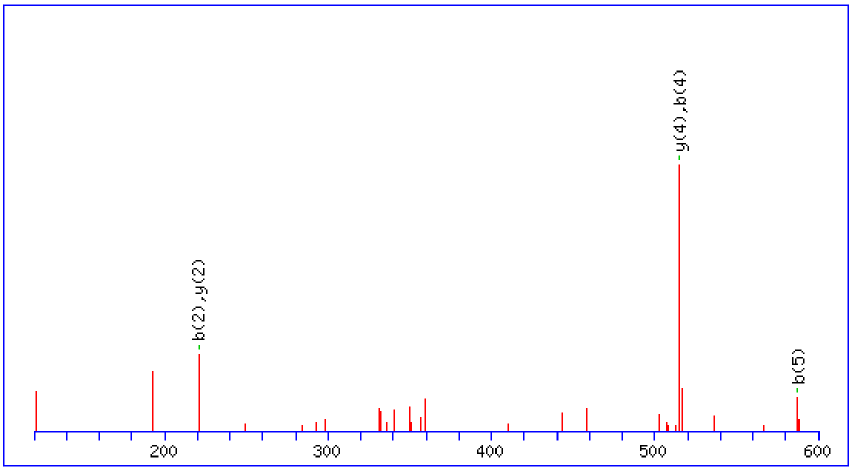
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFYQAK**
Found in **AT1G62960.1** in **TAIR_Arabidopsis**, Symbols: ACS10 | ACS10 (ACC SYNTHASE 10); 1-aminocyclopropane-1-carboxylate synthase | chr1:23321936-23323894 REVERSE

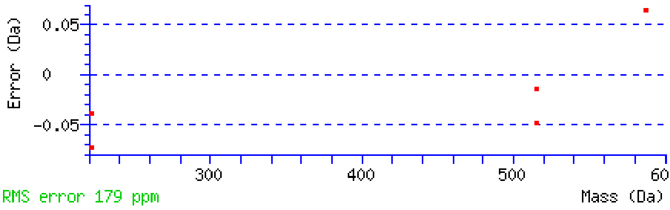
Match to Query 640: 734.345894 from(368.180223,2+) index(492)
Title: Elution from: 10.770 to 10.770 scan no 777 cid35.00 polarity:+
Data file D1d-2_3.mgf

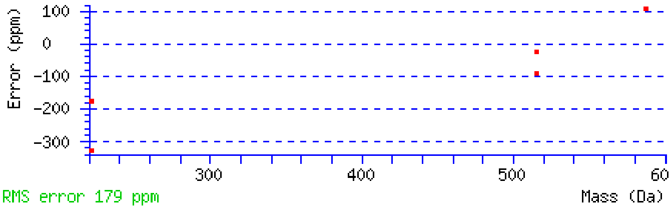
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 734.3463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.023
Matches : 5/34 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	73.0414	37.0244			**A**					**6**
2	***221.1069***	111.0571			**F**	663.3195	332.1634	645.2959	323.1516	**5**
3	385.1672	193.0873			**Y**	**515.2540**	258.1307	497.2305	249.1189	**4**
4	***515.2199***	258.1136	497.1963	249.1018	**Q**	351.1937	176.1005	333.1701	167.0887	**3**
5	***587.2540***	294.1307	569.2305	285.1189	**A**	**221.1410**	111.0741	203.1174	102.0624	**2**
6					**K**	149.1069	75.0571	131.0833	66.0453	**1**





NCBI **BLAST** search of AFYQAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.0	734.3463	-0.0004	AFYQAK
8.9	734.3463	-0.0004	AYFQAK
8.9	734.3441	0.0018	IEEHAK

AT1G62960.1

8.9	734.3463	-0.0004	NFTFAK
0.9	734.3468	-0.0009	KSHSHK
0.9	734.3441	0.0018	NPAAEPK

Mascot: http://www.matrixscience.com/

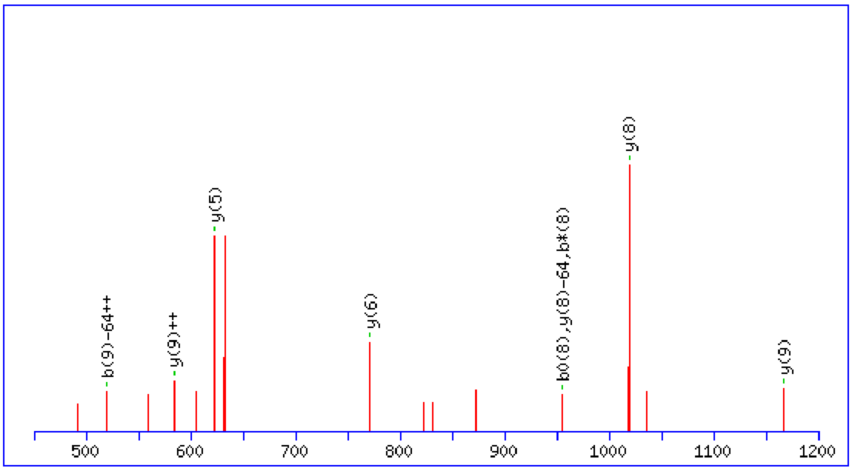
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFSRMVDPER**
Found in **AT1G63680.1** in **TAIR_Arabidopsis**, Symbols: ATMURE, PDE316 | ATMURE/PDE316 (PIGMENT DEFECTIVE EMBRYO); ATP binding / ligase | chr1:23618124-23620764 FORWARD

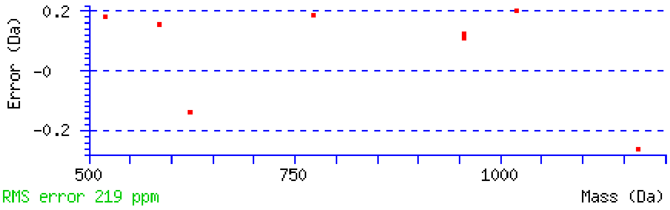
Match to Query 4827: 1280.575904 from(641.295228,2+) index(3123)
Title: Elution from: 31.316 to 31.316 scan no 3889 cid35.00 polarity:+
Data file C7-3_1.mgf

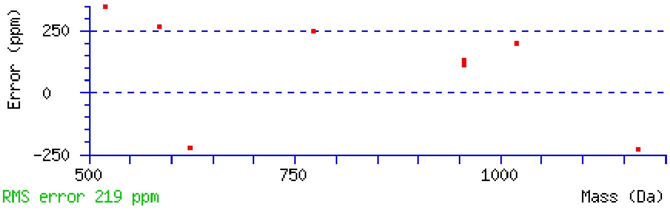
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1280.5760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.028
Matches : 9/150 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							10
2	263.1538	132.0805					F	***1167.5021***	584.2547	1149.4786	575.2429	1149.4916	575.2494	9
3	351.1829	176.0951			333.1723	167.0898	S	***1019.4367***	510.2220	1001.4131	501.2102	1001.4261	501.2167	8
4	511.2721	256.1397	493.2486	247.1279	493.2616	247.1344	R	931.4076	466.2075	913.3840	457.1957	913.3971	457.2022	7
5	659.3046	330.1559	641.2810	321.1441	641.2940	321.1506	M	***771.3184***	386.1628	753.2948	377.1510	753.3078	377.1575	6
6	759.3700	380.1886	741.3464	371.1769	741.3595	371.1834	V	***623.2859***	312.1466	605.2624	303.1348	605.2754	303.1413	5
7	875.3940	438.2006	857.3704	429.1888	857.3834	429.1954	D	523.2205	262.1139	505.1969	253.1021	505.2099	253.1086	4
8	973.4438	487.2255	955.4202	478.2137	955.4332	478.2203	P	407.1965	204.1019	389.1729	195.0901	389.1860	195.0966	3
9	1103.4834	552.2454	1085.4598	543.2336	1085.4729	543.2401	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LFSRMVDPER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G63680.1

Score	Mr(calc)	Delta	Sequence
25.3	1280.5760	-0.0001	LFSRMVDPER
4.0	1280.5789	-0.0030	CYIVLDDMIK
3.9	1280.5733	0.0026	LMDELDKNFK
3.1	1280.5760	-0.0001	SFRGPGMAEGLK
3.1	1280.5733	0.0026	CYEEKLDALK
2.7	1280.5733	0.0026	EQMGYTIDALK
2.3	1280.5759	-0.0000	FLQGEMQQLR
1.8	1280.5764	-0.0005	MEQGSLRERR
1.6	1280.5784	-0.0025	TGSNKTATTDAAK
1.5	1280.5733	0.0026	NEDMKVFLEK

AT1G63710.1

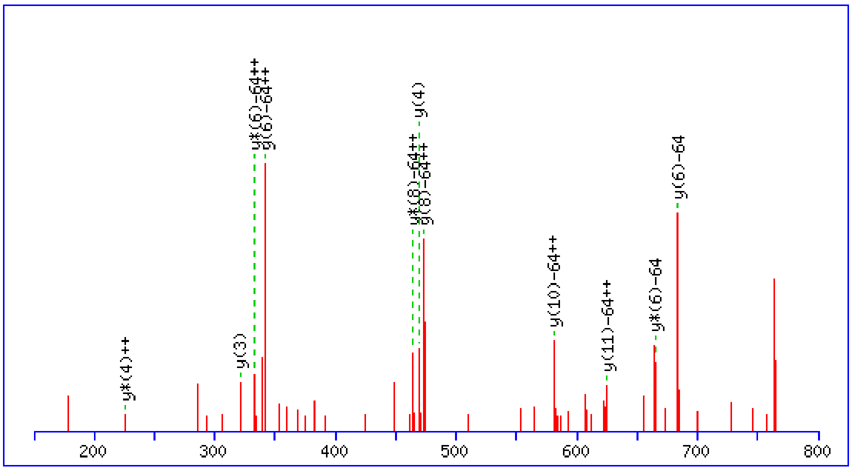
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSLTLFMKFGLK**
Found in **AT1G63710.1** in **TAIR_Arabidopsis**, Symbols: CYP86A7 | CYP86A7 (cytochrome P450, family 86, subfamily A, polypeptide 7); oxygen binding | chr1:23636023-23637594 REVERSE

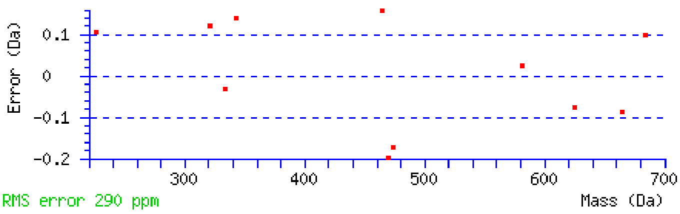
Match to Query 5870: 1444.721217 from(482.581015,3+) index(859)
Title: Elution from: 13.640 to 13.640 scan no 1206 cid35.00 polarity:+
Data file C7-3_2.mgf

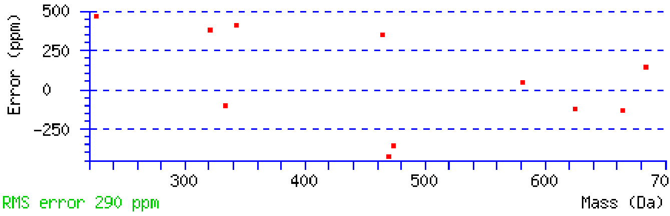
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1444.7251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.039
Matches : 12/158 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							12
2	221.0739	111.0406			203.0633	102.0353	S	1249.6965	625.3519	1231.6729	616.3401	1231.6860	616.3466	11
3	335.1550	168.0811			317.1444	159.0758	L	1161.6675	581.3374	1143.6439	572.3256	1143.6569	572.3321	10
4	437.1997	219.1035			419.1891	210.0982	T	1047.5864	524.2968	1029.5628	515.2850	1029.5758	515.2915	9
5	551.2808	276.1440			533.2702	267.1387	L	945.5417	473.2745	927.5181	464.2627			8
6	699.3462	350.1767			681.3357	341.1715	F	831.4606	416.2339	813.4370	407.2221			7
7	783.3804	392.1938			765.3698	383.1885	M	***683.3951***	342.2012	665.3715	333.1894			6
8	913.4694	457.2383	895.4458	448.2265	895.4588	448.2331	K	599.3610	300.1841	581.3374	291.1723			5
9	1061.5349	531.2711	1043.5113	522.2593	1043.5243	522.2658	F	***469.2719***	235.1396	451.2483	226.1278			4
10	1119.5534	560.2803	1101.5298	551.2685	1101.5428	551.2750	G	***321.2065***	161.1069	303.1829	152.0951			3
11	1233.6344	617.3209	1215.6109	608.3091	1215.6239	608.3156	L	263.1880	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MSLTLFMKFGLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G63710.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.7	1444.7251	-0.0038	MSLTLFMKFGLK
17.0	1444.7199	0.0014	VCVIGAGPAGLVSAR

AT1G63770.1

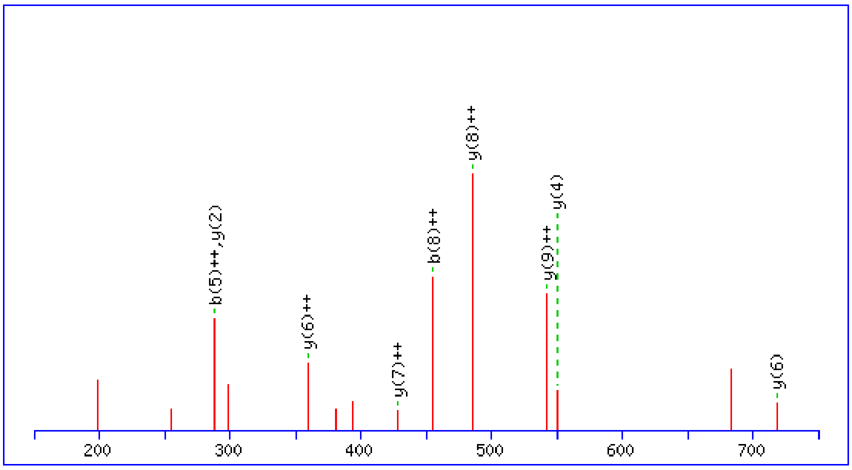
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDHPAFDLR**
Found in **AT1G63770.1** in **TAIR_Arabidopsis**, Symbols: | peptidase M1 family protein | chr1:23661913-23667906 REVERSE

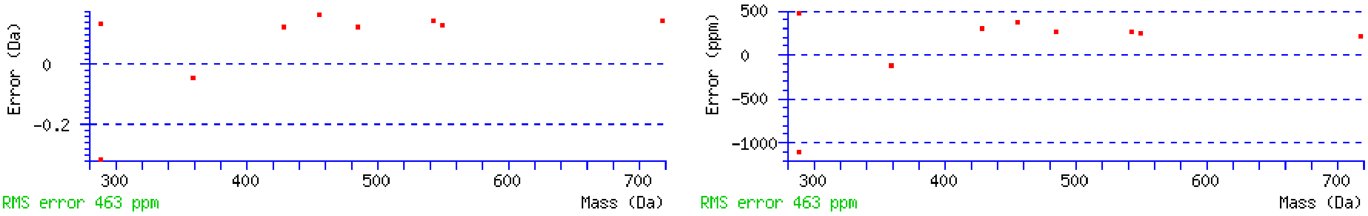
Match to Query 3588: 1195.635273 from(399.552367,3+) index(4964)
Title: Elution from: 47.802 to 47.802 scan no 6378 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1195.6349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0037
Matches : 9/82 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							10
2	227.1754	114.0913			L	1083.5582	542.2827	1066.5316	533.7694	1065.5476	533.2774	9
3	342.2023	171.6048	324.1918	162.5995	D	970.4741	485.7407	953.4476	477.2274	952.4635	476.7354	8
4	479.2613	240.1343	461.2507	231.1290	H	855.4472	428.2272	838.4206	419.7139	837.4366	419.2219	7
5	576.3140	**288.6606**	558.3035	279.6554	P	***718.3883***	359.6978	701.3617	351.1845	700.3777	350.6925	6
6	647.3511	324.1792	629.3406	315.1739	A	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	5
7	794.4196	397.7134	776.4090	388.7081	F	***550.2984***	275.6528	533.2718	267.1395	532.2878	266.6475	4
8	909.4465	**455.2269**	891.4359	446.2216	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	1022.5306	511.7689	1004.5200	502.7636	L	***288.2030***	144.6051	271.1765	136.0919			2
10					R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of LLDHPAFDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G63770.1

30.0	1195.6349	0.0003	LLDHPAFDLR
4.1	1195.6356	-0.0004	RHLMTGGPRR
3.2	1195.6349	0.0003	ILKNGDFYAR
2.9	1195.6350	0.0003	TWVVPDPNLR
0.6	1195.6349	0.0003	YFQQLASALR

AT1G63770.2

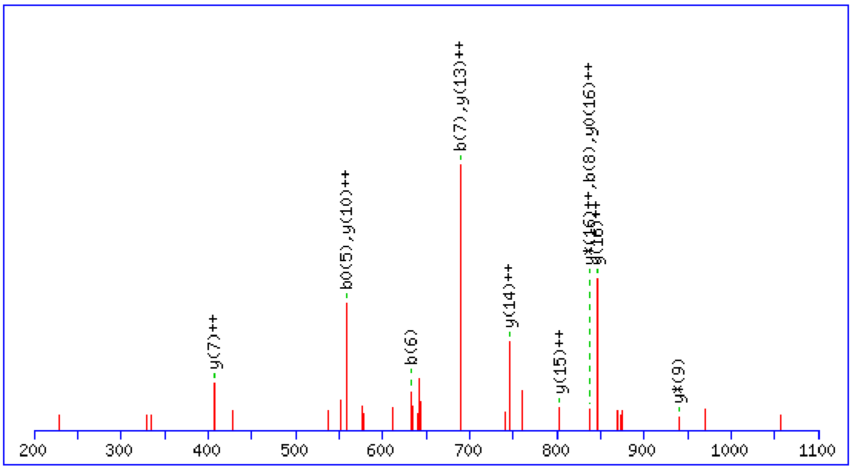
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYSLIGGFCGSPVNFHAK**
Found in **AT1G63770.2** in **TAIR_Arabidopsis**, Symbols: | peptidase M1 family protein | chr1:23661828-23667906 REVERSE

Match to Query 9190: 1951.959804 from(651.660544,3+) index(7867)
Title: Elution from: 68.775 to 68.775 scan no 10296 cid35.00 polarity:+
Data file C7-3_2.mgf

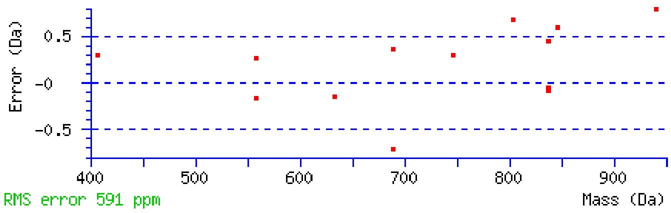
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

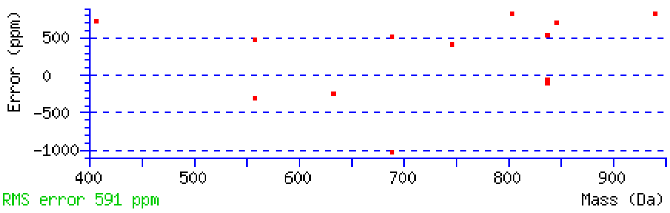


Monoisotopic mass of neutral peptide Mr(calc): 1951.9615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0035
Matches : 13/160 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							18
2	263.1390	132.0731					Y	1853.9003	927.4538	1836.8738	918.9405	1835.8898	918.4485	17
3	350.1710	175.5892			332.1605	166.5839	S	1690.8370	845.9221	1673.8104	837.4089	1672.8264	836.9168	16
4	463.2551	232.1312			445.2445	223.1259	L	1603.8050	802.4061	1586.7784	793.8928	1585.7944	793.4008	15
5	576.3392	288.6732			558.3286	279.6679	I	1490.7209	745.8641	1473.6943	737.3508	1472.7103	736.8588	14
6	**633.3606**	317.1840			615.3501	308.1787	G	1377.6368	689.3221	1360.6103	680.8088	1359.6263	680.3168	13
7	**690.3821**	345.6947			672.3715	336.6894	G	1320.6154	660.8113	1303.5888	652.2980	1302.6048	651.8060	12
8	**837.4505**	419.2289			819.4400	410.2236	F	1263.5939	632.3006	1246.5674	623.7873	1245.5833	623.2953	11
9	997.4812	499.2442			979.4706	490.2389	C	1116.5255	558.7664	1099.4989	550.2531	1098.5149	549.7611	10
10	1054.5026	527.7550			1036.4921	518.7497	G	956.4948	478.7511	939.4683	470.2378	938.4843	469.7458	9
11	1141.5347	571.2710			1123.5241	562.2657	S	899.4734	450.2403	882.4468	441.7271	881.4628	441.2350	8
12	1238.5874	619.7973			1220.5769	610.7921	P	812.4413	406.7243	795.4148	398.2110			7
13	1337.6558	669.3316			1319.6453	660.3263	V	715.3886	358.1979	698.3620	349.6847			6
14	1451.6988	726.3530	1434.6722	717.8397	1433.6882	717.3477	N	616.3202	308.6637	599.2936	300.1504			5
15	1598.7672	799.8872	1581.7406	791.3740	1580.7566	790.8819	F	502.2772	251.6423	485.2507	243.1290			4
16	1735.8261	868.4167	1718.7995	859.9034	1717.8155	859.4114	H	355.2088	178.1081	338.1823	169.5948			3
17	1806.8632	903.9352	1789.8367	895.4220	1788.8526	894.9300	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT1G63770.2





NCBI **BLAST** search of VYSLIGGFCGSPVNFHAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1951.9615	-0.0017	VYSLIGGFCGSPVNFHAK
5.4	1951.9594	0.0004	LNSLVMELDNMAKLSDK
2.4	1951.9608	-0.0010	MDMIKPDFQQIRRDK
2.4	1951.9561	0.0037	NIQEYMVQKLGIEEDK
1.1	1951.9599	-0.0001	GESEPIAAAAAVAGPSSPQSR
0.6	1951.9601	-0.0003	VFDLKNYTMLYSISDK

Mascot: http://www.matrixscience.com/

AT1G63880.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQQMGKR**
Found in **AT1G63880.1** in **TAIR_Arabidopsis**, Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr1:23716177-23719710 REVERSE

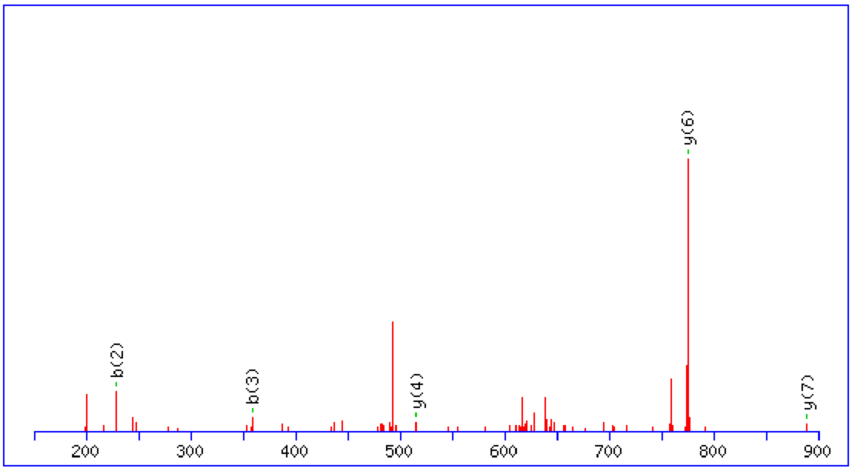
Match to Query 2313: 1002.506992 from(502.260772,2+) index(4293)
Title: Elution from: 39.011 to 39.011 scan no 5400 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

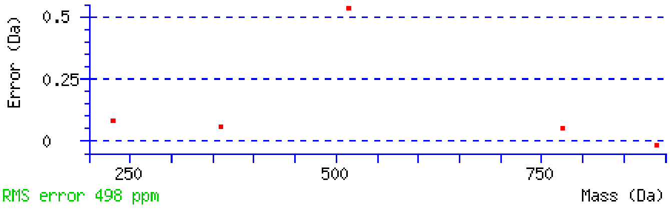
Label all possible matches ○ Label matches used for scoring ●

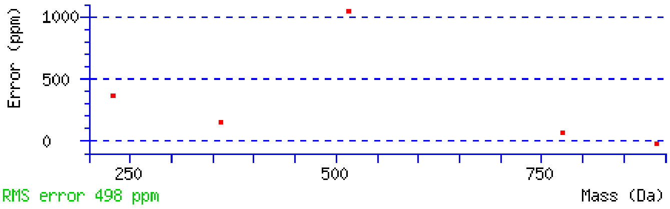
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1002.5073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.04
Matches : 5/80 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	115.0884	58.0478			L					8
2	***229.1695***	115.0884			L	***889.4335***	445.2204	871.4099	436.2086	7
3	***359.2221***	180.1147	341.1985	171.1029	Q	***775.3524***	388.1798	757.3288	379.1680	6
4	489.2748	245.1410	471.2512	236.1292	Q	645.2997	323.1535	627.2761	314.1417	5
5	637.3072	319.1572	619.2836	310.1454	M	***515.2471***	258.1272	497.2235	249.1154	4
6	695.3257	348.1665	677.3021	339.1547	G	367.2146	184.1109	349.1910	175.0992	3
7	825.4147	413.2110	807.3912	404.1992	K	309.1961	155.1017	291.1725	146.0899	2
8					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of LLQQMGKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G63880.1

23.8	1002.5073	-0.0003	LLQQMGKR
14.2	1002.5073	-0.0003	LLQRNMSK
9.5	1002.5046	0.0024	IQKMISEK
9.5	1002.5046	0.0024	LQKMISEK
1.1	1002.5073	-0.0003	LKMNEARK

AT1G63940.1

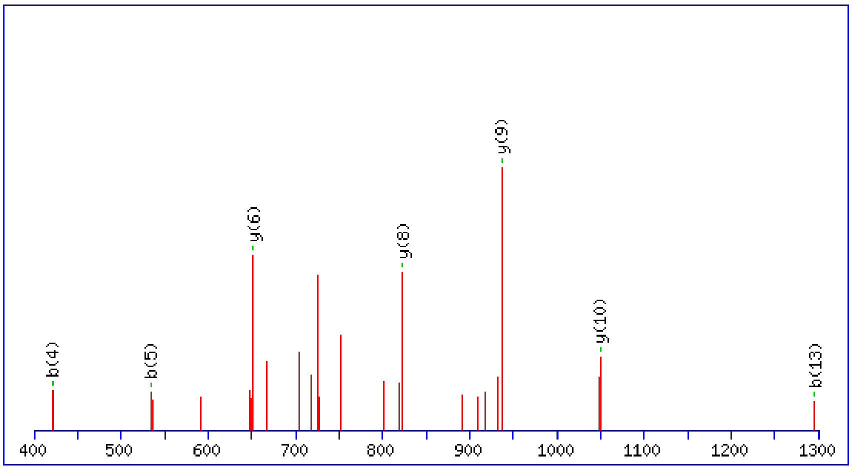
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGSLIIATGCTASR**
Found in **AT1G63940.1** in **TAIR_Arabidopsis**, Symbols: | monodehydroascorbate reductase, putative | chr1:23733869-23737197 FORWARD

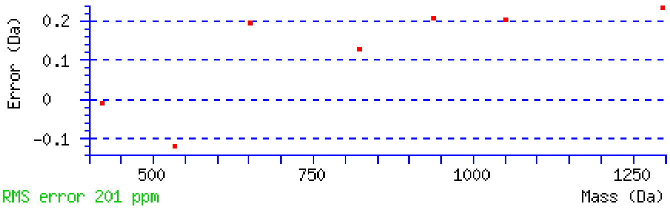
Match to Query 6262: 1468.733034 from(735.373793,2+) index(4664)
Title: Elution from: 42.559 to 42.559 scan no 5813 cid35.00 polarity:+
Data file C7-3_1.mgf

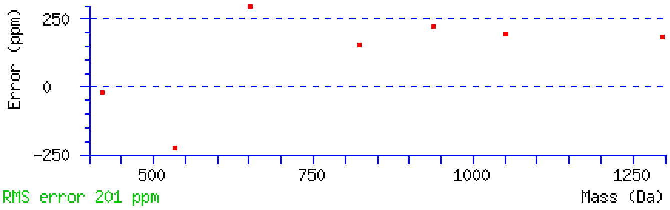
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.7344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00051
Matches : 7/124 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							14
2	221.0921	111.0497			G	1306.6784	653.8428	1289.6518	645.3295	1288.6678	644.8375	13
3	308.1241	154.5657	290.1135	145.5604	S	1249.6569	625.3321	1232.6304	616.8188	1231.6463	616.3268	12
4	***421.2082***	211.1077	403.1976	202.1024	L	1162.6249	581.8161	1145.5983	573.3028	1144.6143	572.8108	11
5	***534.2922***	267.6498	516.2817	258.6445	I	***1049.5408***	525.2740	1032.5143	516.7608	1031.5302	516.2688	10
6	647.3763	324.1918	629.3657	315.1865	I	***936.4567***	468.7320	919.4302	460.2187	918.4462	459.7267	9
7	718.4134	359.7103	700.4028	350.7051	A	***823.3727***	412.1900	806.3461	403.6767	805.3621	403.1847	8
8	819.4611	410.2342	801.4505	401.2289	T	752.3356	376.6714	735.3090	368.1581	734.3250	367.6661	7
9	876.4825	438.7449	858.4720	429.7396	G	***651.2879***	326.1476	634.2613	317.6343	633.2773	317.1423	6
10	1036.5132	518.7602	1018.5026	509.7550	C	594.2664	297.6368	577.2399	289.1236	576.2559	288.6316	5
11	1137.5609	569.2841	1119.5503	560.2788	T	434.2358	217.6215	417.2092	209.1083	416.2252	208.6162	4
12	1208.5980	604.8026	1190.5874	595.7973	A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
13	***1295.6300***	648.3186	1277.6195	639.3134	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YGSLIIATGCTASR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G63940.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.1	1468.7344	-0.0014	YGSLIIATGCTASR
0.9	1468.7305	0.0025	YELKDILGMEMK

AT1G63940.3

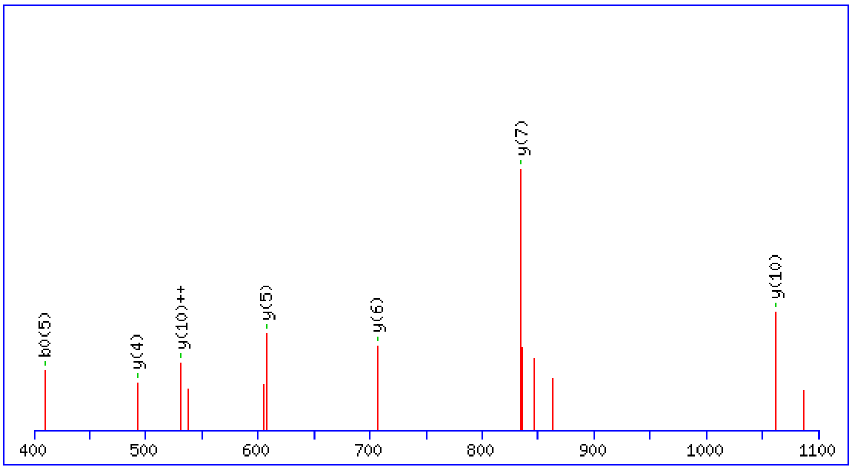
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIGGIQVDGLFR**
Found in **AT1G63940.3** in **TAIR_Arabidopsis**, Symbols: | monodehydroascorbate reductase, putative | chr1:23733869-23736580 FORWARD

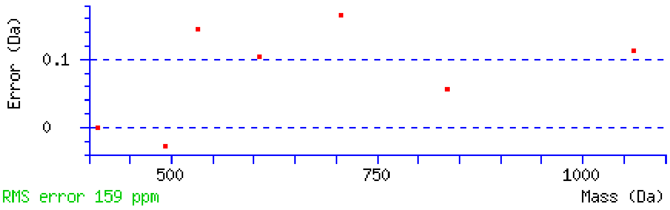
Match to Query 4455: 1260.681830 from(631.348191,2+) index(8037)
Title: Elution from: 70.391 to 70.391 scan no 10625 cid35.00 polarity:+
Data file C7-2_3.mgf

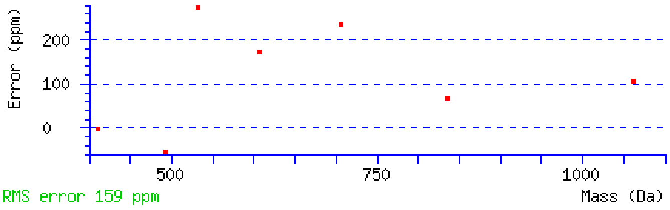
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1260.6826
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.002
Matches : 7/114 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	201.1234	101.0653			183.1128	92.0600	I	1174.6579	587.8326	1157.6313	579.3193	1156.6473	578.8273	11
3	258.1448	129.5761			240.1343	120.5708	G	***1061.5738***	531.2905	1044.5473	522.7773	1043.5633	522.2853	10
4	315.1663	158.0868			297.1557	149.0815	G	1004.5524	502.7798	987.5258	494.2665	986.5418	493.7745	9
5	428.2504	214.6288			410.2398	205.6235	I	947.5309	474.2691	930.5043	465.7558	929.5203	465.2638	8
6	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	Q	***834.4468***	417.7271	817.4203	409.2138	816.4363	408.7218	7
7	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	V	***706.3883***	353.6978	689.3617	345.1845	688.3777	344.6925	6
8	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	D	***607.3198***	304.1636	590.2933	295.6503	589.3093	295.1583	5
9	827.4258	414.2165	810.3992	405.7032	809.4152	405.2112	G	***492.2929***	246.6501	475.2663	238.1368			4
10	940.5098	470.7585	923.4833	462.2453	922.4993	461.7533	L	435.2714	218.1394	418.2449	209.6261			3
11	1087.5782	544.2928	1070.5517	535.7795	1069.5677	535.2875	F	322.1874	161.5973	305.1608	153.0840			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SIGGIQVDGLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G63940.3

Score	Mr(calc)	Delta	Sequence
32.2	1260.6826	-0.0008	SIGGIQVDGLFR
2.8	1260.6786	0.0032	SVTQDLSRISR

Mascot: http://www.matrixscience.com/

AT1G64050.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LILLDETVR**
Found in **AT1G64050.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO65897.1) | chr1:23766247-23769377 FORWARD

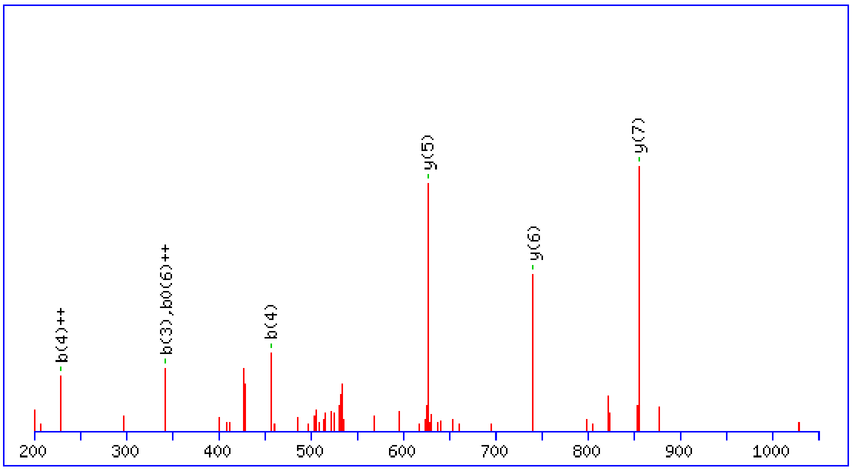
Match to Query 3152: 1082.597950 from(542.306251,2+) index(5868)
Title: Elution from: 52.624 to 52.624 scan no 7492 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

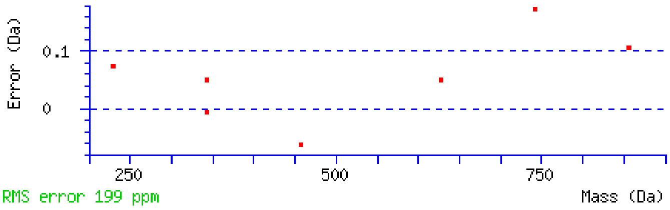
Label all possible matches ○ Label matches used for scoring ●

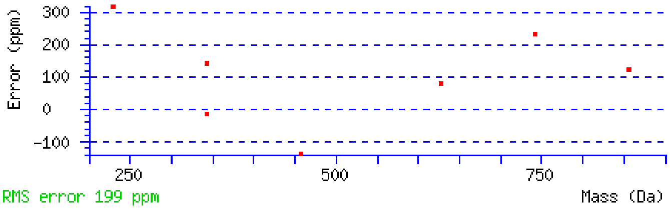
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1082.5980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.015
Matches : 8/68 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							9
2	***229.1695***	115.0884			I	969.5242	485.2657	951.5006	476.2539	951.5136	476.2604	8
3	***343.2506***	172.1289			L	***855.4431***	428.2252	837.4195	419.2134	837.4325	419.2199	7
4	***457.3317***	229.1695			L	***741.3620***	371.1846	723.3384	362.1728	723.3514	362.1793	6
5	573.3556	287.1815	555.3451	278.1762	D	***627.2809***	314.1441	609.2573	305.1323	609.2703	305.1388	5
6	703.3953	352.2013	685.3847	343.1960	E	511.2569	256.1321	493.2333	247.1203	493.2463	247.1268	4
7	805.4400	403.2236	787.4294	394.2184	T	381.2173	191.1123	363.1937	182.1005	363.2067	182.1070	3
8	905.5054	453.2564	887.4949	444.2511	V	279.1725	140.0899	261.1490	131.0781			2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LILLDETVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G64050.1

25.3	1082.5980	-0.0000	LILLDETVR
24.9	1082.5980	-0.0000	IILLGDSGVGK
24.9	1082.5980	-0.0000	ILLIGDSGVGK
24.9	1082.5980	-0.0000	LLLIGDSGVGK

AT1G64090.1

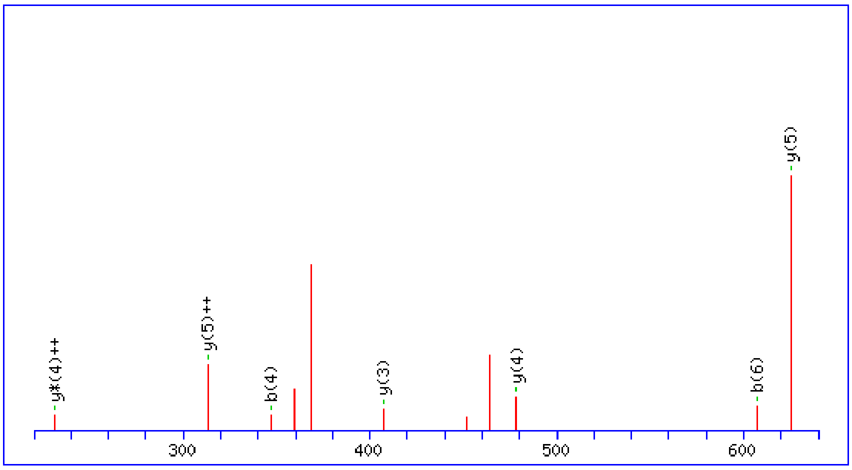
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAFAFIK**
Found in **AT1G64090.1** in **TAIR_Arabidopsis**, Symbols: | reticulon family protein (RTNLB3) | chr1:23793058-23794332 FORWARD

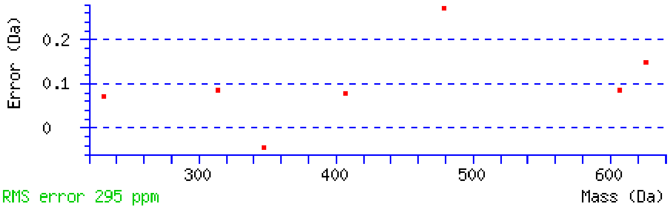
Match to Query 742: 752.420994 from(377.217773,2+) index(5214)
Title: Elution from: 47.743 to 47.743 scan no 6537 cid35.00 polarity:+
Data file D6h-2_2.mgf

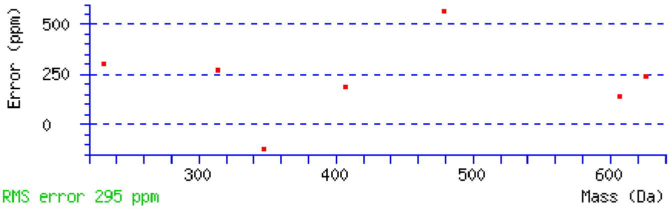
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 640 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 752.4221
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.0039
Matches : 7/36 fragment ions using 11 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	58.0287	29.5180	G					7
2	129.0659	65.0366	A	696.4079	348.7076	679.3814	340.1943	6
3	276.1343	138.5708	F	*625.3708*	313.1890	608.3443	304.6758	5
4	*347.1714*	174.0893	A	*478.3024*	239.6548	461.2758	231.1416	4
5	494.2398	247.6235	F	*407.2653*	204.1363	390.2387	195.6230	3
6	*607.3239*	304.1656	I	260.1969	130.6021	243.1703	122.0888	2
7			K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of GAFAFIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.1	752.4221	-0.0011	GAFAFIK
12.5	752.4221	-0.0011	FQAFIK
7.7	752.4221	-0.0011	FPSFKK

AT1G64090.1

1.1	752.4221	-0.0011	VGFFGVK

Mascot: http://www.matrixscience.com/

AT1G64180.1

Mascot Search Results

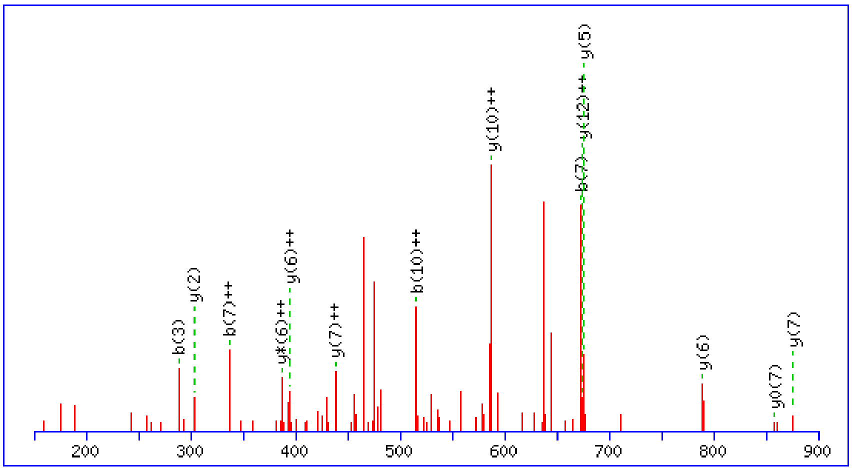
Peptide View

MS/MS Fragmentation of **LSSAVQSLEDERK**
Found in **AT1G64180.1** in **TAIR_Arabidopsis**, Symbols: | intracellular protein transport protein USO1-related | chr1:23825303-23827856 FORWARD

Match to Query 5886: 1460.750739 from(487.924189,3+) index(7216)
Title: Elution from: 63.484 to 63.484 scan no 9390 cid35.00 polarity:+
Data file D6h-3_2.mgf

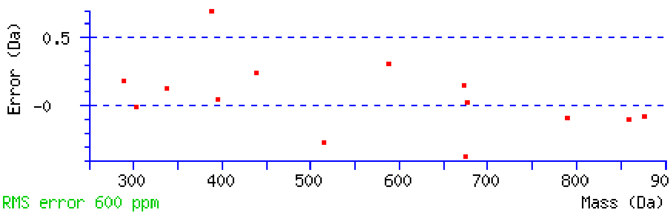
Click mouse within plot area to zoom in by factor of two about that point

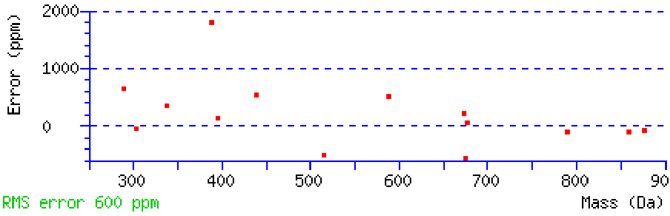
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1460.7471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.015
Matches : 14/128 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**13**
2	201.1234	101.0653			183.1128	92.0600	**S**	1348.6703	674.8388	1331.6437	666.3255	1330.6597	665.8335	**12**
3	**288.1554**	144.5813			270.1448	135.5761	**S**	1261.6383	631.3228	1244.6117	622.8095	1243.6277	622.3175	**11**
4	359.1925	180.0999			341.1819	171.0946	**A**	1174.6062	587.8068	1157.5797	579.2935	1156.5957	578.8015	**10**
5	458.2609	229.6341			440.2504	220.6288	**V**	1103.5691	552.2882	1086.5426	543.7749	1085.5586	543.2829	**9**
6	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	**Q**	1004.5007	502.7540	987.4742	494.2407	986.4901	493.7487	**8**
7	**673.3515**	**337.1794**	656.3250	328.6661	655.3410	328.1741	**S**	***876.4421***	438.7247	859.4156	430.2114	858.4316	429.7194	**7**
8	786.4356	393.7214	769.4090	385.2082	768.4250	384.7162	**L**	***789.4101***	395.2087	772.3836	386.6954	771.3995	386.2034	**6**
9	915.4782	458.2427	898.4516	449.7295	897.4676	449.2374	**E**	***676.3260***	338.6667	659.2995	330.1534	658.3155	329.6614	**5**
10	1030.5051	**515.7562**	1013.4786	507.2429	1012.4946	506.7509	**D**	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	**4**
11	1159.5477	580.2775	1142.5212	571.7642	1141.5372	571.2722	**E**	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	**3**
12	1315.6488	658.3281	1298.6223	649.8148	1297.6383	649.3228	**R**	***303.2139***	152.1106	286.1874	143.5973			**2**
13							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LSSAVQSLEDERK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G64180.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.5	1460.7471	0.0037	LSSAVQSLEDERK
5.6	1460.7511	-0.0004	TLTSVLGWQEEAK
4.8	1460.7524	-0.0017	HNPILPQDPFQR
3.2	1460.7518	-0.0010	RLDGTMSLAARDR
3.2	1460.7470	0.0037	KSSEQLEDLEKR
2.7	1460.7518	-0.0010	LLEQTRMERNR
2.4	1460.7486	0.0022	VYMSSKLWYLR
1.6	1460.7471	0.0037	DENVESSIKQKGK
0.4	1460.7518	-0.0010	MAQSSLVAAAGRSGR
0.2	1460.7470	0.0037	ATNGGEAEKSLKEK

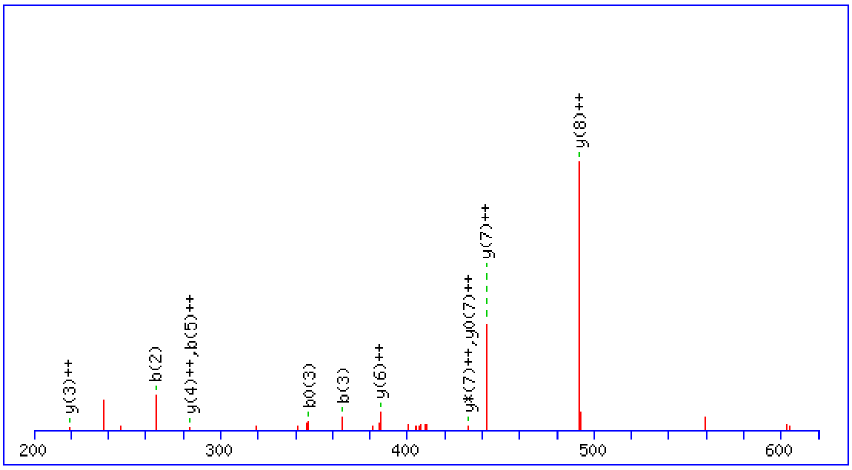
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFVLSIQRPR**
Found in **AT1G64190.1** in **TAIR_Arabidopsis**, Symbols: | 6-phosphogluconate dehydrogenase family protein | chr1:23829212-23830675 REVERSE

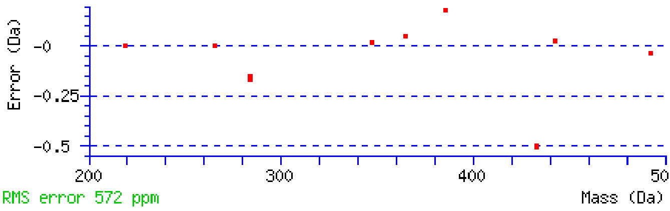
Match to Query 3878: 1246.636665 from(416.552831,3+) index(4876)
Title: Elution from: 46.359 to 46.359 scan no 6278 cid35.00 polarity:+
Data file D1d-1_3.mgf

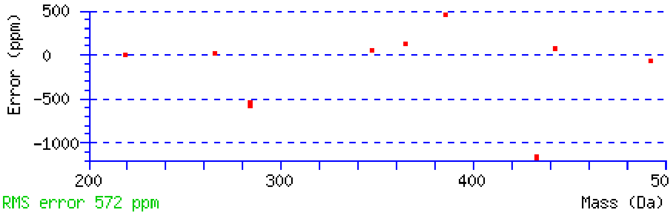
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 620 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.6376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0067
Matches : 11/86 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							10
2	**265.0967**	133.0520			247.0861	124.0467	F	1131.6209	566.3141	1113.5974	557.3023	1113.6104	557.3088	9
3	**365.1622**	183.0847			347.1516	174.0794	V	983.5555	492.2814	965.5319	483.2696	965.5449	483.2761	8
4	479.2433	240.1253			461.2327	231.1200	L	883.4901	442.2487	865.4665	433.2369	865.4795	433.2434	7
5	567.2723	284.1398			549.2617	275.1345	S	769.4090	385.2081	751.3854	376.1963	751.3984	376.2028	6
6	681.3534	341.1803			663.3428	332.1751	I	681.3799	341.1936	663.3563	332.1818			5
7	811.4061	406.2067	793.3825	397.1949	793.3955	397.2014	Q	567.2988	284.1530	549.2752	275.1412			4
8	971.4953	486.2513	953.4717	477.2395	953.4847	477.2460	R	437.2461	219.1267	419.2226	210.1149			3
9	1069.5451	535.2762	1051.5215	526.2644	1051.5345	526.2709	P	277.1569	139.0821	259.1333	130.0703			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DFVLSIQRPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G64190.1

31.3	1246.6376	-0.0010	DFVLSIQRPR
21.2	1246.6383	-0.0017	CTVLEAAIKTK
7.3	1246.6372	-0.0005	VLSWNFLIDK
6.7	1246.6354	0.0013	SNAQKRAVLDK
3.0	1246.6372	-0.0005	YVGLELWQVK
1.3	1246.6349	0.0017	IADFGVAKVADK
0.1	1246.6372	-0.0005	TLFITDFIHK

AT1G64200.1

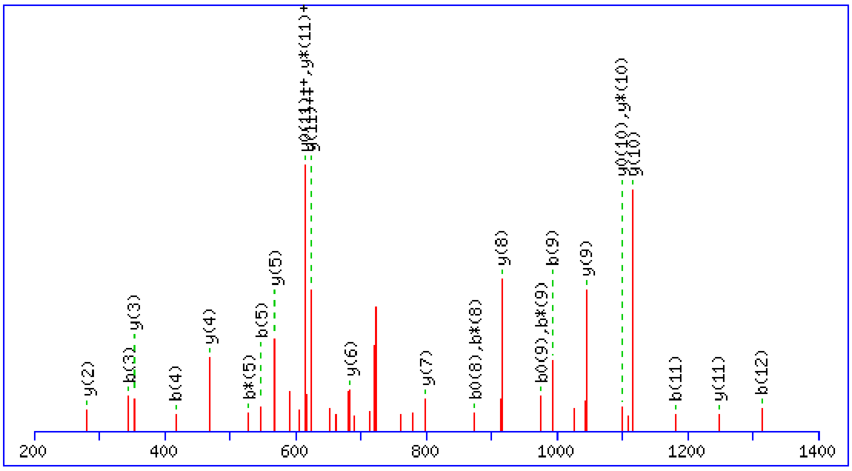
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLQAQDDIVNAMK**
Found in **AT1G64200.1** in **TAIR_Arabidopsis**, Symbols: VHA-E3 | VHA-E3 (VACUOLAR H+-ATPASE SUBUNIT E ISOFORM 3); hydrogen ion transporting ATPase, rotational mechanism | chr1:23832200-23833665 REVERSE

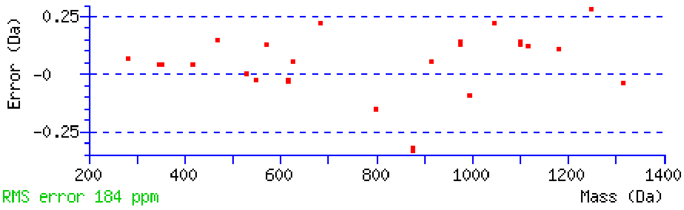
Match to Query 5661: 1460.685996 from(731.350274,2+) index(5470)
Title: Elution from: 48.871 to 48.871 scan no 6970 cid35.00 polarity:+
Data file D6h-2_3.mgf

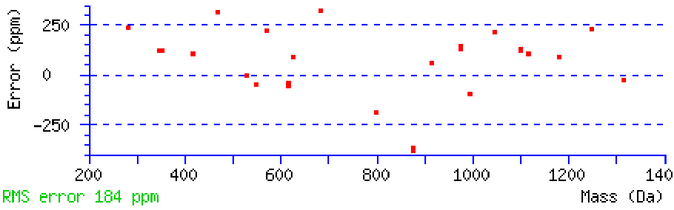
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1460.6887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 99 **Expect:** 1e-009
Matches : 26/118 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							13
2	215.1538	108.0805					L	1361.6306	681.3189	1343.6070	672.3071	1343.6200	672.3136	12
3	**345.2065**	173.1069	327.1829	164.0951			Q	***1247.5495***	624.2784	1229.5259	615.2666	1229.5389	615.2731	11
4	**417.2406**	209.1239	399.2170	200.1122			A	***1117.4968***	559.2521	1099.4733	550.2403	1099.4863	550.2468	10
5	**547.2933**	274.1503	529.2697	265.1385			Q	***1045.4627***	523.2350	1027.4391	514.2232	1027.4521	514.2297	9
6	663.3172	332.1623	645.2937	323.1505	645.3067	323.1570	D	***915.4100***	458.2087	897.3865	449.1969	897.3995	449.2034	8
7	779.3412	390.1742	761.3176	381.1625	761.3307	381.1690	D	***799.3861***	400.1967	781.3625	391.1849	781.3755	391.1914	7
8	893.4223	447.2148	875.3987	438.2030	875.4118	438.2095	I	***683.3621***	342.1847	665.3385	333.1729			6
9	**993.4878**	497.2475	975.4642	488.2357	975.4772	488.2422	V	***569.2810***	285.1441	551.2574	276.1323			5
10	1109.5248	555.2660	1091.5012	546.2542	1091.5142	546.2607	N	***469.2155***	235.1114	451.1920	226.0996			4
11	**1181.5589**	591.2831	1163.5353	582.2713	1163.5484	582.2778	A	***353.1785***	177.0929	335.1550	168.0811			3
12	**1313.5964**	657.3019	1295.5729	648.2901	1295.5859	648.2966	M	***281.1444***	141.0758	263.1208	132.0640			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VLQAQDDIVNAMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G64200.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
98.5	1460.6887	-0.0027	VLQAQDDIVNAMK
2.9	1460.6867	-0.0007	MAMFVRRALSSR
2.5	1460.6854	0.0006	WIDQNIDPSKTK
2.3	1460.6862	-0.0003	KMGLDWMLPPTR

Mascot: http://www.matrixscience.com/

AT1G64260.1

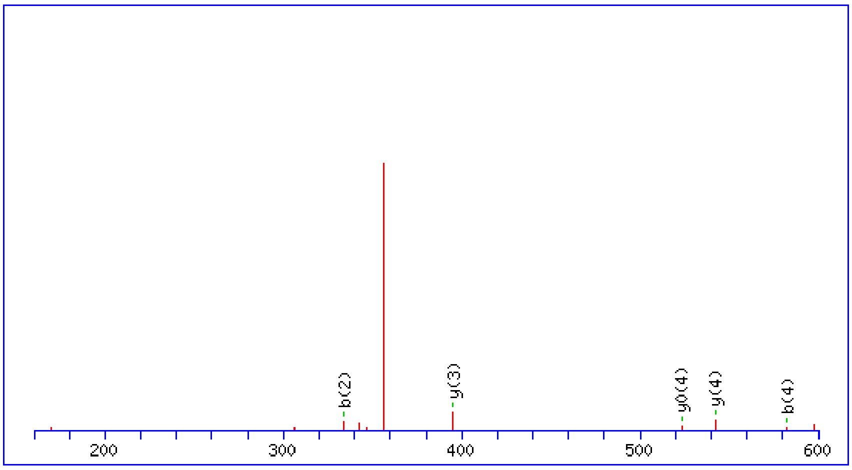
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WFFTK**
Found in **AT1G64260.1** in **TAIR_Arabidopsis**

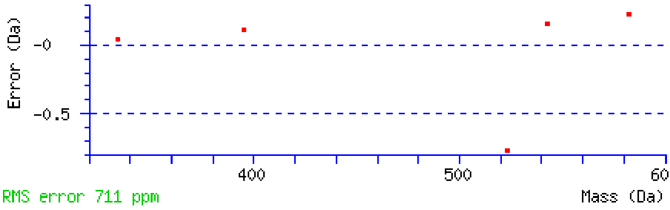
Match to Query 747: 727.369096 from(364.691824,2+) index(6103)
Title: Elution from: 53.483 to 53.483 scan no 7716 cid35.00 polarity:+
Data file C7-2_2.mgf

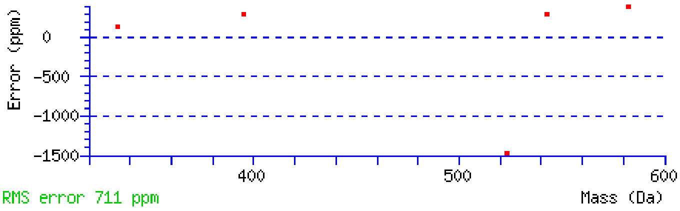
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 727.3694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.014
Matches : 5/32 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469			**W**							**5**
2	***334.1550***	167.5811			**F**	***542.2973***	271.6523	525.2708	263.1390	524.2867	262.6470	**4**
3	481.2234	241.1153			**F**	***395.2289***	198.1181	378.2023	189.6048	377.2183	189.1128	**3**
4	***582.2711***	291.6392	564.2605	282.6339	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
5					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of WFFTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.8	727.3694	-0.0003	WFFTK
5.8	727.3694	-0.0003	FWTFK

Mascot: http://www.matrixscience.com/

AT1G64300.1

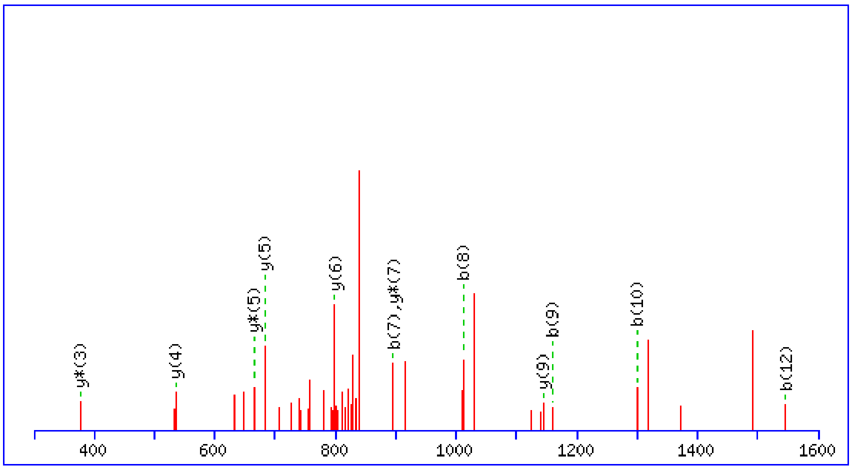
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWWGKVINFHQNK**
Found in **AT1G64300.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:23867206-23869439 FORWARD

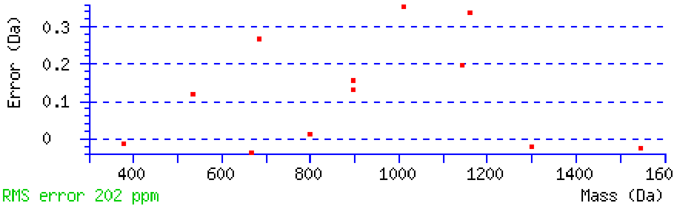
Match to Query 7685: 1692.768316 from(847.391434,2+) index(5956)
Title: Elution from: 52.855 to 52.855 scan no 7635 cid35.00 polarity:+
Data file D6h-2_3.mgf

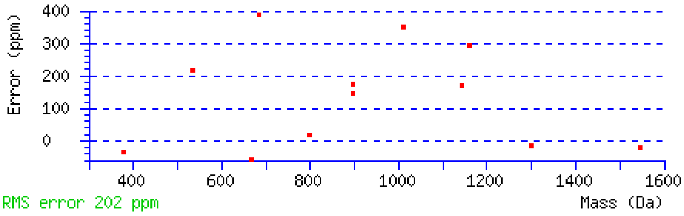
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1692.7665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.012
Matches : 12/112 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	117.0313	59.0193			99.0207	50.0140	D					13
2	305.1046	153.0560			287.0941	144.0507	W	1577.7498	789.3786	1559.7262	780.3668	12
3	493.1780	247.0926			475.1675	238.0874	W	1389.6764	695.3419	1371.6529	686.3301	11
4	551.1965	276.1019			533.1860	267.0966	G	1201.6031	601.3052	1183.5795	592.2934	10
5	681.2856	341.1464	663.2620	332.1346	663.2750	332.1411	K	***1143.5846***	572.2959	1125.5610	563.2841	9
6	781.3510	391.1791	763.3274	382.1673	763.3404	382.1739	V	1013.4955	507.2514	995.4719	498.2396	8
7	***895.4321***	448.2197	877.4085	439.2079	877.4215	439.2144	I	913.4301	457.2187	895.4065	448.2069	7
8	***1011.4691***	506.2382	993.4455	497.2264	993.4585	497.2329	N	***799.3490***	400.1781	781.3254	391.1663	6
9	***1159.5345***	580.2709	1141.5110	571.2591	1141.5240	571.2656	F	***683.3120***	342.1596	665.2884	333.1478	5
10	***1299.5846***	650.2959	1281.5610	641.2841	1281.5740	641.2906	H	***535.2465***	268.1269	517.2230	259.1151	4
11	1429.6372	715.3222	1411.6136	706.3105	1411.6266	706.3170	Q	395.1965	198.1019	377.1729	189.0901	3
12	***1545.6742***	773.3407	1527.6506	764.3289	1527.6636	764.3355	N	265.1439	133.0756	247.1203	124.0638	2
13							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of DWWGKVINFHQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G64300.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.5	1692.7665	0.0018	DWWGKVINFHQNK
11.9	1692.7675	0.0008	NSIEVGKVGNVEDDAK
6.2	1692.7645	0.0038	EVLMGKAEYFESFK
3.1	1692.7650	0.0033	FTADELRRIMDYK
3.0	1692.7675	0.0008	NLSSVNVGLDTENPSK
0.8	1692.7650	0.0033	SGPPLRCFTPGEIDK
0.2	1692.7645	0.0038	FTAYKVSGFMVEEGI

AT1G64510.1

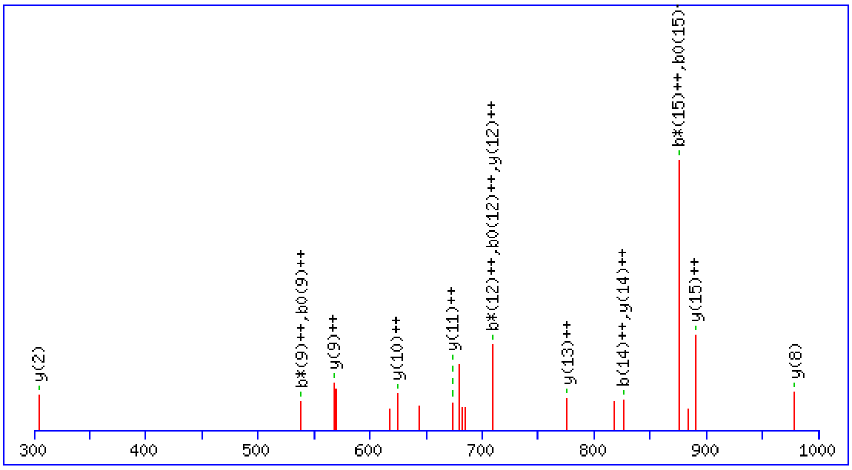
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYETMAVLRPDMSEDER**
Found in **AT1G64510.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein S6 family protein | chr1:23958656-23959868 REVERSE

Match to Query 9151: 2068.916616 from(690.646148,3+) index(5233)
Title: Elution from: 46.154 to 46.154 scan no 6622 cid35.00 polarity:+
Data file 0-2_3.mgf

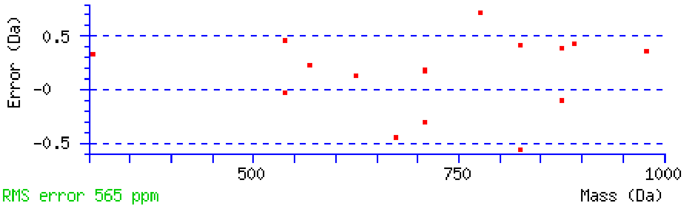
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

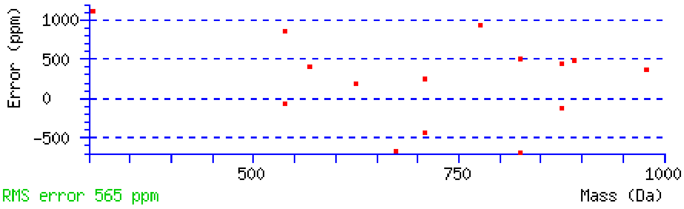


Monoisotopic mass of neutral peptide Mr(calc): 2068.9194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 2.9e-005
Matches : 16/186 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							17
2	292.1292	146.5682	275.1026	138.0550			Y	1941.8681	971.4377	1924.8415	962.9244	1923.8575	962.4324	16
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	E	1778.8048	889.9060	1761.7782	881.3927	1760.7942	880.9007	15
4	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	T	1649.7622	825.3847	1632.7356	816.8714	1631.7516	816.3794	14
5	653.2599	327.1336	636.2334	318.6203	635.2494	318.1283	M	1548.7145	774.8609	1531.6879	766.3476	1530.7039	765.8556	13
6	724.2971	362.6522	707.2705	354.1389	706.2865	353.6469	A	1417.6740	709.3406	1400.6475	700.8274	1399.6634	700.3354	12
7	823.3655	412.1864	806.3389	403.6731	805.3549	403.1811	V	1346.6369	673.8221	1329.6103	665.3088	1328.6263	664.8168	11
8	936.4495	468.7284	919.4230	460.2151	918.4390	459.7231	L	1247.5685	624.2879	1230.5419	615.7746	1229.5579	615.2826	10
9	1092.5506	546.7790	1075.5241	538.2657	1074.5401	537.7737	R	1134.4844	567.7458	1117.4579	559.2326	1116.4738	558.7406	9
10	1189.6034	595.3053	1172.5769	586.7921	1171.5928	586.3001	P	**978.3833**	489.6953	961.3568	481.1820	960.3727	480.6900	8
11	1304.6304	652.8188	1287.6038	644.3055	1286.6198	643.8135	D	881.3305	441.1689	864.3040	432.6556	863.3200	432.1636	7
12	1435.6708	718.3391	1418.6443	709.8258	1417.6603	709.3338	M	766.3036	383.6554	749.2770	375.1422	748.2930	374.6502	6
13	1522.7029	761.8551	1505.6763	753.3418	1504.6923	752.8498	S	635.2631	318.1352	618.2366	309.6219	617.2525	309.1299	5
14	1651.7455	826.3764	1634.7189	817.8631	1633.7349	817.3711	E	548.2311	274.6192	531.2045	266.1059	530.2205	265.6139	4
15	1766.7724	883.8898	1749.7459	875.3766	1748.7618	874.8846	D	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
16	1895.8150	948.4111	1878.7884	939.8979	1877.8044	939.4059	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
17							R	175.1190	88.0631	158.0924	79.5498			1

AT1G64510.1





NCBI **BLAST** search of QYETMAVLRPDMSEDER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.9	2068.9194	-0.0027	QYETMAVLRPDMSEDER

Mascot: http://www.matrixscience.com/

AT1G64625.1

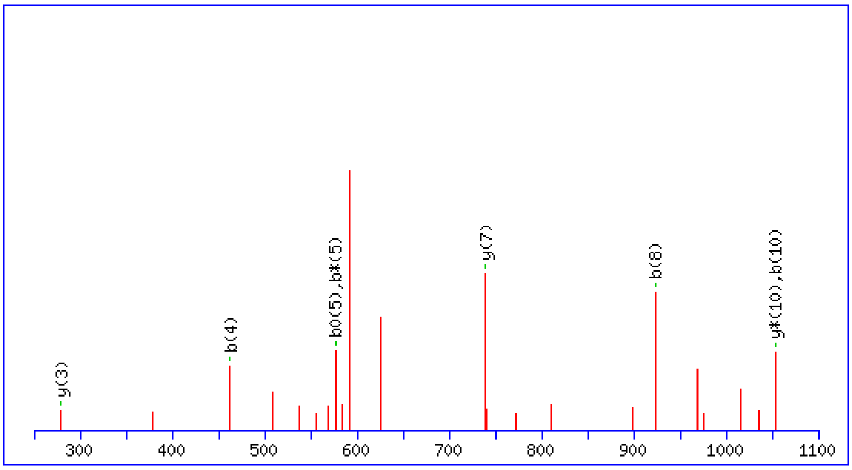
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELRGMIPNGAK**
Found in **AT1G64625.1** in **TAIR_Arabidopsis**, Symbols: | transcription factor | chr1:24020541-24022844 FORWARD

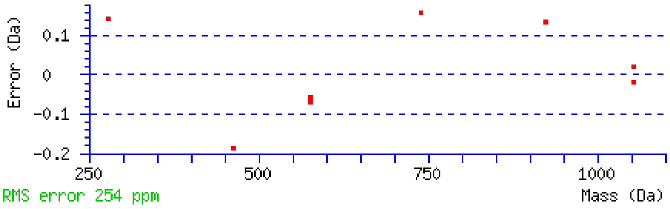
Match to Query 4165: 1200.583644 from(601.299098,2+) index(4015)
Title: Elution from: 37.402 to 37.402 scan no 4975 cid35.00 polarity:+
Data file D12h-1_2.mgf

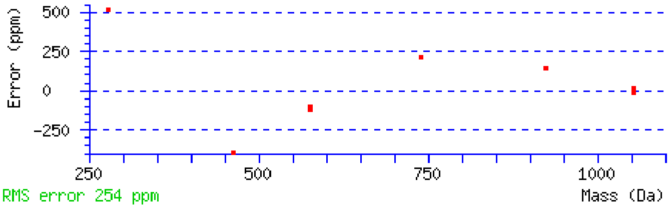
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [250] to [1100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1200.5861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.043
Matches : 8/96 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	131.0469	66.0271			113.0363	57.0218	E					11
2	245.1280	123.0676			227.1174	114.0624	L	1071.5538	536.2805	1053.5302	527.2687	10
3	405.2173	203.1123	387.1937	194.1005	387.2067	194.1070	R	957.4727	479.2400	939.4491	470.2282	9
4	***463.2358***	232.1215	445.2122	223.1097	445.2252	223.1162	G	797.3834	399.1954	779.3599	390.1836	8
5	595.2733	298.1403	577.2497	289.1285	577.2627	289.1350	M	**739.3649**	370.1861	721.3414	361.1743	7
6	709.3544	355.1808	691.3308	346.1690	691.3438	346.1755	I	607.3274	304.1673	589.3038	295.1556	6
7	807.4042	404.2057	789.3806	395.1939	789.3936	395.2004	P	493.2463	247.1268	475.2227	238.1150	5
8	***923.4412***	462.2242	905.4176	453.2124	905.4306	453.2189	N	395.1965	198.1019	377.1729	189.0901	4
9	981.4597	491.2335	963.4361	482.2217	963.4491	482.2282	G	**279.1595**	140.0834	261.1359	131.0716	3
10	***1053.4938***	527.2505	1035.4702	518.2388	1035.4833	518.2453	A	221.1410	111.0741	203.1174	102.0624	2
11							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of ELRGMIPNGAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G64625.1

Score	Mr(calc)	Delta	Sequence
22.3	1200.5861	-0.0025	ELRGMIPNGAK
6.9	1200.5805	0.0031	ARSEGPAEIVR
2.3	1200.5857	-0.0021	MLLFVPNDPK
2.3	1200.5828	0.0009	GWKGSVNPNVK
1.8	1200.5827	0.0009	ATQVIFNHQK
1.8	1200.5801	0.0036	DPFLTPQDKK
1.8	1200.5861	-0.0025	HALLSMRTEK
1.8	1200.5857	-0.0020	IIEWMELQK
1.8	1200.5861	-0.0025	LPGRMDQLQK
1.8	1200.5801	0.0036	LPKFDPTDQK

Mascot: http://www.matrixscience.com/

AT1G64860.1

Mascot Search Results

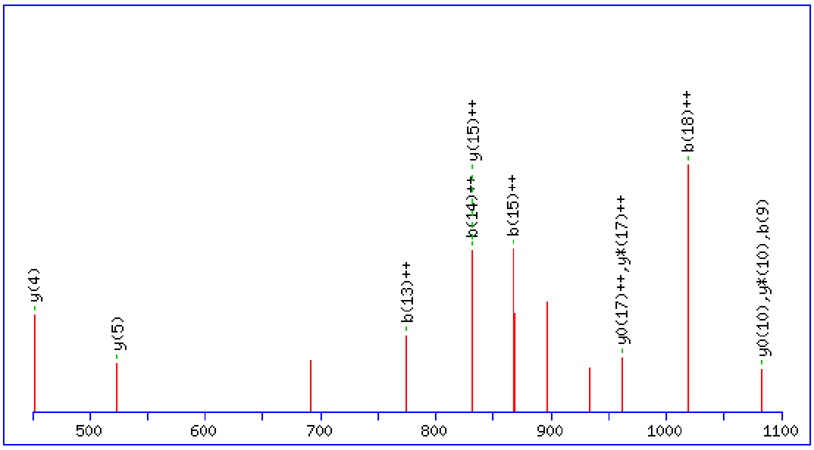
Peptide View

MS/MS Fragmentation of **LKDRLGCEPSDEQLAVSLK**
Found in **AT1G64860.1** in **TAIR_Arabidopsis**, Symbols: SIG1, SIG2, SIGB, RPOD1, SIGA | SIGA (SIGMA FACTOR A); DNA binding / DNA-directed RNA polymerase/ transcription factor | chr1:24102160-24104409 FORWARD

Match to Query 9711: 2183.035146 from(728.685658,3+) index(10827)
Title: Elution from: 116.799 to 116.799 scan no 15896 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

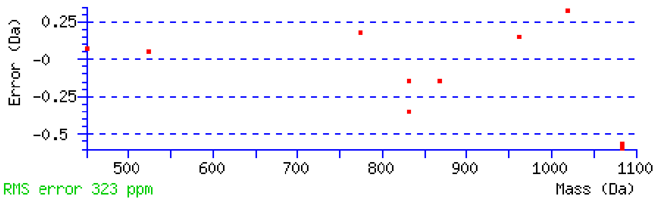
Or, Plot from 450 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

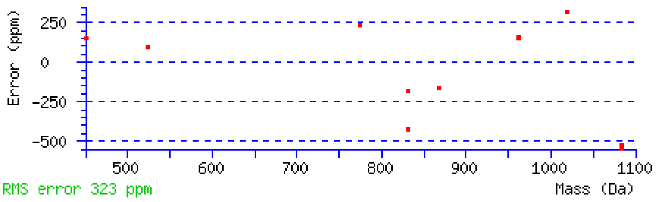


Monoisotopic mass of neutral peptide Mr(calc): 2183.0329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0038
Matches : 13/206 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							19
2	245.1774	123.0923	227.1538	114.0805			K	2069.9591	1035.4832	2051.9355	1026.4714	2051.9485	1026.4779	18
3	361.2014	181.1043	343.1778	172.0925	343.1908	172.0990	D	1939.8700	970.4386	1921.8464	961.4269	1921.8595	961.4334	17
4	521.2906	261.1490	503.2671	252.1372	503.2801	252.1437	R	1823.8460	912.4267	1805.8225	903.4149	1805.8355	903.4214	16
5	635.3717	318.1895	617.3482	309.1777	617.3612	309.1842	L	1663.7568	832.3820	1645.7332	823.3702	1645.7462	823.3768	15
6	693.3902	347.1988	675.3667	338.1870	675.3797	338.1935	G	1549.6757	775.3415	1531.6521	766.3297	1531.6651	766.3362	14
7	855.4150	428.2111	837.3914	419.1993	837.4044	419.2058	C	1491.6572	746.3322	1473.6336	737.3204	1473.6466	737.3270	13
8	985.4546	493.2309	967.4310	484.2191	967.4440	484.2256	E	1329.6325	665.3199	1311.6089	656.3081	1311.6219	656.3146	12
9	1083.5044	542.2558	1065.4808	533.2440	1065.4938	533.2505	P	1199.5928	600.3001	1181.5693	591.2883	1181.5823	591.2948	11
10	1171.5334	586.2704	1153.5099	577.2586	1153.5229	577.2651	S	1101.5430	551.2752	1083.5195	542.2634	1083.5325	542.2699	10
11	1287.5574	644.2823	1269.5338	635.2706	1269.5469	635.2771	D	1013.5140	507.2606	995.4904	498.2488	995.5034	498.2553	9
12	1417.5970	709.3022	1399.5735	700.2904	1399.5865	700.2969	E	897.4900	449.2486	879.4664	440.2369	879.4794	440.2434	8
13	1547.6497	***774.3285***	1529.6261	765.3167	1529.6391	765.3232	Q	767.4504	384.2288	749.4268	375.2170	749.4398	375.2235	7
14	1661.7308	***831.3690***	1643.7072	822.3572	1643.7202	822.3638	L	637.3977	319.2025	619.3741	310.1907	619.3872	310.1972	6
15	1733.7649	***867.3861***	1715.7414	858.3743	1715.7544	858.3808	A	**523.3166**	262.1620	505.2931	253.1502	505.3061	253.1567	5
16	1833.8304	917.4188	1815.8068	908.4070	1815.8198	908.4136	V	**451.2825**	226.1449	433.2589	217.1331	433.2719	217.1396	4
17	1921.8595	***961.4334***	1903.8359	952.4216	1903.8489	952.4281	S	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
18	2035.9406	***1018.4739***	2017.9170	1009.4621	2017.9300	1009.4686	L	263.1880	132.0976	245.1644	123.0858			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT1G64860.1





NCBI **BLAST** search of LKDRLGCEPSDEQLAVSLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.3	2183.0329	0.0023	LKDRLGCEPSDEQLAVSLK
7.4	2183.0295	0.0057	FTPNEDPVDTNANVAKGIKK
7.0	2183.0329	0.0023	AAKPAVKAAMDDVNADQSVLK
7.0	2183.0317	0.0034	SPVDYSRAPGEVNLVEWLK
6.4	2183.0329	0.0023	PVMERVAEETVATNNIQLK
6.0	2183.0351	0.0000	ASPTSSVNELHLEIMKFQK
5.7	2183.0351	0.0000	LNYSSNTRFMLEAIDKLK
5.1	2183.0304	0.0048	ASVGKFIEQSMSHMIVHLK
5.1	2183.0304	0.0048	ASVGKFIEQSMSHMIVHLK
4.4	2183.0373	-0.0022	GCDLLEGEWGKVGSILLWK

Mascot: http://www.matrixscience.com/

AT1G65260.1

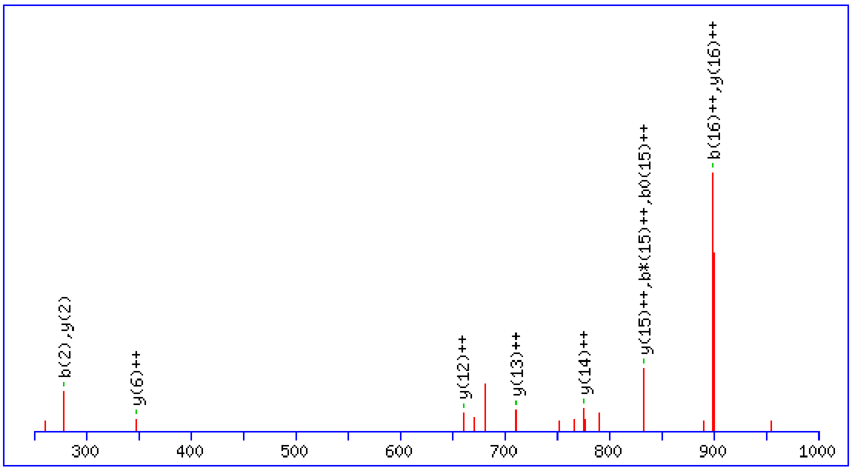
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQMLETSSVDDDLADLKK**
Found in **AT1G65260.1** in **TAIR_Arabidopsis**, Symbols: PTAC4 | PTAC4 (PLASTID TRANSCRIPTIONALLY ACTIVE4) | chr1:24239992-24244091 FORWARD

Match to Query 9787: 2074.927866 from(692.649898,3+) index(8146)
Title: Elution from: 70.985 to 70.985 scan no 10636 cid35.00 polarity:+
Data file D1d-3_1.mgf

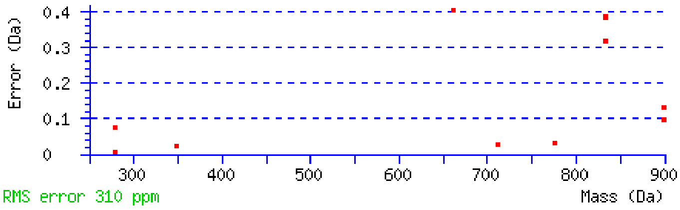
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

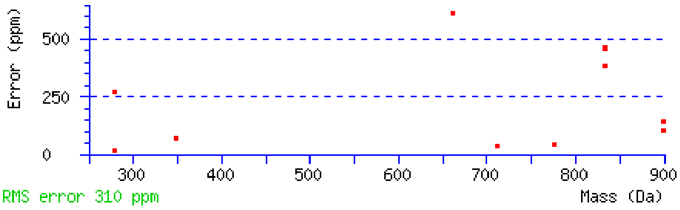


Monoisotopic mass of neutral peptide Mr(calc): 2074.9255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00021
Matches : 11/188 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							18
2	279.1254	140.0663	261.1018	131.0545			Q	1927.8673	964.4373	1909.8438	955.4255	1909.8568	955.4320	17
3	411.1629	206.0851	393.1393	197.0733			M	1797.8147	899.4110	1779.7911	890.3992	1779.8041	890.4057	16
4	525.2440	263.1256	507.2204	254.1138			L	1665.7772	833.3922	1647.7536	824.3804	1647.7666	824.3869	15
5	655.2836	328.1454	637.2600	319.1337	637.2731	319.1402	E	1551.6961	776.3517	1533.6725	767.3399	1533.6855	767.3464	14
6	757.3283	379.1678	739.3047	370.1560	739.3178	370.1625	T	1421.6565	711.3319	1403.6329	702.3201	1403.6459	702.3266	13
7	845.3574	423.1823	827.3338	414.1705	827.3468	414.1771	S	1319.6117	660.3095	1301.5882	651.2977	1301.6012	651.3042	12
8	933.3865	467.1969	915.3629	458.1851	915.3759	458.1916	S	1231.5827	616.2950	1213.5591	607.2832	1213.5721	607.2897	11
9	1033.4519	517.2296	1015.4283	508.2178	1015.4413	508.2243	V	1143.5536	572.2804	1125.5300	563.2687	1125.5430	563.2752	10
10	1149.4759	575.2416	1131.4523	566.2298	1131.4653	566.2363	D	1043.4882	522.2477	1025.4646	513.2359	1025.4776	513.2424	9
11	1265.4999	633.2536	1247.4763	624.2418	1247.4893	624.2483	D	927.4642	464.2357	909.4406	455.2239	909.4536	455.2304	8
12	1381.5238	691.2656	1363.5003	682.2538	1363.5133	682.2603	D	811.4402	406.2237	793.4166	397.2120	793.4296	397.2185	7
13	1495.6049	748.3061	1477.5814	739.2943	1477.5944	739.3008	L	695.4162	348.2118	677.3926	339.2000	677.4057	339.2065	6
14	1567.6391	784.3232	1549.6155	775.3114	1549.6285	775.3179	A	581.3351	291.1712	563.3115	282.1594	563.3246	282.1659	5
15	1683.6631	842.3352	1665.6395	833.3234	1665.6525	833.3299	D	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	4
16	1797.7442	899.3757	1779.7206	890.3639	1779.7336	890.3704	L	393.2770	197.1421	375.2534	188.1303			3
17	1927.8332	964.4202	1909.8096	955.4084	1909.8226	955.4150	K	279.1959	140.1016	261.1723	131.0898			2
18							K	149.1069	75.0571	131.0833	66.0453			1

AT1G65260.1





NCBI **BLAST** search of FQMLETSSVDDDLADLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.6	2074.9255	0.0024	FQMLETSSVDDDLADLKK
9.9	2074.9329	-0.0051	AEYETLSQESRELIQEK
9.3	2074.9338	-0.0059	AACYTKLGAMPEGLKDAEK
6.6	2074.9248	0.0031	DYKLYEEIGDGVSATVHR
4.8	2074.9290	-0.0012	EVICKCIPCQGIGYVQK
4.5	2074.9338	-0.0059	MLQGLTGMPSAAFQEESKK
4.4	2074.9248	0.0030	WDVQSFIRSSPELSGSEK
4.4	2074.9221	0.0058	FTDLTADETSDLWLTAQK
4.1	2074.9281	-0.0003	LTTFEIQGCENVTVDGLR
3.7	2074.9268	0.0011	SVKLGCGEGGCGACLVVLSK

Mascot: http://www.matrixscience.com/

AT1G65290.1

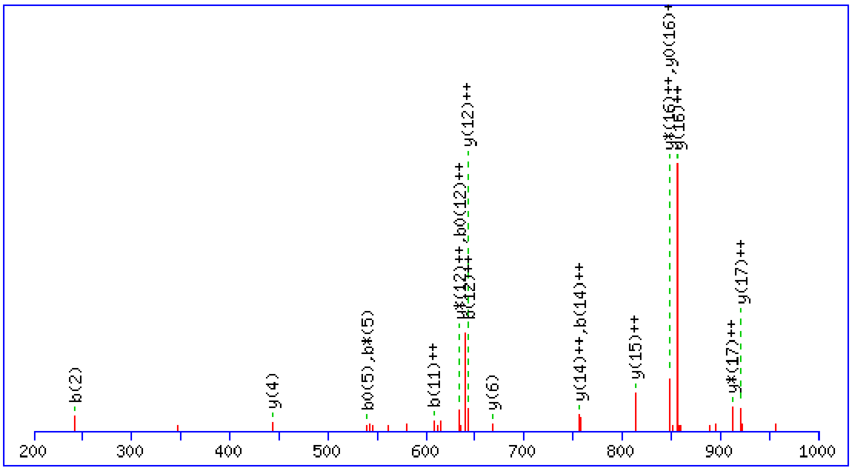
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQSIDLAVDFIASHPQAK**
Found in **AT1G65290.1** in **TAIR_Arabidopsis**, Symbols: MTACP2 | MTACP2 (MITOCHONDRIAL ACYL CARRIER PROTEIN 2); acyl carrier | chr1:24252751-24254029 REVERSE

Match to Query 9319: 1952.034000 from(651.685276,3+) index(8994)
Title: Elution from: 81.238 to 81.238 scan no 12081 cid35.00 polarity:+
Data file 0-3_1.mgf

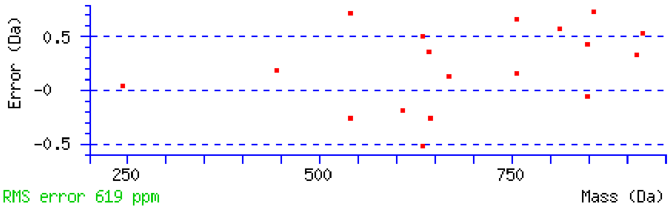
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

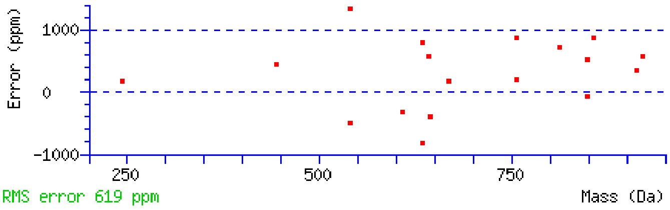


Monoisotopic mass of neutral peptide Mr(calc): 1952.0367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0046
Matches : 18/188 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							18
2	242.1499	121.5786	225.1234	113.0653			Q	1839.9599	920.4836	1822.9334	911.9703	1821.9494	911.4783	17
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	S	1711.9014	856.4543	1694.8748	847.9410	1693.8908	847.4490	16
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	I	1624.8693	812.9383	1607.8428	804.4250	1606.8588	803.9330	15
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	D	1511.7853	756.3963	1494.7587	747.8830	1493.7747	747.3910	14
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	L	1396.7583	698.8828	1379.7318	690.3695	1378.7478	689.8775	13
7	741.4141	371.2107	724.3876	362.6974	723.4036	362.2054	A	1283.6743	642.3408	1266.6477	633.8275	1265.6637	633.3355	12
8	840.4825	420.7449	823.4560	412.2316	822.4720	411.7396	V	1212.6371	606.8222	1195.6106	598.3089	1194.6266	597.8169	11
9	955.5095	478.2584	938.4829	469.7451	937.4989	469.2531	D	1113.5687	557.2880	1096.5422	548.7747	1095.5582	548.2827	10
10	1102.5779	551.7926	1085.5514	543.2793	1084.5673	542.7873	F	998.5418	499.7745	981.5152	491.2613	980.5312	490.7693	9
11	1215.6620	***608.3346***	1198.6354	599.8213	1197.6514	599.3293	I	851.4734	426.2403	834.4468	417.7271	833.4628	417.2350	8
12	1286.6991	***643.8532***	1269.6725	635.3399	1268.6885	634.8479	A	738.3893	369.6983	721.3628	361.1850	720.3787	360.6930	7
13	1373.7311	687.3692	1356.7046	678.8559	1355.7205	678.3639	S	**667.3522**	334.1797	650.3257	325.6665	649.3416	325.1745	6
14	1510.7900	***755.8986***	1493.7635	747.3854	1492.7795	746.8934	H	580.3202	290.6637	563.2936	282.1504			5
15	1607.8428	804.4250	1590.8162	795.9118	1589.8322	795.4197	P	**443.2613**	222.1343	426.2347	213.6210			4
16	1735.9014	868.4543	1718.8748	859.9410	1717.8908	859.4490	Q	346.2085	173.6079	329.1819	165.0946			3
17	1806.9385	903.9729	1789.9119	895.4596	1788.9279	894.9676	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT1G65290.1





NCBI **BLAST** search of IQSIDLAVDFIASHPQAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.8	1952.0367	-0.0027	IQSIDLAVDFIASHPQAK
1.8	1952.0302	0.0038	ELRQLFSPFGQIKSMR

Mascot: http://www.matrixscience.com/

AT1G65350.1

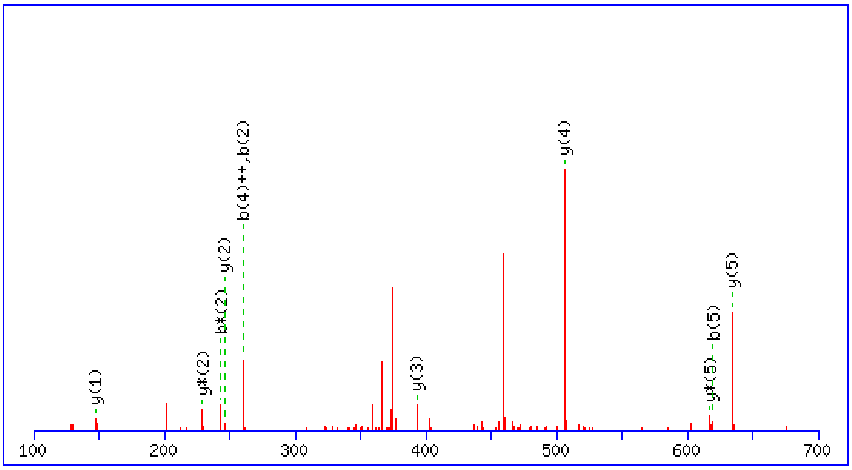
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQIFVK**
Found in **AT1G65350.1** in **TAIR_Arabidopsis**, Symbols: UBQ13 | UBQ13 (ubiquitin 13) | chr1:24280054-24280938 REVERSE

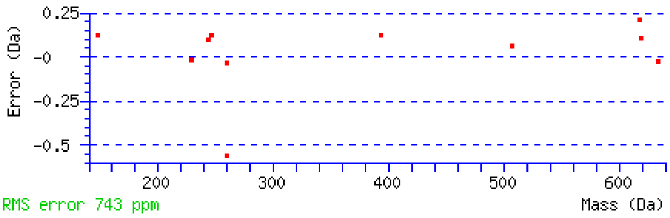
Match to Query 827: 764.425488 from(383.220020,2+) index(3275)
Title: Elution from: 31.911 to 31.911 scan no 4061 cid35.00 polarity:+
Data file 0-1_3.mgf

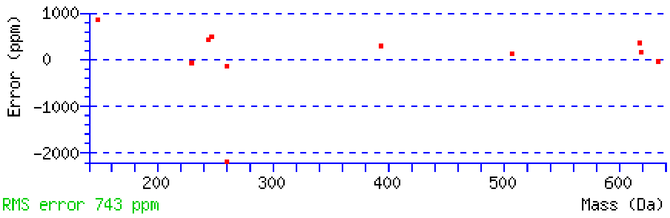
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 764.4255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00014
Matches : 11/38 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	132.0478	66.5275			M					6
2	**260.1063**	130.5568	243.0798	122.0435	Q	***634.3923***	317.6998	617.3657	309.1865	5
3	373.1904	187.0988	356.1639	178.5856	I	***506.3337***	253.6705	489.3071	245.1572	4
4	520.2588	260.6330	503.2323	252.1198	F	***393.2496***	197.1285	376.2231	188.6152	3
5	**619.3272**	310.1673	602.3007	301.6540	V	***246.1812***	123.5942	229.1547	115.0810	2
6					K	***147.1128***	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of MQIFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.0	764.4255	0.0000	MQIFVK
19.0	764.4255	0.0000	MGIAFVK
17.2	764.4255	0.0000	MYPKVK
15.5	764.4255	0.0000	MVGFALK

AT1G65350.1

4.4	764.4255	0.0000	FMIGVAK
1.1	764.4255	-0.0000	VFIVCK
1.1	764.4255	-0.0000	VFVLCK

Mascot: http://www.matrixscience.com/

AT1G65930.1

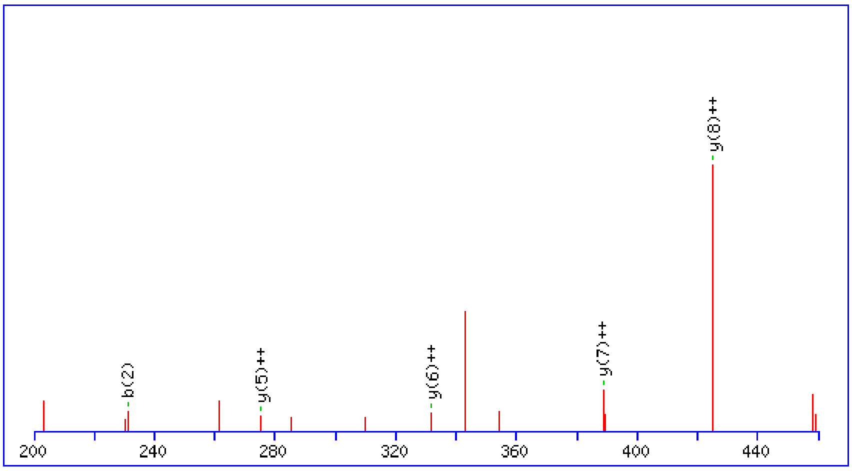
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLALIIHGSK**
Found in **AT1G65930.1** in **TAIR_Arabidopsis**, Symbols: | isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative | chr1:24542751-24545524 FORWARD

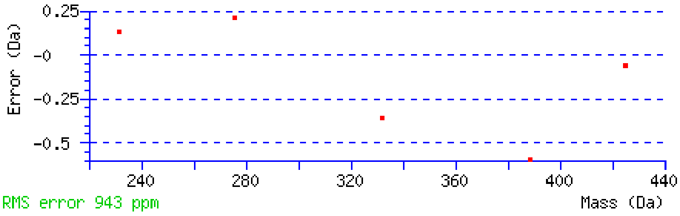
Match to Query 3130: 1078.577163 from(360.532997,3+) index(4535)
Title: Elution from: 40.687 to 40.687 scan no 5702 cid35.00 polarity:+
Data file 0-2_3.mgf

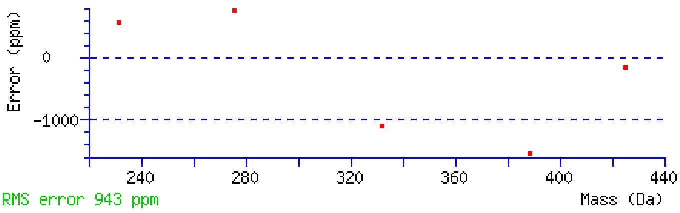
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 460 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1078.5797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.033
Matches : 5/88 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							10
2	231.1124	116.0598	213.1018	107.0545	L	963.5630	482.2851	945.5394	473.2733	945.5524	473.2799	9
3	303.1465	152.0769	285.1359	143.0716	A	849.4819	425.2446	831.4583	416.2328	831.4713	416.2393	8
4	417.2276	209.1174	399.2170	200.1122	L	777.4478	389.2275	759.4242	380.2157	759.4372	380.2222	7
5	531.3087	266.1580	513.2981	257.1527	I	663.3667	332.1870	645.3431	323.1752	645.3561	323.1817	6
6	645.3898	323.1985	627.3792	314.1933	I	549.2856	275.1464	531.2620	266.1346	531.2750	266.1411	5
7	785.4398	393.2235	767.4293	384.2183	H	435.2045	218.1059	417.1809	209.0941	417.1939	209.1006	4
8	843.4583	422.2328	825.4478	413.2275	G	295.1544	148.0809	277.1309	139.0691	277.1439	139.0756	3
9	931.4874	466.2473	913.4768	457.2420	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DLALIIHGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G65930.1

Score	Mr(calc)	Delta	Sequence
18.5	1078.5797	-0.0025	DLALIIHGSK
9.9	1078.5797	-0.0025	VKAIEHLEK

AT1G65960.1

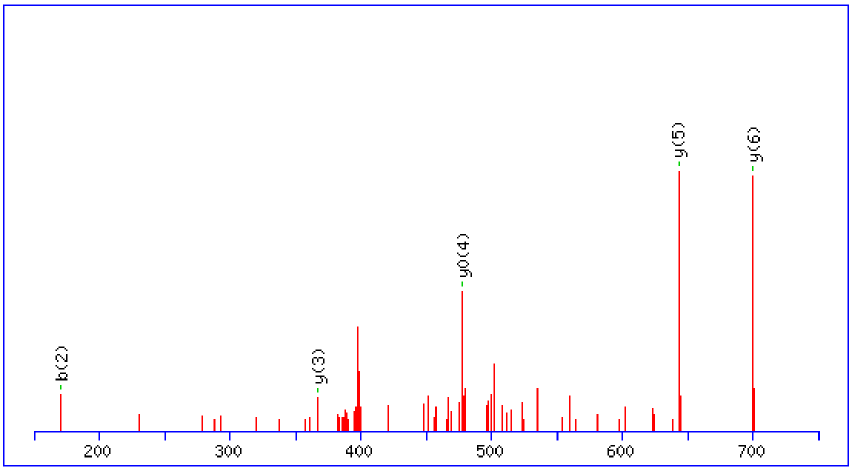
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGFEGYK**
Found in **AT1G65960.1** in **TAIR_Arabidopsis**, Symbols: GAD2 | GAD2 (GLUTAMATE DECARBOXYLASE 2); calmodulin binding | chr1:24559531-24560916 FORWARD

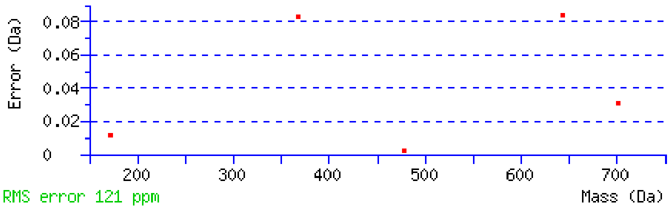
Match to Query 1113: 812.404970 from(407.209761,2+) index(3173)
Title: Elution from: 31.118 to 31.118 scan no 3930 cid35.00 polarity:+
Data file C7-2_2.mgf

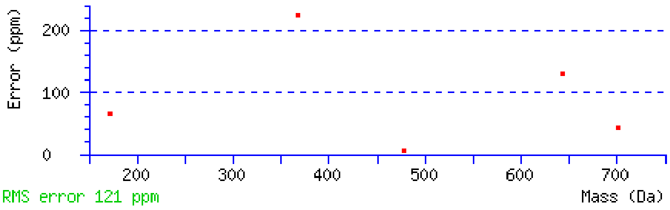
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 812.4068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.013
Matches : 5/48 fragment ions using 6 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493			L							7
2	171.1128	86.0600			G	***700.3301***	350.6687	683.3035	342.1554	682.3195	341.6634	6
3	318.1812	159.5942			F	***643.3086***	322.1579	626.2821	313.6447	625.2980	313.1527	5
4	447.2238	224.1155	429.2132	215.1103	E	496.2402	248.6237	479.2136	240.1105	478.2296	239.6185	4
5	504.2453	252.6263	486.2347	243.6210	G	***367.1976***	184.1024	350.1710	175.5892			3
6	667.3086	334.1579	649.2980	325.1527	Y	310.1761	155.5917	293.1496	147.0784			2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LGFEGYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	812.4068	-0.0019	LGFEGYK
8.0	812.4069	-0.0019	IGDFFSK

AT1G65960.1

8.0	812.4028	0.0022	IGTEHEK

Mascot: http://www.matrixscience.com/

AT1G65960.2

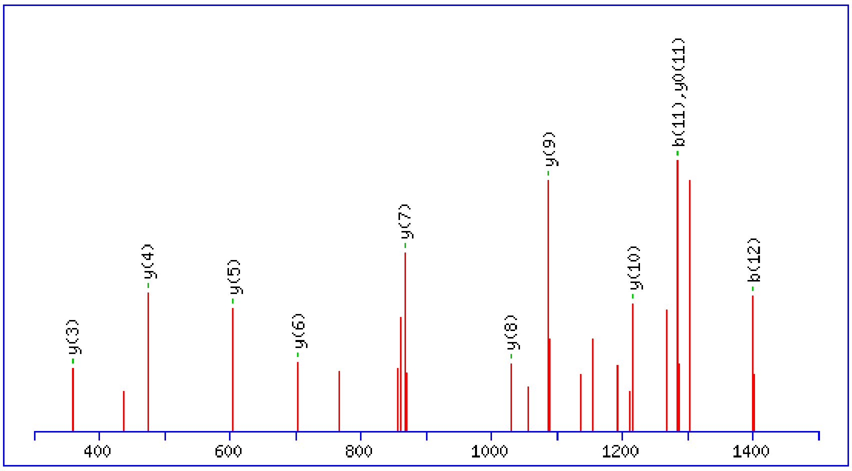
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVNLSEGYYVMDPDK**
Found in **AT1G65960.2** in **TAIR_Arabidopsis**, Symbols: GAD2 | GAD2 (GLUTAMATE DECARBOXYLASE 2) | chr1:24555757-24560916 FORWARD

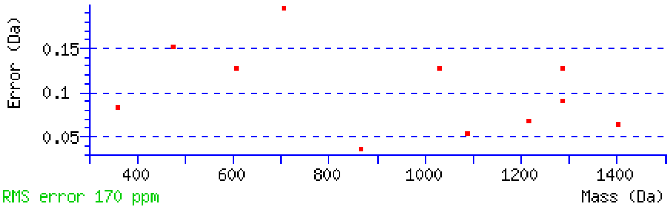
Match to Query 8386: 1757.779192 from(879.896872,2+) index(7067)
Title: Elution from: 64.633 to 64.633 scan no 9262 cid35.00 polarity:+
Data file D1d-2_1.mgf

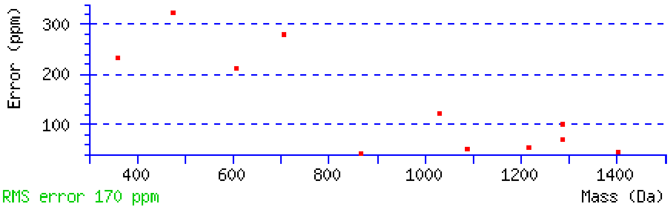
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1757.7818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 4.1e-008
Matches : 11/162 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**15**
2	229.1183	115.0628			211.1077	106.0575	**V**	1629.7465	815.3769	1612.7200	806.8636	1611.7359	806.3716	**14**
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	**N**	1530.6781	765.8427	1513.6515	757.3294	1512.6675	756.8374	**13**
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	**L**	1416.6352	708.8212	1399.6086	700.3079	1398.6246	699.8159	**12**
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	**S**	1303.5511	652.2792	1286.5245	643.7659	1285.5405	643.2739	**11**
6	672.3199	336.6636	655.2933	328.1503	654.3093	327.6583	**E**	***1216.5191***	608.7632	1199.4925	600.2499	1198.5085	599.7579	**10**
7	729.3414	365.1743	712.3148	356.6610	711.3308	356.1690	**G**	***1087.4765***	544.2419	1070.4499	535.7286	1069.4659	535.2366	**9**
8	892.4047	446.7060	875.3781	438.1927	874.3941	437.7007	**Y**	***1030.4550***	515.7311	1013.4285	507.2179	1012.4444	506.7259	**8**
9	1055.4680	528.2376	1038.4415	519.7244	1037.4575	519.2324	**Y**	***867.3917***	434.1995	850.3651	425.6862	849.3811	425.1942	**7**
10	1154.5364	577.7719	1137.5099	569.2586	1136.5259	568.7666	**V**	***704.3284***	352.6678	687.3018	344.1545	686.3178	343.6625	**6**
11	**1285.5769**	643.2921	1268.5504	634.7788	1267.5664	634.2868	**M**	***605.2599***	303.1336	588.2334	294.6203	587.2494	294.1283	**5**
12	**1400.6039**	700.8056	1383.5773	692.2923	1382.5933	691.8003	**D**	***474.2195***	237.6134	457.1929	229.1001	456.2089	228.6081	**4**
13	1497.6566	749.3319	1480.6301	740.8187	1479.6461	740.3267	**P**	***359.1925***	180.0999	342.1660	171.5866	341.1819	171.0946	**3**
14	1612.6836	806.8454	1595.6570	798.3321	1594.6730	797.8401	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
15							**K**	147.1128	74.0600	130.0863	65.5468			**1**





AT1G65960.2

NCBI **BLAST** search of EVNLSEGYYVMDPDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.8	1757.7818	-0.0026	EVNLSEGYYVMDPDK
8.8	1757.7834	-0.0042	HHKSDCMCAICVLK

Mascot: http://www.matrixscience.com/

AT1G65980.1

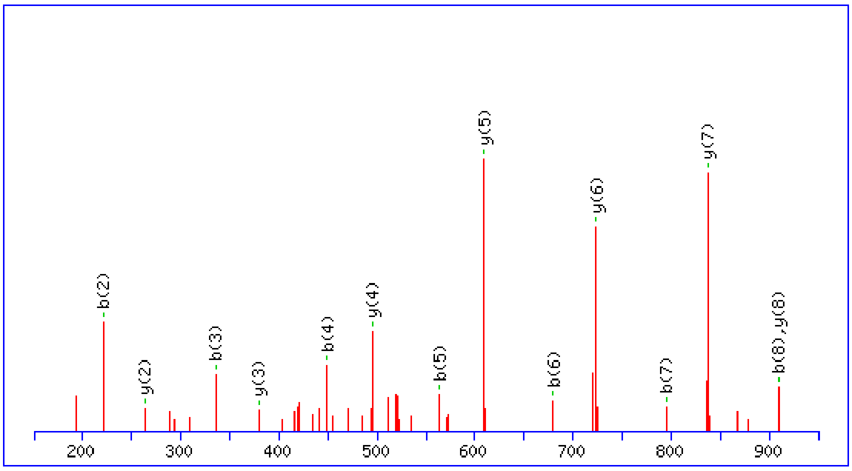
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FALLLDDLK**
Found in **AT1G65980.1** in **TAIR_Arabidopsis**, Symbols: TPX1 | TPX1 (THIOREDOXIN-DEPENDENT PEROXIDASE 1); antioxidant | chr1:24563187-24564416 REVERSE

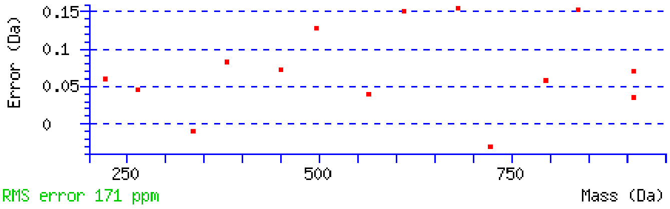
Match to Query 3001: 1056.570370 from(529.292461,2+) index(8835)
Title: Elution from: 79.117 to 79.117 scan no 11899 cid35.00 polarity:+
Data file 0-1_3.mgf

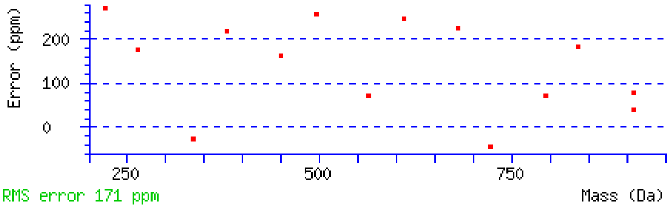
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.5715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 6.5e-006
Matches : 14/66 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0727	75.0400			F							9
2	***221.1069***	111.0571			A	**909.5134**	455.2603	891.4898	446.2485	891.5028	446.2550	8
3	***335.1880***	168.0976			L	**837.4792**	419.2433	819.4556	410.2315	819.4687	410.2380	7
4	***449.2691***	225.1382			L	**723.3981**	362.2027	705.3745	353.1909	705.3876	353.1974	6
5	***563.3502***	282.1787			L	**609.3170**	305.1622	591.2934	296.1504	591.3065	296.1569	5
6	***679.3741***	340.1907	661.3636	331.1854	D	**495.2359**	248.1216	477.2123	239.1098	477.2254	239.1163	4
7	***795.3981***	398.2027	777.3876	389.1974	D	**379.2120**	190.1096	361.1884	181.0978	361.2014	181.1043	3
8	***909.4792***	455.2433	891.4687	446.2380	L	**263.1880**	132.0976	245.1644	123.0858			2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FALLLDDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G65980.1

60.6	1056.5715	-0.0012	FALLLDDLK
27.2	1056.5693	0.0011	DSKLIETIK
15.4	1056.5693	0.0011	DKSLTLLEK
15.4	1056.5720	-0.0016	RDGIDKLVK
15.0	1056.5693	0.0011	ITQTIETLK
14.2	1056.5720	-0.0016	SRKLDSPIK
4.7	1056.5720	-0.0016	RITVNEALK
3.7	1056.5720	-0.0016	RDGVDKLLK
1.8	1056.5672	0.0031	CAALPRKVK
1.1	1056.5720	-0.0016	QRTTPSLLK

AT1G66200.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMREEGGYEIIKK**
Found in **AT1G66200.1** in **TAIR_Arabidopsis**, Symbols: ATGSR2 | ATGSR2 (Arabidopsis thaliana glutamine synthase clone R2); glutamate-ammonia ligase | chr1:24659183-24661183 REVERSE

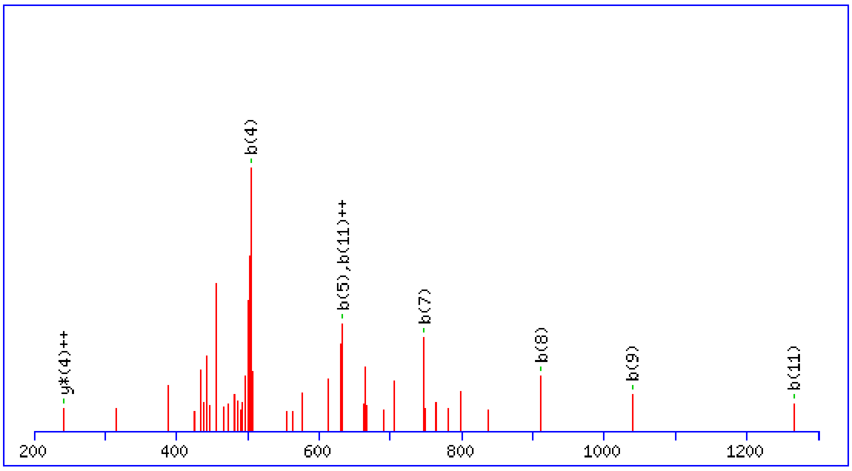
Match to Query 6968: 1538.776050 from(513.932626,3+) index(1872)
Title: Elution from: 22.366 to 22.366 scan no 2434 cid35.00 polarity:+
Data file C7-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

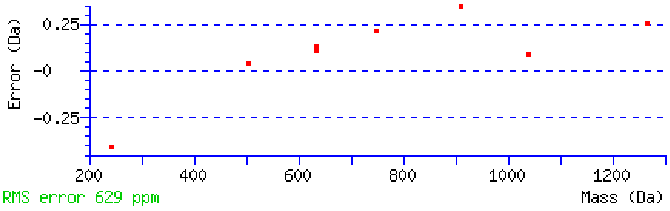
Label all possible matches ○ Label matches used for scoring ●

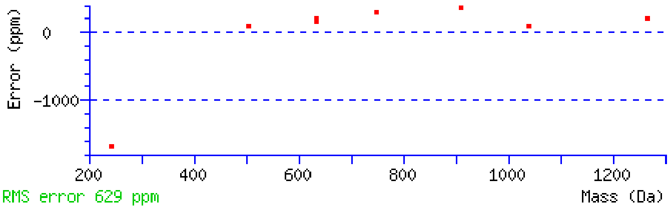
Show Y-axis ☐



`Monoisotopic mass of neutral peptide Mr(calc): 1538.7762`
`Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)`
`Ions Score: 41  Expect: 0.00042`
`Matches : 8/132 fragment ions using 9 most intense peaks  (help)`

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	219.0798	110.0435			201.0692	101.0382	M	1452.7515	726.8794	1435.7250	718.3661	1434.7410	717.8741	12
3	375.1809	188.0941	358.1544	179.5808	357.1703	179.0888	R	1321.7110	661.3592	1304.6845	652.8459	1303.7005	652.3539	11
4	***504.2235***	252.6154	487.1969	244.1021	486.2129	243.6101	E	1165.6099	583.3086	1148.5834	574.7953	1147.5994	574.3033	10
5	***633.2661***	317.1367	616.2395	308.6234	615.2555	308.1314	E	1036.5673	518.7873	1019.5408	510.2740	1018.5568	509.7820	9
6	690.2876	345.6474	673.2610	337.1341	672.2770	336.6421	G	907.5247	454.2660	890.4982	445.7527	889.5142	445.2607	8
7	***747.3090***	374.1581	730.2825	365.6449	729.2984	365.1529	G	850.5033	425.7553	833.4767	417.2420	832.4927	416.7500	7
8	***910.3723***	455.6898	893.3458	447.1765	892.3618	446.6845	Y	793.4818	397.2445	776.4553	388.7313	775.4713	388.2393	6
9	***1039.4149***	520.2111	1022.3884	511.6978	1021.4044	511.2058	E	630.4185	315.7129	613.3919	307.1996	612.4079	306.7076	5
10	1152.4990	576.7531	1135.4725	568.2399	1134.4884	567.7479	I	501.3759	251.1916	484.3493	242.6783			4
11	***1265.5831***	633.2952	1248.5565	624.7819	1247.5725	624.2899	I	388.2918	194.6496	371.2653	186.1363			3
12	1393.6780	697.3427	1376.6515	688.8294	1375.6675	688.3374	K	275.2078	138.1075	258.1812	129.5942			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SMREEGGYEIIKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G66200.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.8	1538.7762	-0.0002	SMREEGGYEIIKK
6.3	1538.7796	-0.0036	MSEASNKQMKLIK
5.7	1538.7763	-0.0002	LKMGTVEDEFSRK
5.2	1538.7763	-0.0002	MVLPDQIDDTHKK

Mascot: http://www.matrixscience.com/

AT1G66240.1

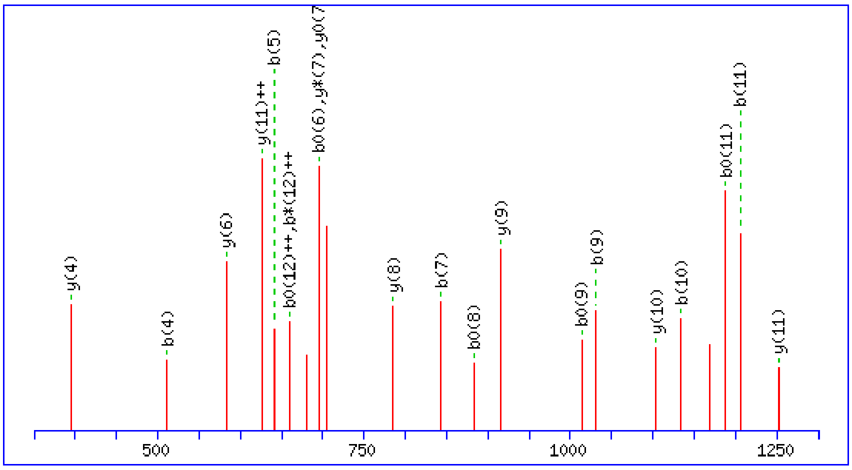
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFWEAEGETAKA**
Found in **AT1G66240.1** in **TAIR_Arabidopsis**, Symbols: ATX1 | ATX1; metal ion binding | chr1:24690108-24690990 REVERSE

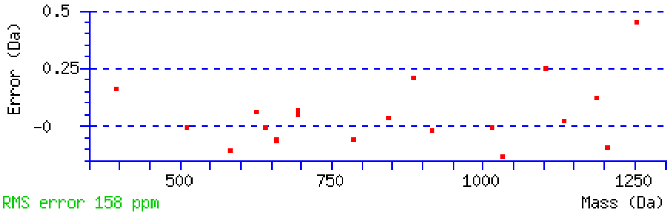
Match to Query 5400: 1424.603022 from(713.308787,2+) index(4760)
Title: Elution from: 42.473 to 42.473 scan no 5984 cid35.00 polarity:+
Data file D6h-3_3.mgf

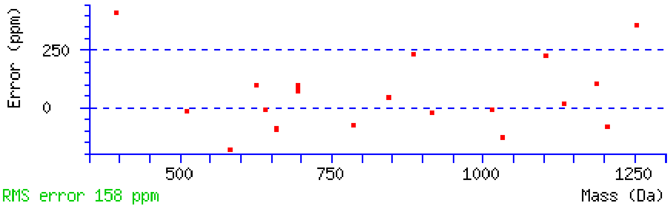
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



`Monoisotopic mass of neutral peptide Mr(calc): 1424.6018`
`Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)`
`Ions Score: 61  Expect: 4.7e-006`
`Matches : 21/114 fragment ions using 21 most intense peaks  (help)`

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	103.0520	52.0296			85.0414	43.0244	T							13
2	175.0861	88.0467			157.0756	79.0414	A	1323.5644	662.2858	1305.5408	653.2740	1305.5538	653.2806	12
3	323.1516	162.0794			305.1410	153.0741	F	***1251.5302***	626.2688	1233.5067	617.2570	1233.5197	617.2635	11
4	***511.2250***	256.1161			493.2144	247.1108	W	***1103.4648***	552.2360	1085.4412	543.2242	1085.4542	543.2308	10
5	***641.2646***	321.1359			623.2540	312.1307	E	***915.3914***	458.1993	897.3678	449.1876	897.3809	449.1941	9
6	713.2987	357.1530			695.2882	348.1477	A	***785.3518***	393.1795	767.3282	384.1677	767.3412	384.1743	8
7	***843.3384***	422.1728			825.3278	413.1675	E	713.3176	357.1625	695.2941	348.1507	695.3071	348.1572	7
8	901.3569	451.1821			883.3463	442.1768	G	***583.2780***	292.1426	565.2544	283.1309	565.2674	283.1374	6
9	***1031.3965***	516.2019			1013.3859	507.1966	E	525.2595	263.1334	507.2359	254.1216	507.2489	254.1281	5
10	***1133.4412***	567.2242			1115.4307	558.2190	T	***395.2199***	198.1136	377.1963	189.1018	377.2093	189.1083	4
11	***1205.4754***	603.2413			1187.4648	594.2360	A	293.1752	147.0912	275.1516	138.0794			3
12	1335.5644	668.2858	1317.5408	659.2740	1317.5538	659.2806	K	221.1410	111.0741	203.1174	102.0624			2
13							A	91.0520	46.0296					1





NCBI **BLAST** search of TAFWEAEGETAKA
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G66240.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.9	1424.6018	0.0012	TAFWEAEGETAKA
10.2	1424.6056	-0.0026	MNEDALEAVRSR
8.9	1424.5996	0.0035	FLRDDEEDDKK
8.9	1424.6057	-0.0026	MEAEASRKNENK
2.9	1424.6052	-0.0022	SEPYAQSAGELMK
2.2	1424.6005	0.0026	NQMVSMQEIWK
0.9	1424.6027	0.0003	DEESRRQVGGNR
0.7	1424.6031	-0.0001	SHTCRFLPNMK

Mascot: http://www.matrixscience.com/

AT1G66410.1

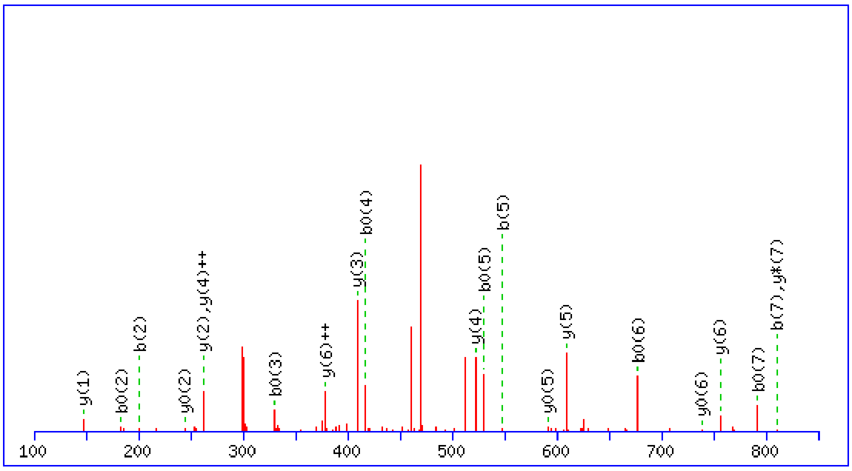
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAFSLFDK**
Found in **AT1G66410.1** in **TAIR_Arabidopsis**, Symbols: ACAM-4, CAM4 | CAM4 (CALMODULIN 4); calcium ion binding | chr1:24778094-24779448 REVERSE

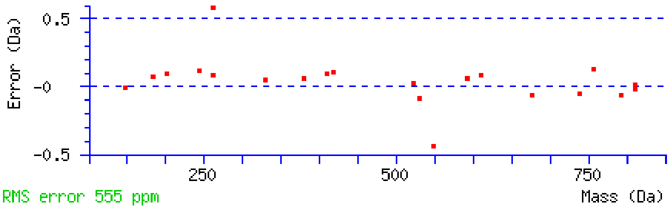
Match to Query 2127: 955.465892 from(478.740222,2+) index(6424)
Title: Elution from: 56.635 to 56.635 scan no 8216 cid35.00 polarity:+
Data file D12h-1_2.mgf

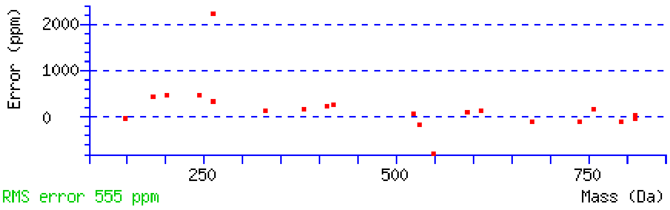
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 955.4651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00051
Matches : 21/68 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							8
2	**201.0870**	101.0471	183.0764	92.0418	A	827.4298	414.2185	810.4032	405.7053	809.4192	405.2132	7
3	348.1554	174.5813	330.1448	165.5761	F	***756.3927***	378.7000	739.3661	370.1867	738.3821	369.6947	6
4	435.1874	218.0974	417.1769	209.0921	S	***609.3243***	305.1658	592.2977	296.6525	591.3137	296.1605	5
5	**548.2715**	274.6394	530.2609	265.6341	L	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
6	695.3399	348.1736	677.3293	339.1683	F	***409.2082***	205.1077	392.1816	196.5944	391.1976	196.1024	3
7	**810.3668**	405.6871	792.3563	396.6818	D	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
8					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EAFSLFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.4	955.4651	0.0008	EAFSLFDK

AT1G66410.1

18.6	955.4651	0.0008	SLFEFADK
10.3	955.4684	-0.0026	EAMYLVSK
6.7	955.4657	0.0001	HAAMERNK
2.8	955.4685	-0.0026	KSFLDMLS
2.2	955.4685	-0.0026	TMIDAYVK
1.6	955.4685	-0.0026	MESTTFLK
1.6	955.4651	0.0008	AFDSFLEK
0.0	955.4685	-0.0026	DFSMSILK

AT1G66580.1

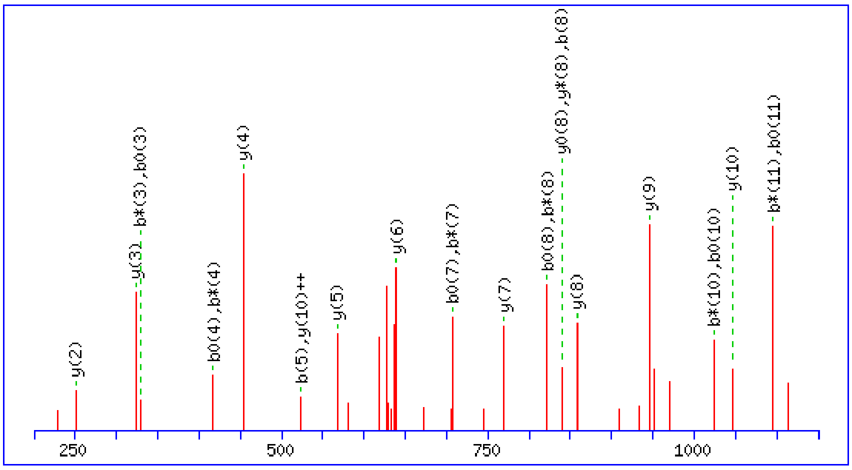
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENVSSEALEAAR**
Found in **AT1G66580.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L10 (RPL10C) | chr1:24842871-24844102 FORWARD

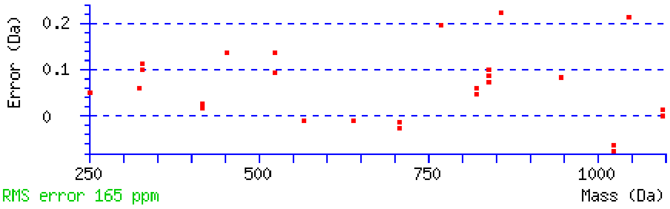
Match to Query 4632: 1290.564184 from(646.289368,2+) index(2748)
Title: Elution from: 28.965 to 28.965 scan no 3461 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

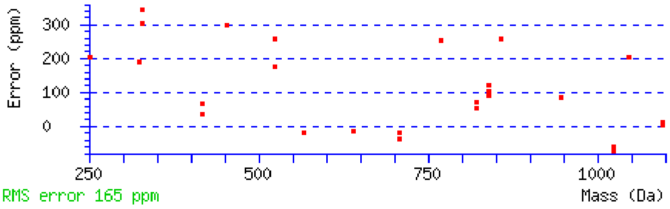


Monoisotopic mass of neutral peptide Mr(calc): 1290.5628
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 2.7e-010
Matches : 26/124 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							12
2	247.0839	124.0456	229.0603	115.0338	229.0733	115.0403	N	1161.5305	581.2689	1143.5069	572.2571	1143.5199	572.2636	11
3	347.1493	174.0783	329.1258	165.0665	329.1388	165.0730	V	***1045.4935***	523.2504	1027.4699	514.2386	1027.4829	514.2451	10
4	435.1784	218.0928	417.1548	209.0811	417.1678	209.0876	S	***945.4280***	473.2176	927.4044	464.2059	927.4175	464.2124	9
5	**523.2075**	262.1074	505.1839	253.0956	505.1969	253.1021	S	***857.3990***	429.2031	839.3754	420.1913	839.3884	420.1978	8
6	653.2471	327.1272	635.2235	318.1154	635.2365	318.1219	E	***769.3699***	385.1886	751.3463	376.1768	751.3593	376.1833	7
7	725.2813	363.1443	707.2577	354.1325	707.2707	354.1390	A	***639.3303***	320.1688	621.3067	311.1570	621.3197	311.1635	6
8	**839.3624**	420.1848	821.3388	411.1730	821.3518	411.1795	L	***567.2961***	284.1517	549.2725	275.1399	549.2856	275.1464	5
9	969.4020	485.2046	951.3784	476.1928	951.3914	476.1993	E	***453.2150***	227.1111	435.1914	218.0994	435.2045	218.1059	4
10	1041.4361	521.2217	1023.4125	512.2099	1023.4256	512.2164	A	***323.1754***	162.0913	305.1518	153.0795			3
11	1113.4703	557.2388	1095.4467	548.2270	1095.4597	548.2335	A	***251.1412***	126.0743	233.1177	117.0625			2
12							R	179.1071	90.0572	161.0835	81.0454			1



RMS error 165 ppm



RMS error 165 ppm

NCBI **BLAST** search of ENVSSEALEAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G66580.1

Score	Mr(calc)	Delta	Sequence
102.9	1290.5628	0.0014	ENVSSEALEAAR
11.4	1290.5673	-0.0031	FVDSDHFSVPK
5.5	1290.5637	0.0005	LATHMEMIAAR
0.0	1290.5637	0.0005	NCLPMELNLR

AT1G66670.1

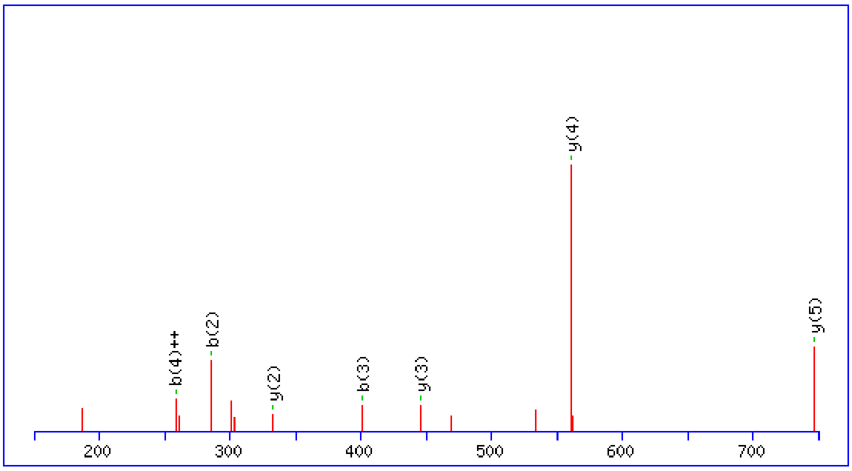
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VWDLWK**
Found in **AT1G66670.1** in **TAIR_Arabidopsis**, Symbols: NCLPP4, CLPP3 | CLPP3 (Clp protease proteolytic subunit 3); endopeptidase Clp | chr1:24867658-24869309 REVERSE

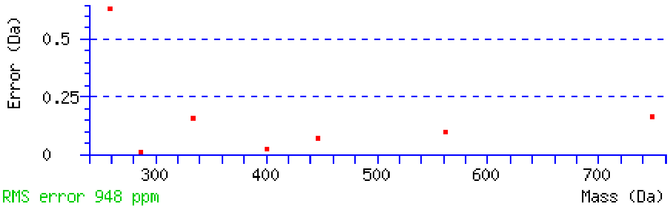
Match to Query 1267: 845.443978 from(423.729265,2+) index(7121)
Title: Elution from: 63.303 to 63.303 scan no 9309 cid35.00 polarity:+
Data file 0-2_2.mgf

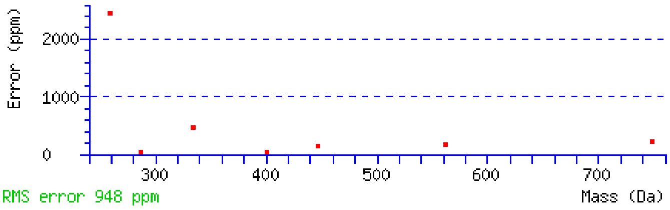
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 845.4436
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.003
Matches : 7/40 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							6
2	**286.1550**	143.5811			W	***747.3824***	374.1949	730.3559	365.6816	729.3719	365.1896	5
3	**401.1819**	201.0946	383.1714	192.0893	D	***561.3031***	281.1552	544.2766	272.6419	543.2926	272.1499	4
4	514.2660	257.6366	496.2554	248.6314	L	***446.2762***	223.6417	429.2496	215.1285			3
5	700.3453	350.6763	682.3348	341.6710	W	***333.1921***	167.0997	316.1656	158.5864			2
6					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VWDLWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.9	845.4436	0.0004	VWDLWK

Mascot: http://www.matrixscience.com/

AT1G66860.1

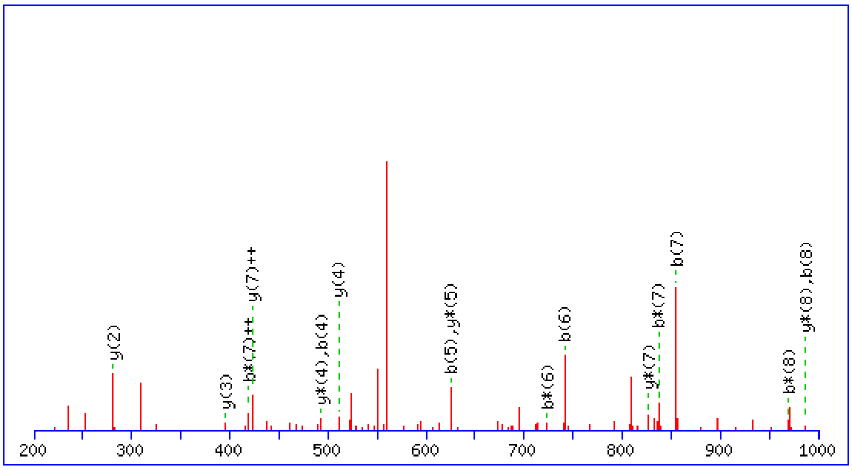
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QRKAMNIMK**
Found in **AT1G66860.1** in **TAIR_Arabidopsis**, Symbols: | hydrolase | chr1:24945903-24948015 FORWARD

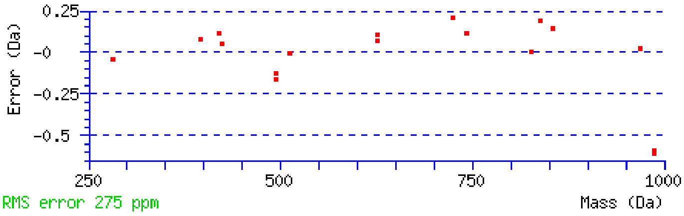
Match to Query 3683: 1134.556600 from(568.285576,2+) index(5301)
Title: Elution from: 46.341 to 46.341 scan no 6653 cid35.00 polarity:+
Data file C7-2_3.mgf

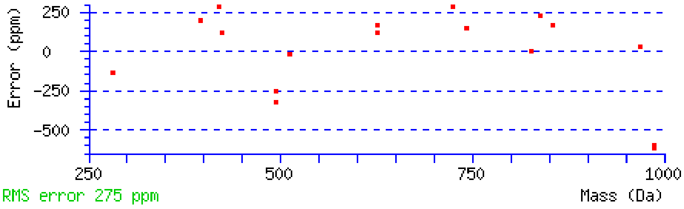
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1134.5578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.027
Matches : 17/64 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	131.0599	66.0336	113.0363	57.0218	Q					9
2	291.1492	146.0782	273.1256	137.0664	R	1005.5124	503.2599	987.4889	494.2481	8
3	421.2382	211.1227	403.2146	202.1109	K	845.4232	423.2152	827.3996	414.2034	7
4	***493.2724***	247.1398	475.2488	238.1280	A	715.3342	358.1707	697.3106	349.1589	6
5	***625.3099***	313.1586	607.2863	304.1468	M	643.3000	322.1536	625.2764	313.1419	5
6	***741.3469***	371.1771	723.3233	362.1653	N	**511.2625**	256.1349	493.2389	247.1231	4
7	***855.4280***	428.2176	837.4044	419.2058	I	**395.2255**	198.1164	377.2019	189.1046	3
8	***987.4655***	494.2364	969.4419	485.2246	M	**281.1444**	141.0758	263.1208	132.0640	2
9					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of QRKAMNIMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.3	1134.5578	-0.0012	QRKAMNIMK

AT1G66860.1

16.7	1134.5599	-0.0033	MLEKTISSKA
14.6	1134.5565	0.0001	DITELYLTR
10.7	1134.5587	-0.0021	DVYKLDFPK
8.0	1134.5592	-0.0026	YIAAAAEQRK
6.3	1134.5592	-0.0026	VQYGSPVSRK
5.3	1134.5551	0.0015	LLETTMMRK
1.0	1134.5565	0.0001	LYETLKDNK
0.9	1134.5544	0.0022	RTMLWLAGR
0.7	1134.5565	0.0001	LYELSNVSAK

AT1G66930.1

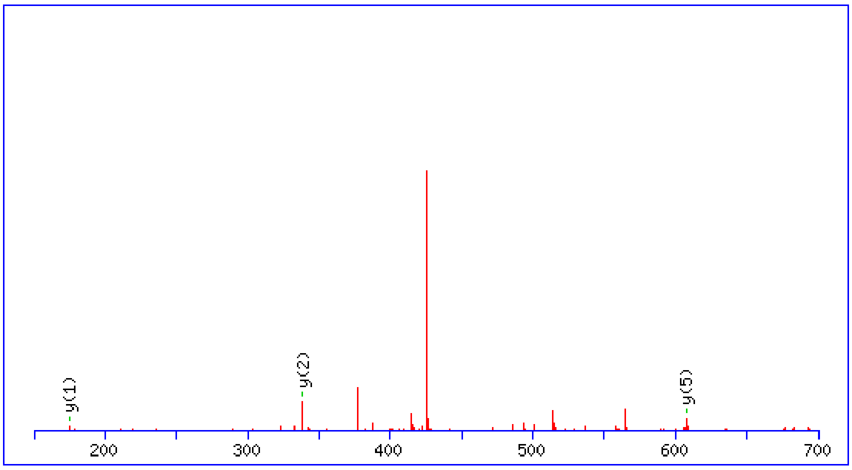
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGFGIVYR**
Found in **AT1G66930.1** in **TAIR_Arabidopsis**, Symbols: | serine/threonine protein kinase family protein | chr1:24974186-24976732 FORWARD

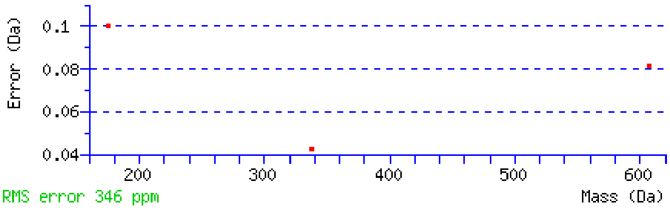
Match to Query 1401: 867.458820 from(434.736686,2+) index(2856)
Title: Elution from: 28.991 to 28.991 scan no 3577 cid35.00 polarity:+
Data file C7-3_3.mgf

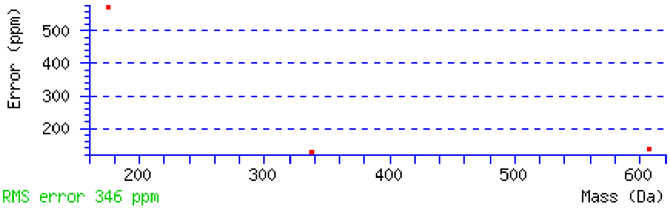
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 867.4603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.025
Matches : 3/42 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.5180	G					8
2	115.0502	58.0287	G	811.4461	406.2267	794.4196	397.7134	7
3	262.1186	131.5629	F	754.4246	377.7160	737.3981	369.2027	6
4	319.1401	160.0737	G	***607.3562***	304.1817	590.3297	295.6685	5
5	432.2241	216.6157	I	550.3348	275.6710	533.3082	267.1577	4
6	531.2926	266.1499	V	437.2507	219.1290	420.2241	210.6157	3
7	694.3559	347.6816	Y	***338.1823***	169.5948	321.1557	161.0815	2
8			R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of GGFGIVYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.0	867.4603	-0.0015	GGFGIVYR
20.8	867.4603	-0.0015	QGFVVYR

AT1G66930.1

9.9	867.4563	0.0026	GSIPPNQR
9.8	867.4603	-0.0015	FVGGAVYR
3.0	867.4563	0.0026	LHPTSASR
2.4	867.4603	-0.0015	IFFTGGAR
1.3	867.4603	-0.0015	SAIAGFFR
1.2	867.4603	-0.0015	QFGTIFR

AT1G66970.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVSIDFISSPEVNFFK**
Found in **AT1G66970.1** in **TAIR_Arabidopsis**, Symbols: | glycerophosphoryl diester phosphodiesterase family protein | chr1:24996409-24999668 REVERSE

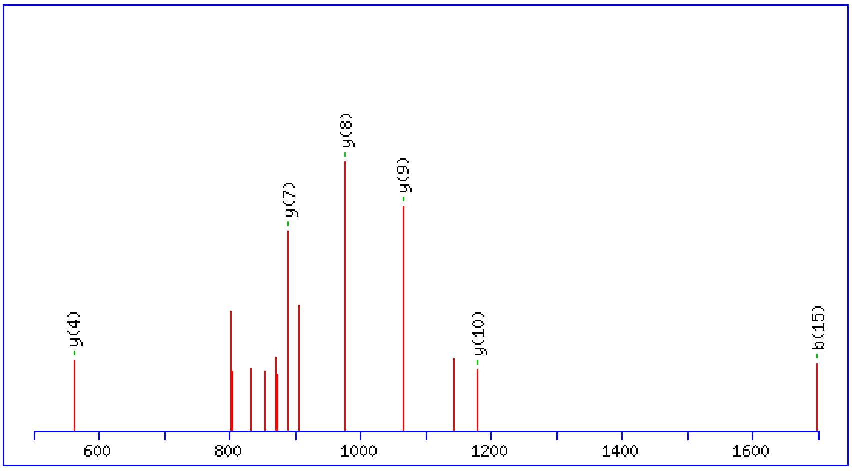
Match to Query 9274: 1846.870268 from(924.442410,2+) index(10768)
Title: Elution from: 99.626 to 99.626 scan no 15092 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

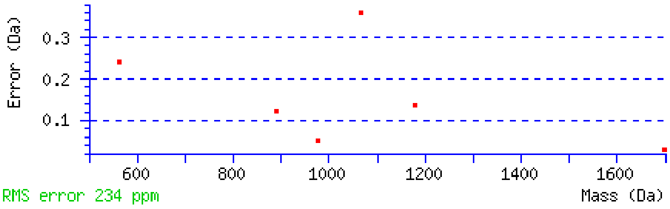
Show Y-axis ☐

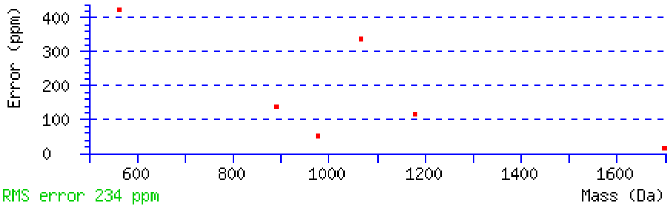


Monoisotopic mass of neutral peptide Mr(calc): 1846.8713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0028
Matches : 6/146 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							16
2	203.1174	102.0624			185.1069	93.0571	V	1745.8339	873.4206	1727.8103	864.4088	1727.8233	864.4153	15
3	291.1465	146.0769			273.1359	137.0716	S	1645.7685	823.3879	1627.7449	814.3761	1627.7579	814.3826	14
4	405.2276	203.1174			387.2170	194.1122	I	1557.7394	779.3733	1539.7158	770.3615	1539.7288	770.3681	13
5	521.2516	261.1294			503.2410	252.1241	D	1443.6583	722.3328	1425.6347	713.3210	1425.6477	713.3275	12
6	669.3170	335.1622			651.3065	326.1569	F	1327.6343	664.3208	1309.6107	655.3090	1309.6238	655.3155	11
7	783.3981	392.2027			765.3876	383.1974	I	***1179.5689***	590.2881	1161.5453	581.2763	1161.5583	581.2828	10
8	871.4272	436.2172			853.4166	427.2120	S	***1065.4878***	533.2475	1047.4642	524.2357	1047.4772	524.2422	9
9	959.4563	480.2318			941.4457	471.2265	S	***977.4587***	489.2330	959.4351	480.2212	959.4481	480.2277	8
10	1057.5061	529.2567			1039.4955	520.2514	P	***889.4296***	445.2185	871.4061	436.2067	871.4191	436.2132	7
11	1187.5457	594.2765			1169.5351	585.2712	E	791.3798	396.1936	773.3563	387.1818	773.3693	387.1883	6
12	1287.6111	644.3092			1269.6006	635.3039	V	661.3402	331.1737	643.3166	322.1620			5
13	1403.6481	702.3277	1385.6245	693.3159	1385.6376	693.3224	N	***561.2748***	281.1410	543.2512	272.1292			4
14	1551.7136	776.3604	1533.6900	767.3486	1533.7030	767.3551	F	445.2378	223.1225	427.2142	214.1107			3
15	1699.7790	850.3931	1681.7554	841.3814	1681.7685	841.3879	F	297.1723	149.0898	279.1487	140.0780			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT1G66970.1





NCBI **BLAST** search of TVSIDFISSPEVNFFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.9	1846.8713	-0.0011	TVSIDFISSPEVNFFK
5.7	1846.8699	0.0003	GFFDTDKLMIMLVGNK
1.9	1846.8722	-0.0019	HGEPLKKSSGPQSGGVTR
1.4	1846.8752	-0.0049	IEKTENLIIADHMNGK
1.1	1846.8747	-0.0045	LEMPPPFSVVIQESEK
0.4	1846.8670	0.0032	YKMQRVPFVEEQVR

AT1G67090.1

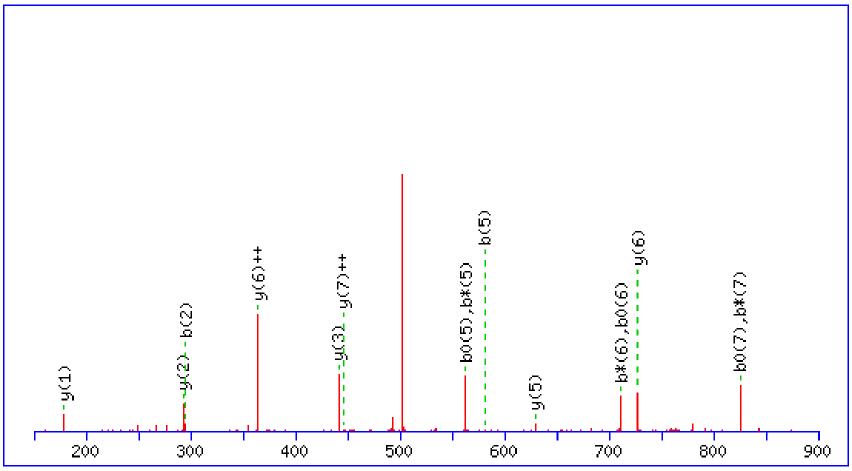
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYPNAFIR**
Found in **AT1G67090.1** in **TAIR_Arabidopsis**, Symbols: RBCS1A | RBCS1A; ribulose-bisphosphate carboxylase | chr1:25052128-25052912 REVERSE

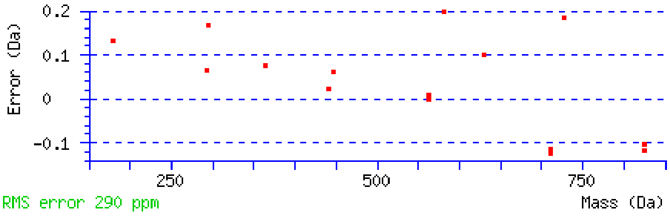
Match to Query 2800: 1020.467052 from(511.240802,2+) index(4136)
Title: Elution from: 38.635 to 38.635 scan no 5141 cid35.00 polarity:+
Data file C7-3_1.mgf

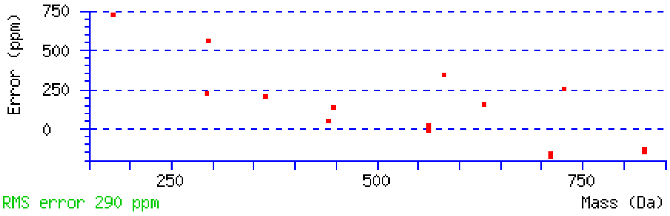
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1020.4673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0019
Matches : 15/64 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	131.0469	66.0271			113.0363	57.0218	E					8
2	**295.1073**	148.0573			277.0967	139.0520	Y	891.4349	446.2211	873.4114	437.2093	7
3	393.1571	197.0822			375.1465	188.0769	P	***727.3746***	364.1909	709.3510	355.1791	6
4	509.1941	255.1007	491.1705	246.0889	491.1835	246.0954	N	***629.3248***	315.1660	611.3012	306.1542	5
5	**581.2282**	291.1177	563.2046	282.1060	563.2176	282.1125	A	513.2878	257.1475	495.2642	248.1357	4
6	729.2937	365.1505	711.2701	356.1387	711.2831	356.1452	F	***441.2536***	221.1305	423.2301	212.1187	3
7	843.3748	422.1910	825.3512	413.1792	825.3642	413.1857	I	***293.1882***	147.0977	275.1646	138.0859	2
8							R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of EYPNAFIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.3	1020.4673	-0.0002	EYPNAFIR

AT1G67090.1

15.6	1020.4650	0.0020	GSFVSDQIR
10.9	1020.4655	0.0016	TNGKRDASR
9.9	1020.4650	0.0020	GSEGYVQIR
9.1	1020.4655	0.0016	SRSIDRDR
7.8	1020.4700	-0.0029	WNDRFLR
7.7	1020.4651	0.0020	EKIYGENR
5.7	1020.4655	0.0016	QSNGIRSSR
5.2	1020.4684	-0.0014	KASVMDVSR
4.2	1020.4650	0.0020	YQKDLEGR

Mascot: http://www.matrixscience.com/

AT1G67120.1

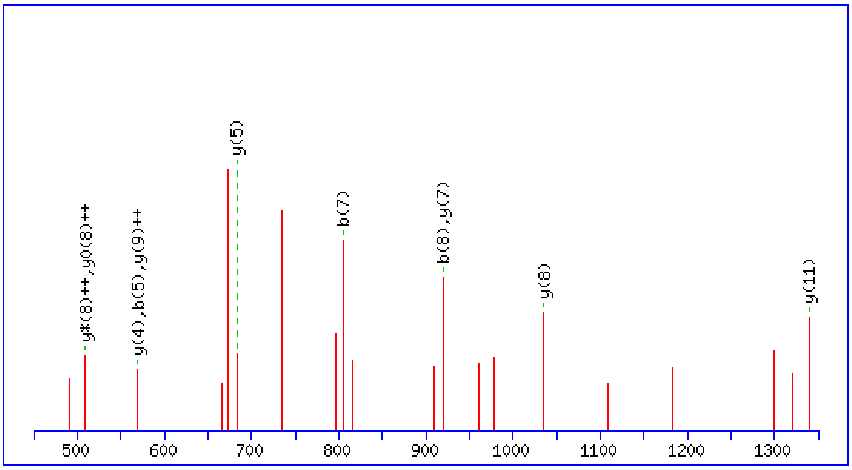
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEATDAYLLCLR**
Found in **AT1G67120.1** in **TAIR_Arabidopsis**, Symbols: | midasin-related | chr1:25073390-25099189 REVERSE

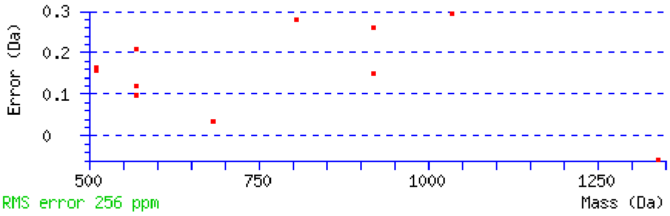
Match to Query 6513: 1486.635346 from(744.324949,2+) index(7322)
Title: Elution from: 63.391 to 63.391 scan no 9404 cid35.00 polarity:+
Data file C7-1_1.mgf

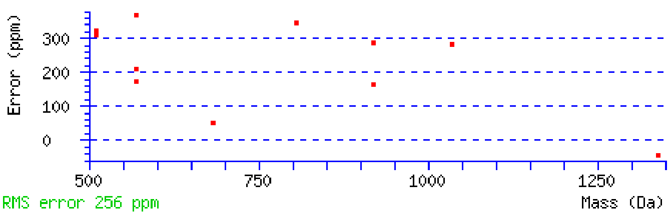
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



`Monoisotopic mass of neutral peptide Mr(calc): 1486.6372`
`Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)`
`Variable modifications:`
`M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983`
`Ions Score: 28 Expect: 0.0076`
`Matches : 11/136 fragment ions using 14 most intense peaks (help)`

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235			**M**							**12**
2	279.0793	140.0433	261.0688	131.0380	**E**	***1339.6121***	670.3097	1321.5885	661.2979	1321.6015	661.3044	**11**
3	351.1135	176.0604	333.1029	167.0551	**A**	1209.5725	605.2899	1191.5489	596.2781	1191.5619	596.2846	**10**
4	453.1582	227.0827	435.1476	218.0775	**T**	1137.5383	569.2728	1119.5147	560.2610	1119.5277	560.2675	**9**
5	**569.1822**	285.0947	551.1716	276.0894	**D**	***1035.4936***	518.2504	1017.4700	509.2386	1017.4830	509.2452	**8**
6	641.2163	321.1118	623.2058	312.1065	**A**	***919.4696***	460.2384	901.4460	451.2267			**7**
7	**805.2767**	403.1420	787.2661	394.1367	**Y**	847.4355	424.2214	829.4119	415.2096			**6**
8	**919.3578**	460.1825	901.3472	451.1773	**L**	***683.3751***	342.1912	665.3515	333.1794			**5**
9	1033.4389	517.2231	1015.4283	508.2178	**L**	***569.2940***	285.1506	551.2704	276.1388			**4**
10	1195.4636	598.2354	1177.4530	589.2302	**C**	455.2129	228.1101	437.1893	219.0983			**3**
11	1309.5447	655.2760	1291.5341	646.2707	**L**	293.1882	147.0977	275.1646	138.0859			**2**
12					**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of MEATDAYLLCLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G67120.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.9	1486.6372	-0.0019	MEATDAYLLCLR
13.3	1486.6339	0.0015	DFEGAYNMLGNLK
10.7	1486.6309	0.0044	AENTSYFGASRHK
4.8	1486.6339	0.0015	SGTYLYKHEMDK
3.6	1486.6358	-0.0005	HHGLNNFWVADR
3.5	1486.6343	0.0011	ICTAGRFSEAEAR
3.3	1486.6390	-0.0037	GKQVAGSDSYSGGQK
2.0	1486.6390	-0.0037	NLKNDDHEQDLK
1.2	1486.6372	-0.0019	GAFELMREMVEK
0.3	1486.6352	0.0002	WIMSRQNMVMR

AT1G67140.1

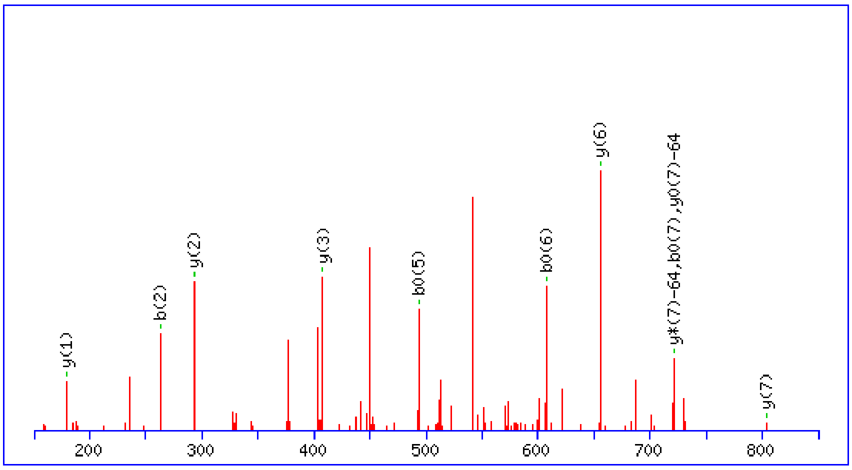
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMTSGIIR**
Found in **AT1G67140.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr1:25104679-25121035 REVERSE

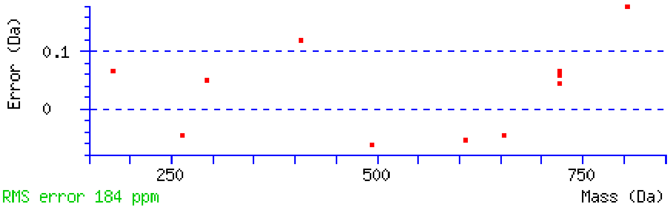
Match to Query 1712: 916.466252 from(459.240402,2+) index(4239)
Title: Elution from: 39.380 to 39.380 scan no 5332 cid35.00 polarity:+
Data file 0-3_2.mgf

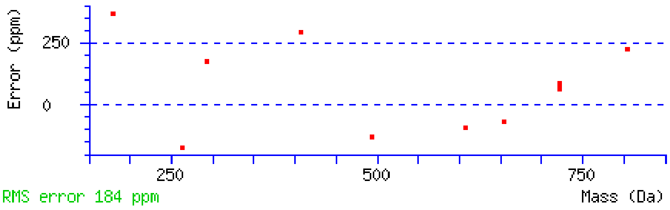
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 916.4678
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 0.022
Matches : 11/86 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			**I**							**8**
2	263.1208	132.0640			**M**	***803.3940***	402.2006	785.3704	393.1888	785.3834	393.1954	**7**
3	365.1655	183.0864	347.1550	174.0811	**T**	***655.3616***	328.1844	637.3380	319.1726	637.3510	319.1791	**6**
4	453.1946	227.1009	435.1840	218.0956	**S**	553.3169	277.1621	535.2933	268.1503	535.3063	268.1568	**5**
5	511.2131	256.1102	493.2025	247.1049	**G**	465.2878	233.1475	447.2642	224.1357			**4**
6	625.2942	313.1507	607.2836	304.1454	**I**	***407.2693***	204.1383	389.2457	195.1265			**3**
7	739.3753	370.1913	721.3647	361.1860	**I**	***293.1882***	147.0977	275.1646	138.0859			**2**
8					**R**	***179.1071***	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of IMTSGIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.3	916.4678	-0.0016	IMTSGIIR

AT1G67140.1

18.5	916.4649	0.0014	NGSISRIR
9.2	916.4671	-0.0009	IEHHVLR
9.0	916.4644	0.0018	VELGYGIR
7.8	916.4644	0.0018	YPGLSTLR
7.2	916.4644	0.0018	LFAIAESR
7.2	916.4644	0.0018	IFDLRDK
6.8	916.4644	0.0018	IFGLVSDR
6.8	916.4644	0.0018	IFSGEVVR
6.8	916.4678	-0.0016	LMKTLER

Mascot: http://www.matrixscience.com/

AT1G67190.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **CPNLKK**
Found in **AT1G67190.1** in **TAIR_Arabidopsis**, Symbols: | F-box family protein | chr1:25136717-25137976 FORWARD

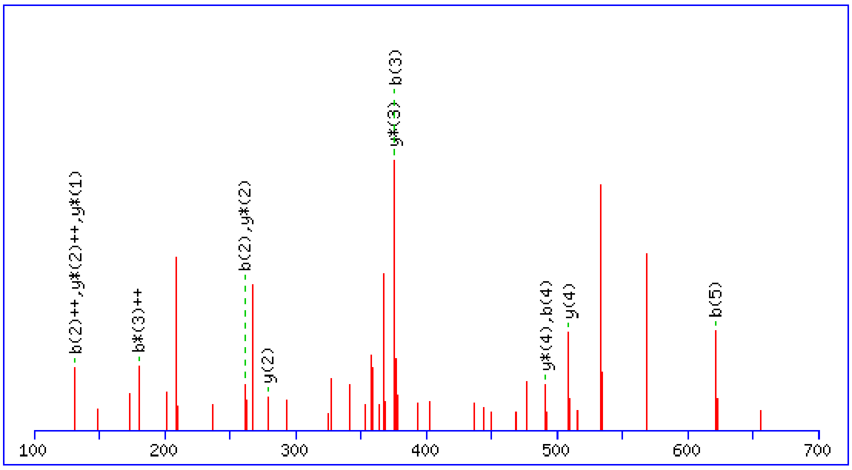
Match to Query 891: 768.381678 from(385.198115,2+) index(456)
Title: Elution from: 10.573 to 10.573 scan no 739 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

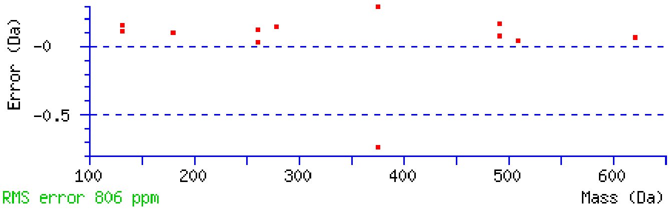
Label all possible matches ○ Label matches used for scoring ●

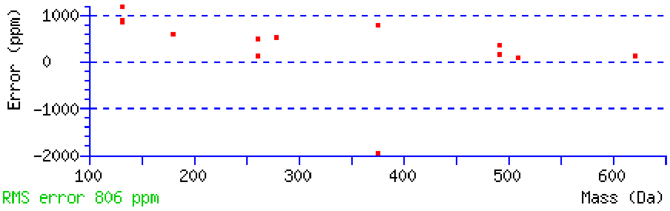
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 768.3813
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.038
Matches : 13/36 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	163.0320	82.0196			C					6
2	***261.0818***	131.0445			P	607.3638	304.1855	589.3402	295.1737	5
3	***377.1188***	189.0630	359.0952	180.0512	N	**509.3140**	255.1606	491.2904	246.1488	4
4	***491.1999***	246.1036	473.1763	237.0918	L	393.2770	197.1421	375.2534	188.1303	3
5	***621.2889***	311.1481	603.2653	302.1363	K	**279.1959**	140.1016	261.1723	131.0898	2
6					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of CPNLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.2	768.3813	0.0004	CPNLKK
11.2	768.3813	0.0004	KMISHK
6.2	768.3813	0.0004	KCPNLK
3.8	768.3813	0.0004	KSHMIK

AT1G67190.1

3.8	768.3812	0.0004	GAMVPIR

Mascot: http://www.matrixscience.com/

AT1G67230.1

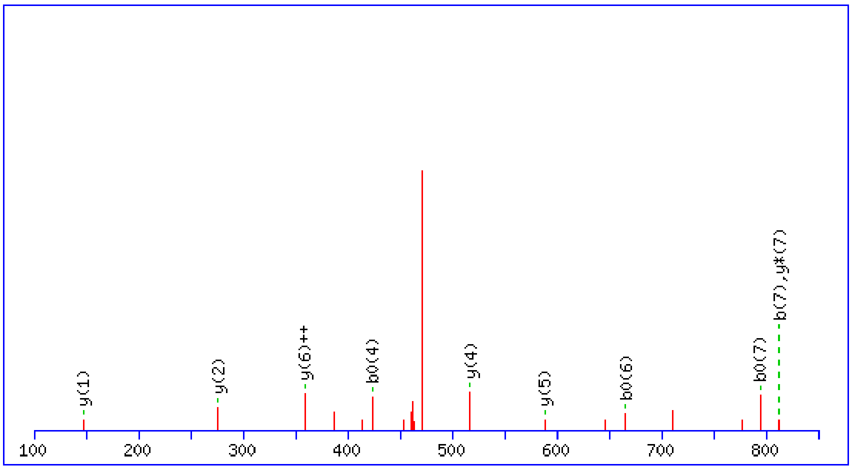
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELQALQEK**
Found in **AT1G67230.1** in **TAIR_Arabidopsis**, Symbols: LINC1 | LINC1 (LITTLE NUCLEI1) | chr1:25155224-25159695 REVERSE

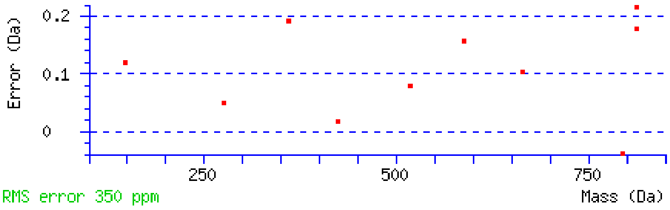
Match to Query 2237: 957.512954 from(479.763753,2+) index(935)
Title: Elution from: 15.139 to 15.139 scan no 1333 cid35.00 polarity:+
Data file C7-3_1.mgf

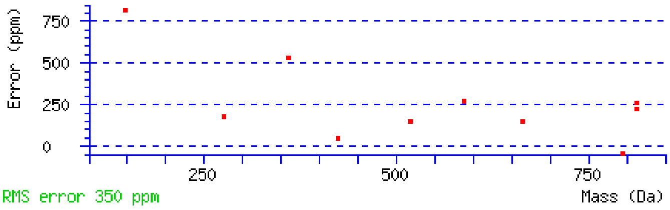
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 957.5131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.033
Matches : 10/78 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							8
2	243.1339	122.0706			225.1234	113.0653	L	829.4778	415.2425	812.4512	406.7293	811.4672	406.2373	7
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	Q	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	A	***588.3352***	294.6712	571.3086	286.1579	570.3246	285.6659	5
5	555.3137	278.1605	538.2871	269.6472	537.3031	269.1552	L	***517.2980***	259.1527	500.2715	250.6394	499.2875	250.1474	4
6	683.3723	342.1898	666.3457	333.6765	665.3617	333.1845	Q	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
7	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
8							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ELQALQEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	957.5131	-0.0001	ELQALQEK
14.9	957.5131	-0.0001	AIGEVDLNK

AT1G67230.1

13.3	957.5131	-0.0001	ELAQQIEK
11.1	957.5131	-0.0001	TNPEKEIK
11.1	957.5131	-0.0002	ISAVQTDPK
8.9	957.5131	-0.0001	AIADVDLNK
5.5	957.5131	-0.0001	EDLQNLVK
4.5	957.5131	-0.0001	EDQINVLK
4.5	957.5131	-0.0002	QIQDDVLK
4.3	957.5131	-0.0001	AQSVSPIEK

Mascot Search Results

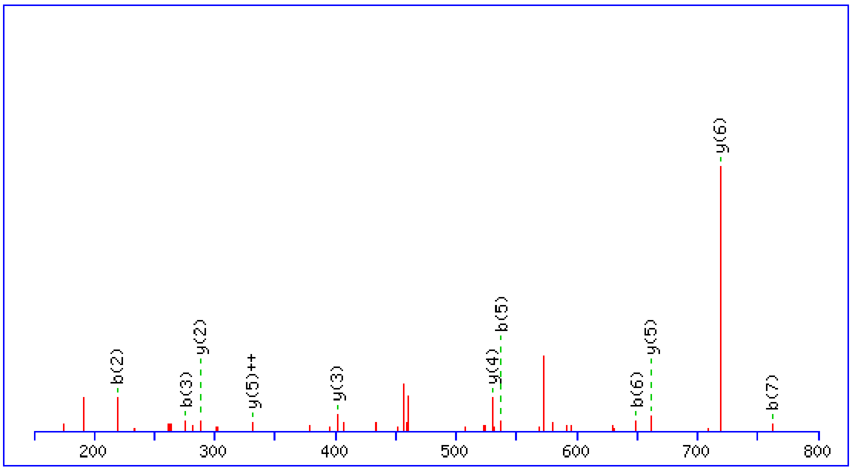
Peptide View

MS/MS Fragmentation of **AFGMELLR**
Found in **AT1G67280.1** in **TAIR_Arabidopsis**, Symbols: | lactoylglutathione lyase, putative / glyoxalase I, putative | chr1:25192226-25194210 REVERSE

Match to Query 1554: 935.490266 from(468.752409,2+) index(6617)
Title: Elution from: 62.501 to 62.501 scan no 8745 cid35.00 polarity:+
Data file D1d-1-2.mgf

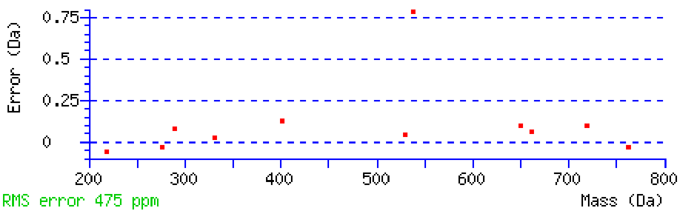
Click mouse within plot area to zoom in by factor of two about that point

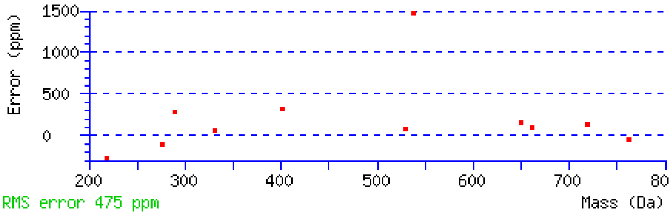
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 935.4899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0004
Matches : 11/56 fragment ions using 18 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258			A							8
2	***219.1128***	110.0600			F	865.4600	433.2337	848.4335	424.7204	847.4495	424.2284	7
3	***276.1343***	138.5708			G	***718.3916***	359.6994	701.3651	351.1862	700.3811	350.6942	6
4	407.1748	204.0910			M	***661.3702***	331.1887	644.3436	322.6754	643.3596	322.1834	5
5	***536.2173***	268.6123	518.2068	259.6070	E	***530.3297***	265.6685	513.3031	257.1552	512.3191	256.6632	4
6	***649.3014***	325.1543	631.2908	316.1491	L	***401.2871***	201.1472	384.2605	192.6339			3
7	***762.3855***	381.6964	744.3749	372.6911	L	***288.2030***	144.6051	271.1765	136.0919			2
8					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AFGMELLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.6	935.4899	0.0004	AFGMELLR

AT1G67280.1

8.8	935.4899	0.0004	AFIDAMIR
3.0	935.4899	0.0004	QFELMLR
1.9	935.4899	0.0004	YPGLMSLR

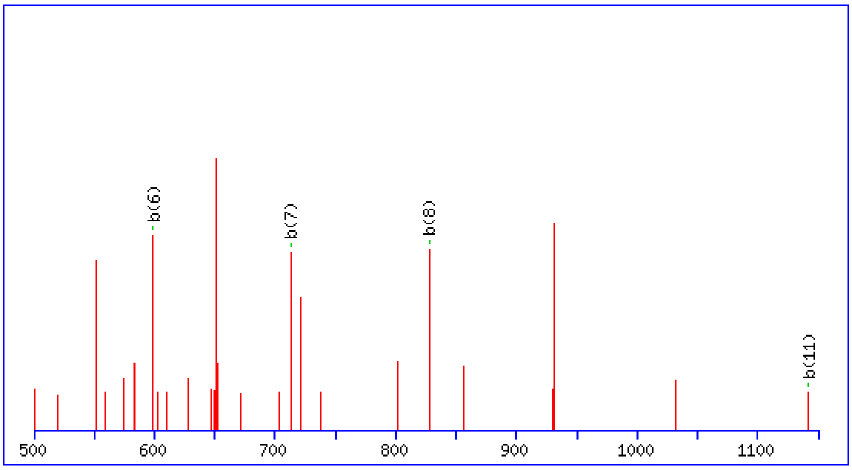
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGDGSIIINHGR**
Found in **AT1G67550.1** in **TAIR_Arabidopsis**, Symbols: URE | URE (UREASE); urease | chr1:25316505-25320574 FORWARD

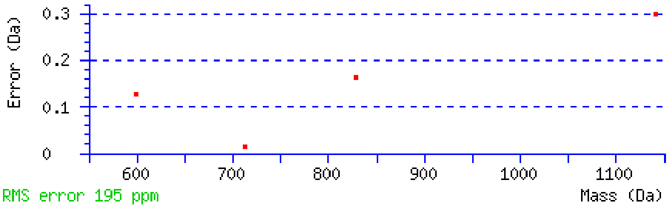
Match to Query 4456: 1318.596750 from(660.305651,2+) index(3107)
Title: Elution from: 31.824 to 31.824 scan no 3924 cid35.00 polarity:+
Data file D12h-2_3.mgf

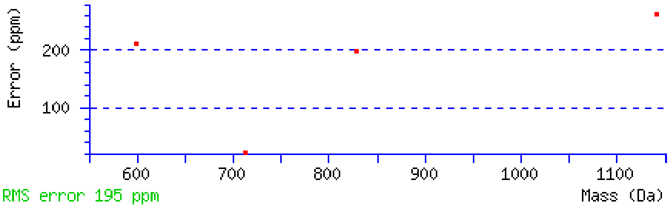
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1318.5990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.033
Matches : 4/98 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							12
2	223.0861	112.0467					G	1155.5459	578.2766	1137.5224	569.2648	1137.5354	569.2713	11
3	339.1101	170.0587			321.0996	161.0534	D	1097.5274	549.2674	1079.5039	540.2556	1079.5169	540.2621	10
4	397.1286	199.0679			379.1181	190.0627	G	981.5035	491.2554	963.4799	482.2436	963.4929	482.2501	9
5	485.1577	243.0825			467.1471	234.0772	S	923.4850	462.2461	905.4614	453.2343	905.4744	453.2408	8
6	***599.2388***	300.1230			581.2282	291.1177	I	835.4559	418.2316	817.4323	409.2198			7
7	***713.3199***	357.1636			695.3093	348.1583	I	721.3748	361.1910	703.3512	352.1792			6
8	***827.4010***	414.2041			809.3904	405.1988	I	607.2937	304.1505	589.2701	295.1387			5
9	943.4380	472.2226	925.4144	463.2108	925.4274	463.2173	N	493.2126	247.1099	475.1890	238.0981			4
10	1083.4880	542.2476	1065.4644	533.2358	1065.4774	533.2424	H	377.1756	189.0914	359.1520	180.0796			3
11	***1141.5065***	571.2569	1123.4829	562.2451	1123.4959	562.2516	G	237.1256	119.0664	219.1020	110.0546			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of YGDGSIIINHGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G67550.1

Score	Mr(calc)	Delta	Sequence
23.1	1318.5990	-0.0023	YGDGSIIINHGR
3.1	1318.5941	0.0026	VANVSIGETEER
0.8	1318.5941	0.0027	TLLVDDGSAEGAR

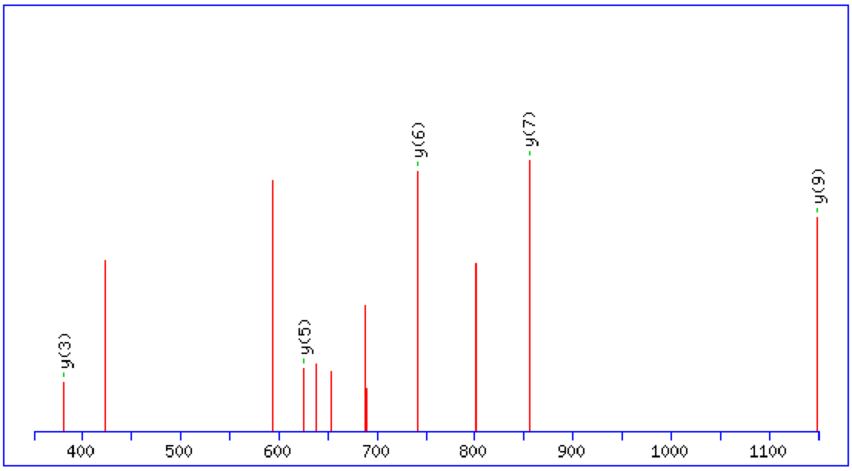
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKYEIDELSLR**
Found in **AT1G67690.1** in **TAIR_Arabidopsis**, Symbols: | peptidase M3 family protein / thimet oligopeptidase family protein | chr1:25372749-25377393 FORWARD

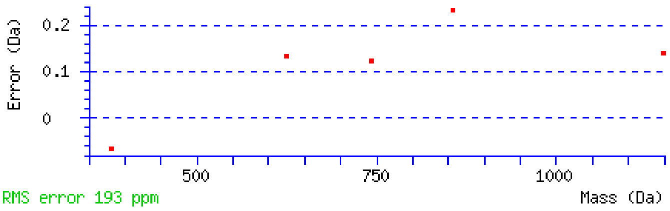
Match to Query 5237: 1392.708048 from(697.361300,2+) index(8108)
Title: Elution from: 71.651 to 71.651 scan no 10689 cid35.00 polarity:+
Data file 0-3_2.mgf

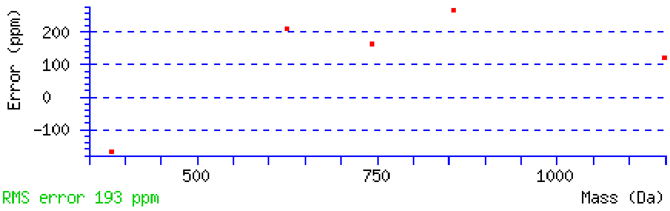
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1392.7059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0096
Matches : 5/108 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							11
2	245.1774	123.0923	227.1538	114.0805			K	1279.6321	640.3197	1261.6085	631.3079	1261.6215	631.3144	10
3	409.2378	205.1225	391.2142	196.1107			Y	***1149.5431***	575.2752	1131.5195	566.2634	1131.5325	566.2699	9
4	539.2774	270.1423	521.2538	261.1305	521.2668	261.1371	E	985.4827	493.2450	967.4591	484.2332	967.4721	484.2397	8
5	653.3585	327.1829	635.3349	318.1711	635.3479	318.1776	I	***855.4431***	428.2252	837.4195	419.2134	837.4325	419.2199	7
6	769.3825	385.1949	751.3589	376.1831	751.3719	376.1896	D	***741.3620***	371.1846	723.3384	362.1728	723.3514	362.1793	6
7	899.4221	450.2147	881.3985	441.2029	881.4115	441.2094	E	***625.3380***	313.1726	607.3144	304.1608	607.3274	304.1673	5
8	1013.5032	507.2552	995.4796	498.2434	995.4926	498.2500	L	495.2984	248.1528	477.2748	239.1410	477.2878	239.1475	4
9	1101.5323	551.2698	1083.5087	542.2580	1083.5217	542.2645	S	***381.2173***	191.1123	363.1937	182.1005	363.2067	182.1070	3
10	1215.6134	608.3103	1197.5898	599.2985	1197.6028	599.3050	L	293.1882	147.0977	275.1646	138.0859			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LKYEIDELSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G67690.1

Score	Mr(calc)	Delta	Sequence
29.7	1392.7059	0.0021	LKYEIDELSLR
2.9	1392.7085	-0.0005	IDRFIVDDVRK
2.5	1392.7086	-0.0005	IKNTERFKPDK
2.4	1392.7045	0.0035	KLMGVTMLDVVR
2.1	1392.7119	-0.0039	MRIVGLTGGIASGK
1.5	1392.7086	-0.0005	LQSLNEQFLRK
0.1	1392.7063	0.0017	DTTIGRVVRETK

AT1G67700.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALSTSDVIELPTQDQLK**
Found in **AT1G67700.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown [Populus trichocarpa] (GB:ABK95743.1); contains domain PTHR11804:SF2 (PTHR11804:SF2); contains domain PTHR11804 (PTHR11804) | chr1:25377958-25379379 FORWARD

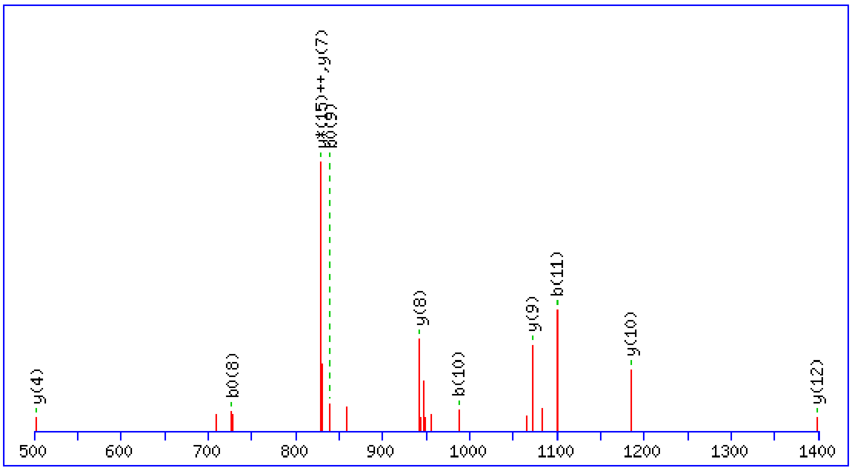
Match to Query 9384: 1928.006566 from(965.010559,2+) index(8003)
Title: Elution from: 69.683 to 69.683 scan no 10422 cid35.00 polarity:+
Data file D1d-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1400 Da Full range

Label all possible matches ○ Label matches used for scoring ●

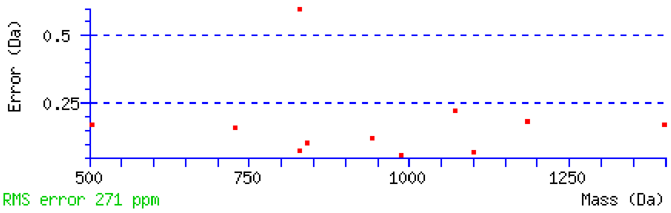
Show Y-axis ☐

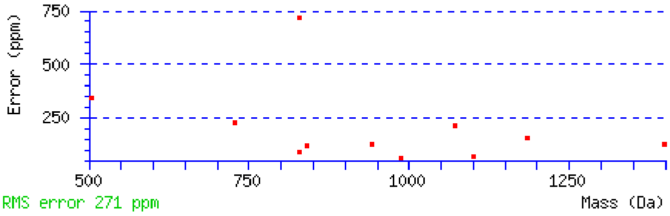


Monoisotopic mass of neutral peptide Mr(calc): 1928.0102
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00033
Matches : 11/166 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**18**
2	143.0815	72.0444					**A**	1857.9804	929.4938	1840.9539	920.9806	1839.9698	920.4886	**17**
3	256.1656	128.5864					**L**	1786.9433	893.9753	1769.9167	885.4620	1768.9327	884.9700	**16**
4	343.1976	172.1024			325.1870	163.0972	**S**	1673.8592	837.4332	1656.8327	828.9200	1655.8487	828.4280	**15**
5	444.2453	222.6263			426.2347	213.6210	**T**	1586.8272	793.9172	1569.8006	785.4040	1568.8166	784.9120	**14**
6	531.2773	266.1423			513.2667	257.1370	**S**	1485.7795	743.3934	1468.7530	734.8801	1467.7690	734.3881	**13**
7	646.3042	323.6558			628.2937	314.6505	**D**	***1398.7475***	699.8774	1381.7209	691.3641	1380.7369	690.8721	**12**
8	745.3727	373.1900			727.3621	364.1847	**V**	1283.7205	642.3639	1266.6940	633.8506	1265.7100	633.3586	**11**
9	858.4567	429.7320			840.4462	420.7267	**I**	***1184.6521***	592.8297	1167.6256	584.3164	1166.6416	583.8244	**10**
10	**987.4993**	494.2533			969.4888	485.2480	**E**	***1071.5681***	536.2877	1054.5415	527.7744	1053.5575	527.2824	**9**
11	**1100.5834**	550.7953			1082.5728	541.7900	**L**	***942.5255***	471.7664	925.4989	463.2531	924.5149	462.7611	**8**
12	1197.6361	599.3217			1179.6256	590.3164	**P**	***829.4414***	415.2243	812.4149	406.7111	811.4308	406.2191	**7**
13	1298.6838	649.8456			1280.6733	640.8403	**T**	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	**6**
14	1426.7424	713.8748	1409.7159	705.3616	1408.7318	704.8696	**Q**	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	**5**
15	1541.7693	771.3883	1524.7428	762.8750	1523.7588	762.3830	**D**	***503.2824***	252.1448	486.2558	243.6316	485.2718	243.1395	**4**
16	1669.8279	835.4176	1652.8014	826.9043	1651.8174	826.4123	**Q**	388.2554	194.6314	371.2289	186.1181			**3**
17	1782.9120	891.9596	1765.8854	883.4464	1764.9014	882.9543	**L**	260.1969	130.6021	243.1703	122.0888			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT1G67700.1





NCBI **BLAST** search of AALSTSDVIELPTQDQLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.1	1928.0102	-0.0037	AALSTSDVIELPTQDQLK
1.2	1928.0116	-0.0050	KSGDSGEKPSISLAHFLR

Mascot: http://www.matrixscience.com/

AT1G68010.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

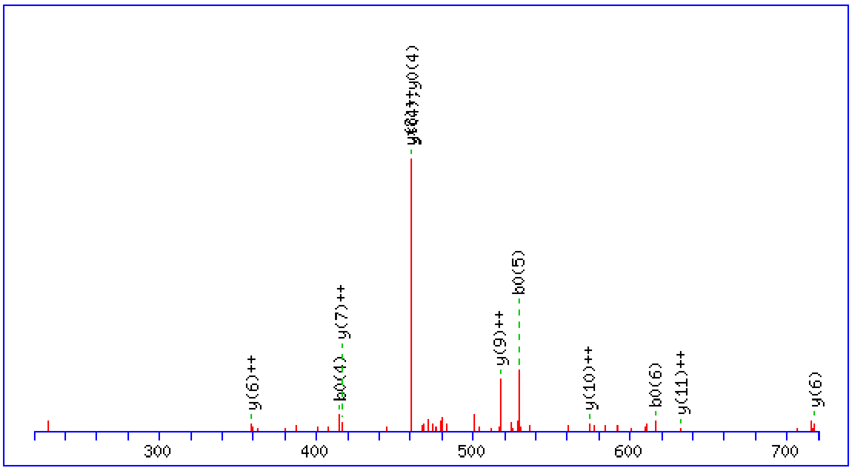
MS/MS Fragmentation of **EADLISLHPVLDK**
Found in **AT1G68010.1** in **TAIR_Arabidopsis**, Symbols: HPR | HPR (HYDROXYPYRUVATE REDUCTASE); glycerate dehydrogenase/ poly(U) binding | chr1:25497081-25499383 FORWARD

Match to Query 5640: 1464.735723 from(489.252517,3+) index(6107)
Title: Elution from: 54.424 to 54.424 scan no 7873 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

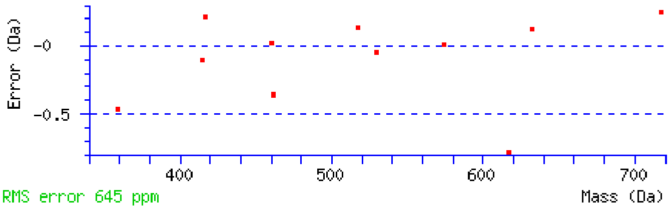
Or, Plot from 220 to 720 Da Full range

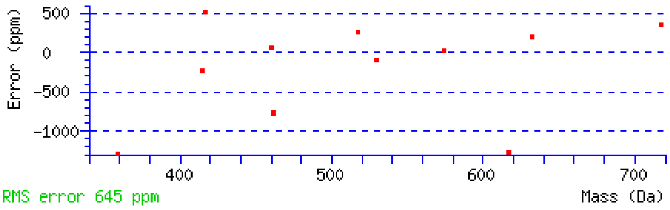
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1464.7401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0016
Matches : 12/118 fragment ions using 13 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0469	66.0271	113.0363	57.0218	E							13
2	203.0811	102.0442	185.0705	93.0389	A	1335.7077	668.3575	1317.6841	659.3457	1317.6971	659.3522	12
3	319.1050	160.0562	301.0945	151.0509	D	1263.6736	632.3404	1245.6500	623.3286	1245.6630	623.3351	11
4	433.1861	217.0967	415.1756	208.0914	L	1147.6496	574.3284	1129.6260	565.3166	1129.6390	565.3231	10
5	547.2672	274.1373	529.2567	265.1320	I	1033.5685	517.2879	1015.5449	508.2761	1015.5579	508.2826	9
6	635.2963	318.1518	617.2857	309.1465	S	919.4874	460.2473	901.4638	451.2355	901.4768	451.2420	8
7	749.3774	375.1923	731.3668	366.1871	L	831.4583	416.2328	813.4347	407.2210	813.4478	407.2275	7
8	889.4274	445.2173	871.4168	436.2121	H	717.3772	359.1922	699.3536	350.1805	699.3667	350.1870	6
9	987.4772	494.2422	969.4666	485.2370	P	577.3272	289.1672	559.3036	280.1554	559.3166	280.1620	5
10	1087.5427	544.2750	1069.5321	535.2697	V	479.2774	240.1423	461.2538	231.1305	461.2668	231.1371	4
11	1201.6238	601.3155	1183.6132	592.3102	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	1317.6477	659.3275	1299.6372	650.3222	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EADLISLHPVLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G68010.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.0	1464.7401	-0.0043	EADLISLHPVLDK
16.7	1464.7401	-0.0044	TSSSIFSISKPPAK
8.5	1464.7319	0.0038	HTDGKLSFLGFVK
0.8	1464.7331	0.0026	LLETMNTNIKVR

AT1G68150.1

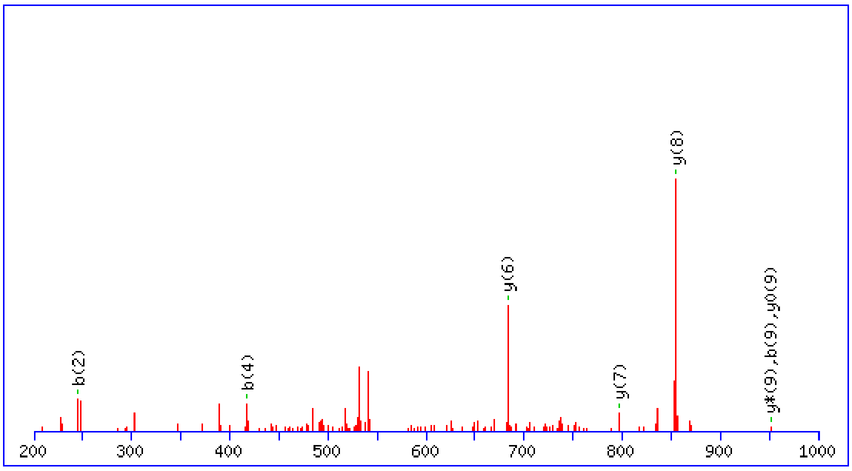
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIGLSLSLEK**
Found in **AT1G68150.1** in **TAIR_Arabidopsis**, Symbols: ATWRKY9, WRKY9 | WRKY9 (WRKY DNA-binding protein 9); transcription factor | chr1:25547633-25549278 FORWARD

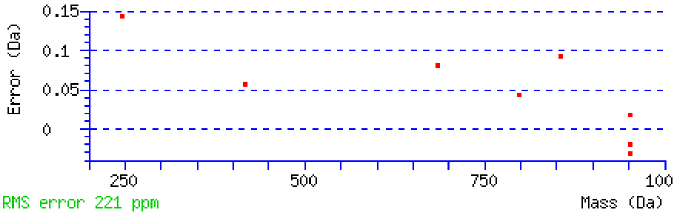
Match to Query 3455: 1098.578222 from(550.296387,2+) index(5207)
Title: Elution from: 47.173 to 47.173 scan no 6528 cid35.00 polarity:+
Data file D12h-3_1.mgf

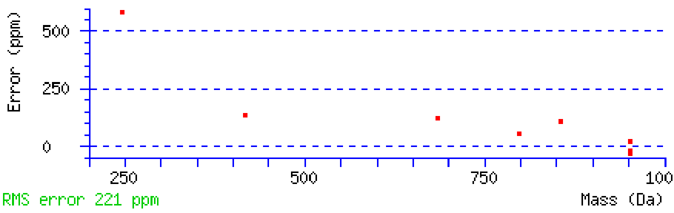
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1098.5799
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0058
Matches : 8/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							10
2	***245.1280***	123.0676	227.1174	114.0624	I	969.5475	485.2774	951.5239	476.2656	951.5370	476.2721	9
3	303.1465	152.0769	285.1359	143.0716	G	***855.4664***	428.2369	837.4428	419.2251	837.4559	419.2316	8
4	***417.2276***	209.1174	399.2170	200.1122	L	***797.4479***	399.2276	779.4243	390.2158	779.4374	390.2223	7
5	505.2567	253.1320	487.2461	244.1267	S	***683.3668***	342.1871	665.3432	333.1753	665.3563	333.1818	6
6	619.3378	310.1725	601.3272	301.1672	L	595.3378	298.1725	577.3142	289.1607	577.3272	289.1672	5
7	707.3668	354.1871	689.3563	345.1818	S	481.2567	241.1320	463.2331	232.1202	463.2461	232.1267	4
8	821.4479	411.2276	803.4374	402.2223	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
9	***951.4876***	476.2474	933.4770	467.2421	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EIGLSLSLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G68150.1

Score	Mr(calc)	Delta	Sequence
27.2	1098.5799	-0.0017	EIGLSLSLEK
18.1	1098.5751	0.0031	IKAVGGIAVME
8.5	1098.5799	-0.0017	VSLILESEAK
7.4	1098.5778	0.0004	MLPARGNVVK
5.0	1098.5799	-0.0016	IAVEESTLVK
4.8	1098.5808	-0.0025	MVIGLLMAPK
1.9	1098.5751	0.0031	MSNVTVIVPK
1.3	1098.5774	0.0008	MVKPFLEPK

AT1G68410.1

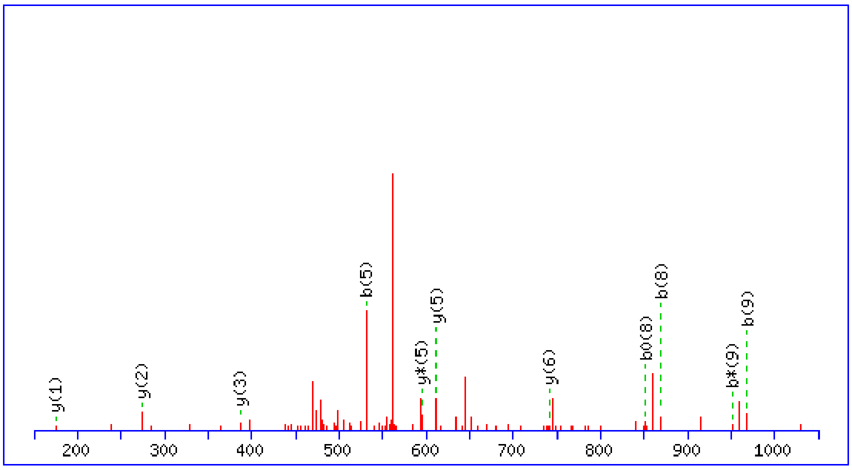
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAKMEKPIVR**
Found in **AT1G68410.1** in **TAIR_Arabidopsis**, Symbols: | protein phosphatase 2C-related / PP2C-related | chr1:25653925-25655918 REVERSE

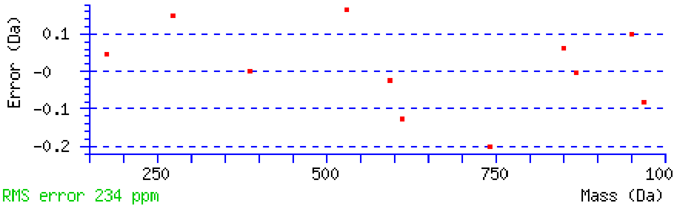
Match to Query 3661: 1141.666870 from(571.840711,2+) index(6073)
Title: Elution from: 54.931 to 54.931 scan no 7744 cid35.00 polarity:+
Data file D6h-2_2.mgf

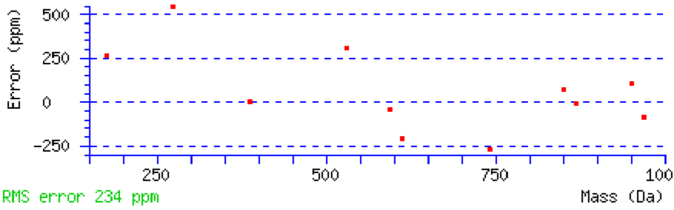
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1141.6641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.026
Matches : 11/86 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**10**
2	143.0815	72.0444					**A**	1071.6343	536.3208	1054.6078	527.8075	1053.6237	527.3155	**9**
3	271.1765	136.0919	254.1499	127.5786			**K**	1000.5972	500.8022	983.5706	492.2890	982.5866	491.7970	**8**
4	402.2170	201.6121	385.1904	193.0988			**M**	872.5022	436.7548	855.4757	428.2415	854.4917	427.7495	**7**
5	**531.2595**	266.1334	514.2330	257.6201	513.2490	257.1281	**E**	***741.4618***	371.2345	724.4352	362.7212	723.4512	362.2292	**6**
6	659.3545	330.1809	642.3280	321.6676	641.3439	321.1756	**K**	***612.4192***	306.7132	595.3926	298.1999			**5**
7	756.4073	378.7073	739.3807	370.1940	738.3967	369.7020	**P**	484.3242	242.6657	467.2976	234.1525			**4**
8	**869.4913**	435.2493	852.4648	426.7360	851.4808	426.2440	**I**	***387.2714***	194.1394	370.2449	185.6261			**3**
9	**968.5598**	484.7835	951.5332	476.2702	950.5492	475.7782	**V**	***274.1874***	137.5973	257.1608	129.0840			**2**
10							**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of AAKMEKPIVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G68410.1

18.3	1141.6641	0.0028	AAKMEKPIVR
5.1	1141.6680	-0.0011	LQRSVDRLR
0.3	1141.6679	-0.0011	ARSIAERALR

AT1G68560.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WIEVGAFYPFSR**
Found in **AT1G68560.1** in **TAIR_Arabidopsis**, Symbols: ATXYL1, XYL1 | ATXYL1/XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase | chr1:25738098-25741560 REVERSE

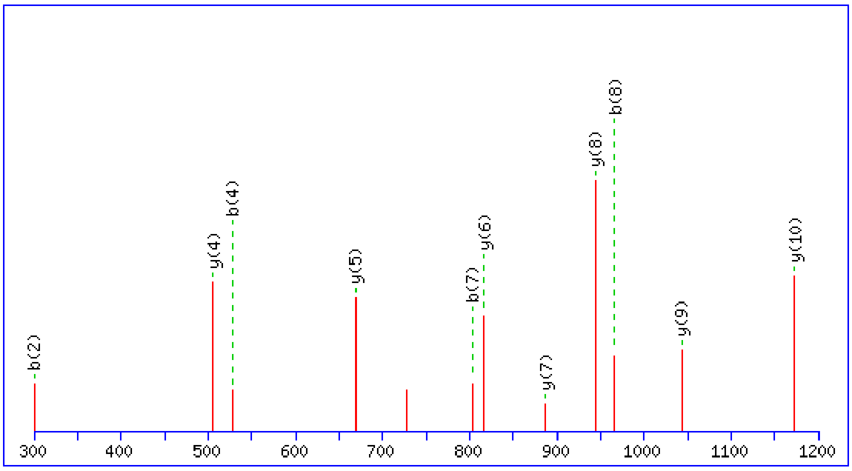
Match to Query 6487: 1470.729186 from(736.371869,2+) index(10497)
Title: Elution from: 95.704 to 95.704 scan no 14534 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1200 Da Full range

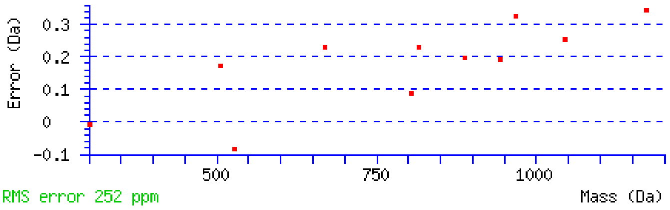
Label all possible matches ○ Label matches used for scoring ●

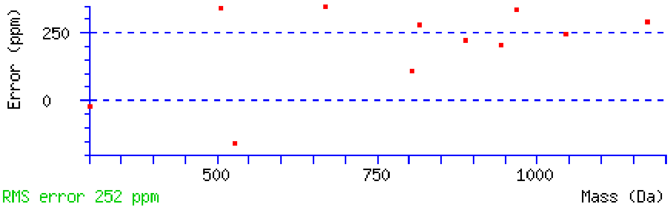
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1470.7296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 2.2e-007
Matches : 11/104 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	187.0866	94.0469			W							12
2	**300.1707**	150.5890			I	1285.6576	643.3324	1268.6310	634.8191	1267.6470	634.3271	11
3	429.2132	215.1103	411.2027	206.1050	E	***1172.5735***	586.7904	1155.5469	578.2771	1154.5629	577.7851	10
4	**528.2817**	264.6445	510.2711	255.6392	V	***1043.5309***	522.2691	1026.5043	513.7558	1025.5203	513.2638	9
5	585.3031	293.1552	567.2926	284.1499	G	***944.4625***	472.7349	927.4359	464.2216	926.4519	463.7296	8
6	656.3402	328.6738	638.3297	319.6685	A	***887.4410***	444.2241	870.4145	435.7109	869.4305	435.2189	7
7	**803.4087**	402.2080	785.3981	393.2027	F	***816.4039***	408.7056	799.3774	400.1923	798.3933	399.7003	6
8	**966.4720**	483.7396	948.4614	474.7343	Y	***669.3355***	335.1714	652.3089	326.6581	651.3249	326.1661	5
9	1063.5247	532.2660	1045.5142	523.2607	P	***506.2722***	253.6397	489.2456	245.1264	488.2616	244.6344	4
10	1210.5932	605.8002	1192.5826	596.7949	F	409.2194	205.1133	392.1928	196.6001	391.2088	196.1081	3
11	1297.6252	649.3162	1279.6146	640.3109	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of WIEVGAFYPFSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G68560.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.0	1470.7296	-0.0004	WIEVGAFYPFSR
1.6	1470.7314	-0.0022	DDAIAIGGNLAANEK

Mascot: http://www.matrixscience.com/

AT1G68710.1

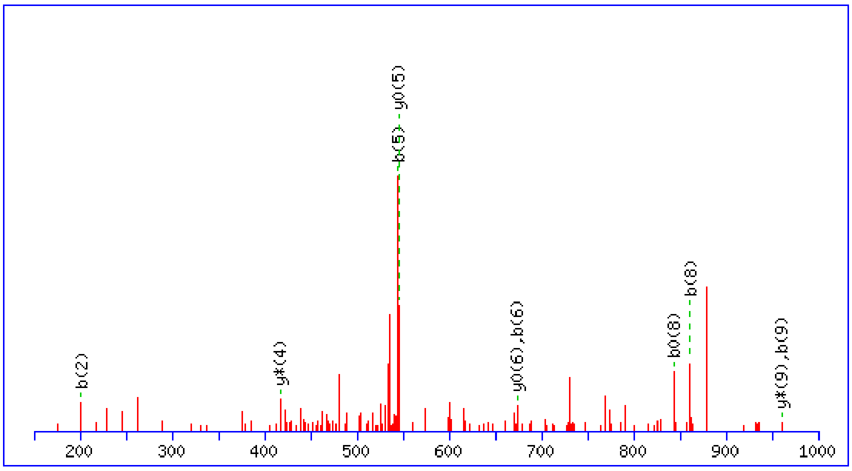
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAITEESTVK**
Found in **AT1G68710.1** in **TAIR_Arabidopsis**, Symbols: | haloacid dehalogenase-like hydrolase family protein | chr1:25797161-25801638 REVERSE

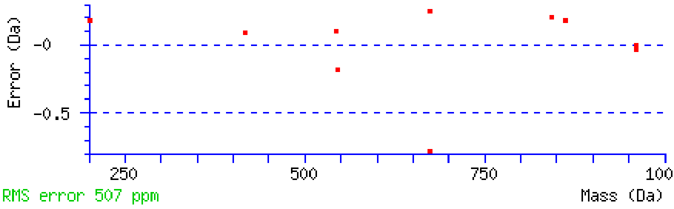
Match to Query 3102: 1105.553192 from(553.783872,2+) index(4984)
Title: Elution from: 48.038 to 48.038 scan no 6415 cid35.00 polarity:+
Data file D12h-2_1.mgf

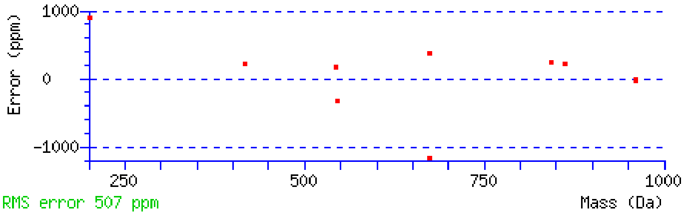
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1105.5503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.036
Matches : 10/86 fragment ions using 16 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	***201.0870***	101.0471	183.0764	92.0418	A	977.5150	489.2611	960.4884	480.7478	959.5044	480.2558	9
3	314.1710	157.5892	296.1605	148.5839	I	906.4779	453.7426	889.4513	445.2293	888.4673	444.7373	8
4	415.2187	208.1130	397.2082	199.1077	T	793.3938	397.2005	776.3672	388.6873	775.3832	388.1953	7
5	***544.2613***	272.6343	526.2508	263.6290	E	692.3461	346.6767	675.3196	338.1634	674.3355	337.6714	6
6	***673.3039***	337.1556	655.2933	328.1503	E	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
7	760.3359	380.6716	742.3254	371.6663	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
8	***861.3836***	431.1954	843.3731	422.1902	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	***960.4520***	480.7297	942.4415	471.7244	V	246.1812	123.5942	229.1547	115.0810			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EAITEESTVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G68710.1

Score	Mr(calc)	Delta	Sequence
21.8	1105.5503	0.0029	EAITEESTVK
11.5	1105.5550	-0.0018	MGSRGIINDK
9.0	1105.5556	-0.0025	NFHFIDSVK
7.4	1105.5516	0.0016	RYIPSEGER
5.6	1105.5550	-0.0018	KADMQVRDK
5.0	1105.5516	0.0016	LYNNPDKSR
4.3	1105.5550	-0.0018	ENSKILSCR
3.2	1105.5550	-0.0018	CTPSARSSLK
1.7	1105.5556	-0.0025	IVGFHGYADK
1.3	1105.5549	-0.0018	RAMNEKTEK

AT1G68890.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CGLEMALLNAMAVR**
Found in **AT1G68890.1** in **TAIR_Arabidopsis**, Symbols: | 2-oxoglutarate decarboxylase/ hydro-lyase/ magnesium ion binding / thiamin pyrophosphate binding | chr1:25900651-25910216 FORWARD

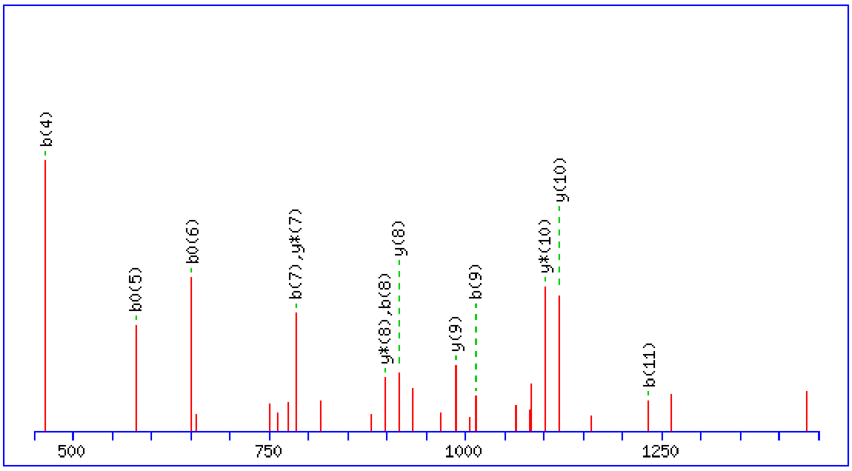
Match to Query 7331: 1582.698034 from(792.356293,2+) index(3723)
Title: Elution from: 35.678 to 35.678 scan no 4602 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1450 Da Full range

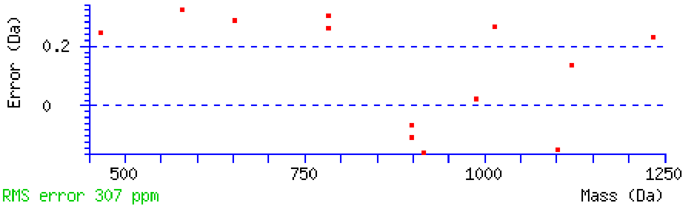
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

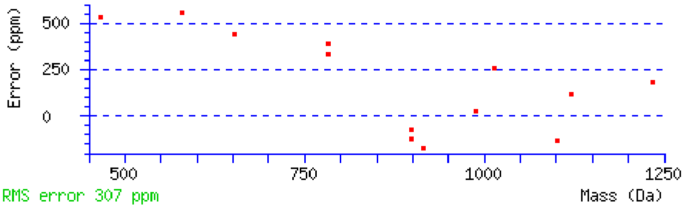


Monoisotopic mass of neutral peptide Mr(calc): 1582.7008
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 **Expect:** 0.0021
Matches : 13/178 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	163.0320	82.0196					C							14
2	221.0505	111.0289					G	1421.6834	711.3453	1403.6598	702.3335	1403.6728	702.3400	13
3	335.1316	168.0694					L	1363.6649	682.3361	1345.6413	673.3243	1345.6543	673.3308	12
4	***465.1712***	233.0892			447.1607	224.0840	E	1249.5838	625.2955	1231.5602	616.2837	1231.5732	616.2902	11
5	597.2087	299.1080			579.1982	290.1027	M	***1119.5441***	560.2757	1101.5206	551.2639			10
6	669.2429	335.1251			651.2323	326.1198	A	***987.5066***	494.2569	969.4830	485.2452			9
7	***783.3240***	392.1656			765.3134	383.1603	L	***915.4725***	458.2399	897.4489	449.2281			8
8	***897.4051***	449.2062			879.3945	440.2009	L	801.3914	401.1993	783.3678	392.1875			7
9	***1013.4421***	507.2247	995.4185	498.2129	995.4315	498.2194	N	687.3103	344.1588	669.2867	335.1470			6
10	1085.4762	543.2418	1067.4526	534.2300	1067.4657	534.2365	A	571.2733	286.1403	553.2497	277.1285			5
11	***1233.5087***	617.2580	1215.4851	608.2462	1215.4981	608.2527	M	499.2391	250.1232	481.2155	241.1114			4
12	1305.5428	653.2750	1287.5192	644.2633	1287.5323	644.2698	A	351.2067	176.1070	333.1831	167.0952			3
13	1405.6083	703.3078	1387.5847	694.2960	1387.5977	694.3025	V	279.1725	140.0899	261.1490	131.0781			2
14							R	179.1071	90.0572	161.0835	81.0454			1



RMS error 307 ppm



RMS error 307 ppm

AT1G68890.1

NCBI **BLAST** search of CGLEMALLNAMAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.7	1582.7008	-0.0028	CGLEMALLNAMAVR	Oxidation M11 99.95%
11.8	1582.6965	0.0015	DFSEEGPSGRVKEK	
9.5	1582.7026	-0.0045	DGAKVVVNCSGRGDK	
4.2	1582.7014	-0.0034	RFPGTVNWSEGGQK	
4.0	1582.7008	-0.0028	CGLEMALLNAMAVR	Oxidation M5 0.05%
3.5	1582.7021	-0.0041	SMQADELKTTWQK	
1.8	1582.6936	0.0044	VSEFQGYVYFMAK	
1.5	1582.6999	-0.0019	RKQMLETTTSEQP	
0.8	1582.6952	0.0028	DCLNRIISCGEVK	
0.6	1582.7022	-0.0041	NNNFDMKIEDVVK	

AT1G68960.1

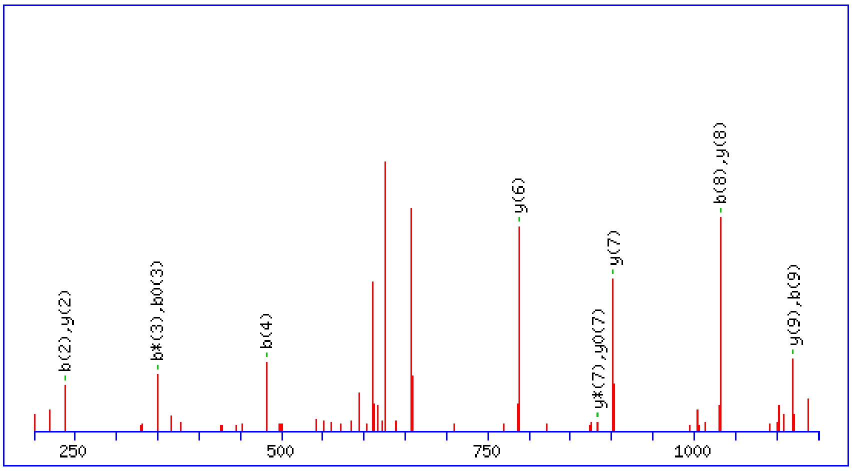
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSQLLCRISK**
Found in **AT1G68960.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03390.1); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR005174) | chr1:25933606-25934806 FORWARD

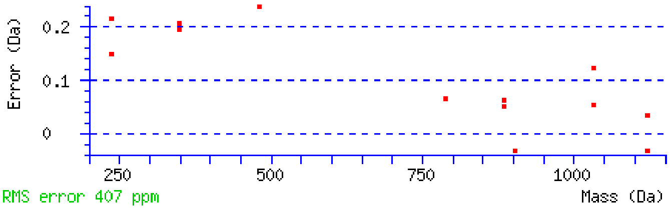
Match to Query 4752: 1266.600524 from(634.307538,2+) index(1725)
Title: Elution from: 22.198 to 22.198 scan no 2292 cid35.00 polarity:+
Data file 0-2_1.mgf

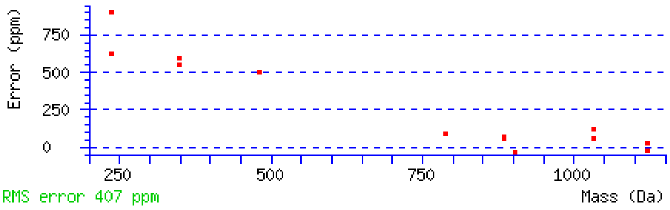
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1266.6001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 48 **Expect:** 0.00015
Matches : 13/148 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							10
2	***237.0688***	119.0380			219.0582	110.0327	S	***1119.5749***	560.2911	1101.5513	551.2793	1101.5643	551.2858	9
3	367.1214	184.0643	349.0978	175.0526	349.1109	175.0591	Q	***1031.5459***	516.2766	1013.5223	507.2648	1013.5353	507.2713	8
4	***481.2025***	241.1049	463.1789	232.0931	463.1920	232.0996	L	***901.4932***	451.2502	883.4696	442.2384	883.4826	442.2450	7
5	595.2836	298.1454	577.2600	289.1337	577.2731	289.1402	L	***787.4121***	394.2097	769.3885	385.1979	769.4015	385.2044	6
6	757.3083	379.1578	739.2848	370.1460	739.2978	370.1525	C	673.3310	337.1691	655.3074	328.1573	655.3204	328.1639	5
7	917.3976	459.2024	899.3740	450.1906	899.3870	450.1971	R	511.3063	256.1568	493.2827	247.1450	493.2957	247.1515	4
8	***1031.4787***	516.2430	1013.4551	507.2312	1013.4681	507.2377	I	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
9	***1119.5078***	560.2575	1101.4842	551.2457	1101.4972	551.2522	S	***237.1359***	119.0716	219.1124	110.0598	219.1254	110.0663	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MSQLLCRISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G68960.1

Score	Mr(calc)	Delta	Sequence
47.7	1266.6001	0.0004	MSQLLCRISK
46.6	1266.6014	-0.0009	RLTYDEIQSK
15.5	1266.6037	-0.0031	KSFWLETASGK
10.1	1266.6014	-0.0009	RYEELEAKSK
7.0	1266.6014	-0.0009	EITKATNNFSK
5.9	1266.5974	0.0031	KMESLSSITMK
4.4	1266.6041	-0.0036	RGYNLVDAVSR
4.1	1266.6014	-0.0009	KTSGYIEGEIR
2.1	1266.6014	-0.0009	TKDKVNEGAYK
0.7	1266.6041	-0.0036	SRSTGLLSSWR

Mascot: http://www.matrixscience.com/

AT1G68980.1

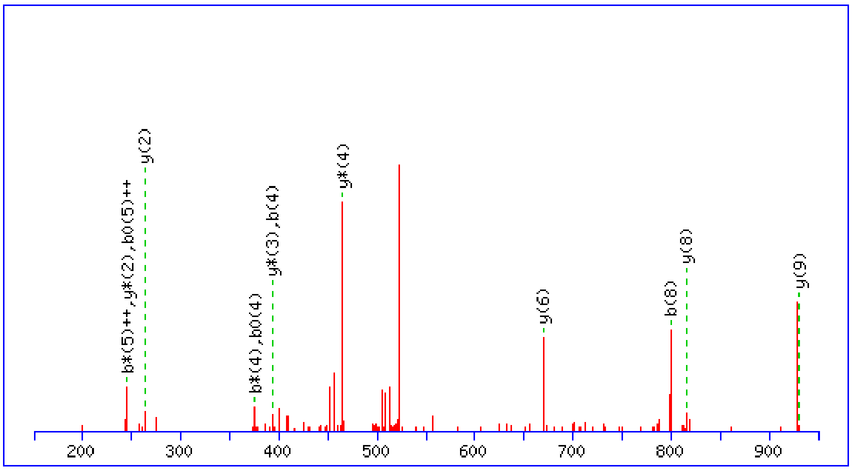
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENGSLAAFLK**
Found in **AT1G68980.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:25936686-25938545 FORWARD

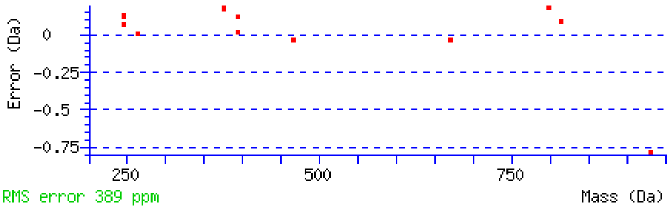
Match to Query 2989: 1060.522262 from(531.268407,2+) index(4876)
Title: Elution from: 43.288 to 43.288 scan no 6142 cid35.00 polarity:+
Data file 0-2_3.mgf

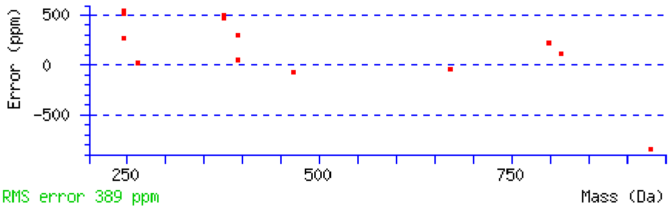
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1060.5197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.03
Matches : 13/94 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							10
2	247.0839	124.0456	229.0603	115.0338	229.0733	115.0403	N	***931.4874***	466.2473	913.4638	457.2355	913.4768	457.2420	9
3	305.1024	153.0548	287.0788	144.0430	287.0918	144.0496	G	***815.4504***	408.2288	797.4268	399.2170	797.4398	399.2235	8
4	**393.1315**	197.0694	375.1079	188.0576	375.1209	188.0641	S	757.4319	379.2196	739.4083	370.2078	739.4213	370.2143	7
5	507.2126	254.1099	489.1890	245.0981	489.2020	245.1046	L	***669.4028***	335.2050	651.3792	326.1933			6
6	579.2467	290.1270	561.2231	281.1152	561.2361	281.1217	A	555.3217	278.1645	537.2981	269.1527			5
7	651.2809	326.1441	633.2573	317.1323	633.2703	317.1388	A	483.2876	242.1474	465.2640	233.1356			4
8	**799.3463**	400.1768	781.3227	391.1650	781.3357	391.1715	F	411.2534	206.1303	393.2298	197.1186			3
9	913.4274	457.2173	895.4038	448.2056	895.4168	448.2121	L	***263.1880***	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ENGSLAAFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G68980.1

Score	Mr(calc)	Delta	Sequence
27.0	1060.5197	0.0025	ENGSLAAFLK
17.9	1060.5231	-0.0009	MEKNISISK
14.9	1060.5231	-0.0008	TREALLLMS
13.7	1060.5231	-0.0008	KMKEQELK
13.7	1060.5210	0.0012	QMKPVMRR
12.8	1060.5197	0.0026	IQQFDTGIK
11.3	1060.5197	0.0026	LFEVEVGTR
11.1	1060.5231	-0.0008	GLAMVSQSLK
9.5	1060.5253	-0.0031	KPMFAALEK
8.3	1060.5197	0.0025	ESTSWKAIK

AT1G68990.1

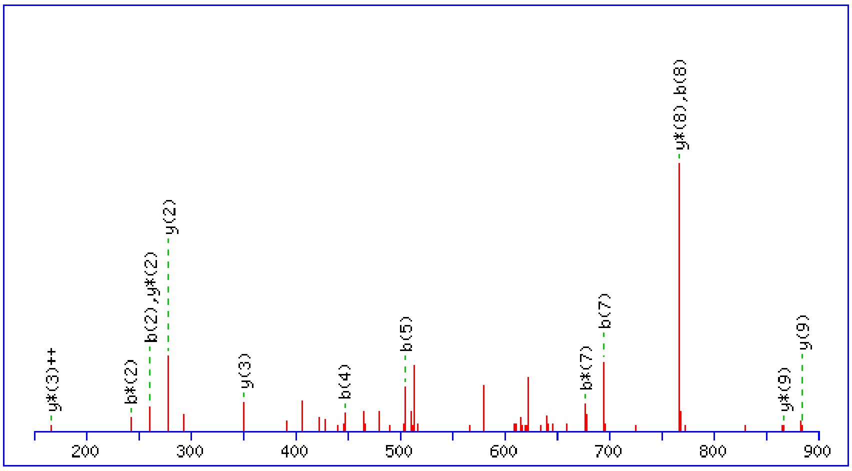
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RVIAGMGAQK**
Found in **AT1G68990.1** in **TAIR_Arabidopsis**, Symbols: | DNA-directed RNA polymerase, mitochondrial (RPOMT) | chr1:25939162-25944418 REVERSE

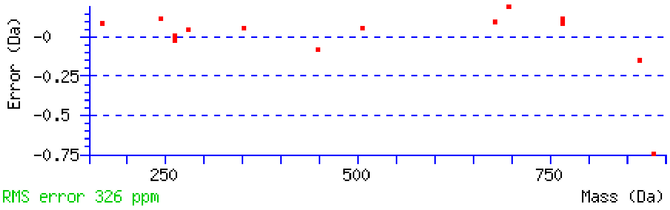
Match to Query 3055: 1044.531084 from(523.272818,2+) index(5807)
Title: Elution from: 50.455 to 50.455 scan no 7328 cid35.00 polarity:+
Data file D1d-3_2.mgf

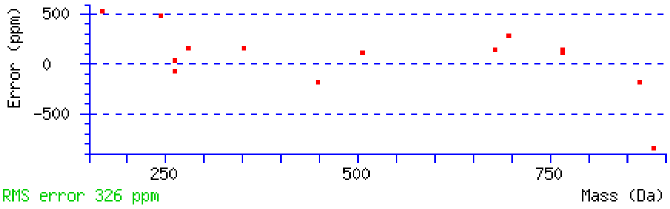
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1044.5308
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0096
Matches : 14/72 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	161.0965	81.0519	143.0729	72.0401	R					10
2	***261.1620***	131.0846	243.1384	122.0728	V	**885.4489**	443.2281	867.4253	434.2163	9
3	375.2431	188.1252	357.2195	179.1134	I	785.3834	393.1954	767.3599	384.1836	8
4	***447.2772***	224.1422	429.2536	215.1305	A	671.3023	336.1548	653.2788	327.1430	7
5	***505.2957***	253.1515	487.2721	244.1397	G	599.2682	300.1377	581.2446	291.1259	6
6	637.3332	319.1703	619.3097	310.1585	M	541.2497	271.1285	523.2261	262.1167	5
7	***695.3517***	348.1795	677.3282	339.1677	G	409.2122	205.1097	391.1886	196.0979	4
8	***767.3859***	384.1966	749.3623	375.1848	A	**351.1937**	176.1005	333.1701	167.0887	3
9	897.4385	449.2229	879.4150	440.2111	Q	**279.1595**	140.0834	261.1359	131.0716	2
10					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of RVIAGMGAQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G68990.1

Score	Mr(calc)	Delta	Sequence
28.8	1044.5308	0.0002	RVIAGMGAQK
17.8	1044.5308	0.0002	MRVLGEAVR
16.6	1044.5309	0.0002	KAGAMNALVR
13.6	1044.5282	0.0029	VLAMAQEKK
11.0	1044.5282	0.0029	VLVTMQAQK
8.0	1044.5309	0.0002	MAQKNAIVR
8.0	1044.5309	0.0002	MAQKNALVR
6.3	1044.5282	0.0029	EMEKLIVR
5.7	1044.5309	0.0002	VLRDMKPR
5.5	1044.5282	0.0029	QMLKIQEK

Mascot: http://www.matrixscience.com/

AT1G69030.1

Mascot Search Results

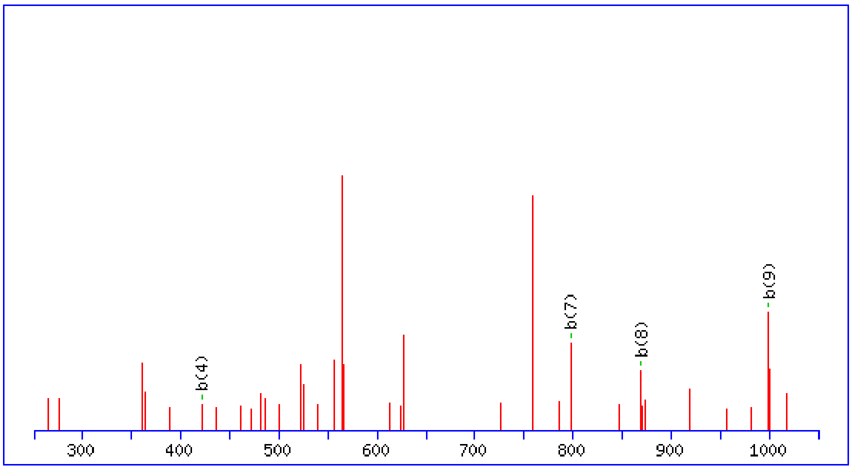
Peptide View

MS/MS Fragmentation of **AESKDEEAKK**
Found in **AT1G69030.1** in **TAIR_Arabidopsis**, Symbols: | similar to BSD domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G26300.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73547.1); contains InterPro domain BSD (InterPro:IPR005607) | chr1:25951092-25952925 REVERSE

Match to Query 3891: 1146.515542 from(574.265047,2+) index(1627)
Title: Elution from: 20.214 to 20.214 scan no 2136 cid35.00 polarity:+
Data file C7-3_2.mgf

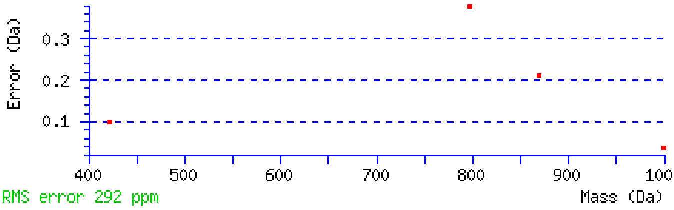
Click mouse within plot area to zoom in by factor of two about that point

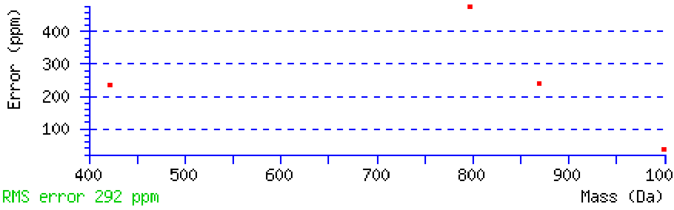
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1146.5179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.037
Matches : 4/94 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							10
2	203.0811	102.0442			185.0705	93.0389	E	1075.4910	538.2491	1057.4674	529.2374	1057.4804	529.2439	9
3	291.1101	146.0587			273.0996	137.0534	S	945.4514	473.2293	927.4278	464.2175	927.4408	464.2240	8
4	***421.1991***	211.1032	403.1756	202.0914	403.1886	202.0979	K	857.4223	429.2148	839.3987	420.2030	839.4118	420.2095	7
5	537.2231	269.1152	519.1995	260.1034	519.2126	260.1099	D	727.3333	364.1703	709.3097	355.1585	709.3227	355.1650	6
6	667.2628	334.1350	649.2392	325.1232	649.2522	325.1297	E	611.3093	306.1583	593.2857	297.1465	593.2987	297.1530	5
7	***797.3024***	399.1548	779.2788	390.1430	779.2918	390.1495	E	481.2697	241.1385	463.2461	232.1267	463.2591	232.1332	4
8	***869.3365***	435.1719	851.3129	426.1601	851.3260	426.1666	A	351.2301	176.1187	333.2065	167.1069			3
9	***999.4256***	500.2164	981.4020	491.2046	981.4150	491.2111	K	279.1959	140.1016	261.1723	131.0898			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AESKDEEAKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G69030.1

Score	Mr(calc)	Delta	Sequence
23.7	1146.5179	-0.0023	AESKDEEAKK
14.4	1146.5179	-0.0023	TLADASTAEQK
12.4	1146.5131	0.0024	GIDLMQNAQK
12.3	1146.5131	0.0024	EDLVNQCKK
12.3	1146.5179	-0.0023	VGISTNETGEK
12.2	1146.5188	-0.0032	MGPDAVAMKAK
11.9	1146.5179	-0.0023	EASQTETLQK
11.0	1146.5154	0.0002	EVMTVGFSHK
10.7	1146.5132	0.0024	MKEESHKTK
8.8	1146.5154	0.0002	MGAEHFSLVK

Mascot: http://www.matrixscience.com/

AT1G69720.1

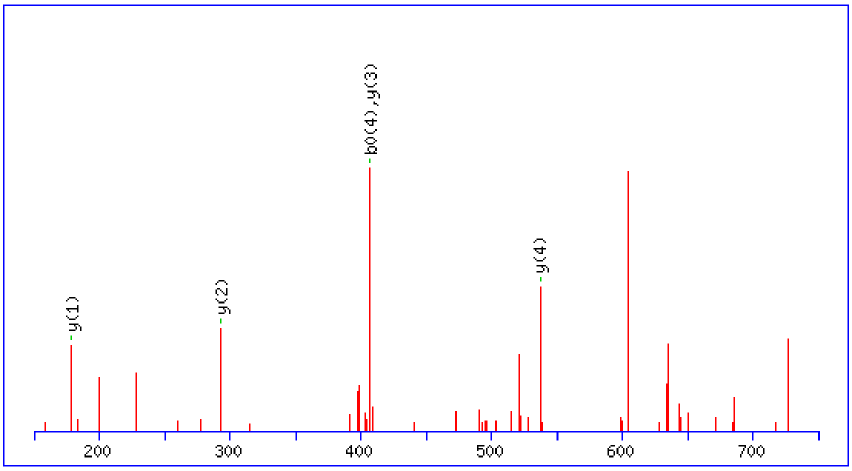
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGEILR**
Found in **AT1G69720.1** in **TAIR_Arabidopsis**, Symbols: HO3 | HO3 (HEME OXYGENASE 3); heme oxygenase (decyclizing) | chr1:26230841-26232082 FORWARD

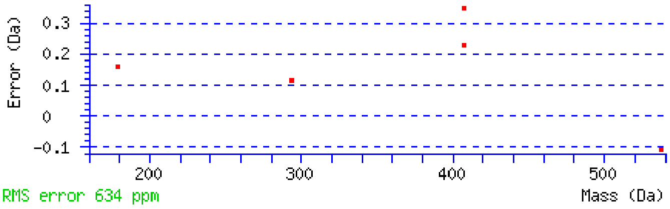
Match to Query 1163: 830.415348 from(416.214950,2+) index(3296)
Title: Elution from: 32.526 to 32.526 scan no 4127 cid35.00 polarity:+
Data file 0-2_2.mgf

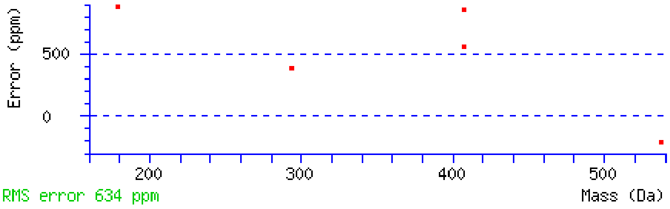
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 830.4146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.02
Matches : 5/52 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400			F							7
2	237.1018	119.0545	219.0912	110.0492	S	683.3565	342.1819	665.3329	333.1701	665.3459	333.1766	6
3	295.1203	148.0638	277.1097	139.0585	G	595.3274	298.1673	577.3038	289.1556	577.3169	289.1621	5
4	425.1599	213.0836	407.1494	204.0783	E	***537.3089***	269.1581	519.2853	260.1463	519.2984	260.1528	4
5	539.2410	270.1241	521.2304	261.1189	I	***407.2693***	204.1383	389.2457	195.1265			3
6	653.3221	327.1647	635.3115	318.1594	L	***293.1882***	147.0977	275.1646	138.0859			2
7					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FSGEILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.6	830.4146	0.0007	FSGEILR
18.2	830.4146	0.0007	FGSLELR

AT1G69720.1

14.1	830.4146	0.0007	DFTGIIR
10.7	830.4178	-0.0024	RNRVNR
9.0	830.4173	-0.0020	WSTRLR
6.3	830.4151	0.0003	RGTAGSIR
6.3	830.4146	0.0007	QYLIER
6.1	830.4151	0.0003	RTASLGGR
6.0	830.4146	0.0007	AFISDIR
6.0	830.4146	0.0007	ALDYAIR

AT1G69740.1

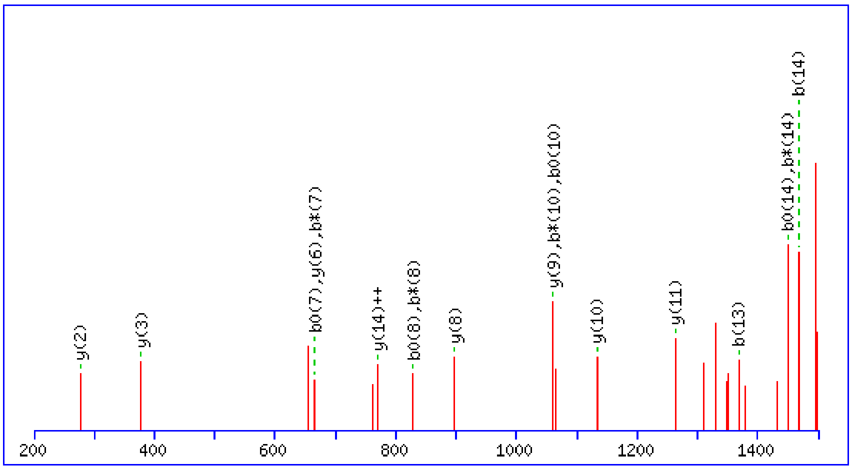
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSTGDEAYNDNGLVPR**
Found in **AT1G69740.1** in **TAIR_Arabidopsis**, Symbols: HEMB1 | HEMB1; porphobilinogen synthase | chr1:26235860-26238376 FORWARD

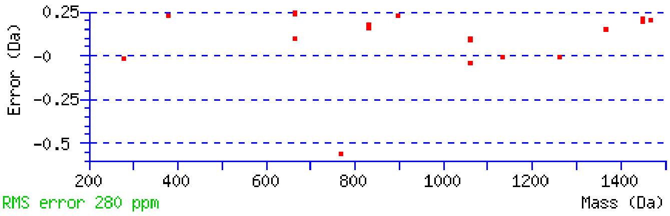
Match to Query 8284: 1742.698580 from(872.356566,2+) index(3422)
Title: Elution from: 33.726 to 33.726 scan no 4278 cid35.00 polarity:+
Data file D6h-1_2.mgf

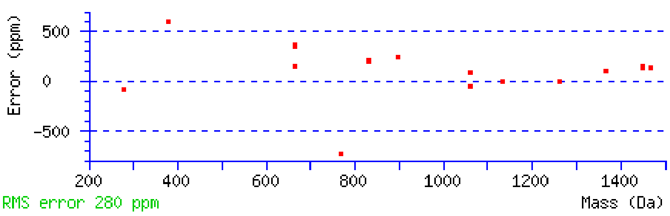
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1742.7000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00012
Matches : 18/166 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							16
2	205.0733	103.0403	187.0498	94.0285	187.0628	94.0350	S	1627.6703	814.3388	1609.6467	805.3270	1609.6597	805.3335	15
3	307.1180	154.0627	289.0945	145.0509	289.1075	145.0574	T	1539.6412	770.3243	1521.6177	761.3125	1521.6307	761.3190	14
4	365.1365	183.0719	347.1130	174.0601	347.1260	174.0666	G	1437.5965	719.3019	1419.5729	710.2901	1419.5860	710.2966	13
5	481.1605	241.0839	463.1369	232.0721	463.1500	232.0786	D	1379.5780	690.2927	1361.5544	681.2809	1361.5675	681.2874	12
6	611.2002	306.1037	593.1766	297.0919	593.1896	297.0984	E	***1263.5541***	632.2807	1245.5305	623.2689	1245.5435	623.2754	11
7	683.2343	342.1208	665.2107	333.1090	665.2237	333.1155	A	***1133.5144***	567.2608	1115.4908	558.2491	1115.5039	558.2556	10
8	847.2947	424.1510	829.2711	415.1392	829.2841	415.1457	Y	***1061.4803***	531.2438	1043.4567	522.2320	1043.4697	522.2385	9
9	963.3317	482.1695	945.3081	473.1577	945.3211	473.1642	N	***897.4199***	449.2136	879.3963	440.2018	879.4093	440.2083	8
10	1079.3556	540.1815	1061.3321	531.1697	1061.3451	531.1762	D	781.3829	391.1951	763.3593	382.1833	763.3723	382.1898	7
11	1195.3926	598.2000	1177.3691	589.1882	1177.3821	589.1947	N	***665.3589***	333.1831	647.3354	324.1713			6
12	1253.4111	627.2092	1235.3876	618.1974	1235.4006	618.2039	G	549.3219	275.1646	531.2984	266.1528			5
13	**1367.4922**	684.2498	1349.4687	675.2380	1349.4817	675.2445	L	491.3034	246.1554	473.2799	237.1436			4
14	**1467.5577**	734.2825	1449.5341	725.2707	1449.5471	725.2772	V	***377.2223***	189.1148	359.1988	180.1030			3
15	1565.6075	783.3074	1547.5839	774.2956	1547.5969	774.3021	P	***277.1569***	139.0821	259.1333	130.0703			2
16							R	179.1071	90.0572	161.0835	81.0454			1





AT1G69740.1

NCBI **BLAST** search of NSTGDEAYNDNGLVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.3	1742.7000	-0.0014	NSTGDEAYNDNGLVPR

Mascot: http://www.matrixscience.com/

AT1G69760.1

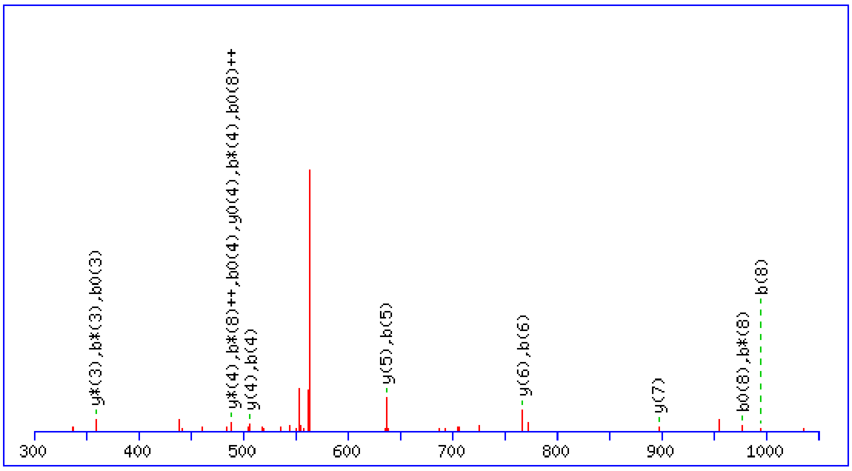
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEQEQEIIK**
Found in **AT1G69760.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G26920.1); similar to hypothetical protein [Ricinus communis] (GB:CAH56540.1) | chr1:26243757-26244290 REVERSE

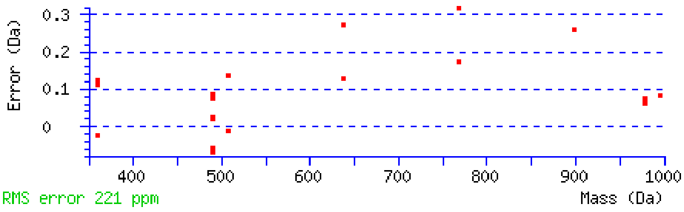
Match to Query 3990: 1142.509622 from(572.262087,2+) index(1980)
Title: Elution from: 24.069 to 24.069 scan no 2583 cid35.00 polarity:+
Data file 0-1_1.mgf

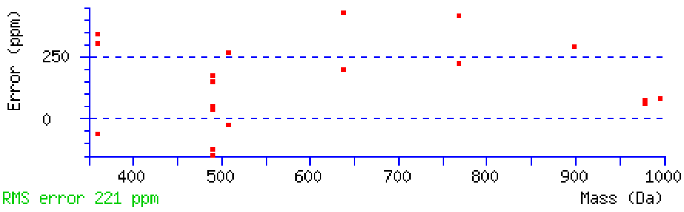
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1142.5099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0022
Matches : 19/86 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							9
2	247.0709	124.0391			229.0603	115.0338	E	1027.4933	514.2503	1009.4697	505.2385	1009.4827	505.2450	8
3	377.1235	189.0654	359.0999	180.0536	359.1130	180.0601	Q	***897.4536***	449.2304	879.4300	440.2187	879.4431	440.2252	7
4	***507.1632***	254.0852	489.1396	245.0734	489.1526	245.0799	E	***767.4010***	384.2041	749.3774	375.1923	749.3904	375.1988	6
5	***637.2158***	319.1115	619.1922	310.0997	619.2052	310.1063	Q	***637.3613***	319.1843	619.3378	310.1725	619.3508	310.1790	5
6	***767.2554***	384.1314	749.2318	375.1196	749.2449	375.1261	E	***507.3087***	254.1580	489.2851	245.1462	489.2981	245.1527	4
7	881.3365	441.1719	863.3129	432.1601	863.3260	432.1666	I	377.2691	189.1382	359.2455	180.1264			3
8	***995.4176***	498.2125	977.3940	489.2007	977.4071	489.2072	I	263.1880	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DEQEQEIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G69760.1

32.7	1142.5099	-0.0003	DEQEQEIIK
26.1	1142.5126	-0.0030	QDQKEPQQK
16.9	1142.5101	-0.0005	MIEEHKWR
11.3	1142.5126	-0.0030	KEDQTDHKK
7.9	1142.5108	-0.0012	SVMLMSYLR
7.8	1142.5099	-0.0003	ETGPDGVEVTK
2.8	1142.5090	0.0006	WFHVHEFK
2.6	1142.5074	0.0022	YIEYMERK
2.5	1142.5074	0.0022	AFDVYKNMK
2.3	1142.5106	-0.0010	HPSCPRSRK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLNDLLSTK**
Found in **AT1G70410.1** in **TAIR_Arabidopsis**, Symbols: | carbonic anhydrase, putative / carbonate dehydratase, putative | chr1:26537830-26540168 REVERSE

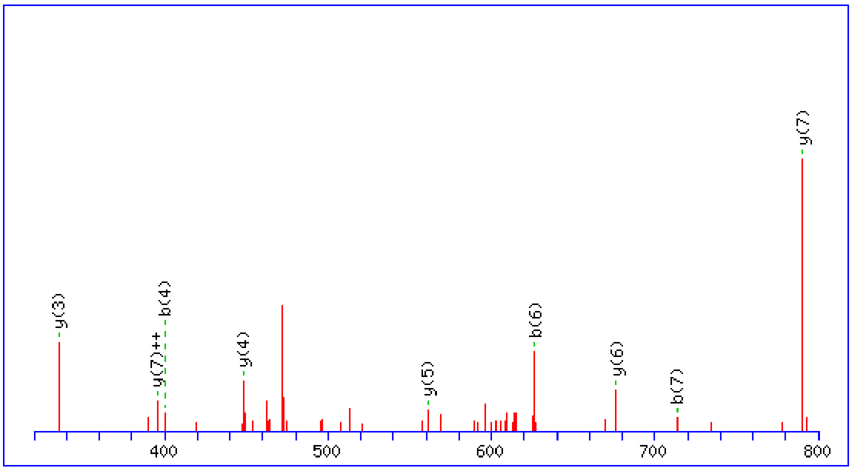
Match to Query 2174: 959.528950 from(480.771751,2+) index(5323)
Title: Elution from: 46.184 to 46.184 scan no 6678 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 320 to 800 Da Full range

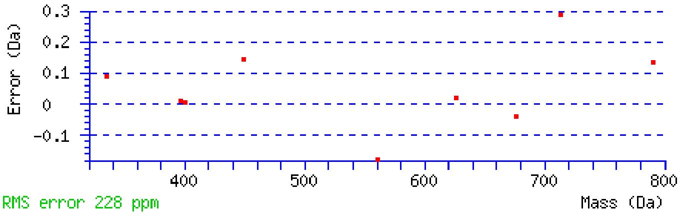
Label all possible matches ○ Label matches used for scoring ●

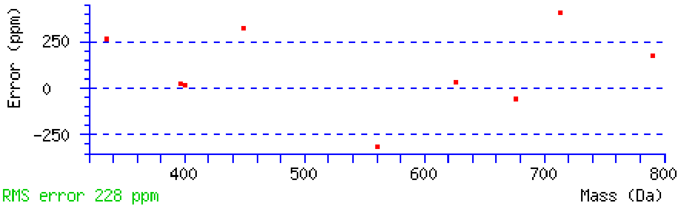
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 959.5287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0014
Matches : 9/84 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							9
2	171.1128	86.0600					L	903.5146	452.2609	886.4880	443.7477	885.5040	443.2556	8
3	285.1557	143.0815	268.1292	134.5682			N	***790.4305***	395.7189	773.4040	387.2056	772.4199	386.7136	7
4	**400.1827**	200.5950	383.1561	192.0817	382.1721	191.5897	D	***676.3876***	338.6974	659.3610	330.1842	658.3770	329.6921	6
5	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	L	***561.3606***	281.1840	544.3341	272.6707	543.3501	272.1787	5
6	**626.3508**	313.6790	609.3243	305.1658	608.3402	304.6738	L	***448.2766***	224.6419	431.2500	216.1287	430.2660	215.6366	4
7	**713.3828**	357.1951	696.3563	348.6818	695.3723	348.1898	S	***335.1925***	168.0999	318.1660	159.5866	317.1819	159.0946	3
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GLNDLLSTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G70410.1

37.1	959.5287	0.0002	GLNDLLSTK

AT1G70430.1

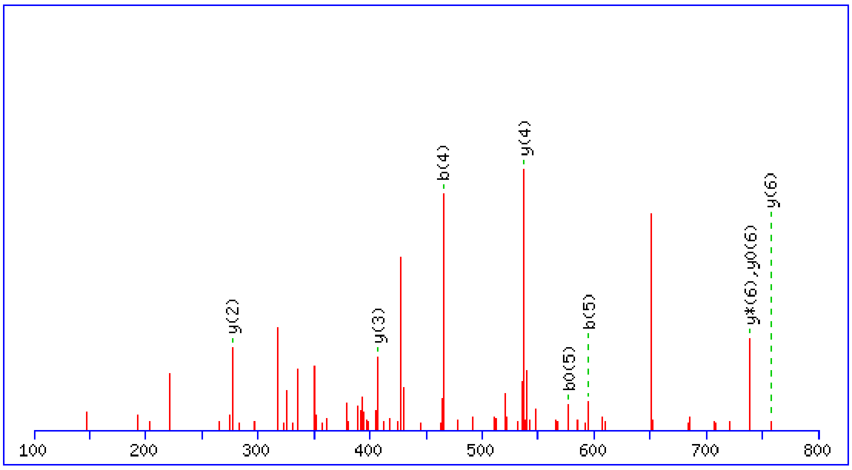
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAFEEPR**
Found in **AT1G70430.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:26549252-26552419 FORWARD

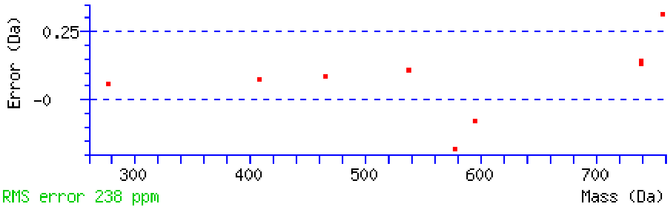
Match to Query 1384: 870.411748 from(436.213150,2+) index(5277)
Title: Elution from: 47.155 to 47.155 scan no 6635 cid35.00 polarity:+
Data file D12h-3_2.mgf

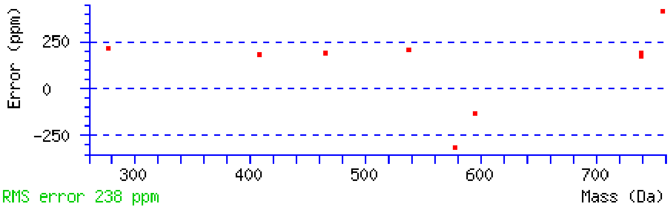
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 870.4096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.014
Matches : 9/50 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							7
2	187.1225	94.0649			A	***757.3357***	379.1715	739.3122	370.1597	739.3252	370.1662	6
3	335.1880	168.0976			F	685.3016	343.1544	667.2780	334.1426	667.2910	334.1492	5
4	**465.2276**	233.1174	447.2170	224.1122	E	***537.2361***	269.1217	519.2126	260.1099	519.2256	260.1164	4
5	**595.2672**	298.1373	577.2567	289.1320	E	***407.1965***	204.1019	389.1729	195.0901	389.1860	195.0966	3
6	693.3170	347.1622	675.3065	338.1569	P	***277.1569***	139.0821	259.1333	130.0703			2
7					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LAFEEPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.2	870.4096	0.0022	LAFEEPR
15.8	870.4100	0.0018	DGREKPR
8.1	870.4129	-0.0012	AEAQMLAK

AT1G70430.1

8.1	870.4129	-0.0012	MALQEAAK
7.4	870.4122	-0.0005	HRYSPAK
6.2	870.4096	0.0022	HYTEAIK
6.1	870.4096	0.0022	SWIDAAAK
6.0	870.4100	0.0018	DRDPRAK
4.0	870.4129	-0.0012	IGNVEMAK
3.7	870.4129	-0.0012	MAPKAAEK

AT1G70730.1

Mascot Search Results

Peptide View

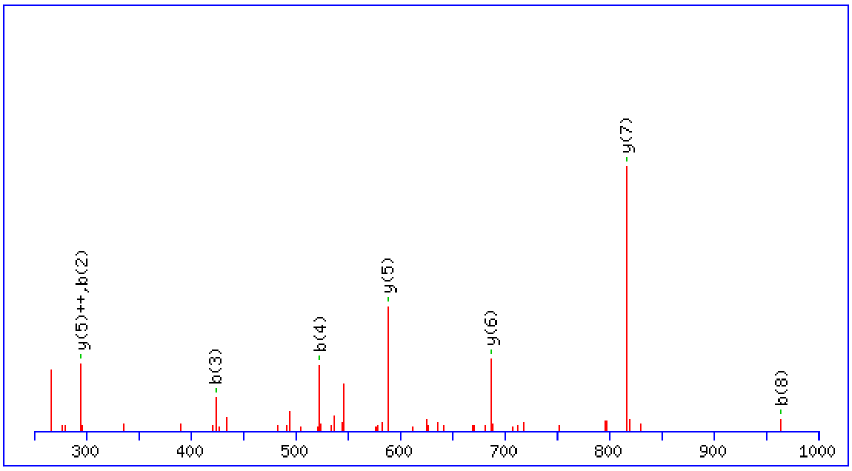
MS/MS Fragmentation of **FFEVPTGWK**
Found in **AT1G70730.1** in **TAIR_Arabidopsis**, Symbols: | phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative | chr1:26672682-26676388 REVERSE

Match to Query 3618: 1109.554956 from(555.784754,2+) index(7704)
Title: Elution from: 67.683 to 67.683 scan no 9976 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

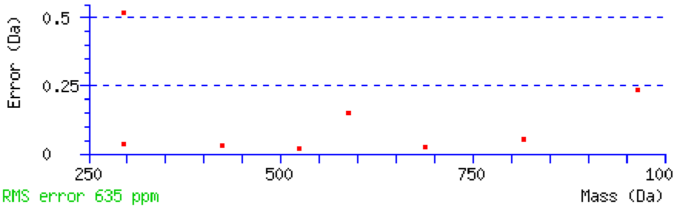
Or, Plot from 250 to 1000 Da Full range

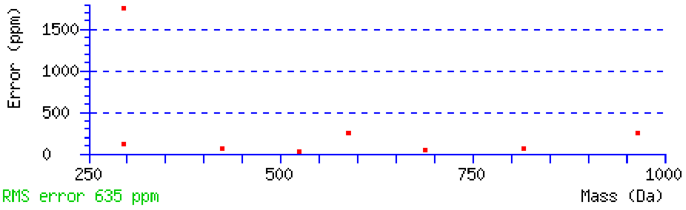
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1109.5546
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00078
Matches : 8/70 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							9
2	***295.1441***	148.0757			F	963.4934	482.2504	946.4669	473.7371	945.4829	473.2451	8
3	***424.1867***	212.5970	406.1761	203.5917	E	**816.4250**	408.7162	799.3985	400.2029	798.4145	399.7109	7
4	***523.2551***	262.1312	505.2445	253.1259	V	**687.3824**	344.1949	670.3559	335.6816	669.3719	335.1896	6
5	620.3079	310.6576	602.2973	301.6523	P	**588.3140**	294.6607	571.2875	286.1474	570.3035	285.6554	5
6	721.3556	361.1814	703.3450	352.1761	T	491.2613	246.1343	474.2347	237.6210	473.2507	237.1290	4
7	778.3770	389.6921	760.3665	380.6869	G	390.2136	195.6104	373.1870	187.0972			3
8	***964.4563***	482.7318	946.4458	473.7265	W	333.1921	167.0997	316.1656	158.5864			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FFEVPTGWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G70730.1

38.1	1109.5546	0.0004	FFEVPTGWK
1.8	1109.5573	-0.0023	MIKNLSNMK

Mascot: http://www.matrixscience.com/

AT1G70830.3

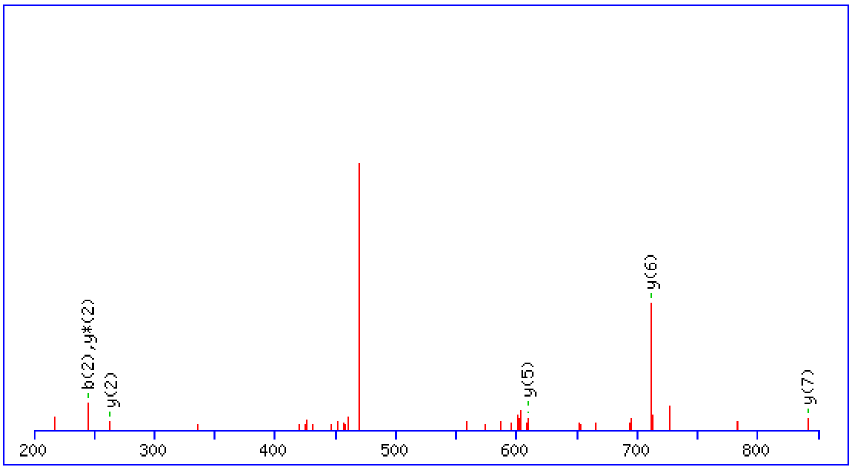
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LETDVEIK**
Found in **AT1G70830.3** in **TAIR_Arabidopsis**, Symbols: MLP28 | MLP28 (MLP-LIKE PROTEIN 28) | chr1:26713865-26715057 REVERSE

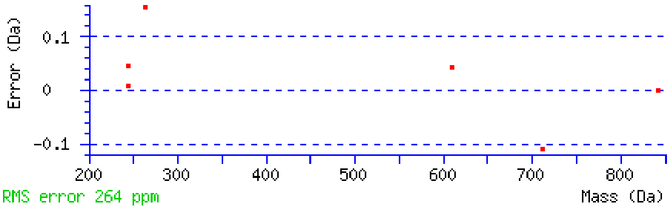
Match to Query 2208: 954.474596 from(478.244574,2+) index(2511)
Title: Elution from: 27.379 to 27.379 scan no 3181 cid35.00 polarity:+
Data file C7-2_1.mgf

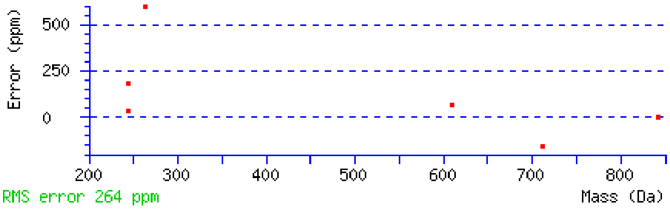
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 954.4752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.024
Matches : 6/64 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	245.1280	123.0676	227.1174	114.0624	E	***841.4014***	421.2043	823.3778	412.1925	823.3908	412.1990	7
3	347.1727	174.0900	329.1622	165.0847	T	***711.3617***	356.1845	693.3382	347.1727	693.3512	347.1792	6
4	463.1967	232.1020	445.1861	223.0967	D	***609.3170***	305.1622	591.2934	296.1504	591.3065	296.1569	5
5	563.2621	282.1347	545.2516	273.1294	V	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
6	693.3018	347.1545	675.2912	338.1492	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	807.3829	404.1951	789.3723	395.1898	I	***263.1880***	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LETDVEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.2	954.4752	-0.0006	LETDVEIK
5.1	954.4731	0.0015	LEMHLKR

AT1G70830.3

3.6	954.4752	-0.0006	LLDEVETK
3.6	954.4752	-0.0006	LLDLDTEK
1.4	954.4752	-0.0006	LSDEEILK
1.4	954.4752	-0.0006	EEESVLLK
1.4	954.4752	-0.0006	EESVEILK
1.3	954.4754	-0.0008	MKARYFK

AT1G70890.1

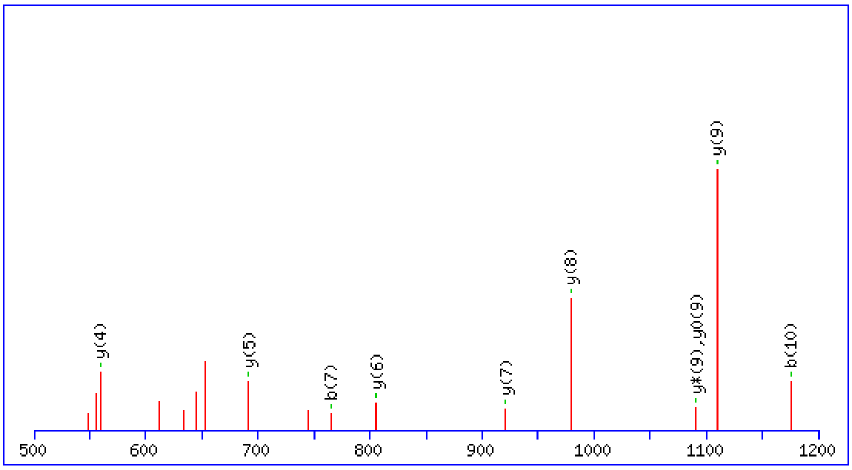
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLEGDLMNEYK**
Found in **AT1G70890.1** in **TAIR_Arabidopsis**, Symbols: MLP43 | MLP43 (MLP-LIKE PROTEIN 43) | chr1:26729574-26730151 REVERSE

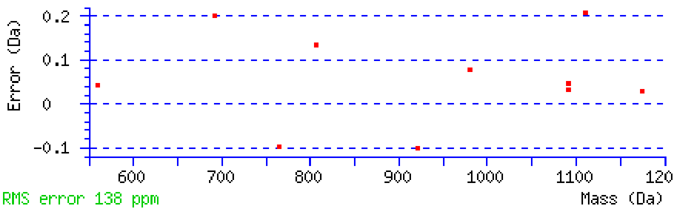
Match to Query 4954: 1322.581084 from(662.297818,2+) index(5260)
Title: Elution from: 46.366 to 46.366 scan no 6598 cid35.00 polarity:+
Data file C7-3_2.mgf

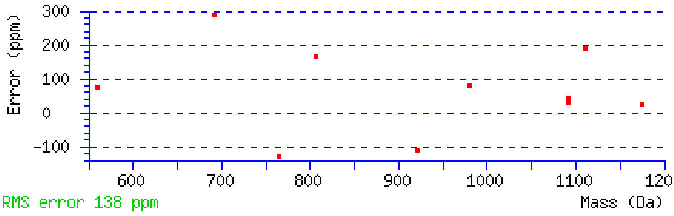
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1322.5838
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 5.6e-006
Matches : 10/98 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							11
2	215.1538	108.0805					L	1223.5257	612.2665	1205.5021	603.2547	1205.5151	603.2612	10
3	345.1935	173.1004			327.1829	164.0951	E	***1109.4446***	555.2259	1091.4210	546.2141	1091.4340	546.2206	9
4	403.2120	202.1096			385.2014	193.1043	G	***979.4050***	490.2061	961.3814	481.1943	961.3944	481.2008	8
5	519.2359	260.1216			501.2254	251.1163	D	***921.3865***	461.1969	903.3629	452.1851	903.3759	452.1916	7
6	633.3170	317.1622			615.3065	308.1569	L	***805.3625***	403.1849	787.3389	394.1731	787.3519	394.1796	6
7	**765.3545**	383.1809			747.3440	374.1756	M	***691.2814***	346.1443	673.2578	337.1325	673.2708	337.1390	5
8	881.3915	441.1994	863.3680	432.1876	863.3810	432.1941	N	***559.2439***	280.1256	541.2203	271.1138	541.2333	271.1203	4
9	1011.4312	506.2192	993.4076	497.2074	993.4206	497.2139	E	443.2069	222.1071	425.1833	213.0953	425.1963	213.1018	3
10	**1175.4915**	588.2494	1157.4680	579.2376	1157.4810	579.2441	Y	313.1672	157.0873	295.1437	148.0755			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VLEGDLMNEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G70890.1

Score	Mr(calc)	Delta	Sequence
62.3	1322.5838	-0.0028	VLEGDLMNEYK
13.5	1322.5809	0.0002	LLDGNADSFAQR
2.7	1322.5805	0.0006	FDLGLPDNYEK
1.6	1322.5838	-0.0027	VLTCGEEFDLK
1.1	1322.5818	-0.0007	VLVGMGQHFMR

AT1G70980.1

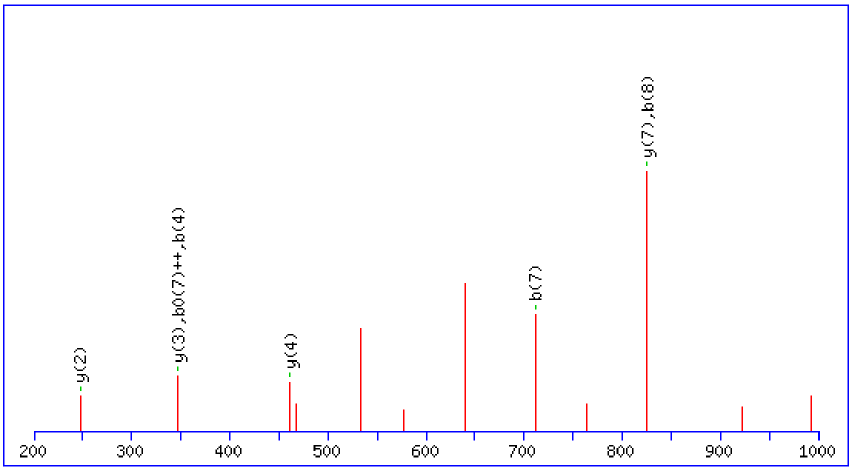
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVAAMDVLVPK**
Found in **AT1G70980.1** in **TAIR_Arabidopsis**, Symbols: SYNC3 | SYNC3; ATP binding / aminoacyl-tRNA ligase/ asparagine-tRNA ligase/ aspartate-tRNA ligase/ nucleic acid binding / nucleotide binding | chr1:26766001-26768056 FORWARD

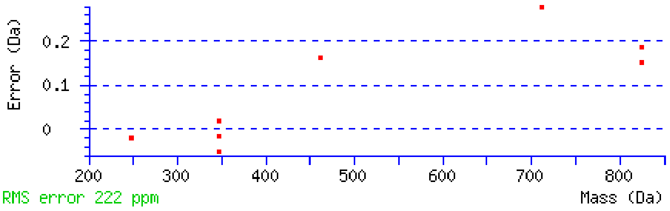
Match to Query 3917: 1170.598556 from(586.306554,2+) index(5522)
Title: Elution from: 49.120 to 49.120 scan no 6976 cid35.00 polarity:+
Data file C7-1_2.mgf

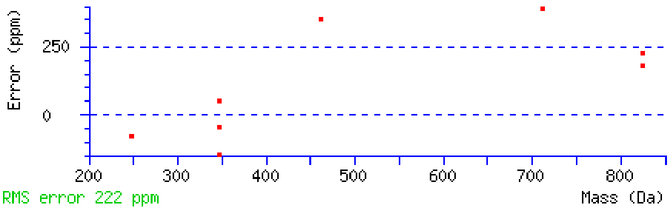
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1170.5963
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.025
Matches : 8/138 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							11
2	203.1174	102.0624	185.1069	93.0571	V	1069.5588	535.2831	1051.5352	526.2713	1051.5483	526.2778	10
3	275.1516	138.0794	257.1410	129.0741	A	969.4934	485.2503	951.4698	476.2385	951.4828	476.2450	9
4	**347.1857**	174.0965	329.1752	165.0912	A	897.4592	449.2333	879.4356	440.2215	879.4487	440.2280	8
5	495.2182	248.1127	477.2076	239.1074	M	***825.4251***	413.2162	807.4015	404.2044	807.4145	404.2109	7
6	611.2421	306.1247	593.2316	297.1194	D	677.3926	339.2000	659.3691	330.1882	659.3821	330.1947	6
7	**711.3076**	356.1574	693.2970	347.1522	V	561.3687	281.1880	543.3451	272.1762			5
8	**825.3887**	413.1980	807.3781	404.1927	L	***461.3032***	231.1552	443.2796	222.1435			4
9	925.4541	463.2307	907.4436	454.2254	V	***347.2221***	174.1147	329.1985	165.1029			3
10	1023.5039	512.2556	1005.4934	503.2503	P	***247.1567***	124.0820	229.1331	115.0702			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TVAAMDVLVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G70980.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.9	1170.5963	0.0023	TVAAMDVLVPK
19.2	1170.6016	-0.0031	RALLIMHQR
13.0	1170.6012	-0.0026	MPIIGLGVWR
8.3	1170.5963	0.0023	IQDVLMSIPK
1.3	1170.6005	-0.0019	KFHLFGHLR
0.1	1170.5960	0.0026	LVNETKRHR

AT1G71020.2

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQRYGSLNSKK**
Found in **AT1G71020.2** in **TAIR_Arabidopsis**, Symbols: | armadillo/beta-catenin repeat family protein / U-box domain-containing protein | chr1:26794487-26796019 REVERSE

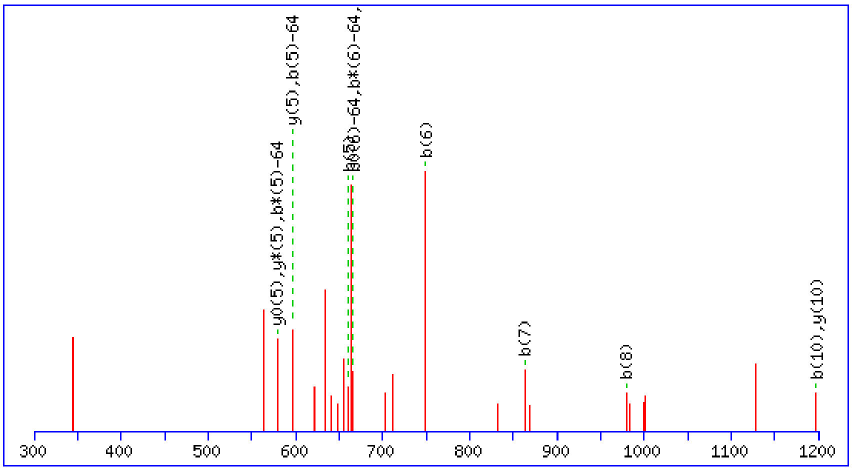
Match to Query 5397: 1344.619138 from(673.316845,2+) index(6304)
Title: Elution from: 55.054 to 55.054 scan no 7865 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1200 Da Full range

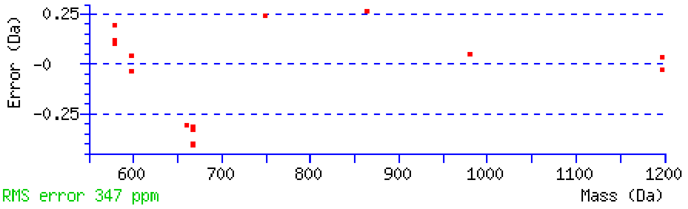
Label all possible matches ○ Label matches used for scoring ●

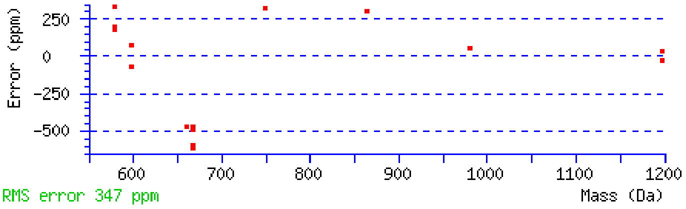
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1344.6181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.04
Matches : 15/152 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							11
2	279.0924	140.0498	261.0688	131.0380			Q	**1197.5929**	599.3001	1179.5693	590.2883	1179.5823	590.2948	10
3	439.1816	220.0944	421.1580	211.0827			R	1067.5402	534.2738	1049.5167	525.2620	1049.5297	525.2685	9
4	603.2420	302.1246	585.2184	293.1128			Y	907.4510	454.2291	889.4274	445.2173	889.4404	445.2239	8
5	***661.2605***	331.1339	643.2369	322.1221			G	743.3906	372.1990	725.3670	363.1872	725.3801	363.1937	7
6	***749.2895***	375.1484	731.2660	366.1366	731.2790	366.1431	S	685.3721	343.1897	667.3485	334.1779	667.3616	334.1844	6
7	***863.3706***	432.1890	845.3470	423.1772	845.3601	423.1837	L	**597.3431**	299.1752	579.3195	290.1634	579.3325	290.1699	5
8	***979.4076***	490.2075	961.3840	481.1957	961.3971	481.2022	N	483.2620	242.1346	465.2384	233.1228	465.2514	233.1293	4
9	1067.4367	534.2220	1049.4131	525.2102	1049.4261	525.2167	S	367.2250	184.1161	349.2014	175.1043	349.2144	175.1108	3
10	***1197.5257***	599.2665	1179.5021	590.2547	1179.5152	590.2612	K	279.1959	140.1016	261.1723	131.0898			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MQRYGSLNSKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G71020.2

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1344.6181	0.0011	MQRYGSLNSKK
2.4	1344.6198	-0.0007	FYSVFVCPVSK
1.2	1344.6154	0.0038	NAMAGEALLPAEK
0.4	1344.6180	0.0011	GRELVDKHMDK
0.1	1344.6198	-0.0007	TYVDVYMKWK
0.0	1344.6203	-0.0011	YGMNFVQGLRK

Mascot: http://www.matrixscience.com/

AT1G71060.1

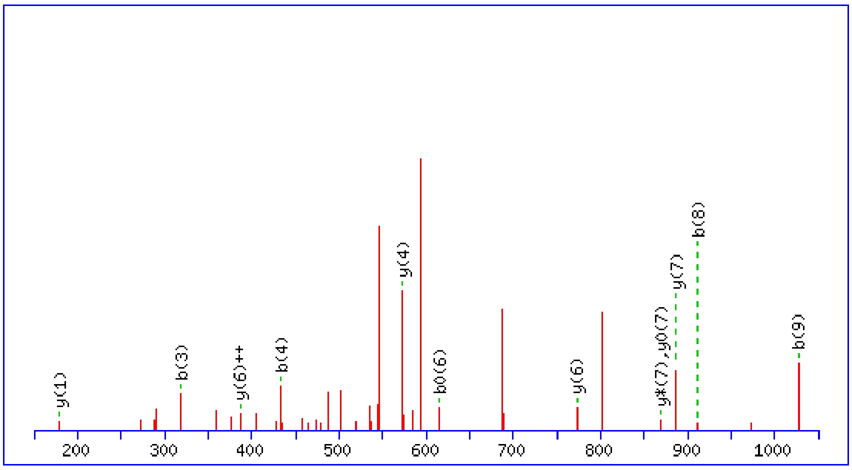
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTDLVVKMDR**
Found in **AT1G71060.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:26809313-26810845 REVERSE

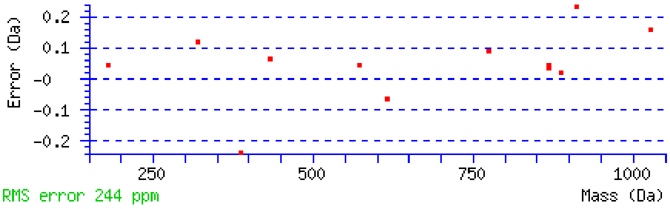
Match to Query 4201: 1204.589460 from(603.302006,2+) index(3452)
Title: Elution from: 34.643 to 34.643 scan no 4358 cid35.00 polarity:+
Data file 0-3_1.mgf

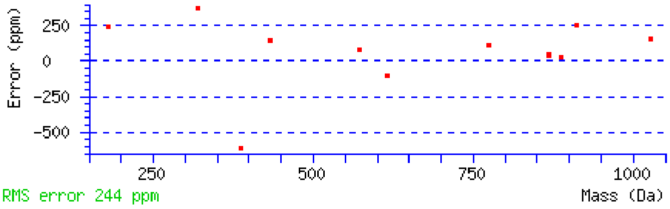
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1204.5914
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.025
Matches : 12/146 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							10
2	203.1174	102.0624			185.1069	93.0571	T	1105.5332	553.2703	1087.5096	544.2585	1087.5227	544.2650	9
3	***319.1414***	160.0743			301.1309	151.0691	D	1003.4885	502.2479	985.4649	493.2361	985.4779	493.2426	8
4	***433.2225***	217.1149			415.2120	208.1096	L	***887.4645***	444.2359	869.4410	435.2241	869.4540	435.2306	7
5	533.2880	267.1476			515.2774	258.1423	V	***773.3834***	387.1954	755.3599	378.1836	755.3729	378.1901	6
6	633.3534	317.1803			615.3428	308.1751	V	673.3180	337.1626	655.2944	328.1508	655.3074	328.1573	5
7	763.4424	382.2249	745.4189	373.2131	745.4319	373.2196	K	***573.2525***	287.1299	555.2290	278.1181	555.2420	278.1246	4
8	***911.4749***	456.2411	893.4513	447.2293	893.4643	447.2358	M	443.1635	222.0854	425.1399	213.0736	425.1529	213.0801	3
9	***1027.4989***	514.2531	1009.4753	505.2413	1009.4883	505.2478	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
10							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VTDLVVKMDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G71060.1

Score	Mr(calc)	Delta	Sequence
26.5	1204.5914	-0.0019	VTDLVVKMDR
8.9	1204.5914	-0.0020	ISNIIAVSSCK
7.7	1204.5884	0.0010	LREETLRDR
7.5	1204.5859	0.0035	MVGATLFHRR
7.3	1204.5880	0.0014	LVIGNEEYVR
6.0	1204.5880	0.0015	DLTVDFGVLGR
5.8	1204.5903	-0.0008	LIEWIFSER
4.4	1204.5907	-0.0012	RPDLAAKFDR
2.2	1204.5907	-0.0012	DKYSAKAHIR
1.9	1204.5884	0.0010	IKRDTVENGR

AT1G71100.1

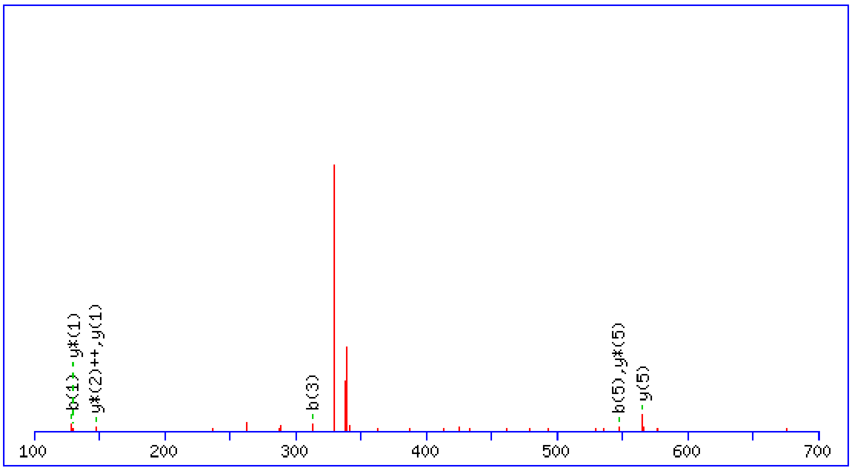
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KIAAYK**
Found in **AT1G71100.1** in **TAIR_Arabidopsis**, Symbols: RSW10 | RSW10 (RADIAL SWELLING 10); ribose-5-phosphate isomerase | chr1:26818388-26819191 FORWARD

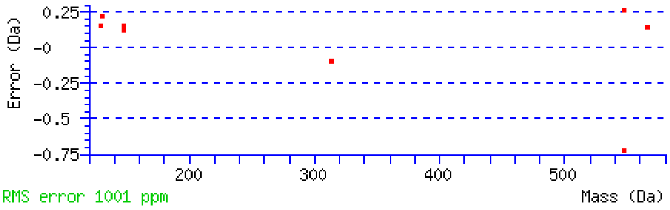
Match to Query 635: 692.421960 from(347.218256,2+) index(734)
Title: Elution from: 13.541 to 13.541 scan no 1094 cid35.00 polarity:+
Data file D6h-1_1.mgf

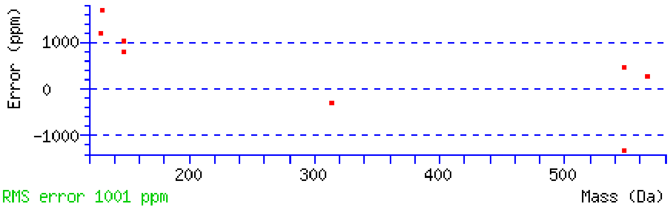
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 692.4221
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.027
Matches : 8/40 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	***129.1022***	65.0548	112.0757	56.5415	K					6
2	242.1863	121.5968	225.1598	113.0835	I	**565.3344**	283.1709	548.3079	274.6576	5
3	***313.2234***	157.1153	296.1969	148.6021	A	452.2504	226.6288	435.2238	218.1155	4
4	384.2605	192.6339	367.2340	184.1206	A	381.2132	191.1103	364.1867	182.5970	3
5	***547.3239***	274.1656	530.2973	265.6523	Y	310.1761	155.5917	293.1496	147.0784	2
6					K	**147.1128**	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of KIAAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.1	692.4221	-0.0001	KIAAYK
19.0	692.4221	-0.0001	KFGTLK
19.0	692.4221	-0.0001	KGFTLK

AT1G71100.1

19.0	692.4221	-0.0001	KLSFAK
17.7	692.4221	-0.0001	KSIAFK
17.7	692.4221	-0.0001	KTVFAK
16.6	692.4221	-0.0001	KTGIFK
14.2	692.4221	-0.0001	ASKFIK
14.2	692.4221	-0.0001	ASKFLK
10.4	692.4221	-0.0001	KFTLGK

AT1G71220.1

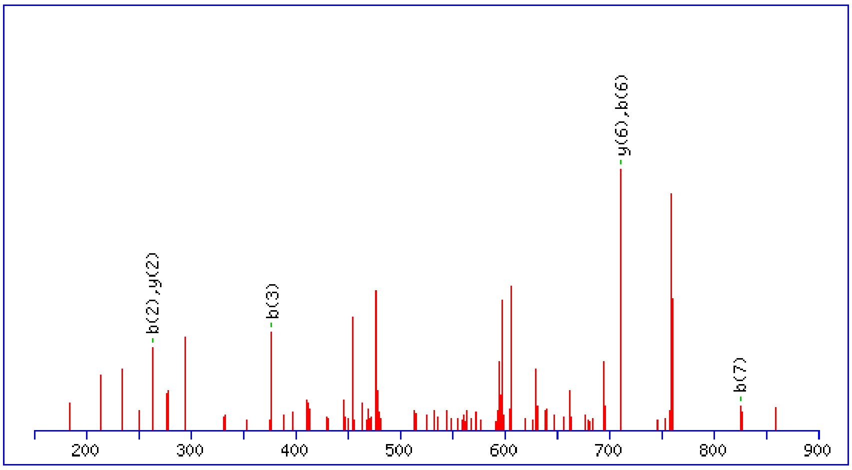
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKLNESIK**
Found in **AT1G71220.1** in **TAIR_Arabidopsis**, Symbols: EBS1 | EBS1 (EMS-MUTAGENIZED BRI1 SUPPRESSOR 1); UDP-glucose:glycoprotein glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr1:26845326-26855392 FORWARD

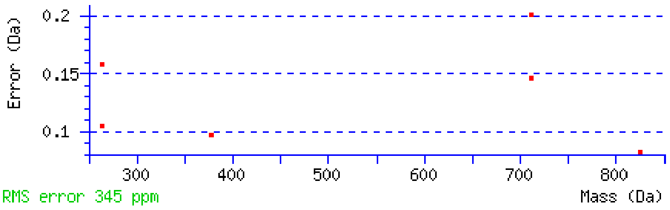
Match to Query 1906: 972.491404 from(487.252978,2+) index(5649)
Title: Elution from: 53.526 to 53.526 scan no 7312 cid35.00 polarity:+
Data file D1d-1_1.mgf

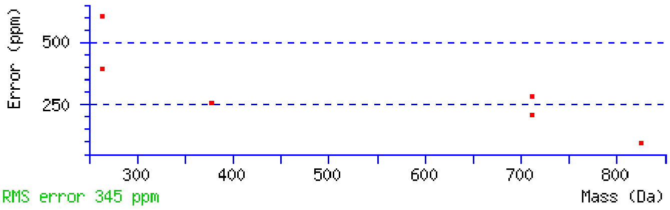
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.031
Matches : 6/70 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	133.0448	67.0260					M							8
2	**263.1338**	132.0706	245.1102	123.0588			K	841.4638	421.2355	823.4402	412.2237	823.4532	412.2303	7
3	**377.2149**	189.1111	359.1913	180.0993			L	**711.3748**	356.1910	693.3512	347.1792	693.3642	347.1857	6
4	493.2519	247.1296	475.2283	238.1178			N	597.2937	299.1505	579.2701	290.1387	579.2831	290.1452	5
5	623.2916	312.1494	605.2680	303.1376	605.2810	303.1441	E	481.2567	241.1320	463.2331	232.1202	463.2461	232.1267	4
6	**711.3206**	356.1639	693.2970	347.1522	693.3101	347.1587	S	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
7	**825.4017**	413.2045	807.3781	404.1927	807.3911	404.1992	I	**263.1880**	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MKLNESIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G71220.1

26.7	972.4940	-0.0026	MKLNESIK
19.2	972.4906	0.0008	IFLIADDR
15.9	972.4940	-0.0026	QMAKDLIK
13.7	972.4940	-0.0026	MKVDTKPK
13.2	972.4940	-0.0026	KMTVQDLK
12.8	972.4907	0.0007	IPSSFGNLK
12.3	972.4940	-0.0026	VCLSVKEK
11.4	972.4940	-0.0026	MGSGEKILK
10.6	972.4907	0.0007	YPPDSKKK
9.2	972.4911	0.0003	IVNDRSVR

AT1G71500.1

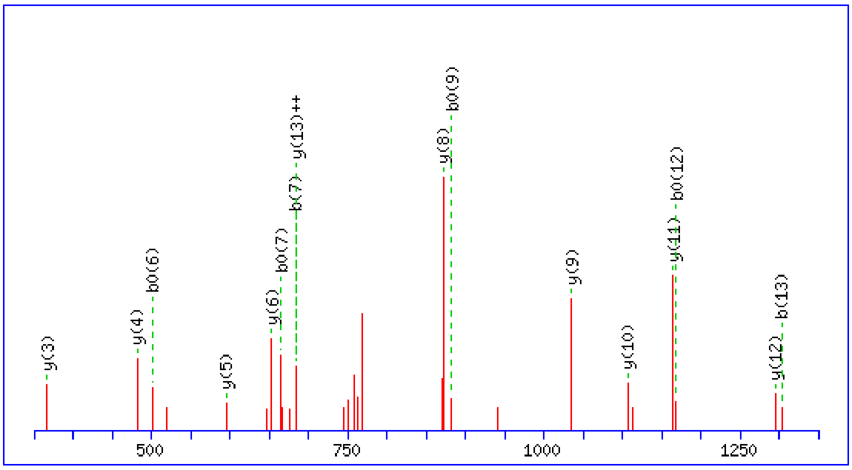
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPAEGAYSEGLLNAR**
Found in **AT1G71500.1** in **TAIR_Arabidopsis**, Symbols: | Rieske (2Fe-2S) domain-containing protein | chr1:26939746-26940993 FORWARD

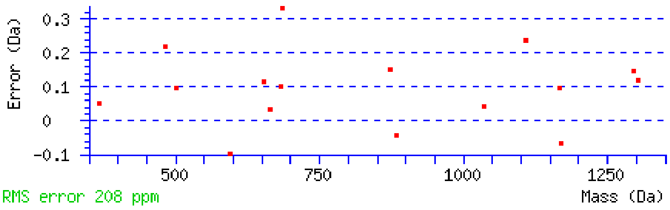
Match to Query 6570: 1552.688516 from(777.351534,2+) index(4479)
Title: Elution from: 40.786 to 40.786 scan no 5604 cid35.00 polarity:+
Data file D12h-1_3.mgf

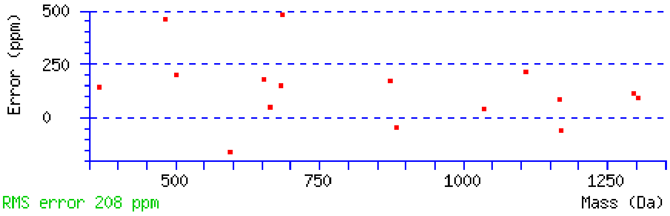
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1552.6860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 83  Expect: 4e-008
Matches : 16/132 fragment ions using 23 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							15
2	187.0861	94.0467			169.0756	85.0414	P	1465.6642	733.3357	1447.6406	724.3240	1447.6536	724.3305	14
3	259.1203	130.0638			241.1097	121.0585	A	1367.6144	684.3108	1349.5908	675.2991	1349.6039	675.3056	13
4	389.1599	195.0836			371.1493	186.0783	E	***1295.5803***	648.2938	1277.5567	639.2820	1277.5697	639.2885	12
5	447.1784	224.0928			429.1678	215.0876	G	***1165.5406***	583.2740	1147.5171	574.2622	1147.5301	574.2687	11
6	519.2126	260.1099			501.2020	251.1046	A	***1107.5221***	554.2647	1089.4986	545.2529	1089.5116	545.2594	10
7	**683.2729**	342.1401			665.2624	333.1348	Y	***1035.4880***	518.2476	1017.4644	509.2358	1017.4774	509.2424	9
8	771.3020	386.1546			753.2914	377.1494	S	***871.4276***	436.2175	853.4040	427.2057	853.4171	427.2122	8
9	901.3416	451.1744			883.3311	442.1692	E	783.3986	392.2029	765.3750	383.1911	765.3880	383.1976	7
10	959.3601	480.1837			941.3496	471.1784	G	***653.3589***	327.1831	635.3354	318.1713			6
11	1073.4412	537.2242			1055.4307	528.2190	L	***595.3404***	298.1739	577.3169	289.1621			5
12	1187.5223	594.2648			1169.5117	585.2595	L	***481.2593***	241.1333	463.2358	232.1215			4
13	**1303.5593**	652.2833	1285.5357	643.2715	1285.5487	643.2780	N	***367.1782***	184.0928	349.1547	175.0810			3
14	1375.5935	688.3004	1357.5699	679.2886	1357.5829	679.2951	A	251.1412	126.0743	233.1177	117.0625			2
15							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SPAEGAYSEGLLNAR

AT1G71500.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.0	1552.6860	0.0025	SPAEGAYSEGLLNAR
6.1	1552.6882	0.0003	FKAETVSPGEWER
0.1	1552.6894	-0.0009	TCNVSLPLQNSSSK

Mascot Search Results

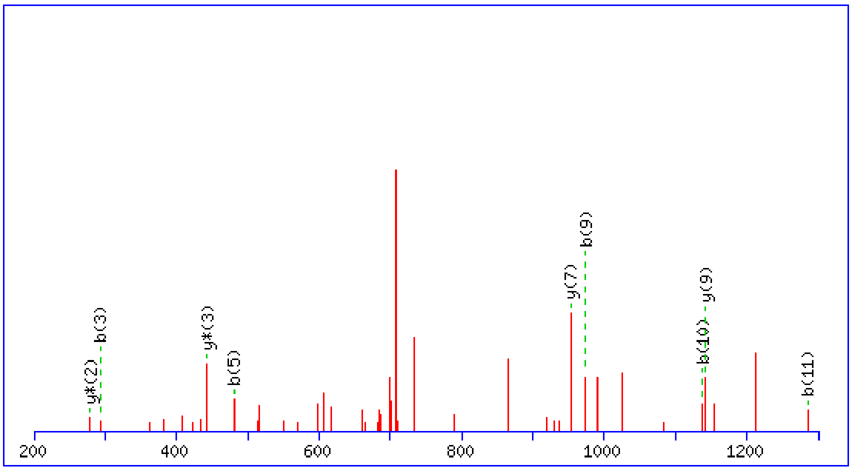
Peptide View

MS/MS Fragmentation of **GTMEGMIDKYMK**
Found in **AT1G71692.1** in **TAIR_Arabidopsis**, Symbols: XAL1, AGL12 | AGL12 (AGAMOUS-LIKE 12); transcription factor | chr1:26956565-26958601 REVERSE

Match to Query 5804: 1432.585946 from(717.300249,2+) index(3330)
Title: Elution from: 32.178 to 32.178 scan no 4111 cid35.00 polarity:+
Data file C7-2_2.mgf

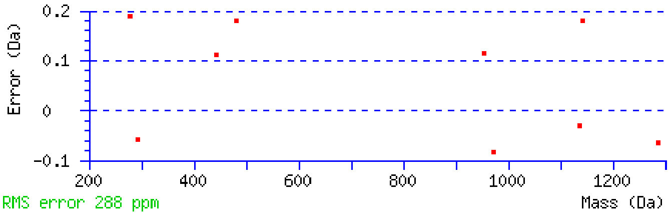
Click mouse within plot area to zoom in by factor of two about that point

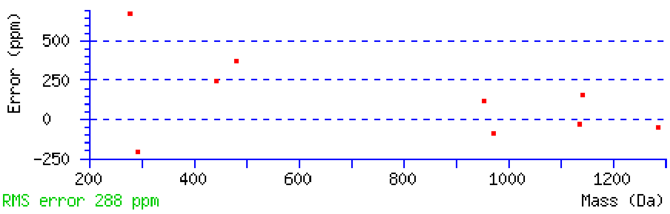
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1432.5829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.02
Matches : 9/166 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							12
2	161.0705	81.0389			143.0599	72.0336	T	1375.5717	688.2895	1357.5481	679.2777	1357.5611	679.2842	11
3	***293.1080***	147.0576			275.0974	138.0524	M	1273.5269	637.2671	1255.5034	628.2553	1255.5164	628.2618	10
4	423.1476	212.0775			405.1371	203.0722	E	**1141.4894**	571.2484	1123.4658	562.2366	1123.4789	562.2431	9
5	***481.1661***	241.0867			463.1556	232.0814	G	1011.4498	506.2285	993.4262	497.2167	993.4392	497.2233	8
6	613.2037	307.1055			595.1931	298.1002	M	**953.4313**	477.2193	935.4077	468.2075	935.4207	468.2140	7
7	727.2848	364.1460			709.2742	355.1407	I	821.3938	411.2005	803.3702	402.1887	803.3832	402.1952	6
8	843.3087	422.1580			825.2982	413.1527	D	707.3127	354.1600	689.2891	345.1482	689.3021	345.1547	5
9	***973.3978***	487.2025	955.3742	478.1907	955.3872	478.1972	K	591.2887	296.1480	573.2651	287.1362			4
10	***1137.4581***	569.2327	1119.4345	560.2209	1119.4476	560.2274	Y	461.1997	231.1035	443.1761	222.0917			3
11	***1285.4906***	643.2489	1267.4670	634.2371	1267.4800	634.2436	M	297.1393	149.0733	279.1157	140.0615			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GTMEGMIDKYMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G71692.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
22.0	1432.5829	0.0031	GTMEGMIDKYMK	Oxidation M11 95.96%
7.7	1432.5829	0.0031	GTMEGMIDKYMK	Oxidation M6 3.56%
5.7	1432.5826	0.0033	KCNERCYINR	
3.7	1432.5829	0.0031	FTATSMMDMLQK	
3.7	1432.5829	0.0031	FTATSMMDMLQK	
0.0	1432.5873	-0.0014	MDRSYRDLEGR	

AT1G71695.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGLFTSDQDLFVDK**
Found in **AT1G71695.1** in **TAIR_Arabidopsis**, Symbols: | peroxidase 12 (PER12) (P12) (PRXR6) | chr1:26968021-26970219 FORWARD

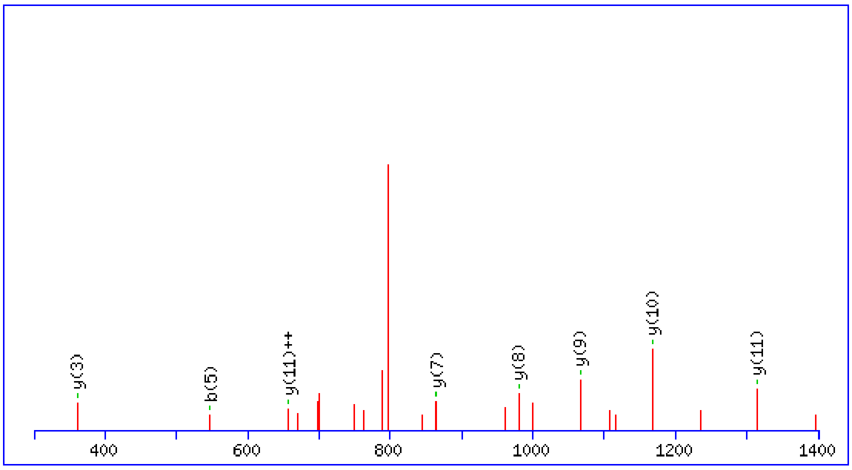
Match to Query 7098: 1611.778034 from(806.896293,2+) index(7939)
Title: Elution from: 69.307 to 69.307 scan no 10498 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1400 Da Full range

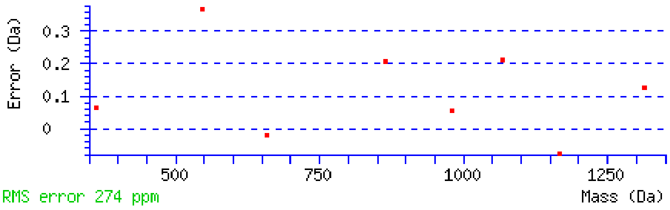
Label all possible matches ○ Label matches used for scoring ●

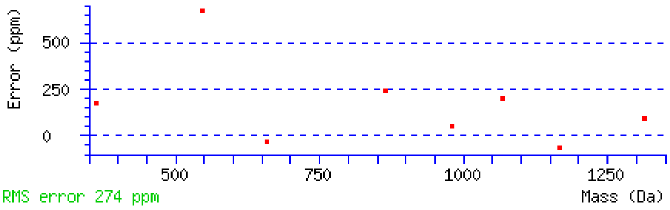
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1611.7781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00028
Matches : 8/146 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							14
2	186.0873	93.5473	169.0608	85.0340			G	1484.7268	742.8670	1467.7002	734.3537	1466.7162	733.8617	13
3	299.1714	150.0893	282.1448	141.5761			L	1427.7053	714.3563	1410.6787	705.8430	1409.6947	705.3510	12
4	446.2398	223.6235	429.2132	215.1103			F	***1314.6212***	657.8143	1297.5947	649.3010	1296.6107	648.8090	11
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	T	***1167.5528***	584.2800	1150.5263	575.7668	1149.5422	575.2748	10
6	634.3195	317.6634	617.2930	309.1501	616.3089	308.6581	S	***1066.5051***	533.7562	1049.4786	525.2429	1048.4946	524.7509	9
7	749.3464	375.1769	732.3199	366.6636	731.3359	366.1716	D	***979.4731***	490.2402	962.4466	481.7269	961.4625	481.2349	8
8	877.4050	439.2062	860.3785	430.6929	859.3945	430.2009	Q	***864.4462***	432.7267	847.4196	424.2134	846.4356	423.7214	7
9	992.4320	496.7196	975.4054	488.2063	974.4214	487.7143	D	736.3876	368.6974	719.3610	360.1842	718.3770	359.6921	6
10	1105.5160	553.2617	1088.4895	544.7484	1087.5055	544.2564	L	621.3606	311.1840	604.3341	302.6707	603.3501	302.1787	5
11	1252.5844	626.7959	1235.5579	618.2826	1234.5739	617.7906	F	508.2766	254.6419	491.2500	246.1287	490.2660	245.6366	4
12	1351.6529	676.3301	1334.6263	667.8168	1333.6423	667.3248	V	***361.2082***	181.1077	344.1816	172.5944	343.1976	172.1024	3
13	1466.6798	733.8435	1449.6533	725.3303	1448.6692	724.8383	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of QGLFTSDQDLFVDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G71695.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	1611.7781	-0.0000	QGLFTSDQDLFVDK
1.8	1611.7827	-0.0047	TNLSQAFSQKMWR

Mascot: http://www.matrixscience.com/

AT1G72130.2

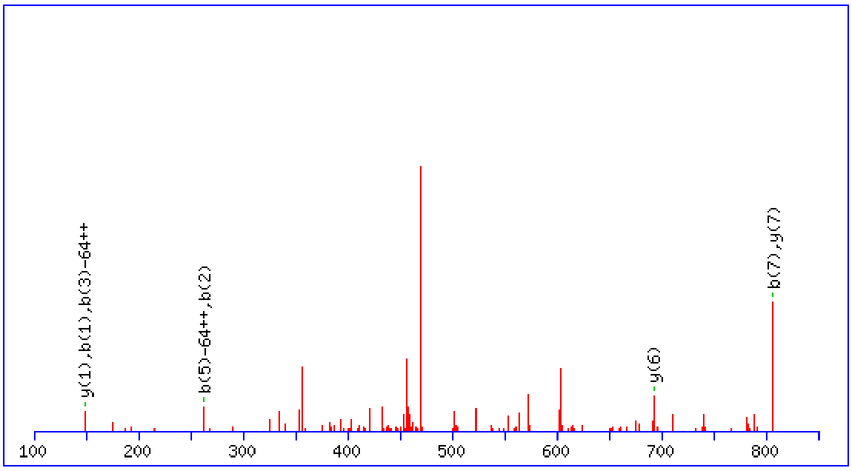
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MIPSHQSK**
Found in **AT1G72130.2** in **TAIR_Arabidopsis**, Symbols: | proton-dependent oligopeptide transport (POT) family protein | chr1:27141425-27142885 FORWARD

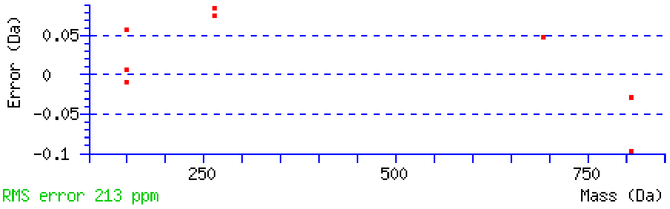
Match to Query 1943: 954.424096 from(478.219324,2+) index(3015)
Title: Elution from: 29.619 to 29.619 scan no 3743 cid35.00 polarity:+
Data file 0-3_3.mgf

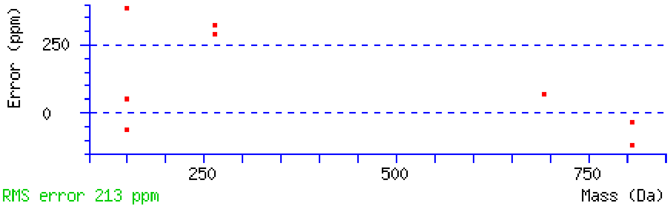
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 954.4237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.025
Matches : 8/92 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	*149.0397*	75.0235					M							8
2	*263.1208*	132.0640					I	*807.3986*	404.2029	789.3750	395.1911	789.3880	395.1976	7
3	361.1706	181.0889					P	*693.3175*	347.1624	675.2939	338.1506	675.3069	338.1571	6
4	449.1997	225.1035			431.1891	216.0982	S	595.2677	298.1375	577.2441	289.1257	577.2571	289.1322	5
5	589.2497	295.1285			571.2391	286.1232	H	507.2386	254.1229	489.2150	245.1111	489.2280	245.1177	4
6	719.3023	360.1548	701.2788	351.1430	701.2918	351.1495	Q	367.1886	184.0979	349.1650	175.0861	349.1780	175.0926	3
7	*807.3314*	404.1693	789.3078	395.1575	789.3208	395.1641	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
8							K	*149.1069*	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MIPSHQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G72130.2

20.8	954.4237	0.0004	MHGLGDGLK
20.8	954.4237	0.0004	MIPSHQSK
11.3	954.4237	0.0004	LMVNHEGK
11.3	954.4237	0.0004	MIEHLER
2.6	954.4237	0.0004	MHEILER
1.4	954.4237	0.0004	GAIPSMPDR
1.0	954.4259	-0.0019	MFLSQFR
0.6	954.4226	0.0015	FFFSSPGR
0.5	954.4259	-0.0019	HIEWMTK
0.4	954.4264	-0.0023	CHKPDRK

AT1G72150.1

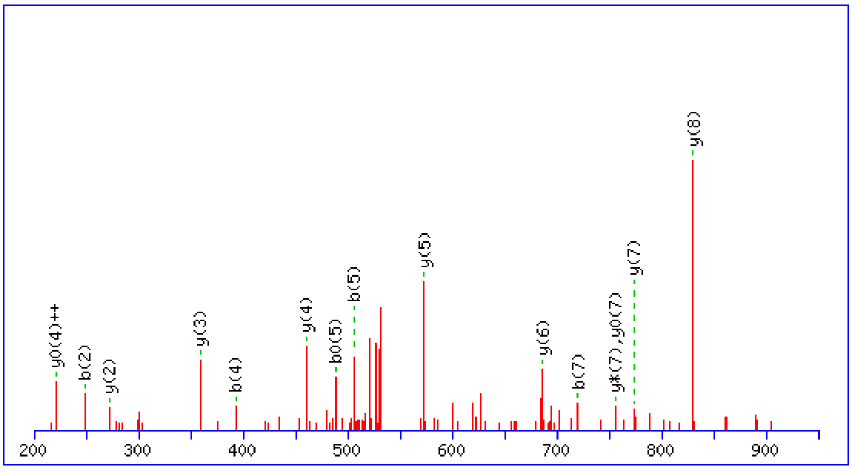
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFGSIITSPR**
Found in **AT1G72150.1** in **TAIR_Arabidopsis**, Symbols: PATL1 | PATL1 (PATELLIN 1); transporter | chr1:27152220-27154314 FORWARD

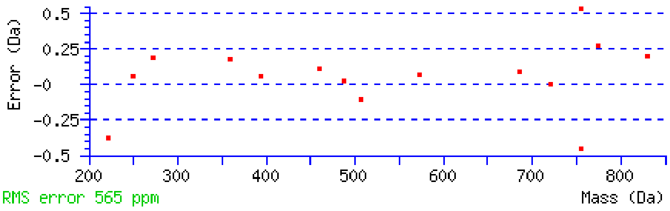
Match to Query 3221: 1077.583106 from(539.798829,2+) index(4801)
Title: Elution from: 42.978 to 42.978 scan no 5975 cid35.00 polarity:+
Data file C7-1_1.mgf

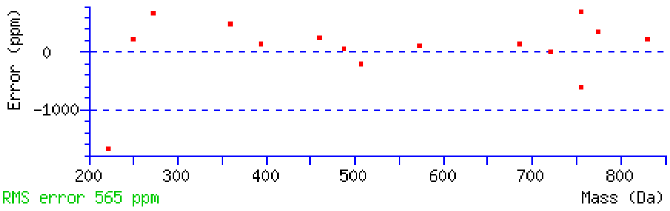
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1077.5819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 6.6e-006
Matches : 15/86 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	**249.1234**	125.0653	231.1128	116.0600	F	977.5415	489.2744	960.5149	480.7611	959.5309	480.2691	9
3	306.1448	153.5761	288.1343	144.5708	G	***830.4730***	415.7402	813.4465	407.2269	812.4625	406.7349	8
4	**393.1769**	197.0921	375.1663	188.0868	S	***773.4516***	387.2294	756.4250	378.7162	755.4410	378.2241	7
5	**506.2609**	253.6341	488.2504	244.6288	I	***686.4196***	343.7134	669.3930	335.2001	668.4090	334.7081	6
6	619.3450	310.1761	601.3344	301.1709	I	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	5
7	**720.3927**	360.7000	702.3821	351.6947	T	***460.2514***	230.6293	443.2249	222.1161	442.2409	221.6241	4
8	807.4247	404.2160	789.4141	395.2107	S	***359.2037***	180.1055	342.1772	171.5922	341.1932	171.1002	3
9	904.4775	452.7424	886.4669	443.7371	P	***272.1717***	136.5895	255.1452	128.0762			2
10					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TFGSIITSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G72150.1

59.7	1077.5819	0.0012	TFGSIITSPR
20.5	1077.5818	0.0013	AFSAELTAIR
6.5	1077.5818	0.0013	DYNLNKLAK
0.6	1077.5819	0.0012	DNVGLKGFTK

AT1G72370.1

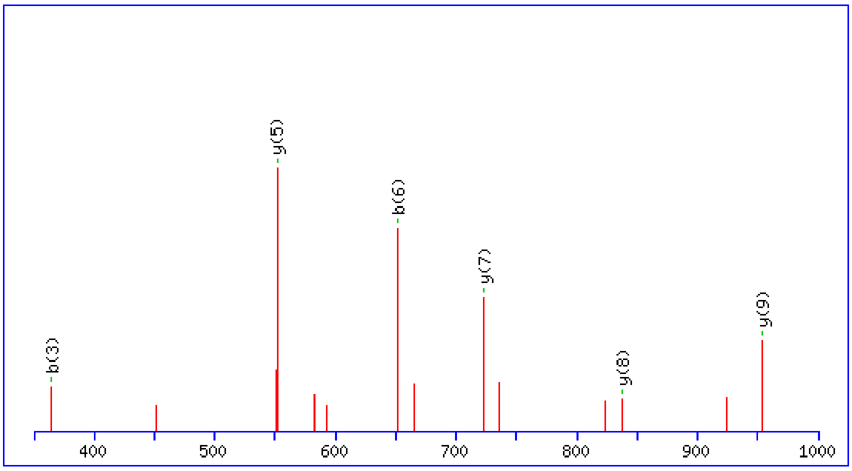
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVDIGIPANNK**
Found in **AT1G72370.1** in **TAIR_Arabidopsis**, Symbols: AP40, RP40, RPSAA, P40 | P40 (40S ribosomal protein SA); structural constituent of ribosome | chr1:27246810-27248504 REVERSE

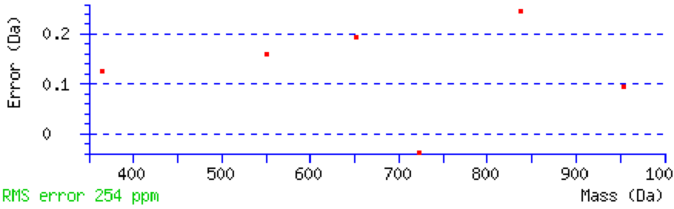
Match to Query 4301: 1200.595076 from(601.304814,2+) index(5135)
Title: Elution from: 46.090 to 46.090 scan no 6406 cid35.00 polarity:+
Data file C7-3_1.mgf

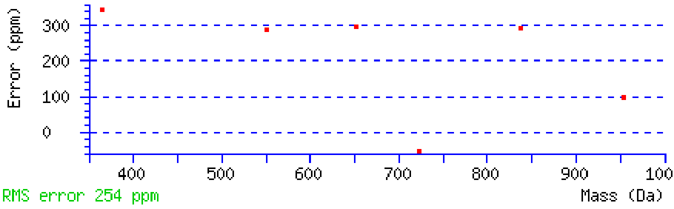
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1200.5931
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0011
Matches : 6/84 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					**F**							**11**
2	249.1382	125.0727					**V**	1053.5349	527.2711	1035.5114	518.2593	1035.5244	518.2658	**10**
3	**365.1622**	183.0847			347.1516	174.0794	**D**	***953.4695***	477.2384	935.4459	468.2266	935.4589	468.2331	**9**
4	479.2433	240.1253			461.2327	231.1200	**I**	***837.4455***	419.2264	819.4219	410.2146			**8**
5	537.2618	269.1345			519.2512	260.1292	**G**	***723.3644***	362.1858	705.3408	353.1741			**7**
6	**651.3428**	326.1751			633.3323	317.1698	**I**	665.3459	333.1766	647.3223	324.1648			**6**
7	749.3926	375.2000			731.3821	366.1947	**P**	***551.2648***	276.1360	533.2412	267.1243			**5**
8	821.4268	411.2170			803.4162	402.2118	**A**	453.2150	227.1111	435.1914	218.0994			**4**
9	937.4638	469.2355	919.4402	460.2237	919.4532	460.2303	**N**	381.1809	191.0941	363.1573	182.0823			**3**
10	1053.5008	527.2540	1035.4772	518.2422	1035.4902	518.2488	**N**	265.1439	133.0756	247.1203	124.0638			**2**
11							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of FVDIGIPANNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G72370.1

Score	Mr(calc)	Delta	Sequence
37.8	1200.5931	0.0020	FVDIGIPANNK
11.6	1200.5958	-0.0007	GKFVIHGSPSR
4.2	1200.5931	0.0020	DIKSSIPYHK
0.8	1200.5935	0.0015	SKRVGVSHEGK
0.0	1200.5936	0.0015	VTPSPGNISRR

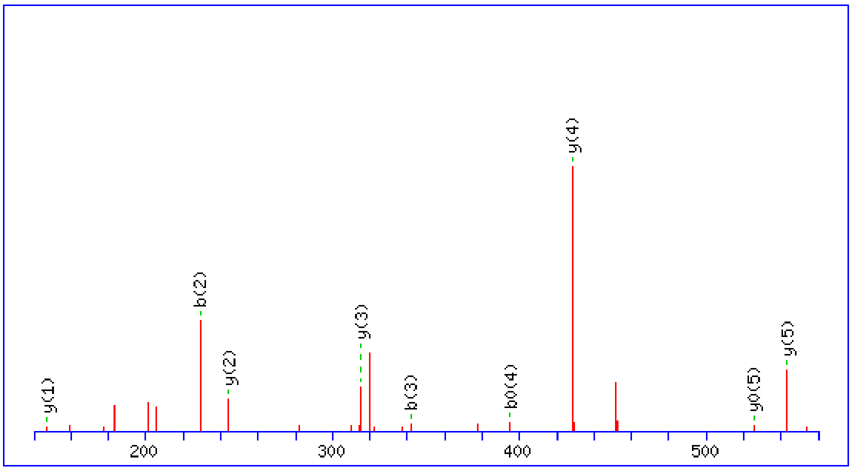
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDLAPK**
Found in **AT1G72610.1** in **TAIR_Arabidopsis**, Symbols: GLP1 | GLP1 (GERMIN-LIKE PROTEIN 1); manganese ion binding / metal ion binding / nutrient reservoir | chr1:27342964-27343590 REVERSE

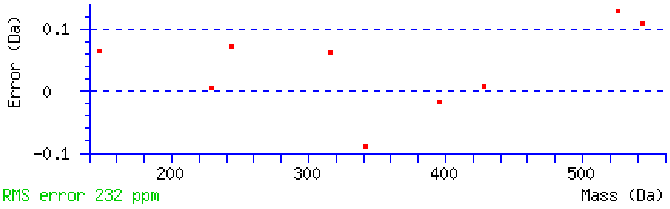
Match to Query 514: 655.390632 from(328.702592,2+) index(1481)
Title: Elution from: 20.361 to 20.361 scan no 2001 cid35.00 polarity:+
Data file C7-1_3.mgf

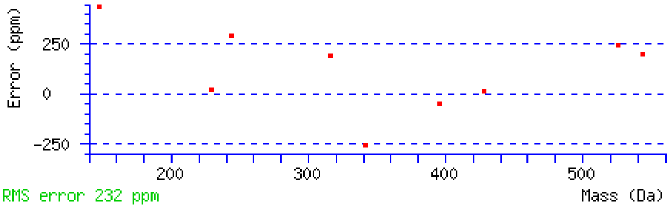
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 560 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 655.3905
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0012
Matches : 9/40 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							6
2	**229.1183**	115.0628	211.1077	106.0575	D	***543.3137***	272.1605	526.2871	263.6472	525.3031	263.1552	5
3	**342.2023**	171.6048	324.1918	162.5995	L	***428.2867***	214.6470	411.2602	206.1337			4
4	413.2395	207.1234	395.2289	198.1181	A	***315.2027***	158.1050	298.1761	149.5917			3
5	510.2922	255.6498	492.2817	246.6445	P	***244.1656***	122.5864	227.1390	114.0731			2
6					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LDLAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.3	655.3905	0.0002	LDLAPK
13.6	655.3905	0.0002	LEVAPK
13.6	655.3905	0.0002	LLDAPK

AT1G72610.1

7.8	655.3905	0.0002	DIALPK
7.7	655.3905	0.0002	EALVPK
5.4	655.3905	0.0002	LPIGEK
5.4	655.3905	0.0002	LPLGEK
4.2	655.3905	0.0002	LLADPK
3.2	655.3905	0.0002	ILEGPK
3.2	655.3905	0.0002	LEGLPK

AT1G72820.1

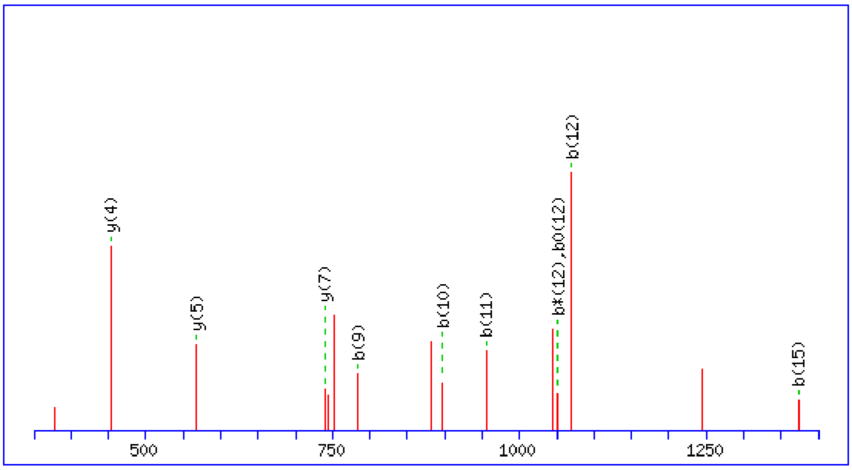
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SNVGSAAVSLGLTEAK**
Found in **AT1G72820.1** in **TAIR_Arabidopsis**, Symbols: | mitochondrial substrate carrier family protein | chr1:27407119-27408168 FORWARD

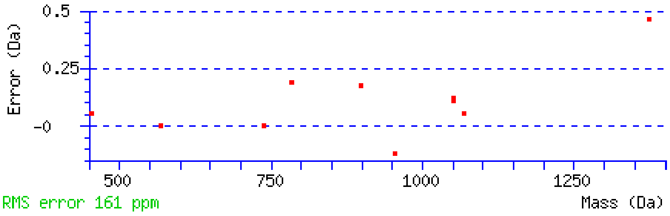
Match to Query 6413: 1520.736908 from(761.375730,2+) index(10860)
Title: Elution from: 108.515 to 108.515 scan no 15918 cid35.00 polarity:+
Data file D6h-3_2.mgf

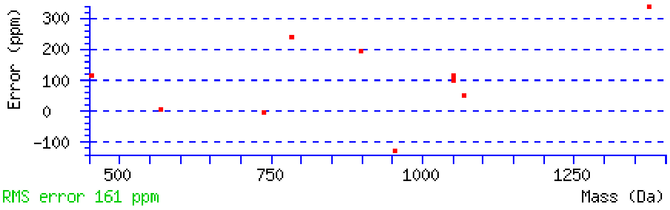
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1520.7407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0064
Matches : 10/174 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							16
2	205.0733	103.0403	187.0498	94.0285	187.0628	94.0350	N	1433.7189	717.3631	1415.6953	708.3513	1415.7083	708.3578	15
3	305.1388	153.0730	287.1152	144.0612	287.1282	144.0677	V	1317.6819	659.3446	1299.6583	650.3328	1299.6713	650.3393	14
4	363.1573	182.0823	345.1337	173.0705	345.1467	173.0770	G	1217.6164	609.3119	1199.5928	600.3001	1199.6059	600.3066	13
5	451.1863	226.0968	433.1628	217.0850	433.1758	217.0915	S	1159.5979	580.3026	1141.5743	571.2908	1141.5874	571.2973	12
6	523.2205	262.1139	505.1969	253.1021	505.2099	253.1086	A	1071.5689	536.2881	1053.5453	527.2763	1053.5583	527.2828	11
7	595.2546	298.1310	577.2311	289.1192	577.2441	289.1257	A	999.5347	500.2710	981.5111	491.2592	981.5242	491.2657	10
8	695.3201	348.1637	677.2965	339.1519	677.3095	339.1584	V	927.5006	464.2539	909.4770	455.2421	909.4900	455.2486	9
9	***783.3492***	392.1782	765.3256	383.1664	765.3386	383.1729	S	827.4351	414.2212	809.4115	405.2094	809.4246	405.2159	8
10	***897.4303***	449.2188	879.4067	440.2070	879.4197	440.2135	L	**739.4061**	370.2067	721.3825	361.1949	721.3955	361.2014	7
11	***955.4488***	478.2280	937.4252	469.2162	937.4382	469.2227	G	625.3250	313.1661	607.3014	304.1543	607.3144	304.1608	6
12	***1069.5299***	535.2686	1051.5063	526.2568	1051.5193	526.2633	L	**567.3065**	284.1569	549.2829	275.1451	549.2959	275.1516	5
13	1171.5746	586.2909	1153.5510	577.2791	1153.5640	577.2856	T	**453.2254**	227.1163	435.2018	218.1045	435.2148	218.1110	4
14	1301.6142	651.3107	1283.5906	642.2989	1283.6036	642.3055	E	351.1807	176.0940	333.1571	167.0822	333.1701	167.0887	3
15	***1373.6483***	687.3278	1355.6248	678.3160	1355.6378	678.3225	A	221.1410	111.0741	203.1174	102.0624			2
16							K	149.1069	75.0571	131.0833	66.0453			1





AT1G72820.1

NCBI **BLAST** search of SNVGSAAVSLGLTEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.3	1520.7407	-0.0038	SNVGSAAVSLGLTEAK
15.6	1520.7334	0.0035	MMISHKALKHYK
11.3	1520.7332	0.0037	TLEEAICEVVSKK
11.2	1520.7334	0.0035	MMISHKALKHYK
9.8	1520.7325	0.0044	YHSQTVGKVIGGEK
9.7	1520.7406	-0.0037	KLEQSSTVADVQAK
7.2	1520.7382	-0.0013	MVKFINNLPENGK
3.0	1520.7359	0.0010	QLNKTDLMNAVQK
3.0	1520.7325	0.0044	RIYQSPTPEVGQK
2.7	1520.7325	0.0044	EIKDRDSLVWNK

Mascot: http://www.matrixscience.com/

AT1G73230.1

Mascot Search Results

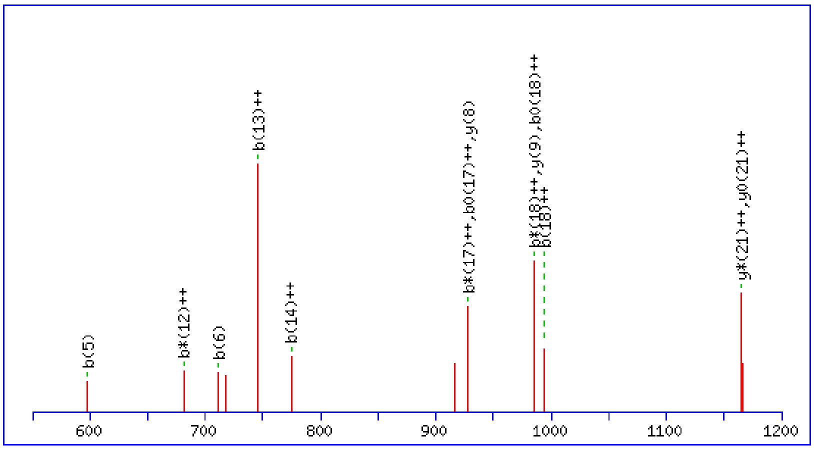
Peptide View

MS/MS Fragmentation of **KLQDILPQIISQLGPDNLDNLK**
Found in **AT1G73230.1** in **TAIR_Arabidopsis**, Symbols: | nascent polypeptide-associated complex (NAC) domain-containing protein | chr1:27544167-27545025 REVERSE

Match to Query 10386: 2474.370507 from(825.797445,3+) index(10817)
Title: Elution from: 110.617 to 110.617 scan no 15828 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

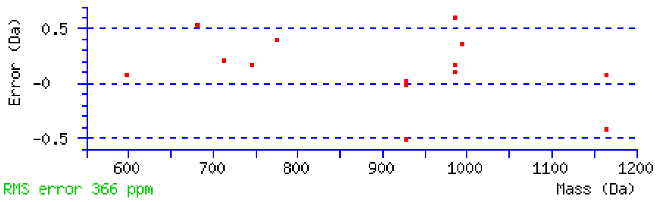
Or, Plot from 550 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

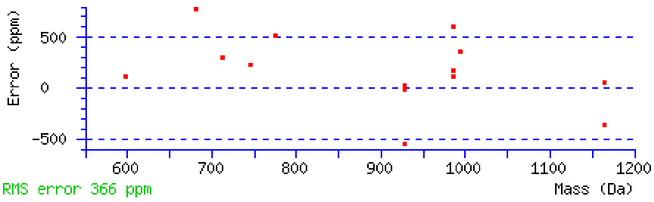


Monoisotopic mass of neutral peptide Mr(calc): 2474.3744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00036
Matches : 15/240 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							22
2	242.1863	121.5968	225.1598	113.0835			L	2347.2868	1174.1470	2330.2602	1165.6337	2329.2762	1165.1417	21
3	370.2449	185.6261	353.2183	177.1128			Q	2234.2027	1117.6050	2217.1761	1109.0917	2216.1921	1108.5997	20
4	485.2718	243.1396	468.2453	234.6263	467.2613	234.1343	D	2106.1441	1053.5757	2089.1176	1045.0624	2088.1335	1044.5704	19
5	***598.3559***	299.6816	581.3293	291.1683	580.3453	290.6763	I	1991.1172	996.0622	1974.0906	987.5489	1973.1066	987.0569	18
6	***711.4400***	356.2236	694.4134	347.7103	693.4294	347.2183	L	1878.0331	939.5202	1861.0066	931.0069	1860.0225	930.5149	17
7	808.4927	404.7500	791.4662	396.2367	790.4822	395.7447	P	1764.9490	882.9782	1747.9225	874.4649	1746.9385	873.9729	16
8	936.5513	468.7793	919.5247	460.2660	918.5407	459.7740	Q	1667.8963	834.4518	1650.8697	825.9385	1649.8857	825.4465	15
9	1049.6354	525.3213	1032.6088	516.8080	1031.6248	516.3160	I	1539.8377	770.4225	1522.8111	761.9092	1521.8271	761.4172	14
10	1162.7194	581.8633	1145.6929	573.3501	1144.7089	572.8581	I	1426.7536	713.8805	1409.7271	705.3672	1408.7431	704.8752	13
11	1249.7515	625.3794	1232.7249	616.8661	1231.7409	616.3741	S	1313.6696	657.3384	1296.6430	648.8251	1295.6590	648.3331	12
12	1377.8100	689.4087	1360.7835	680.8954	1359.7995	680.4034	Q	1226.6375	613.8224	1209.6110	605.3091	1208.6270	604.8171	11
13	1490.8941	***745.9507***	1473.8675	737.4374	1472.8835	736.9454	L	1098.5790	549.7931	1081.5524	541.2798	1080.5684	540.7878	10
14	1547.9156	***774.4614***	1530.8890	765.9481	1529.9050	765.4561	G	**985.4949**	493.2511	968.4684	484.7378	967.4843	484.2458	9
15	1644.9683	822.9878	1627.9418	814.4745	1626.9578	813.9825	P	**928.4734**	464.7404	911.4469	456.2271	910.4629	455.7351	8
16	1759.9953	880.5013	1742.9687	871.9880	1741.9847	871.4960	D	831.4207	416.2140	814.3941	407.7007	813.4101	407.2087	7
17	1874.0382	937.5227	1857.0116	929.0095	1856.0276	928.5175	N	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
18	1987.1223	***994.0648***	1970.0957	985.5515	1969.1117	985.0595	L	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	5
19	2102.1492	1051.5782	2085.1226	1043.0650	2084.1386	1042.5730	D	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	4
20	2216.1921	1108.5997	2199.1656	1100.0864	2198.1816	1099.5944	N	374.2398	187.6235	357.2132	179.1103			3
21	2329.2762	***1165.1417***	2312.2496	1156.6285	2311.2656	1156.1364	L	260.1969	130.6021	243.1703	122.0888			2
22							K	147.1128	74.0600	130.0863	65.5468			1

AT1G73230.1





NCBI **BLAST** search of KLQDILPQIISQLGPDNLDNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.6	2474.3744	-0.0039	KLQDILPQIISQLGPDNLDNLK
1.3	2474.3744	-0.0039	LQDILPQIISQLGPDNLDNLKK
1.1	2474.3719	-0.0014	NALWAVMTVVVVLEFSAGATLRK

Mascot: http://www.matrixscience.com/

AT1G73400.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVIDMLDYMKR**
Found in **AT1G73400.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:27602073-27603473 FORWARD

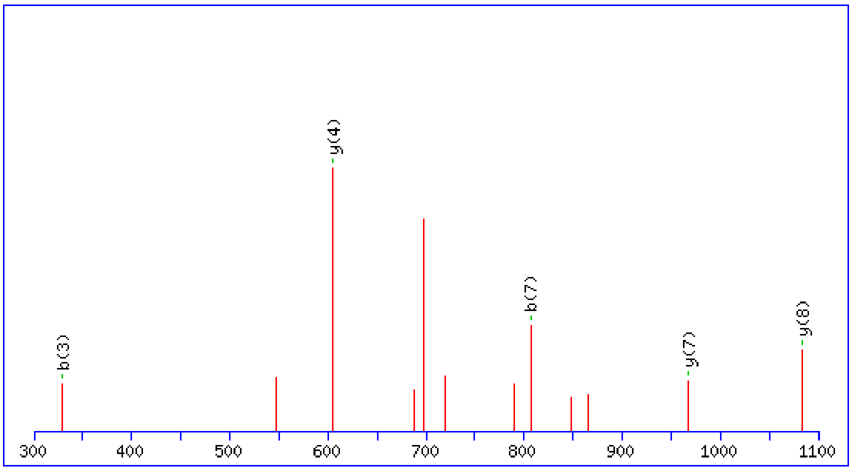
Match to Query 4964: 1410.676840 from(706.345696,2+) index(9629)
Title: Elution from: 93.859 to 93.859 scan no 13742 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1100 Da Full range

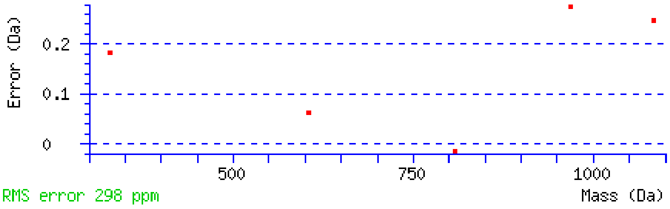
Label all possible matches ○ Label matches used for scoring ●

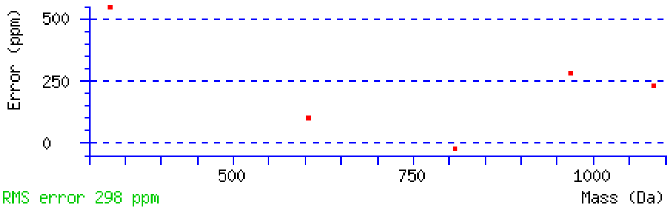
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1410.6809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.047
Matches : 5/88 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							11
2	215.1538	108.0805					V	1297.6071	649.3072	1279.5835	640.2954	1279.5966	640.3019	10
3	**329.2349**	165.1211					I	1197.5417	599.2745	1179.5181	590.2627	1179.5311	590.2692	9
4	445.2589	223.1331			427.2483	214.1278	D	***1083.4606***	542.2339	1065.4370	533.2221	1065.4500	533.2286	8
5	577.2964	289.1518			559.2859	280.1466	M	***967.4366***	484.2219	949.4130	475.2101	949.4260	475.2167	7
6	691.3775	346.1924			673.3670	337.1871	L	835.3991	418.2032	817.3755	409.1914	817.3885	409.1979	6
7	**807.4015**	404.2044			789.3909	395.1991	D	721.3180	361.1626	703.2944	352.1508	703.3074	352.1573	5
8	971.4619	486.2346			953.4513	477.2293	Y	***605.2940***	303.1506	587.2704	294.1389			4
9	1103.4994	552.2533			1085.4888	543.2480	M	441.2336	221.1205	423.2101	212.1087			3
10	1233.5884	617.2978	1215.5648	608.2861	1215.5778	608.2926	K	309.1961	155.1017	291.1725	146.0899			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IVIDMLDYMKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G73400.1

Score	Mr(calc)	Delta	Sequence
22.4	1410.6809	-0.0041	IVIDMLDYMKR
2.3	1410.6801	-0.0032	VTGGSLEVDYKTK
1.7	1410.6780	-0.0012	LPLRQTGSMFAR
1.5	1410.6809	-0.0041	IAAAMVGLGATFMK
1.1	1410.6773	-0.0005	HNRFGLQFSRK

AT1G73620.1

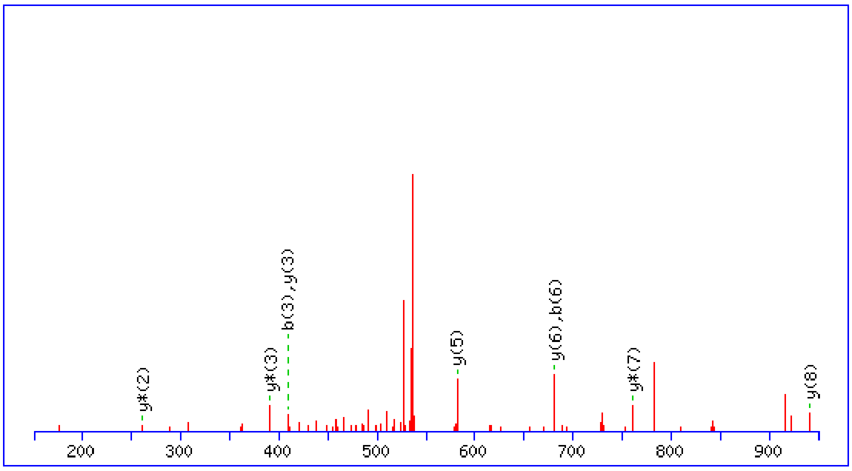
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPVGLQVR**
Found in **AT1G73620.1** in **TAIR_Arabidopsis**, Symbols: | thaumatin-like protein, putative / pathogenesis-related protein, putative | chr1:27685093-27686615 FORWARD

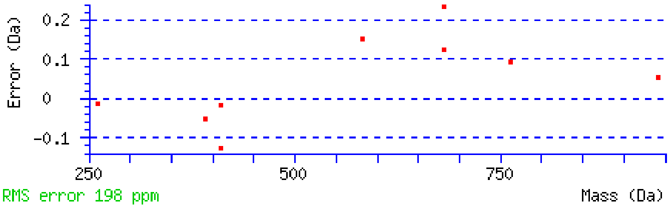
Match to Query 2859: 1088.488256 from(545.251404,2+) index(2371)
Title: Elution from: 28.759 to 28.759 scan no 3099 cid35.00 polarity:+
Data file D1d-1_1.mgf

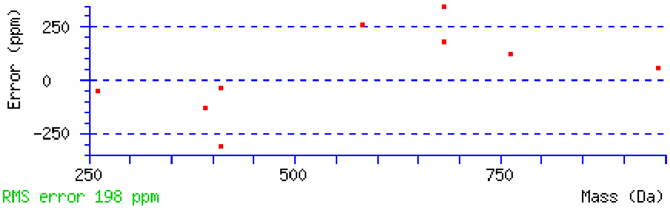
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1088.4899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.039
Matches : 9/72 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	149.0397	75.0235			M					9
2	311.0644	156.0359			C	***941.4648***	471.2360	923.4412	462.2242	8
3	**409.1142**	205.0608			P	779.4400	390.2237	761.4165	381.2119	7
4	509.1797	255.0935			V	***681.3902***	341.1988	663.3667	332.1870	6
5	567.1982	284.1027			G	***581.3248***	291.1660	563.3012	282.1542	5
6	**681.2793**	341.1433			L	523.3063	262.1568	505.2827	253.1450	4
7	811.3319	406.1696	793.3083	397.1578	Q	***409.2252***	205.1162	391.2016	196.1044	3
8	911.3974	456.2023	893.3738	447.1905	V	279.1725	140.0899	261.1490	131.0781	2
9					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of MCPVGLQVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G73620.1

Score	Mr(calc)	Delta	Sequence
23.3	1088.4899	-0.0016	MCPVGLQVR
13.2	1088.4872	0.0010	MAMAELSTPK
8.5	1088.4890	-0.0008	REEQKEEK
8.4	1088.4890	-0.0008	DKKSNGPDSK
8.2	1088.4890	-0.0008	NEENGEKKK
7.3	1088.4913	-0.0030	QEFADTLPR
7.0	1088.4872	0.0010	ETVMLTPCK
6.3	1088.4872	0.0010	MDGDVAMVLK
5.2	1088.4913	-0.0030	KNLDSWDAK
4.8	1088.4864	0.0019	DLESLESASK

Mascot: http://www.matrixscience.com/

AT1G74030.1

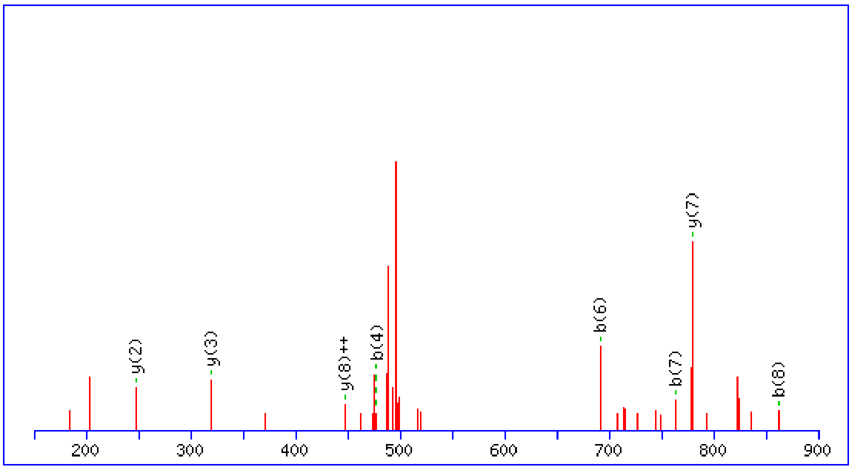
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NINELVAPK**
Found in **AT1G74030.1** in **TAIR_Arabidopsis**, Symbols: | enolase, putative | chr1:27843126-27845562 REVERSE

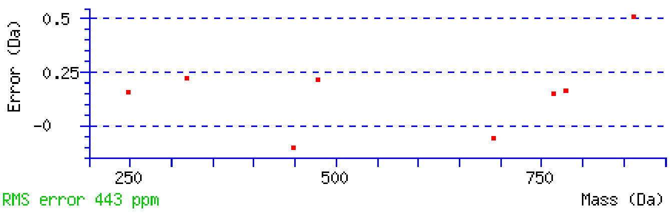
Match to Query 2745: 1008.524234 from(505.269393,2+) index(3185)
Title: Elution from: 31.824 to 31.824 scan no 3965 cid35.00 polarity:+
Data file D12h-1_1.mgf

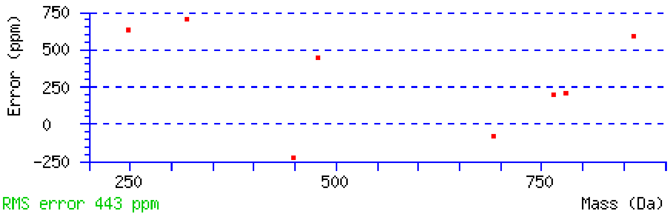
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1008.5248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.033
Matches : 8/80 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	231.1254	116.0663	213.1018	107.0545			I	893.4951	447.2512	875.4715	438.2394	875.4845	438.2459	8
3	347.1624	174.0848	329.1388	165.0730			N	***779.4140***	390.2106	761.3904	381.1988	761.4034	381.2054	7
4	***477.2020***	239.1046	459.1784	230.0928	459.1914	230.0994	E	663.3770	332.1921	645.3534	323.1803	645.3664	323.1869	6
5	591.2831	296.1452	573.2595	287.1334	573.2725	287.1399	L	533.3374	267.1723	515.3138	258.1605			5
6	***691.3485***	346.1779	673.3250	337.1661	673.3380	337.1726	V	419.2563	210.1318	401.2327	201.1200			4
7	***763.3827***	382.1950	745.3591	373.1832	745.3721	373.1897	A	***319.1908***	160.0990	301.1672	151.0873			3
8	***861.4325***	431.2199	843.4089	422.2081	843.4219	422.2146	P	***247.1567***	124.0820	229.1331	115.0702			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NINELVAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.2	1008.5248	-0.0006	NINELVAPK

AT1G74030.1

6.4	1008.5248	-0.0006	VAQAEALAPK
2.5	1008.5248	-0.0006	SGLTGLPQPK

Mascot: http://www.matrixscience.com/

AT1G74050.1

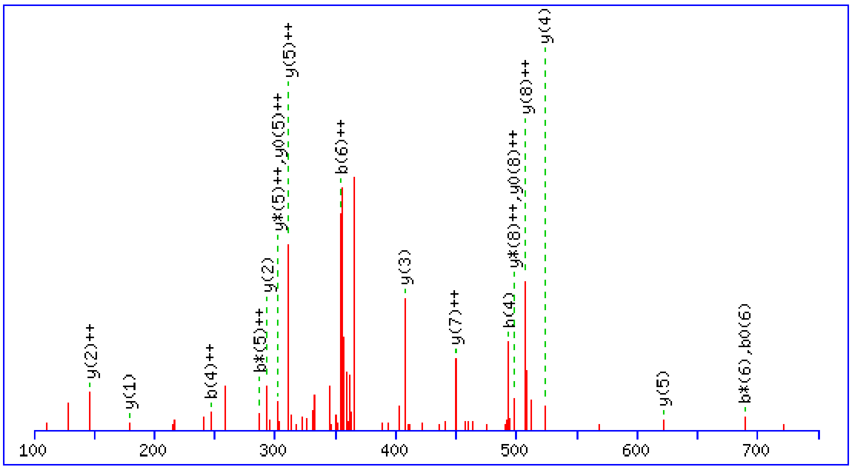
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNRNPDLIR**
Found in **AT1G74050.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L6 (RPL6C) | chr1:27850917-27852341 REVERSE

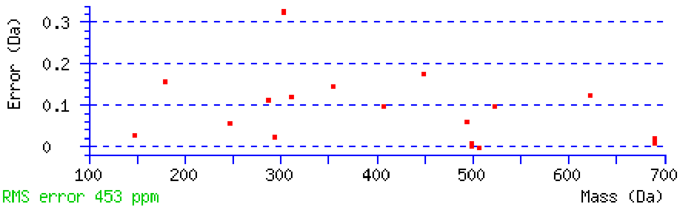
Match to Query 3005: 1112.565465 from(371.862431,3+) index(619)
Title: Elution from: 12.369 to 12.369 scan no 946 cid35.00 polarity:+
Data file D1d-2_3.mgf

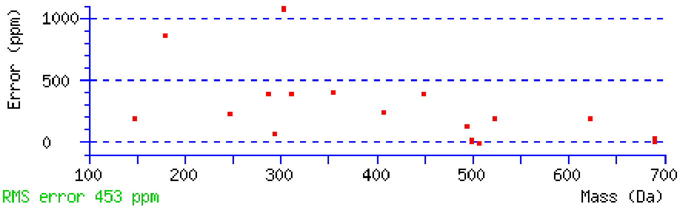
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1112.5645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.004
Matches : 19/78 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400					V							9
2	217.1097	109.0585	199.0861	100.0467			N	1013.5063	507.2568	995.4827	498.2450	995.4957	498.2515	8
3	377.1990	189.1031	359.1754	180.0913			R	897.4693	449.2383	879.4457	440.2265	879.4587	440.2330	7
4	493.2360	**247.1216**	475.2124	238.1098			N	737.3801	369.1937	719.3565	360.1819	719.3695	360.1884	6
5	591.2858	296.1465	573.2622	287.1347			P	***621.3431***	311.1752	603.3195	302.1634	603.3325	302.1699	5
6	707.3097	**354.1585**	689.2862	345.1467	689.2992	345.1532	D	***523.2933***	262.1503	505.2697	253.1385	505.2827	253.1450	4
7	821.3908	411.1991	803.3673	402.1873	803.3803	402.1938	L	***407.2693***	204.1383	389.2457	195.1265			3
8	935.4719	468.2396	917.4484	459.2278	917.4614	459.2343	I	***293.1882***	147.0977	275.1646	138.0859			2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VNRNPDLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.0	1112.5645	0.0010	VNRNPDLIR

AT1G74050.1

0.1	1112.5647	0.0007	EVMELIELK

AT1G74060.1

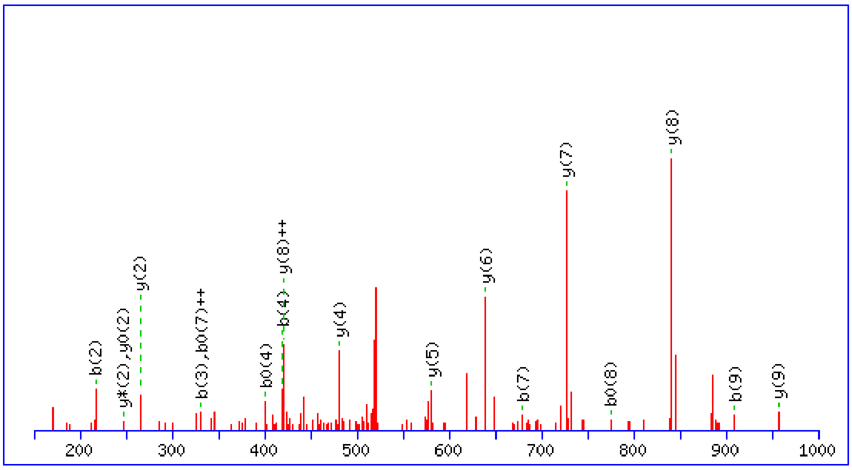
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDISGVTLDK**
Found in **AT1G74060.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L6 (RPL6B) | chr1:27853694-27854960 REVERSE

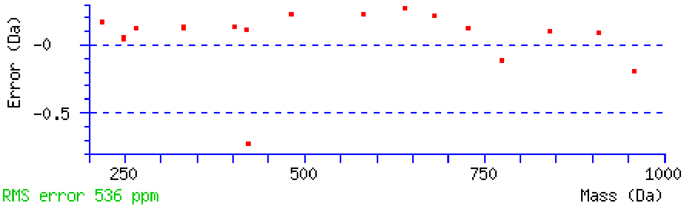
Match to Query 2994: 1056.530752 from(529.272652,2+) index(4544)
Title: Elution from: 43.142 to 43.142 scan no 5741 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

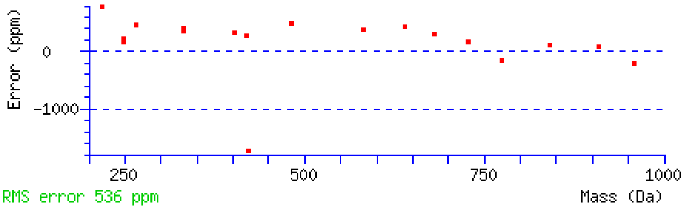


Monoisotopic mass of neutral peptide Mr(calc): 1056.5329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00011
Matches : 18/86 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							10
2	***217.0967***	109.0520	199.0861	100.0467	D	***957.4748***	479.2410	939.4512	470.2292	939.4642	470.2357	9
3	***331.1778***	166.0925	313.1672	157.0873	I	***841.4508***	421.2290	823.4272	412.2172	823.4402	412.2237	8
4	***419.2069***	210.1071	401.1963	201.1018	S	***727.3697***	364.1885	709.3461	355.1767	709.3591	355.1832	7
5	477.2254	239.1163	459.2148	230.1110	G	***639.3406***	320.1739	621.3170	311.1622	621.3300	311.1687	6
6	577.2908	289.1490	559.2802	280.1438	V	***581.3221***	291.1647	563.2985	282.1529	563.3115	282.1594	5
7	***679.3355***	340.1714	661.3250	331.1661	T	***481.2567***	241.1320	463.2331	232.1202	463.2461	232.1267	4
8	793.4166	397.2120	775.4061	388.2067	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
9	***909.4406***	455.2239	891.4300	446.2187	D	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	2
10					K	149.1069	75.0571	131.0833	66.0453			1



RMS error 536 ppm



RMS error 536 ppm

NCBI **BLAST** search of VDISGVTLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G74060.1

47.0	1056.5329	-0.0021	VDISGVTLDK
13.9	1056.5282	0.0026	TIISDMLPR
8.9	1056.5329	-0.0021	VVETEKVDK
1.4	1056.5329	-0.0022	DVSLLISDGK
0.4	1056.5329	-0.0022	VITIPSSSDK
0.2	1056.5329	-0.0022	DLVSLEAATK

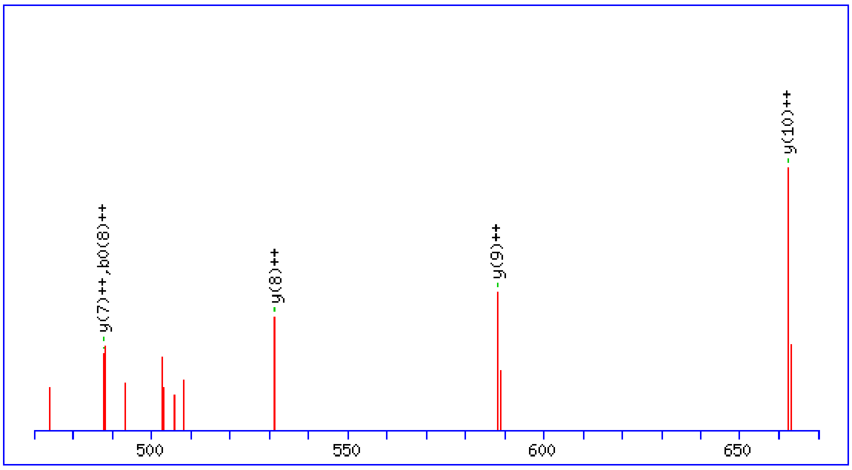
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTFISMWTFLHK**
Found in **AT1G74100.1** in **TAIR_Arabidopsis**, Symbols: | sulfotransferase family protein | chr1:27868150-27869166 REVERSE

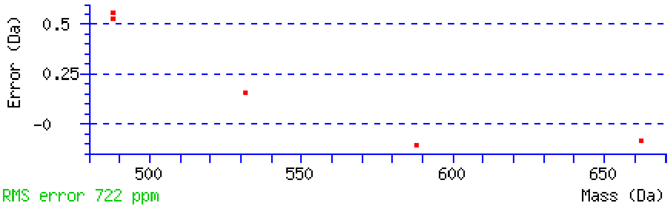
Match to Query 6576: 1540.698285 from(514.573371,3+) index(10271)
Title: Elution from: 95.543 to 95.543 scan no 14463 cid35.00 polarity:+
Data file D6h-3_2.mgf

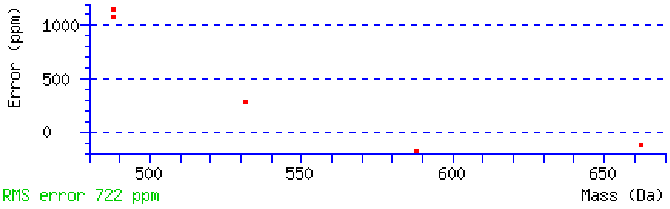
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 470 to 670 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1540.6961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0092
Matches : 5/102 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							12
2	219.0760	110.0416	201.0654	101.0363	T	1425.6794	713.3433	1407.6558	704.3315	1407.6688	704.3380	11
3	367.1414	184.0743	349.1309	175.0691	F	1323.6347	662.3210	1305.6111	653.3092	1305.6241	653.3157	10
4	481.2225	241.1149	463.2120	232.1096	I	1175.5692	588.2882	1157.5456	579.2765	1157.5587	579.2830	9
5	569.2516	285.1294	551.2410	276.1241	S	1061.4881	531.2477	1043.4645	522.2359	1043.4776	522.2424	8
6	701.2891	351.1482	683.2785	342.1429	M	973.4591	487.2332	955.4355	478.2214	955.4485	478.2279	7
7	889.3625	445.1849	871.3519	436.1796	W	841.4215	421.2144	823.3980	412.2026	823.4110	412.2091	6
8	991.4072	496.2072	973.3966	487.2020	T	653.3482	327.1777	635.3246	318.1659	635.3376	318.1724	5
9	1139.4726	570.2400	1121.4621	561.2347	F	551.3034	276.1554	533.2799	267.1436			4
10	1253.5537	627.2805	1235.5432	618.2752	L	403.2380	202.1226	385.2144	193.1108			3
11	1393.6038	697.3055	1375.5932	688.3002	H	289.1569	145.0821	271.1333	136.0703			2
12					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DTFISMWTFLHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G74100.1

Score	Mr(calc)	Delta	Sequence
30.6	1540.6961	0.0022	DTFISMWTFLHK
12.6	1540.6938	0.0045	KSMEEDLFWAIR
8.2	1540.6950	0.0033	CTVDSLSIRPTMK
5.8	1540.6972	0.0011	LNALLDVCMGFQK
4.1	1540.6950	0.0033	MKSLLCLESGDVR
3.2	1540.6941	0.0042	KSGSESEEKASVSAK
2.7	1540.6990	-0.0007	DFQDRITGNIQSK
2.7	1540.7019	-0.0037	ELGIMVVSDEVYR
2.7	1540.6987	-0.0005	LAFHSCVYAIWR
2.6	1540.6950	0.0033	SKANQMASALDMLK

Mascot: http://www.matrixscience.com/

AT1G74230.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFVGGISYSTDEFGLR**
Found in **AT1G74230.1** in **TAIR_Arabidopsis**, Symbols: GR-RBP5 | GR-RBP5 (glycine-rich RNA-binding protein 5); RNA binding | chr1:27919007-27920518 FORWARD

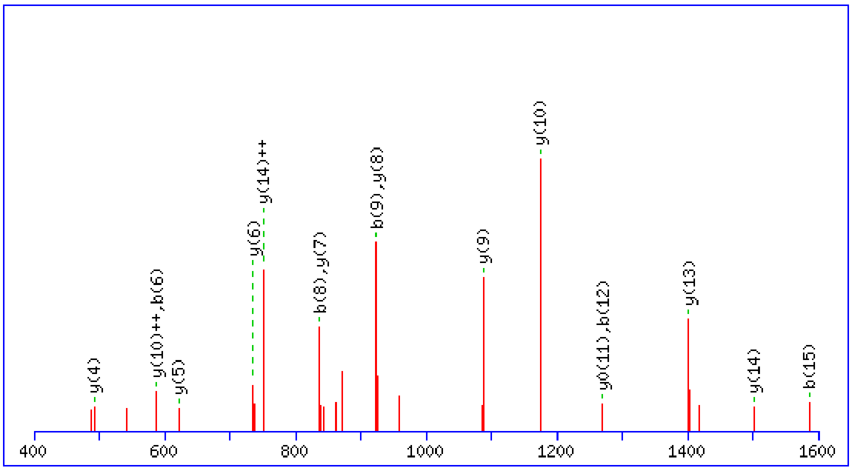
Match to Query 8519: 1759.880228 from(880.947390,2+) index(9319)
Title: Elution from: 83.690 to 83.690 scan no 12612 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

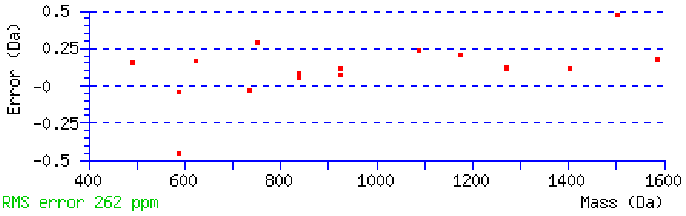
Show Y-axis ☐

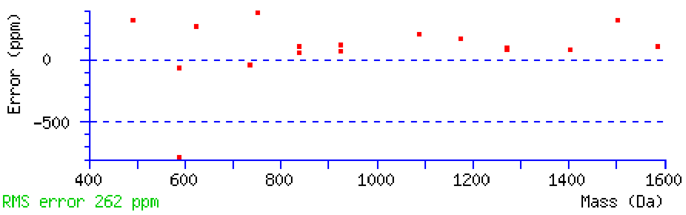


Monoisotopic mass of neutral peptide Mr(calc): 1759.8781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.1e-007
Matches : 17/130 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							16
2	261.1598	131.0835			F	1647.8013	824.4043	1630.7748	815.8910	1629.7907	815.3990	15
3	360.2282	180.6177			V	***1500.7329***	750.8701	1483.7064	742.3568	1482.7223	741.8648	14
4	417.2496	209.1285			G	***1401.6645***	701.3359	1384.6379	692.8226	1383.6539	692.3306	13
5	474.2711	237.6392			G	1344.6430	672.8251	1327.6165	664.3119	1326.6325	663.8199	12
6	**587.3552**	294.1812			I	1287.6216	644.3144	1270.5950	635.8011	1269.6110	635.3091	11
7	674.3872	337.6972	656.3766	328.6919	S	***1174.5375***	587.7724	1157.5109	579.2591	1156.5269	578.7671	10
8	**837.4505**	419.2289	819.4400	410.2236	Y	***1087.5055***	544.2564	1070.4789	535.7431	1069.4949	535.2511	9
9	**924.4825**	462.7449	906.4720	453.7396	S	***924.4421***	462.7247	907.4156	454.2114	906.4316	453.7194	8
10	1025.5302	513.2687	1007.5197	504.2635	T	***837.4101***	419.2087	820.3836	410.6954	819.3995	410.2034	7
11	1140.5572	570.7822	1122.5466	561.7769	D	***736.3624***	368.6849	719.3359	360.1716	718.3519	359.6796	6
12	**1269.5998**	635.3035	1251.5892	626.2982	E	***621.3355***	311.1714	604.3089	302.6581	603.3249	302.1661	5
13	1416.6682	708.8377	1398.6576	699.8324	F	***492.2929***	246.6501	475.2663	238.1368			4
14	1473.6896	737.3485	1455.6791	728.3432	G	345.2245	173.1159	328.1979	164.6026			3
15	**1586.7737**	793.8905	1568.7631	784.8852	L	288.2030	144.6051	271.1765	136.0919			2
16					R	175.1190	88.0631	158.0924	79.5498			1

AT1G74230.1





NCBI **BLAST** search of IFVGGISYSTDEFGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.2	1759.8781	0.0021	IFVGGISYSTDEFGLR
11.7	1759.8839	-0.0037	SDEPKTEETASNLVLK
10.9	1759.8790	0.0012	FLKVVDYPFCIGMR
1.8	1759.8813	-0.0010	DEITKRSSGQELNQR
0.2	1759.8828	-0.0025	WREKNIPCPLYER

Mascot: http://www.matrixscience.com/

AT1G74470.1

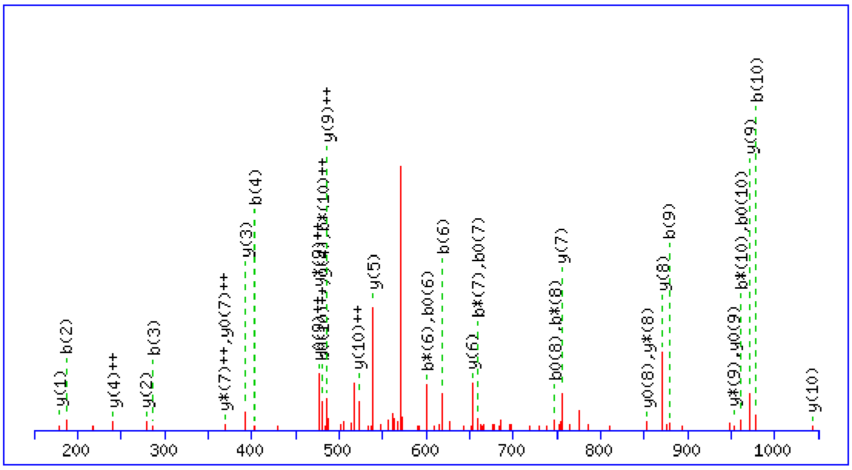
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVNTIGSLVR**
Found in **AT1G74470.1** in **TAIR_Arabidopsis**, Symbols: | geranylgeranyl reductase | chr1:27994909-27996506 FORWARD

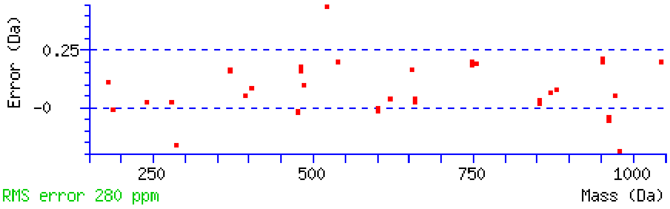
Match to Query 3592: 1156.636786 from(579.325669,2+) index(6123)
Title: Elution from: 56.436 to 56.436 scan no 7915 cid35.00 polarity:+
Data file D1d-2_1.mgf

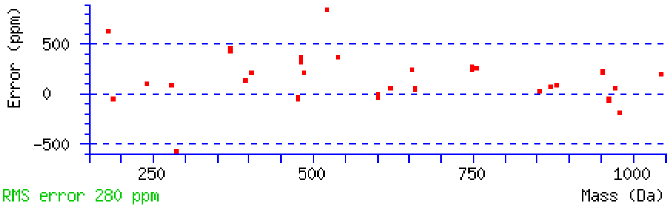
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1156.6374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 1.9e-008
Matches : 37/100 fragment ions using 42 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							11
2	**187.1225**	94.0649					A	***1043.5636***	522.2854	1025.5400	513.2737	1025.5530	513.2802	10
3	**287.1880**	144.0976					V	***971.5295***	486.2684	953.5059	477.2566	953.5189	477.2631	9
4	**403.2250**	202.1161	385.2014	193.1043			N	***871.4640***	436.2356	853.4404	427.2239	853.4534	427.2304	8
5	505.2697	253.1385	487.2461	244.1267	487.2591	244.1332	T	***755.4270***	378.2171	737.4034	369.2054	737.4164	369.2119	7
6	**619.3508**	310.1790	601.3272	301.1672	601.3402	301.1737	I	***653.3823***	327.1948	635.3587	318.1830	635.3717	318.1895	6
7	677.3693	339.1883	659.3457	330.1765	659.3587	330.1830	G	***539.3012***	270.1542	521.2776	261.1424	521.2906	261.1490	5
8	765.3983	383.2028	747.3748	374.1910	747.3878	374.1975	S	***481.2827***	241.1450	463.2591	232.1332	463.2721	232.1397	4
9	**879.4794**	440.2434	861.4559	431.2316	861.4689	431.2381	L	***393.2536***	197.1305	375.2301	188.1187			3
10	**979.5449**	490.2761	961.5213	481.2643	961.5343	481.2708	V	***279.1725***	140.0899	261.1490	131.0781			2
11							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LAVNTIGSLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G74470.1

Score	Mr(calc)	Delta	Sequence
85.5	1156.6374	-0.0006	LAVNTIGSLVR
8.1	1156.6374	-0.0006	LADGTLVAVKR
5.9	1156.6374	-0.0006	LGIIDNKTLR
5.3	1156.6347	0.0020	ALITKLTEEK
3.9	1156.6374	-0.0006	LALLGNNAKTK
3.9	1156.6401	-0.0033	AARGPVKVSVR
0.6	1156.6374	-0.0006	LNGLSLEKLR
0.5	1156.6374	-0.0006	LTGKRPTIEK
0.3	1156.6397	-0.0029	ALGPLLEKFR
0.2	1156.6374	-0.0006	ATIIIQSQIR

Mascot: http://www.matrixscience.com/

AT1G74560.3

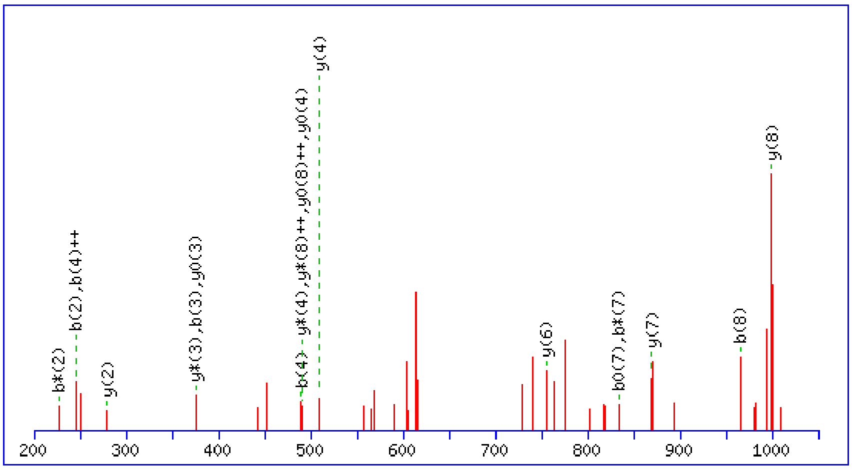
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQEIQDDLEK**
Found in **AT1G74560.3** in **TAIR_Arabidopsis**, Symbols: NRP1 | NRP1 (NAP1-RELATED PROTEIN 1) | chr1:28021424-28023561 REVERSE

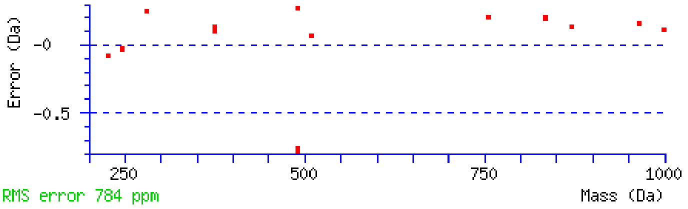
Match to Query 4320: 1242.576090 from(622.295321,2+) index(3299)
Title: Elution from: 32.243 to 32.243 scan no 4096 cid35.00 polarity:+
Data file C7-1_2.mgf

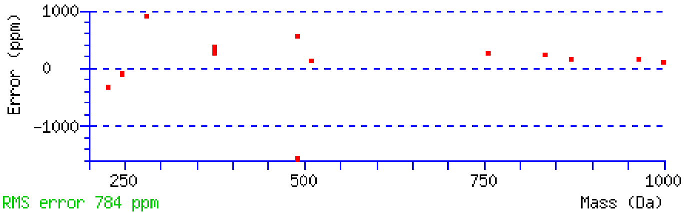
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1242.5754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24  Expect: 0.02
Matches : 19/100 fragment ions using 25 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							10
2	**245.1410**	123.0741	227.1174	114.0624			Q	1129.5016	565.2544	1111.4780	556.2426	1111.4910	556.2491	9
3	**375.1806**	188.0940	357.1571	179.0822	357.1701	179.0887	E	***999.4489***	500.2281	981.4253	491.2163	981.4384	491.2228	8
4	**489.2617**	245.1345	471.2382	236.1227	471.2512	236.1292	I	***869.4093***	435.2083	851.3857	426.1965	851.3987	426.2030	7
5	619.3144	310.1608	601.2908	301.1490	601.3038	301.1556	Q	***755.3282***	378.1677	737.3046	369.1559	737.3176	369.1625	6
6	735.3384	368.1728	717.3148	359.1610	717.3278	359.1675	D	625.2756	313.1414	607.2520	304.1296	607.2650	304.1361	5
7	851.3624	426.1848	833.3388	417.1730	833.3518	417.1795	D	***509.2516***	255.1294	491.2280	246.1176	491.2410	246.1241	4
8	**965.4435**	483.2254	947.4199	474.2136	947.4329	474.2201	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
9	1095.4831	548.2452	1077.4595	539.2334	1077.4725	539.2399	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LQEIQDDLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G74560.3

24.1	1242.5754	0.0007	LQEIQDDLEK
10.9	1242.5781	-0.0020	IEKEHESVTR
2.3	1242.5781	-0.0020	QIEPKEQNGGK

Mascot: http://www.matrixscience.com/

AT1G74690.1

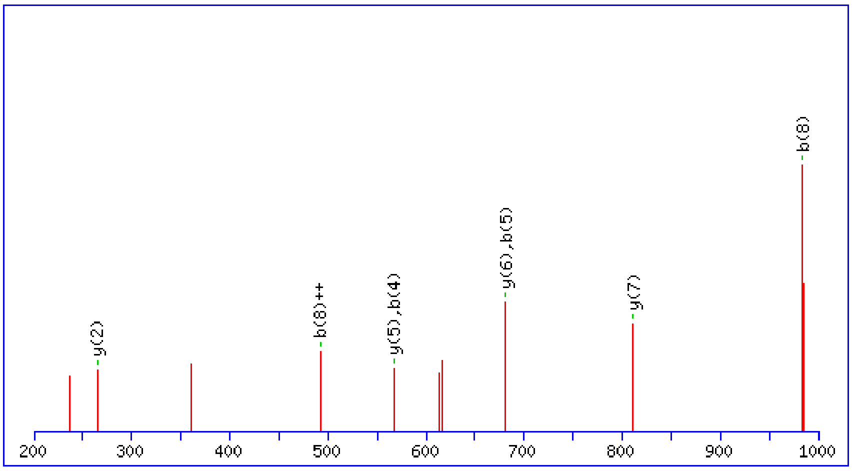
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CRLQLLQGNK**
Found in **AT1G74690.1** in **TAIR_Arabidopsis**, Symbols: IQD31 | IQD31 (IQ-domain 31); calmodulin binding | chr1:28065159-28067585 REVERSE

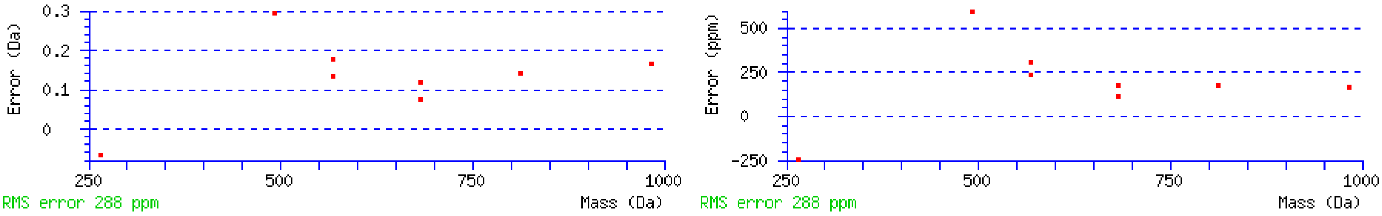
Match to Query 4432: 1246.621146 from(624.317849,2+) index(8588)
Title: Elution from: 76.212 to 76.212 scan no 11403 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.6176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.03
Matches : 8/70 fragment ions using 10 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	163.0320	82.0196			C					10
2	323.1212	162.0643	305.0977	153.0525	R	1085.6002	543.3037	1067.5766	534.2920	9
3	437.2023	219.1048	419.1788	210.0930	L	925.5110	463.2591	907.4874	454.2473	8
4	**567.2550**	284.1311	549.2314	275.1193	Q	***811.4299***	406.2186	793.4063	397.2068	7
5	**681.3361**	341.1717	663.3125	332.1599	L	***681.3772***	341.1922	663.3536	332.1805	6
6	795.4172	398.2122	777.3936	389.2004	L	***567.2961***	284.1517	549.2725	275.1399	5
7	925.4698	463.2386	907.4463	454.2268	Q	453.2150	227.1111	435.1914	218.0994	4
8	**983.4883**	492.2478	965.4648	483.2360	G	323.1624	162.0848	305.1388	153.0730	3
9	1099.5253	550.2663	1081.5017	541.2545	N	***265.1439***	133.0756	247.1203	124.0638	2
10					K	149.1069	75.0571	131.0833	66.0453	1



NCBI **BLAST** search of CRLQLLQGNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G74690.1

Score	Mr(calc)	Delta	Sequence
24.7	1246.6176	0.0035	CRLQLLQGNK
16.5	1246.6219	-0.0008	FVDLVTEAVNK
16.5	1246.6224	-0.0013	NVNKKSEAVNK
12.2	1246.6176	0.0035	RICAGIALAER
11.8	1246.6246	-0.0035	EIDSARKWVK
3.7	1246.6206	0.0005	ILMKNMEINK
3.2	1246.6219	-0.0008	ILLQNYLDDK
0.4	1246.6197	0.0014	ESVTSIVGSNIK
0.4	1246.6206	0.0005	MVNEKKMLPK

Mascot: http://www.matrixscience.com/

AT1G74970.1

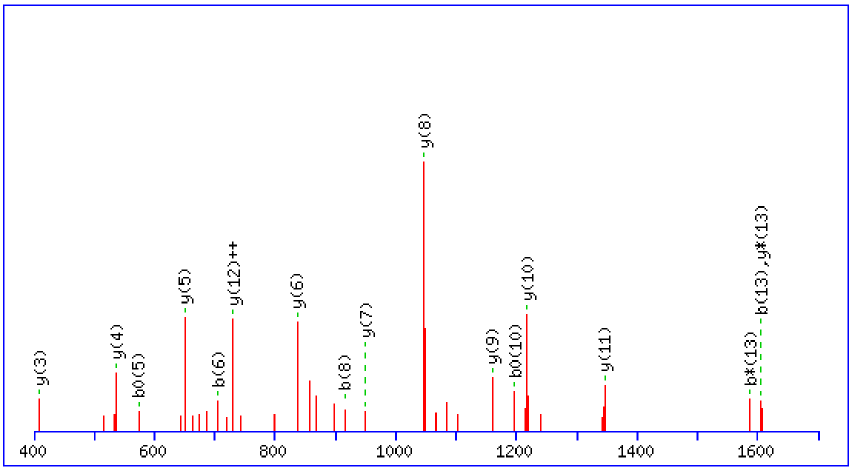
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYLQGNPLWLQYVK**
Found in **AT1G74970.1** in **TAIR_Arabidopsis**, Symbols: TWN3, RPS9 | RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome | chr1:28161422-28162863 REVERSE

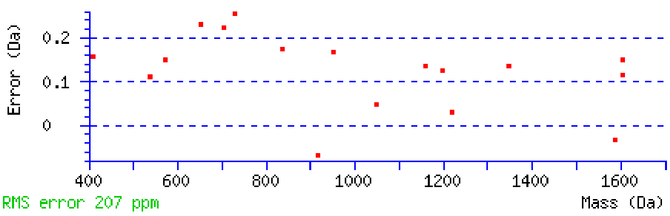
Match to Query 7872: 1749.906778 from(875.960665,2+) index(8960)
Title: Elution from: 85.363 to 85.363 scan no 12433 cid35.00 polarity:+
Data file D1d-1-2.mgf

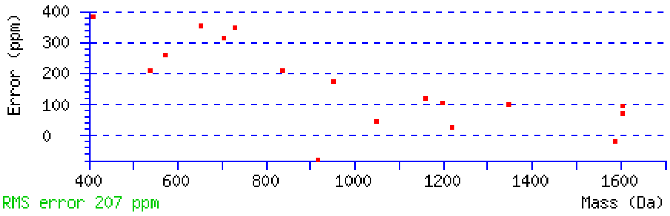
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1749.9090
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 2.1e-007
Matches : 17/124 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	130.0499	65.5286			112.0393	56.5233	E					14
2	293.1132	147.0602			275.1026	138.0550	Y	1621.8737	811.4405	1604.8471	802.9272	13
3	406.1973	203.6023			388.1867	194.5970	L	1458.8104	729.9088	1441.7838	721.3955	12
4	534.2558	267.6316	517.2293	259.1183	516.2453	258.6263	Q	***1345.7263***	673.3668	1328.6998	664.8535	11
5	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	G	***1217.6677***	609.3375	1200.6412	600.8242	10
6	**705.3202**	353.1638	688.2937	344.6505	687.3097	344.1585	N	***1160.6463***	580.8268	1143.6197	572.3135	9
7	802.3730	401.6901	785.3464	393.1769	784.3624	392.6849	P	***1046.6033***	523.8053	1029.5768	515.2920	8
8	**915.4571**	458.2322	898.4305	449.7189	897.4465	449.2269	L	***949.5506***	475.2789	932.5240	466.7656	7
9	1101.5364	551.2718	1084.5098	542.7585	1083.5258	542.2665	W	***836.4665***	418.7369	819.4400	410.2236	6
10	1214.6204	607.8139	1197.5939	599.3006	1196.6099	598.8086	L	***650.3872***	325.6972	633.3606	317.1840	5
11	1342.6790	671.8431	1325.6525	663.3299	1324.6684	662.8379	Q	***537.3031***	269.1552	520.2766	260.6419	4
12	1505.7423	753.3748	1488.7158	744.8615	1487.7318	744.3695	Y	***409.2445***	205.1259	392.2180	196.6126	3
13	**1604.8108**	802.9090	1587.7842	794.3957	1586.8002	793.9037	V	246.1812	123.5942	229.1547	115.0810	2
14							K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of EYLQGNPLWLQYVK

AT1G74970.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.3	1749.9090	-0.0022	EYLQGNPLWLQYVK
0.4	1749.9043	0.0025	TLSSGDAERMLRSSLK

Mascot: http://www.matrixscience.com/

AT1G75330.1

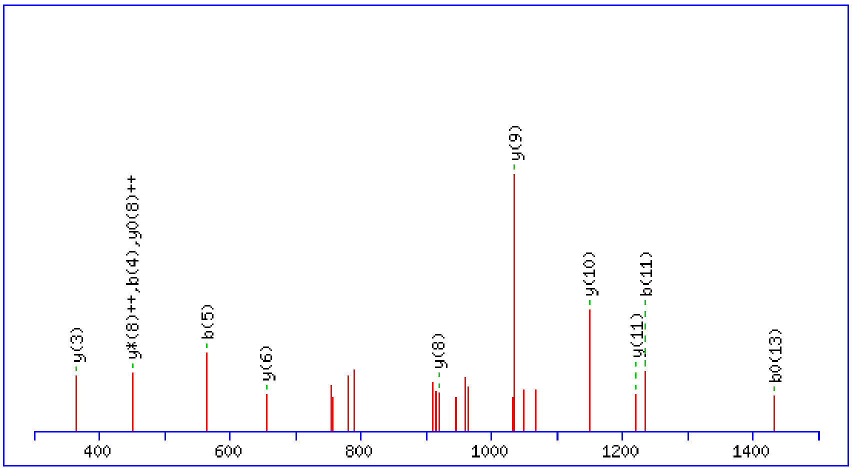
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFLAIDDFDTATIK**
Found in **AT1G75330.1** in **TAIR_Arabidopsis**, Symbols: OTC | OTC (ORNITHINE CARBAMOYLTRANSFERASE); amino acid binding / carboxyl- or carbamoyltransferase | chr1:28270118-28272044 REVERSE

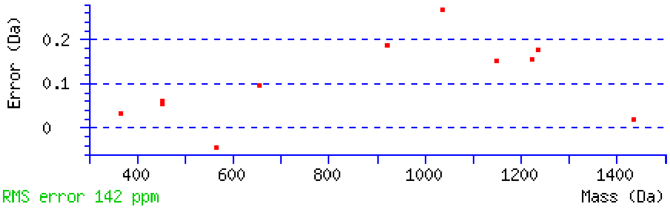
Match to Query 7197: 1598.723406 from(800.368979,2+) index(9786)
Title: Elution from: 90.367 to 90.367 scan no 13594 cid35.00 polarity:+
Data file D6h-1_2.mgf

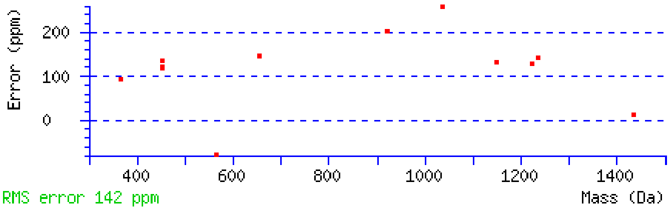
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1598.7274
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0021
Matches : 12/126 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							14
2	265.0967	133.0520	247.0861	124.0467	F	1483.7107	742.3590	1465.6871	733.3472	1465.7002	733.3537	13
3	379.1778	190.0925	361.1672	181.0873	L	1335.6453	668.3263	1317.6217	659.3145	1317.6347	659.3210	12
4	**451.2120**	226.1096	433.2014	217.1043	A	***1221.5642***	611.2857	1203.5406	602.2739	1203.5536	602.2804	11
5	**565.2930**	283.1502	547.2825	274.1449	I	***1149.5300***	575.2687	1131.5064	566.2569	1131.5195	566.2634	10
6	681.3170	341.1622	663.3065	332.1569	D	***1035.4489***	518.2281	1017.4253	509.2163	1017.4384	509.2228	9
7	797.3410	399.1741	779.3304	390.1689	D	***919.4250***	460.2161	901.4014	451.2043	901.4144	451.2108	8
8	945.4065	473.2069	927.3959	464.2016	F	803.4010	402.2041	785.3774	393.1923	785.3904	393.1988	7
9	1061.4304	531.2189	1043.4199	522.2136	D	***655.3355***	328.1714	637.3119	319.1596	637.3250	319.1661	6
10	1163.4751	582.2412	1145.4646	573.2359	T	539.3115	270.1594	521.2880	261.1476	521.3010	261.1541	5
11	**1235.5093**	618.2583	1217.4987	609.2530	A	437.2668	219.1371	419.2433	210.1253	419.2563	210.1318	4
12	1337.5540	669.2806	1319.5434	660.2754	T	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
13	1451.6351	726.3212	1433.6245	717.3159	I	263.1880	132.0976	245.1644	123.0858			2
14					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DFLAIDDFDTATIK

AT1G75330.1
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.3	1598.7274	-0.0040	DFLAIDDFDTATIK
11.0	1598.7252	-0.0018	TSEDYGSITAIAIDK
5.2	1598.7209	0.0025	TDTEIQRSLLCSR
1.8	1598.7280	-0.0046	LAVCGFNVYHKNR
1.2	1598.7279	-0.0045	SDISSVRNYSDLPK
1.1	1598.7254	-0.0020	FVAGGLAGHLYMNSK
0.6	1598.7218	0.0017	MGRKPCCDKIGLK
0.1	1598.7204	0.0030	DLQTSIDYACGVLK

AT1G75950.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEAVEGAATSDDDLK**
Found in **AT1G75950.1** in **TAIR_Arabidopsis**, Symbols: ASK1, ATSKP1, SKP1A, UIP1, SKP1 | SKP1 (ARABIDOPSIS SKP1 HOMOLOGUE); ubiquitin-protein ligase | chr1:28520376-28521115 FORWARD

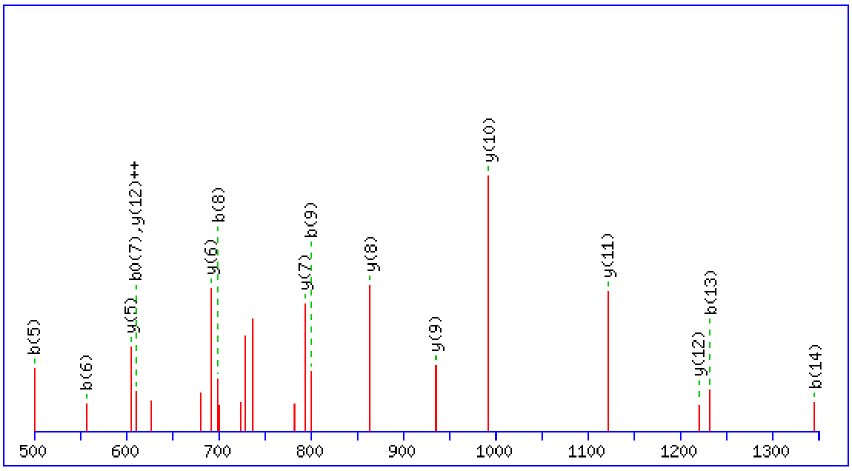
Match to Query 6676: 1490.673204 from(746.343878,2+) index(1944)
Title: Elution from: 22.970 to 22.970 scan no 2513 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1350 Da Full range

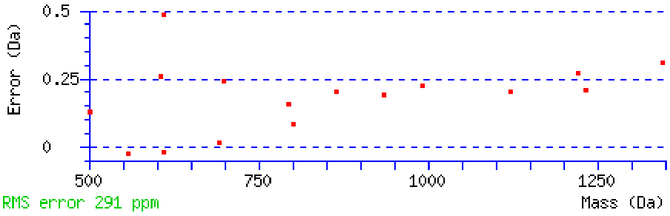
Label all possible matches ○ Label matches used for scoring ●

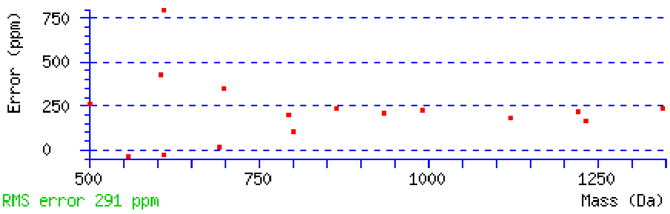
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1490.6736
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 9.7e-010
Matches : 16/134 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							15
2	201.0870	101.0471	183.0764	92.0418	E	1420.6438	710.8255	1403.6173	702.3123	1402.6332	701.8203	14
3	272.1241	136.5657	254.1135	127.5604	A	1291.6012	646.3042	1274.5747	637.7910	1273.5907	637.2990	13
4	371.1925	186.0999	353.1819	177.0946	V	***1220.5641***	610.7857	1203.5376	602.2724	1202.5535	601.7804	12
5	***500.2351***	250.6212	482.2245	241.6159	E	***1121.4957***	561.2515	1104.4691	552.7382	1103.4851	552.2462	11
6	***557.2566***	279.1319	539.2460	270.1266	G	***992.4531***	496.7302	975.4265	488.2169	974.4425	487.7249	10
7	628.2937	314.6505	610.2831	305.6452	A	***935.4316***	468.2195	918.4051	459.7062	917.4211	459.2142	9
8	***699.3308***	350.1690	681.3202	341.1638	A	***864.3945***	432.7009	847.3680	424.1876	846.3840	423.6956	8
9	***800.3785***	400.6929	782.3679	391.6876	T	***793.3574***	397.1823	776.3309	388.6691	775.3468	388.1771	7
10	887.4105	444.2089	869.3999	435.2036	S	***692.3097***	346.6585	675.2832	338.1452	674.2992	337.6532	6
11	1002.4374	501.7224	984.4269	492.7171	D	***605.2777***	303.1425	588.2511	294.6292	587.2671	294.1372	5
12	1117.4644	559.2358	1099.4538	550.2305	D	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
13	***1232.4913***	616.7493	1214.4808	607.7440	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
14	***1345.5754***	673.2913	1327.5648	664.2861	L	260.1969	130.6021	243.1703	122.0888			2
15					K	147.1128	74.0600	130.0863	65.5468			1





AT1G75950.1

NCBI **BLAST** search of AEAVEGAATSDDDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.1	1490.6736	-0.0004	AEAVEGAATSDDDLK

AT1G76030.1

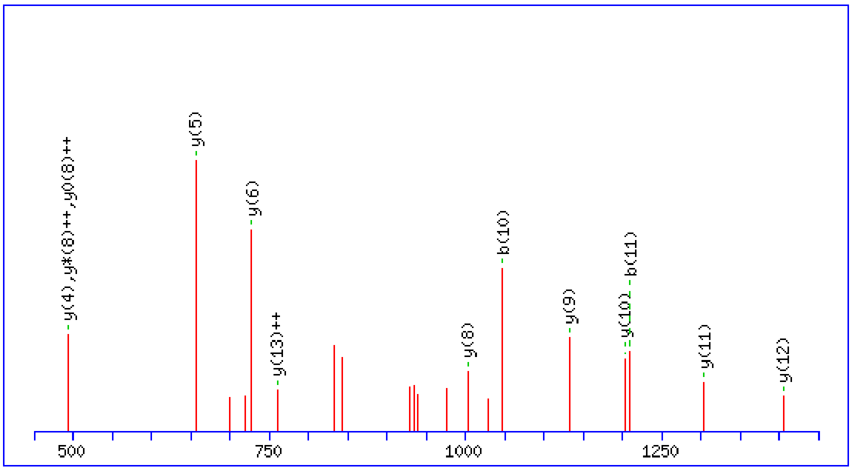
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IALTTAEYLAYECGK**
Found in **AT1G76030.1** in **TAIR_Arabidopsis**, Symbols: | (VACUOLAR ATP SYNTHASE SUBUNIT B1); hydrogen ion transporting ATP synthase, rotational mechanism | chr1:28537795-28540577 FORWARD

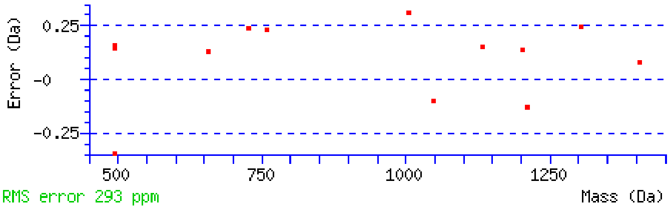
Match to Query 8107: 1701.832654 from(851.923603,2+) index(6989)
Title: Elution from: 61.715 to 61.715 scan no 9071 cid35.00 polarity:+
Data file C7-1_2.mgf

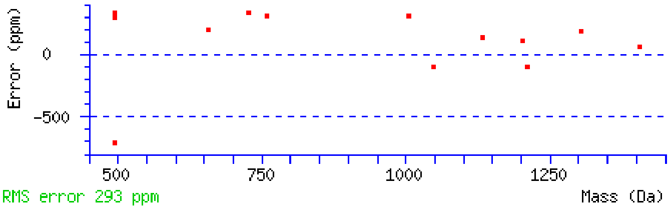
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1701.8283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 6e-007
Matches : 13/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			I							15
2	185.1285	93.0679			A	1589.7516	795.3794	1572.7250	786.8662	1571.7410	786.3742	14
3	298.2125	149.6099			L	1518.7145	759.8609	1501.6879	751.3476	1500.7039	750.8556	13
4	399.2602	200.1337	381.2496	191.1285	T	***1405.6304***	703.3188	1388.6039	694.8056	1387.6198	694.3136	12
5	500.3079	250.6576	482.2973	241.6523	T	***1304.5827***	652.7950	1287.5562	644.2817	1286.5722	643.7897	11
6	571.3450	286.1761	553.3344	277.1709	A	***1203.5351***	602.2712	1186.5085	593.7579	1185.5245	593.2659	10
7	700.3876	350.6974	682.3770	341.6921	E	***1132.4979***	566.7526	1115.4714	558.2393	1114.4874	557.7473	9
8	863.4509	432.2291	845.4403	423.2238	Y	***1003.4553***	502.2313	986.4288	493.7180	985.4448	493.2260	8
9	976.5350	488.7711	958.5244	479.7658	L	840.3920	420.6996	823.3655	412.1864	822.3815	411.6944	7
10	**1047.5721**	524.2897	1029.5615	515.2844	A	***727.3080***	364.1576	710.2814	355.6443	709.2974	355.1523	6
11	**1210.6354**	605.8213	1192.6249	596.8161	Y	***656.2708***	328.6391	639.2443	320.1258	638.2603	319.6338	5
12	1339.6780	670.3426	1321.6674	661.3374	E	***493.2075***	247.1074	476.1810	238.5941	475.1969	238.1021	4
13	1499.7087	750.3580	1481.6981	741.3527	C	364.1649	182.5861	347.1384	174.0728			3
14	1556.7301	778.8687	1538.7196	769.8634	G	204.1343	102.5708	187.1077	94.0575			2
15					K	147.1128	74.0600	130.0863	65.5468			1





AT1G76030.1

NCBI **BLAST** search of IALTTAEYLAYECGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.9	1701.8283	0.0043	IALTTAEYLAYECGK
7.8	1701.8331	-0.0004	SKEFEVIMMRNFR
7.8	1701.8331	-0.0004	SKEFEVIMMRNFR
4.4	1701.8331	-0.0004	HAIYNGACNLTLPMK

AT1G76080.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GELIGEILR**
Found in **AT1G76080.1** in **TAIR_Arabidopsis**, Symbols: ATCDSP32, CDSP32 | ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGHT-INDUCED STRESS PROTEIN OF 32 KD); thiol-disulfide exchange intermediate | chr1:28552957-28554242 REVERSE

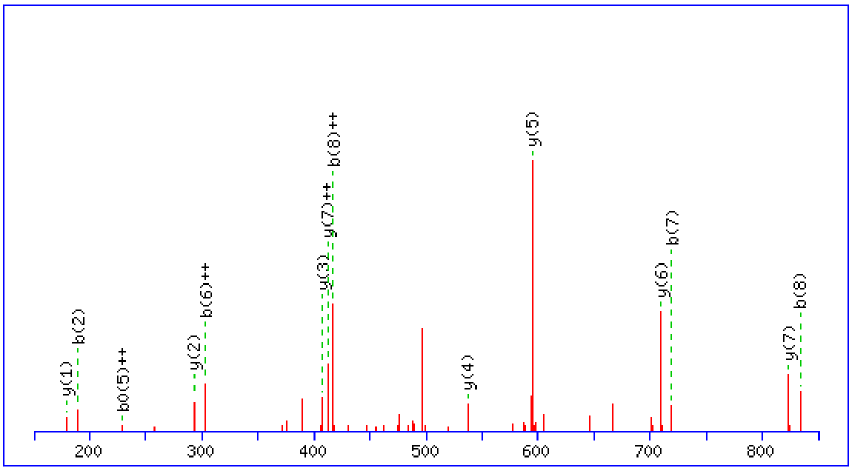
Match to Query 2564: 1010.540572 from(506.277562,2+) index(6700)
Title: Elution from: 58.218 to 58.218 scan no 8633 cid35.00 polarity:+
Data file C7-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

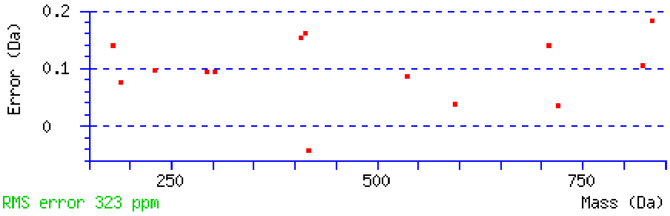
Label all possible matches ○ Label matches used for scoring ●

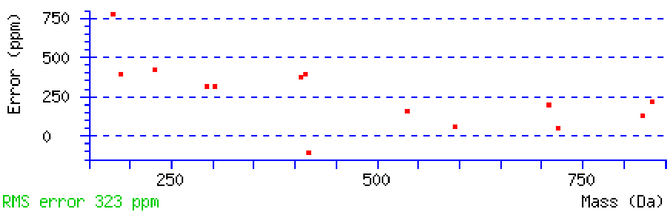
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1010.5405
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.3e-006
Matches : 16/72 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			G							9
2	**189.0654**	95.0363	171.0548	86.0311	E	953.5292	477.2683	935.5057	468.2565	935.5187	468.2630	8
3	**303.1465**	152.0769	285.1359	143.0716	L	***823.4896***	412.2484	805.4660	403.2367	805.4791	403.2432	7
4	**417.2276**	209.1174	399.2170	200.1122	I	***709.4085***	355.2079	691.3849	346.1961	691.3980	346.2026	6
5	475.2461	238.1267	457.2355	229.1214	G	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	5
6	605.2857	**303.1465**	587.2752	294.1412	E	***537.3089***	269.1581	519.2853	260.1463	519.2984	260.1528	4
7	**719.3668**	360.1871	701.3563	351.1818	I	***407.2693***	204.1383	389.2457	195.1265			3
8	**833.4479**	**417.2276**	815.4374	408.2223	L	***293.1882***	147.0977	275.1646	138.0859			2
9					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GELIGEILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G76080.1

66.6	1010.5405	0.0001	GELIGEILR
31.4	1010.5405	0.0001	ELGLAVEIR
31.4	1010.5405	0.0001	ELGLAVELR
28.6	1010.5405	0.0001	TPTLVEALR
18.2	1010.5405	0.0001	ALLDLEGLR
15.8	1010.5405	0.0001	LGEIELAVR
12.8	1010.5431	-0.0025	LQGGPKGAIR
12.4	1010.5404	0.0001	VIVGDDLLR
12.3	1010.5405	0.0001	AQVIAIQEK
12.3	1010.5405	0.0001	IANLEAQIK

AT1G76160.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISNVGLQDSLNFR**
Found in **AT1G76160.1** in **TAIR_Arabidopsis**, Symbols: SKS5 | SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase | chr1:28583105-28585914 REVERSE

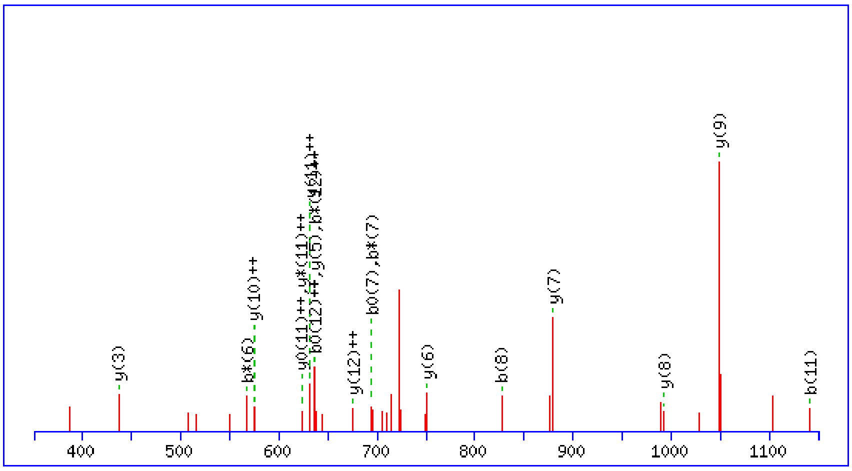
Match to Query 5831: 1461.757460 from(731.886006,2+) index(6357)
Title: Elution from: 56.273 to 56.273 scan no 8171 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1150 Da Full range

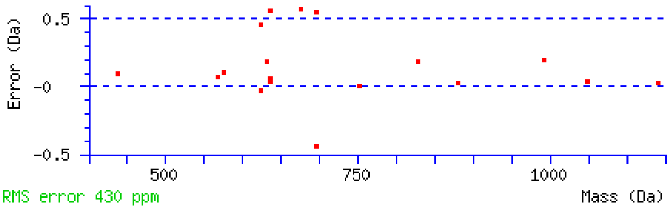
Label all possible matches ○ Label matches used for scoring ●

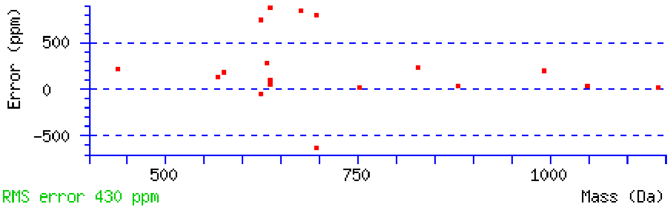
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1461.7576
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00025
Matches : 18/130 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	201.1234	101.0653			183.1128	92.0600	S	1349.6808	675.3440	1332.6543	666.8308	1331.6702	666.3388	12
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	N	1262.6488	631.8280	1245.6222	623.3148	1244.6382	622.8227	11
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	V	1148.6058	574.8066	1131.5793	566.2933	1130.5953	565.8013	10
5	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	G	***1049.5374***	525.2724	1032.5109	516.7591	1031.5269	516.2671	9
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	L	***992.5160***	496.7616	975.4894	488.2483	974.5054	487.7563	8
7	712.3988	356.7030	695.3723	348.1898	694.3882	347.6978	Q	***879.4319***	440.2196	862.4054	431.7063	861.4213	431.2143	7
8	**827.4258**	414.2165	810.3992	405.7032	809.4152	405.2112	D	***751.3733***	376.1903	734.3468	367.6770	733.3628	367.1850	6
9	914.4578	457.7325	897.4312	449.2193	896.4472	448.7272	S	***636.3464***	318.6768	619.3198	310.1636	618.3358	309.6715	5
10	1027.5418	514.2746	1010.5153	505.7613	1009.5313	505.2693	L	549.3144	275.1608	532.2878	266.6475			4
11	**1141.5848**	571.2960	1124.5582	562.7828	1123.5742	562.2907	N	***436.2303***	218.6188	419.2037	210.1055			3
12	1288.6532	644.8302	1271.6266	636.3170	1270.6426	635.8250	F	322.1874	161.5973	305.1608	153.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ISNVGLQDSLNFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G76160.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.8	1461.7576	-0.0001	ISNVGLQDSLNFR
5.2	1461.7610	-0.0035	IVTRDNGAKMDVK
2.7	1461.7610	-0.0035	TDLGRLTSPSIMR
0.2	1461.7537	0.0037	VLIEERMPVYDV

Mascot: http://www.matrixscience.com/

AT1G76180.1

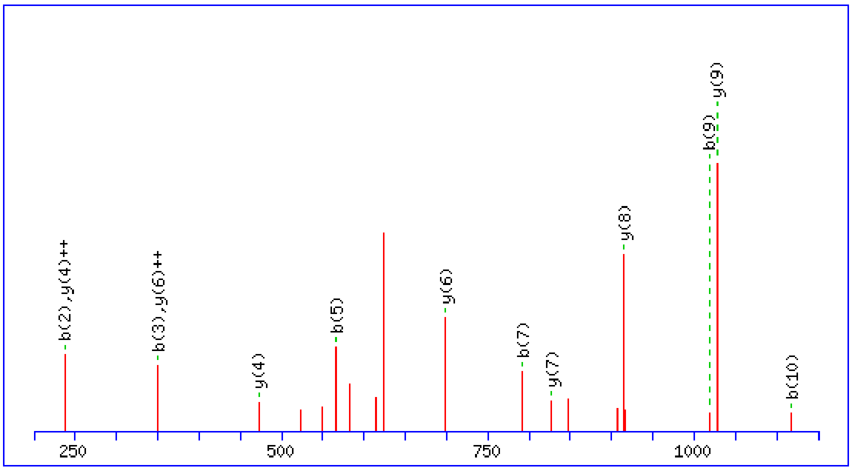
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VHISEPEPEVK**
Found in **AT1G76180.1** in **TAIR_Arabidopsis**, Symbols: ERD14 | ERD14 (EARLY RESPONSE TO DEHYDRATION 14) | chr1:28591907-28592551 REVERSE

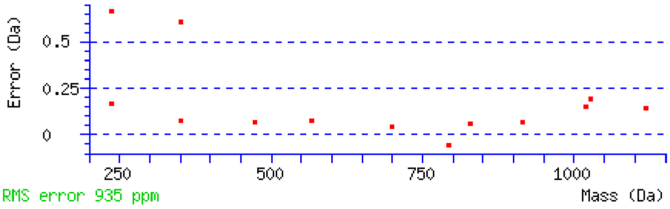
Match to Query 4571: 1262.650136 from(632.332344,2+) index(1816)
Title: Elution from: 21.438 to 21.438 scan no 2345 cid35.00 polarity:+
Data file C7-3_2.mgf

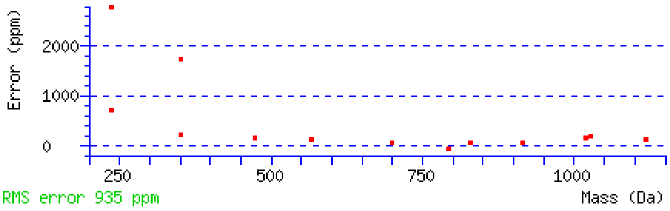
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1262.6507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 9.2e-006
Matches : 13/90 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			**V**							**11**
2	***237.1346***	119.0709			**H**	1164.5895	582.7984	1147.5630	574.2851	1146.5790	573.7931	**10**
3	***350.2187***	175.6130			**I**	***1027.5306***	514.2689	1010.5041	505.7557	1009.5201	505.2637	**9**
4	437.2507	219.1290	419.2401	210.1237	**S**	***914.4466***	457.7269	897.4200	449.2136	896.4360	448.7216	**8**
5	***566.2933***	283.6503	548.2827	274.6450	**E**	***827.4145***	414.2109	810.3880	405.6976	809.4040	405.2056	**7**
6	663.3461	332.1767	645.3355	323.1714	**P**	***698.3719***	349.6896	681.3454	341.1763	680.3614	340.6843	**6**
7	***792.3886***	396.6980	774.3781	387.6927	**E**	601.3192	301.1632	584.2926	292.6499	583.3086	292.1579	**5**
8	889.4414	445.2243	871.4308	436.2191	**P**	***472.2766***	236.6419	455.2500	228.1287	454.2660	227.6366	**4**
9	***1018.4840***	509.7456	1000.4734	500.7404	**E**	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
10	***1117.5524***	559.2798	1099.5419	550.2746	**V**	246.1812	123.5942	229.1547	115.0810			**2**
11					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VHISEPEPEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G76180.1

Score	Mr(calc)	Delta	Sequence
56.5	1262.6507	-0.0005	VHISEPEPEVK
3.8	1262.6507	-0.0005	YGLAGDNVLDVK
2.4	1262.6466	0.0035	KSQQKEDSVSK
0.4	1262.6481	0.0020	YWPLVMDIAR
0.1	1262.6475	0.0026	RMMLTSGQPVK
0.1	1262.6475	0.0026	RMMLTSGQPVK

AT1G76680.1

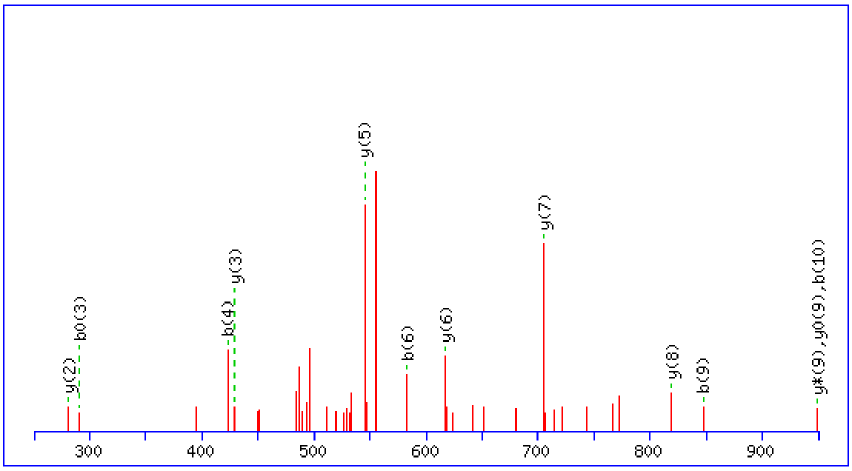
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTFISAGGFTR**
Found in **AT1G76680.1** in **TAIR_Arabidopsis**, Symbols: OPR1 | OPR1 (12-oxophytodienoate reductase 1); 12-oxophytodienoate reductase | chr1:28781876-28783165 FORWARD

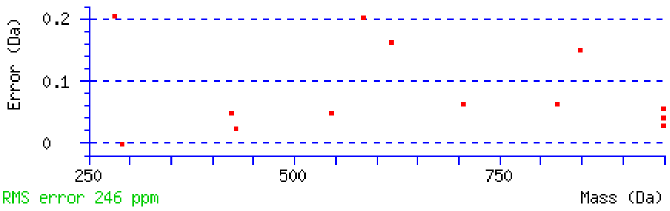
Match to Query 3441: 1126.518862 from(564.266707,2+) index(4758)
Title: Elution from: 43.661 to 43.661 scan no 5988 cid35.00 polarity:+
Data file C7-1_3.mgf

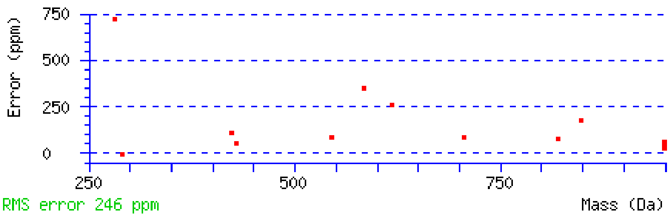
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1126.5199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 8.4e-006
Matches : 13/96 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			G							11
2	161.0705	81.0389	143.0599	72.0336	T	1069.5087	535.2580	1051.4851	526.2462	1051.4982	526.2527	10
3	309.1359	155.0716	291.1254	146.0663	F	967.4640	484.2356	949.4404	475.2239	949.4534	475.2304	9
4	**423.2170**	212.1122	405.2065	203.1069	I	***819.3986***	410.2029	801.3750	401.1911	801.3880	401.1976	8
5	511.2461	256.1267	493.2355	247.1214	S	***705.3175***	353.1624	687.2939	344.1506	687.3069	344.1571	7
6	**583.2802**	292.1438	565.2697	283.1385	A	***617.2884***	309.1478	599.2648	300.1360	599.2778	300.1426	6
7	641.2987	321.1530	623.2882	312.1477	G	***545.2543***	273.1308	527.2307	264.1190	527.2437	264.1255	5
8	699.3172	350.1623	681.3067	341.1570	G	487.2358	244.1215	469.2122	235.1097	469.2252	235.1162	4
9	**847.3827**	424.1950	829.3721	415.1897	F	***429.2173***	215.1123	411.1937	206.1005	411.2067	206.1070	3
10	**949.4274**	475.2173	931.4168	466.2121	T	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	2
11					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GTFISAGGFTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G76680.1

Score	Mr(calc)	Delta	Sequence
56.5	1126.5199	-0.0011	GTFISAGGFTR
1.6	1126.5159	0.0029	SVMLMSYLR
0.7	1126.5199	-0.0011	FDYIKSGQR
0.1	1126.5204	-0.0015	RHSPELQSR

AT1G76825.1

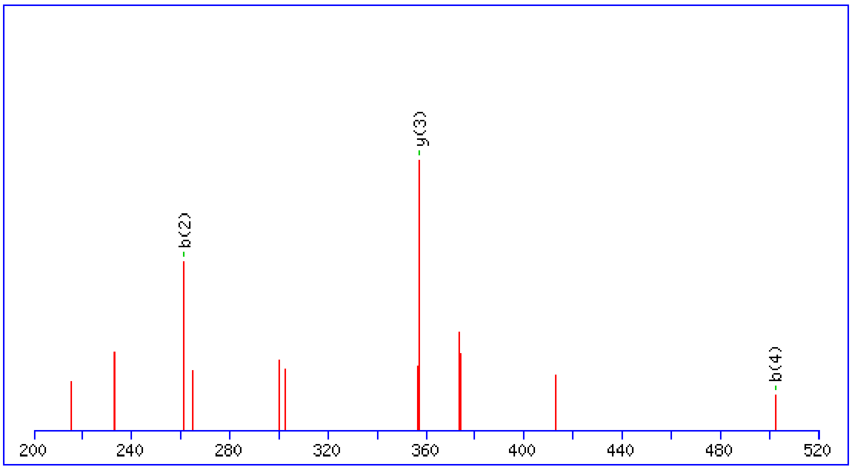
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFKIP**
Found in **AT1G76825.1** in **TAIR_Arabidopsis**

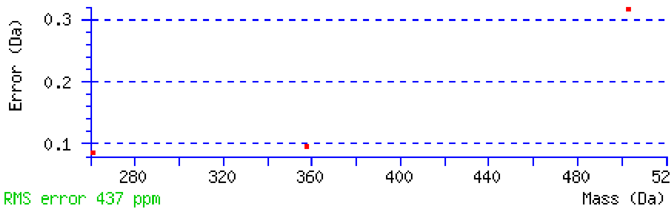
Match to Query 514: 616.394686 from(309.204619,2+) index(2175)
Title: Elution from: 24.705 to 24.705 scan no 2772 cid35.00 polarity:+
Data file D6h-1_3.mgf

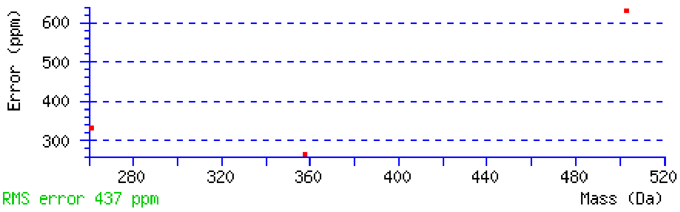
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 520 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 616.3948
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.044
Matches : 3/24 fragment ions using 3 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.0913	57.5493			I					5
2	***261.1598***	131.0835			F	504.3180	252.6627	487.2915	244.1494	4
3	389.2547	195.1310	372.2282	186.6177	K	**357.2496**	179.1285	340.2231	170.6152	3
4	***502.3388***	251.6730	485.3122	243.1598	I	229.1547	115.0810			2
5					P	116.0706	58.5389			1





NCBI **BLAST** search of IFKIP
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.7	616.3948	-0.0001	IFKIP
4.1	616.3948	-0.0001	FIIPK
4.1	616.3948	-0.0001	FLLPK
4.1	616.3948	-0.0001	IFIPK
4.1	616.3948	-0.0001	IFLPK

AT1G76825.1

4.1	616.3948	-0.0001	LFLPK

Mascot: http://www.matrixscience.com/

AT1G77120.1

Mascot Search Results

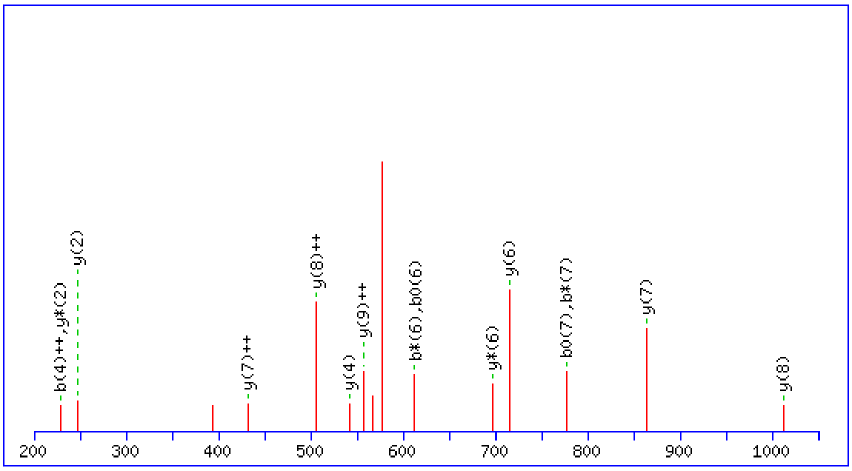
Peptide View

MS/MS Fragmentation of **GTFFGNYKPK**
Found in **AT1G77120.1** in **TAIR_Arabidopsis**, Symbols: ADH, ATADH, ADH1 | ADH1 (ALCOHOL DEHYDROGENASE 1) | chr1:28980403-28982110 FORWARD

Match to Query 3984: 1170.545382 from(586.279967,2+) index(3018)
Title: Elution from: 30.298 to 30.298 scan no 3755 cid35.00 polarity:+
Data file D12h-1_2.mgf

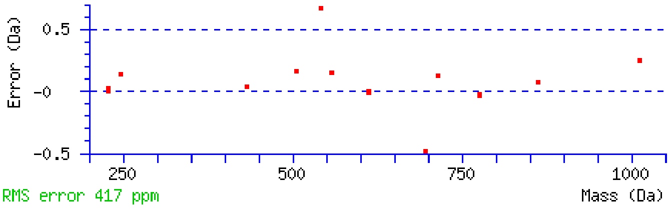
Click mouse within plot area to zoom in by factor of two about that point

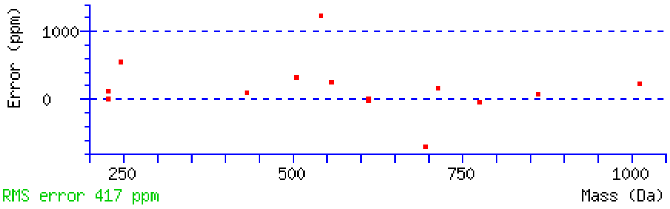
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1170.5484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00088
Matches : 15/80 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					**G**							**10**
2	161.0705	81.0389			143.0599	72.0336	**T**	1113.5372	557.2722	1095.5136	548.2604	1095.5266	548.2669	**9**
3	309.1359	155.0716			291.1254	146.0663	**F**	***1011.4925***	506.2499	993.4689	497.2381			**8**
4	457.2014	229.1043			439.1908	220.0990	**F**	***863.4270***	432.2171	845.4034	423.2054			**7**
5	515.2199	258.1136			497.2093	249.1083	**G**	***715.3616***	358.1844	697.3380	349.1726			**6**
6	631.2569	316.1321	613.2333	307.1203	613.2463	307.1268	**N**	657.3431	329.1752	639.3195	320.1634			**5**
7	795.3172	398.1623	777.2937	389.1505	777.3067	389.1570	**Y**	***541.3061***	271.1567	523.2825	262.1449			**4**
8	925.4063	463.2068	907.3827	454.1950	907.3957	454.2015	**K**	377.2457	189.1265	359.2221	180.1147			**3**
9	1023.4561	512.2317	1005.4325	503.2199	1005.4455	503.2264	**P**	***247.1567***	124.0820	229.1331	115.0702			**2**
10							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of GTFFGNYKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G77120.1

Score	Mr(calc)	Delta	Sequence
37.9	1170.5484	-0.0030	GTFFGNYKPK
9.8	1170.5488	-0.0034	RFKGSNGNFK
3.1	1170.5448	0.0006	MGKYQVMKR
1.9	1170.5462	-0.0008	RVPFSSSYSK
1.8	1170.5466	-0.0012	SANGSLPHSKR
1.7	1170.5469	-0.0015	AIEVLDEMPK
1.5	1170.5466	-0.0012	LDRALSHGER
1.4	1170.5461	-0.0007	TTGFTVYVNR
1.3	1170.5462	-0.0008	GPISDHLQYK
0.9	1170.5484	-0.0030	LLHWDSYPK

Mascot: http://www.matrixscience.com/

AT1G77170.1

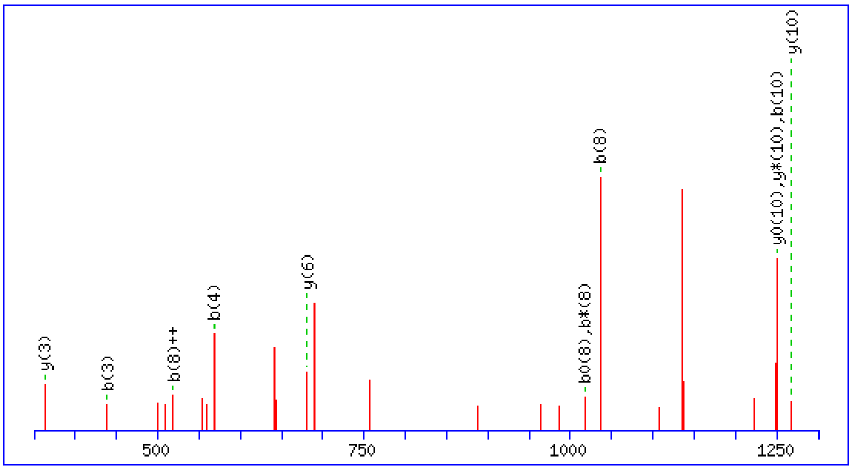
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QMREFGVRPNK**
Found in **AT1G77170.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:29003027-29004430 REVERSE

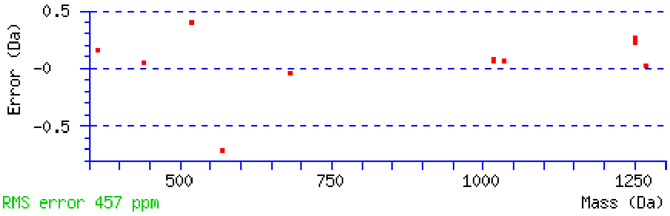
Match to Query 5264: 1396.635640 from(699.325096,2+) index(3229)
Title: Elution from: 31.582 to 31.582 scan no 3995 cid35.00 polarity:+
Data file 0-3_2.mgf

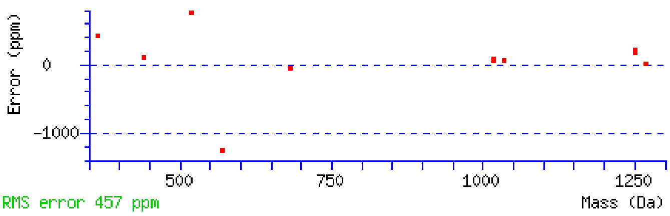
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1396.6390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.023
Matches : 12/156 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							11
2	279.0924	140.0498	261.0688	131.0380			M	***1267.5936***	634.3005	1249.5700	625.2887	1249.5831	625.2952	10
3	***439.1816***	220.0944	421.1580	211.0827			R	1119.5612	560.2842	1101.5376	551.2724	1101.5506	551.2790	9
4	***569.2212***	285.1143	551.1977	276.1025	551.2107	276.1090	E	959.4719	480.2396	941.4484	471.2278	941.4614	471.2343	8
5	717.2867	359.1470	699.2631	350.1352	699.2761	350.1417	F	829.4323	415.2198	811.4087	406.2080			7
6	775.3052	388.1562	757.2816	379.1444	757.2946	379.1509	G	***681.3669***	341.1871	663.3433	332.1753			6
7	875.3706	438.1890	857.3470	429.1772	857.3601	429.1837	V	623.3484	312.1778	605.3248	303.1660			5
8	***1035.4599***	518.2336	1017.4363	509.2218	1017.4493	509.2283	R	523.2829	262.1451	505.2593	253.1333			4
9	1133.5097	567.2585	1115.4861	558.2467	1115.4991	558.2532	P	***363.1937***	182.1005	345.1701	173.0887			3
10	***1249.5467***	625.2770	1231.5231	616.2652	1231.5361	616.2717	N	265.1439	133.0756	247.1203	124.0638			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QMREFGVRPNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G77170.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.8	1396.6390	-0.0034	QMREFGVRPNK
13.7	1396.6370	-0.0014	MTEKKEMEVVK
12.9	1396.6397	-0.0041	MSSEKRVGMVEK
10.9	1396.6336	0.0020	DATASMIFDLTAK
9.7	1396.6359	-0.0002	QDFMEVVEFLK
8.9	1396.6359	-0.0002	VGVFSFIEDMPK
8.5	1396.6390	-0.0033	FRLQAMEQQAR
6.8	1396.6330	0.0027	ENLRSFPNEFK
6.5	1396.6341	0.0015	KSVMGNLQSQSGK
6.2	1396.6329	0.0027	SAEEAFSRWAVK

AT1G77230.1

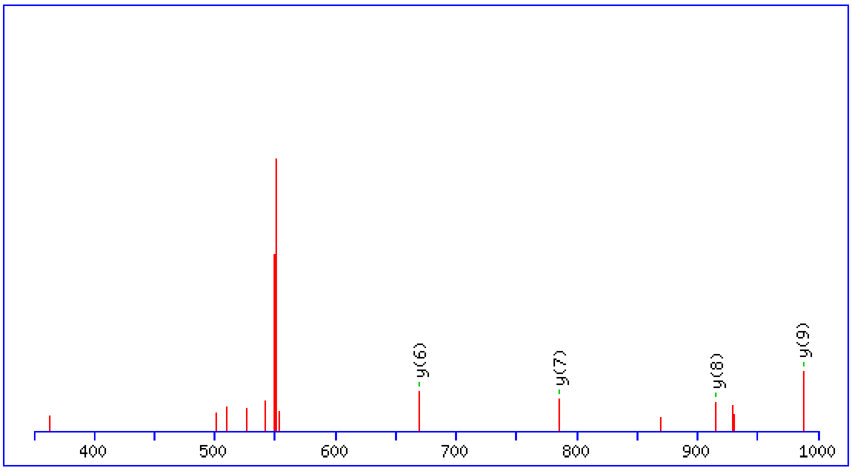
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAKDDLKSAK**
Found in **AT1G77230.1** in **TAIR_Arabidopsis**, Symbols: | tetratricopeptide repeat (TPR)-containing protein | chr1:29021023-29022767 FORWARD

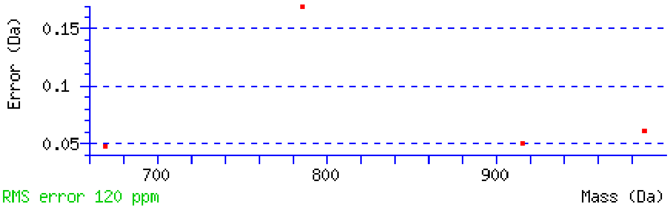
Match to Query 3045: 1116.544592 from(559.279572,2+) index(1442)
Title: Elution from: 20.117 to 20.117 scan no 1967 cid35.00 polarity:+
Data file D1d-2_3.mgf

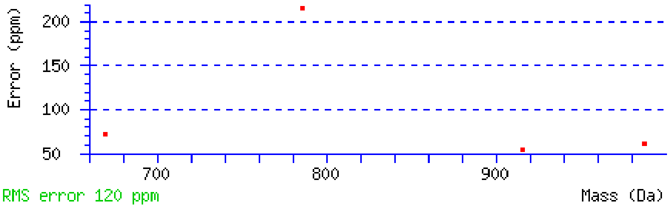
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.006
Matches : 4/100 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							10
2	203.0811	102.0442			185.0705	93.0389	A	***987.5114***	494.2593	969.4878	485.2475	969.5008	485.2540	9
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	K	***915.4772***	458.2422	897.4536	449.2304	897.4666	449.2370	8
4	449.1941	225.1007	431.1705	216.0889	431.1835	216.0954	D	***785.3882***	393.1977	767.3646	384.1859	767.3776	384.1924	7
5	565.2180	283.1127	547.1945	274.1009	547.2075	274.1074	D	***669.3642***	335.1857	651.3406	326.1739	651.3536	326.1805	6
6	679.2991	340.1532	661.2756	331.1414	661.2886	331.1479	L	553.3402	277.1737	535.3166	268.1620	535.3297	268.1685	5
7	809.3882	405.1977	791.3646	396.1859	791.3776	396.1924	K	439.2591	220.1332	421.2355	211.1214	421.2486	211.1279	4
8	897.4172	449.2123	879.3937	440.2005	879.4067	440.2070	S	309.1701	155.0887	291.1465	146.0769	291.1595	146.0834	3
9	969.4514	485.2293	951.4278	476.2175	951.4408	476.2240	A	221.1410	111.0741	203.1174	102.0624			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EAKDDLKSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G77230.1

Score	Mr(calc)	Delta	Sequence
32.0	1116.5437	0.0009	EAKDDLKSAK
16.3	1116.5437	0.0009	EGSKVSASLNI
14.3	1116.5464	-0.0018	EGSSSLLPRR
11.8	1116.5437	0.0009	GEGLSGTVKEK
10.4	1116.5437	0.0009	EATEKAEKAK
10.1	1116.5464	-0.0018	EALLRASADR
5.1	1116.5437	0.0009	EAGTKTVEAAK
5.0	1116.5437	0.0009	ESITVNGEKK
5.0	1116.5437	0.0009	ESLENSIKGK
5.0	1116.5464	-0.0018	KALAREEER

Mascot: http://www.matrixscience.com/

AT1G77510.1

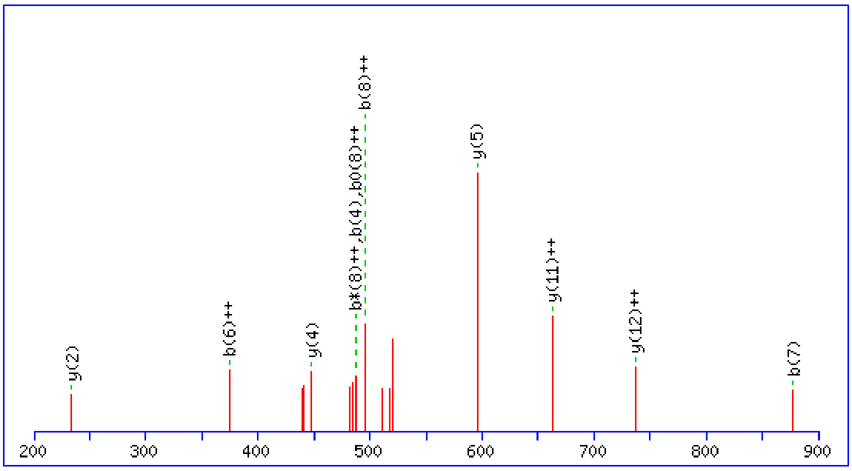
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFKPFDELFVDSK**
Found in **AT1G77510.1** in **TAIR_Arabidopsis**, Symbols: ATPDIL1-2 | ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase | chr1:29131636-29134327 FORWARD

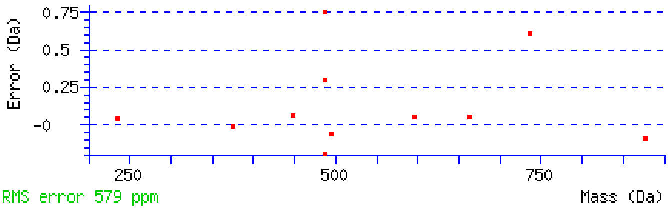
Match to Query 6941: 1583.821497 from(528.947775,3+) index(9126)
Title: Elution from: 82.718 to 82.718 scan no 12442 cid35.00 polarity:+
Data file D12h-3_2.mgf

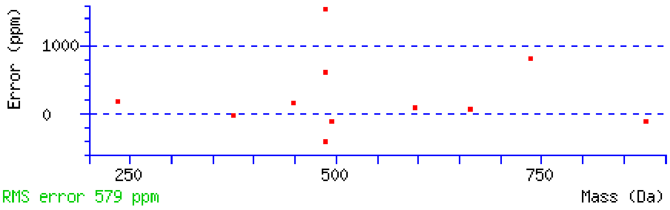
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1583.8235
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0036
Matches : 11/128 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							13
2	261.1598	131.0835					F	1471.7468	736.3770	1454.7202	727.8637	1453.7362	727.3717	12
3	389.2547	195.1310	372.2282	186.6177			K	1324.6783	662.8428	1307.6518	654.3295	1306.6678	653.8375	11
4	***486.3075***	243.6574	469.2809	235.1441			P	1196.5834	598.7953	1179.5568	590.2821	1178.5728	589.7900	10
5	633.3759	317.1916	616.3493	308.6783			F	1099.5306	550.2689	1082.5041	541.7557	1081.5201	541.2637	9
6	748.4028	***374.7051***	731.3763	366.1918	730.3923	365.6998	D	952.4622	476.7347	935.4357	468.2215	934.4516	467.7295	8
7	***877.4454***	439.2264	860.4189	430.7131	859.4349	430.2211	E	837.4353	419.2213	820.4087	410.7080	819.4247	410.2160	7
8	990.5295	***495.7684***	973.5029	487.2551	972.5189	486.7631	L	708.3927	354.7000	691.3661	346.1867	690.3821	345.6947	6
9	1137.5979	569.3026	1120.5714	560.7893	1119.5873	560.2973	F	***595.3086***	298.1579	578.2821	289.6447	577.2980	289.1527	5
10	1236.6663	618.8368	1219.6398	610.3235	1218.6558	609.8315	V	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6185	4
11	1351.6933	676.3503	1334.6667	667.8370	1333.6827	667.3450	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
12	1438.7253	719.8663	1421.6987	711.3530	1420.7147	710.8610	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LFKPFDELFVDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G77510.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1583.8235	-0.0021	LFKPFDELFVDSK
4.0	1583.8242	-0.0027	NMVHLPKGFLDGTR
3.6	1583.8208	0.0006	FLWRTNSSFAISR
2.2	1583.8242	-0.0027	YGRFAEILGRGAMK
2.0	1583.8195	0.0020	NFLLESKSGAYDLK
1.5	1583.8242	-0.0027	GFKAAGMYAGLRAAGK
0.6	1583.8168	0.0047	DKFEGLGHGRNNLK

AT1G77710.1

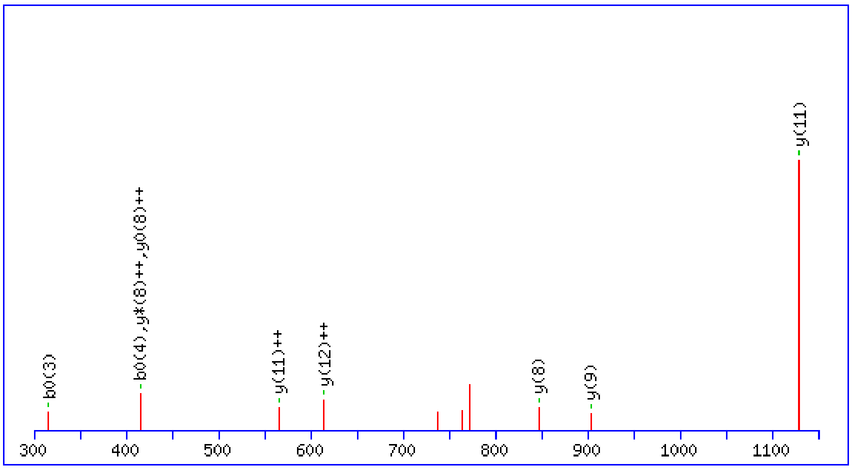
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFSVPEGAPFTAVLK**
Found in **AT1G77710.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Probable ubiquitin-fold modifier 1 precursor [Arabidopsis Thaliana] (GB:Q9CA23); similar to unknown [Populus trichocarpa] (GB:ABK93968.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61814.1); contains InterP

Match to Query 6329: 1560.854946 from(781.434749,2+) index(8753)
Title: Elution from: 82.776 to 82.776 scan no 12040 cid35.00 polarity:+
Data file D1d-1-2.mgf

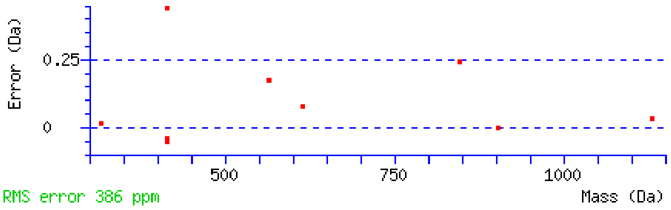
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

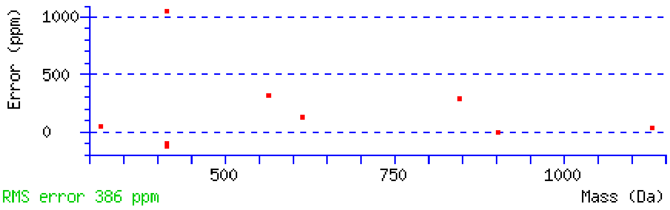


Monoisotopic mass of neutral peptide Mr(calc): 1560.8552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.021
Matches : 9/128 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							15
2	247.1441	124.0757			F	1462.7940	731.9007	1445.7675	723.3874	1444.7835	722.8954	14
3	334.1761	167.5917	316.1656	158.5864	S	1315.7256	658.3665	1298.6991	649.8532	1297.7151	649.3612	13
4	433.2445	217.1259	415.2340	208.1206	V	1228.6936	614.8504	1211.6671	606.3372	1210.6830	605.8452	12
5	530.2973	265.6523	512.2867	256.6470	P	***1129.6252***	565.3162	1112.5986	556.8030	1111.6146	556.3109	11
6	659.3399	330.1736	641.3293	321.1683	E	1032.5724	516.7899	1015.5459	508.2766	1014.5619	507.7846	10
7	716.3614	358.6843	698.3508	349.6790	G	***903.5298***	452.2686	886.5033	443.7553	885.5193	443.2633	9
8	787.3985	394.2029	769.3879	385.1976	A	***846.5084***	423.7578	829.4818	415.2445	828.4978	414.7525	8
9	884.4512	442.7293	866.4407	433.7240	P	775.4713	388.2393	758.4447	379.7260	757.4607	379.2340	7
10	1031.5197	516.2635	1013.5091	507.2582	F	678.4185	339.7129	661.3919	331.1996	660.4079	330.7076	6
11	1132.5673	566.7873	1114.5568	557.7820	T	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
12	1203.6045	602.3059	1185.5939	593.3006	A	430.3024	215.6548	413.2758	207.1416			4
13	1302.6729	651.8401	1284.6623	642.8348	V	359.2653	180.1363	342.2387	171.6230			3
14	1415.7569	708.3821	1397.7464	699.3768	L	260.1969	130.6021	243.1703	122.0888			2
15					K	147.1128	74.0600	130.0863	65.5468			1

AT1G77710.1





NCBI **BLAST** search of VFSVPEGAPFTAVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.6	1560.8552	-0.0002	VFSVPEGAPFTAVLK

AT1G77940.1

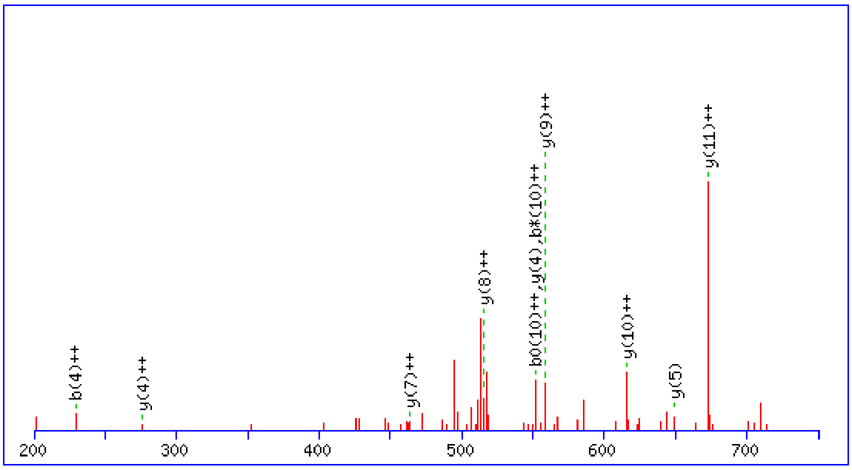
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LILISTNCPPLRR**
Found in **AT1G77940.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L30 (RPL30B) | chr1:29309010-29310182 REVERSE

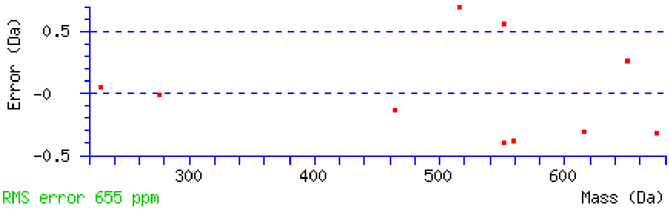
Match to Query 6858: 1572.833436 from(525.285088,3+) index(5275)
Title: Elution from: 46.992 to 46.992 scan no 6621 cid35.00 polarity:+
Data file 0-3_2.mgf

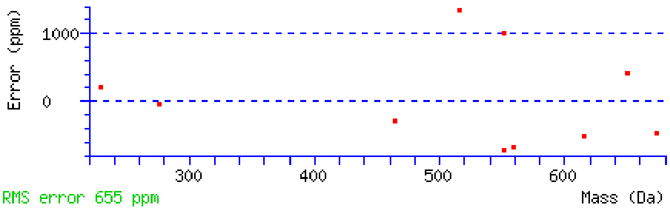
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1572.8297
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.047
Matches : 12/110 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							13
2	229.1695	115.0884					I	1459.7558	730.3816	1441.7322	721.3698	1441.7453	721.3763	12
3	343.2506	172.1289					L	1345.6747	673.3410	1327.6511	664.3292	1327.6642	664.3357	11
4	457.3317	229.1695					I	1231.5936	616.3005	1213.5700	607.2887	1213.5831	607.2952	10
5	545.3607	273.1840			527.3502	264.1787	S	1117.5125	559.2599	1099.4889	550.2481	1099.5020	550.2546	9
6	647.4054	324.2064			629.3949	315.2011	T	1029.4835	515.2454	1011.4599	506.2336	1011.4729	506.2401	8
7	763.4424	382.2249	745.4189	373.2131	745.4319	373.2196	N	927.4388	464.2230	909.4152	455.2112			7
8	925.4672	463.2372	907.4436	454.2254	907.4566	454.2319	C	811.4018	406.2045	793.3782	397.1927			6
9	1023.5170	512.2621	1005.4934	503.2503	1005.5064	503.2568	P	649.3770	325.1922	631.3535	316.1804			5
10	1121.5668	561.2870	1103.5432	552.2752	1103.5562	552.2817	P	551.3272	276.1673	533.3037	267.1555			4
11	1235.6479	618.3276	1217.6243	609.3158	1217.6373	609.3223	L	453.2774	227.1424	435.2539	218.1306			3
12	1395.7371	698.3722	1377.7135	689.3604	1377.7265	689.3669	R	339.1963	170.1018	321.1728	161.0900			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LILISTNCPPLRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G77940.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.9	1572.8297	0.0038	LILISTNCPPLRR
3.3	1572.8371	-0.0036	IPNQRQNLVSILR
2.9	1572.8366	-0.0032	ILGFIPVKAPDGTAR
0.3	1572.8373	-0.0039	LDMIINLLATSLPK

Mascot: http://www.matrixscience.com/

AT1G78020.1

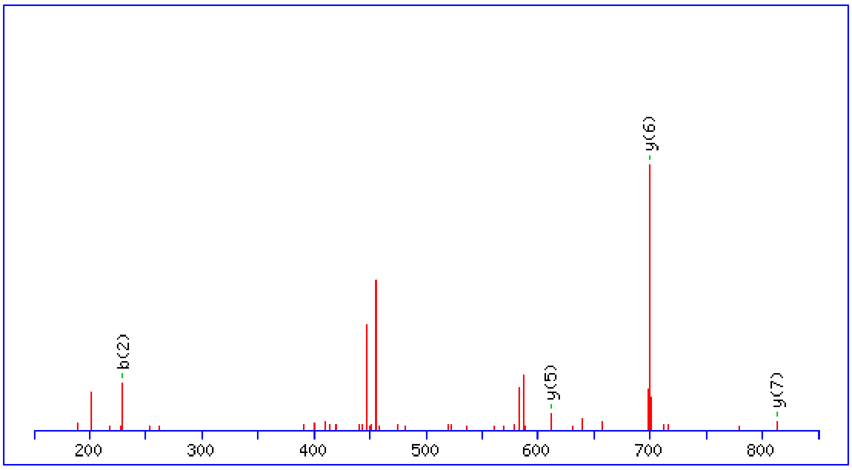
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLSMVTPR**
Found in **AT1G78020.1** in **TAIR_Arabidopsis**, Symbols: | senescence-associated protein-related | chr1:29343681-29344385 FORWARD

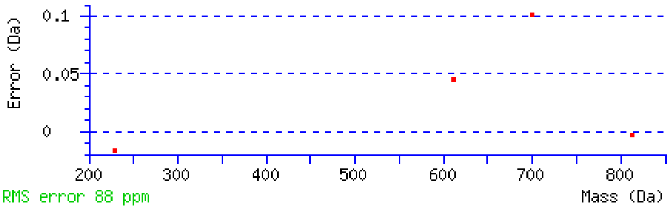
Match to Query 1844: 926.489012 from(464.251782,2+) index(1139)
Title: Elution from: 15.557 to 15.557 scan no 1519 cid35.00 polarity:+
Data file C7-2_3.mgf

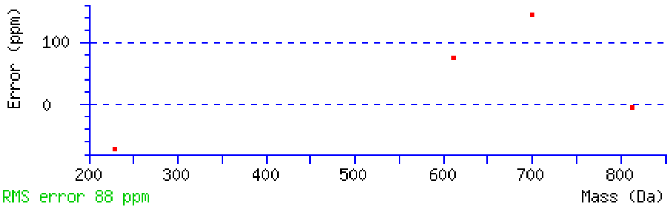
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 926.4886
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.035
Matches : 4/62 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	229.1695	115.0884			L	***813.4147***	407.2110	795.3912	398.1992	795.4042	398.2057	7
3	317.1985	159.1029	299.1880	150.0976	S	***699.3336***	350.1705	681.3101	341.1587	681.3231	341.1652	6
4	449.2361	225.1217	431.2255	216.1164	M	***611.3046***	306.1559	593.2810	297.1441	593.2940	297.1506	5
5	549.3015	275.1544	531.2909	266.1491	V	479.2671	240.1372	461.2435	231.1254	461.2565	231.1319	4
6	651.3462	326.1767	633.3357	317.1715	T	379.2016	190.1044	361.1780	181.0926	361.1910	181.0992	3
7	749.3960	375.2016	731.3855	366.1964	P	277.1569	139.0821	259.1333	130.0703			2
8					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LLSMVTPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.7	926.4886	0.0005	LLSMVTPR
10.4	926.4912	-0.0022	LIQRMPR

AT1G78020.1

8.9	926.4886	0.0005	ILCELLR
4.6	926.4886	0.0004	ISIPAIMR
2.8	926.4885	0.0005	LAMVVEVR
0.1	926.4908	-0.0018	WLNILMK

AT1G78300.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAQDIANAELAPTHPIR**
Found in **AT1G78300.1** in **TAIR_Arabidopsis**, Symbols: GF14 OMEGA, GRF2 | GRF2 (GENERAL REGULATORY FACTOR 2); protein phosphorylated amino acid binding | chr1:29466776-29467945 FORWARD

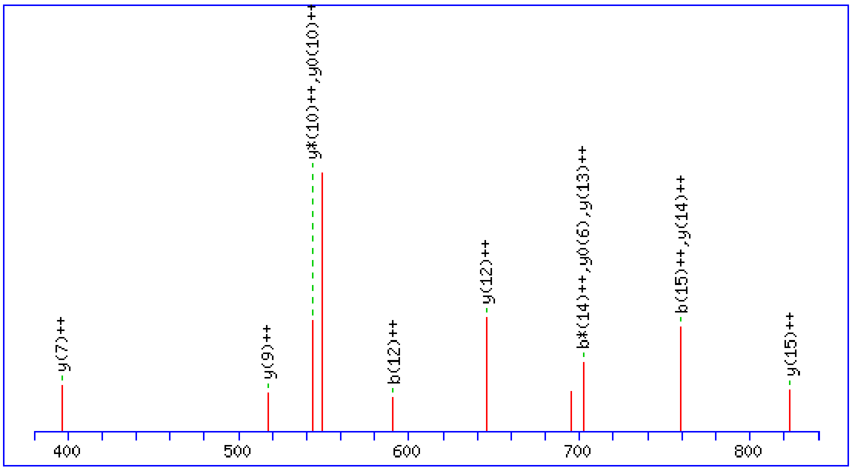
Match to Query 8944: 1802.925609 from(601.982479,3+) index(4536)
Title: Elution from: 40.938 to 40.938 scan no 5645 cid35.00 polarity:+
Data file D1d-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 380 to 840 Da Full range

Label all possible matches ○ Label matches used for scoring ●

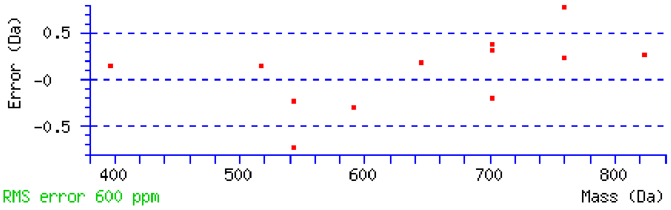
Show Y-axis ☐

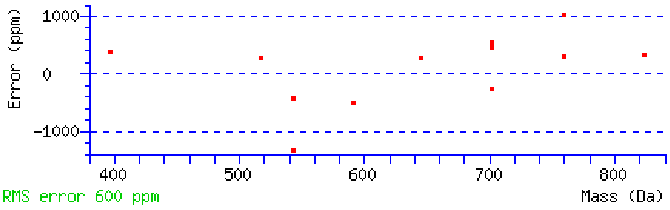


Monoisotopic mass of neutral peptide Mr(calc): 1802.9275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00031
Matches : 12/180 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	159.0764	80.0418			141.0659	71.0366	A	1716.9028	858.9550	1699.8762	850.4417	1698.8922	849.9497	16
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	Q	1645.8656	823.4365	1628.8391	814.9232	1627.8551	814.4312	15
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	D	1517.8071	759.4072	1500.7805	750.8939	1499.7965	750.4019	14
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	I	1402.7801	701.8937	1385.7536	693.3804	1384.7696	692.8884	13
6	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	A	1289.6961	645.3517	1272.6695	636.8384	1271.6855	636.3464	12
7	700.3260	350.6667	683.2995	342.1534	682.3155	341.6614	N	1218.6589	609.8331	1201.6324	601.3198	1200.6484	600.8278	11
8	771.3632	386.1852	754.3366	377.6719	753.3526	377.1799	A	1104.6160	552.8116	1087.5895	544.2984	1086.6055	543.8064	10
9	900.4058	450.7065	883.3792	442.1932	882.3952	441.7012	E	1033.5789	517.2931	1016.5524	508.7798	1015.5683	508.2878	9
10	1013.4898	507.2485	996.4633	498.7353	995.4792	498.2433	L	904.5363	452.7718	887.5098	444.2585	886.5257	443.7665	8
11	1084.5269	542.7671	1067.5004	534.2538	1066.5164	533.7618	A	791.4522	396.2298	774.4257	387.7165	773.4417	387.2245	7
12	1181.5797	**591.2935**	1164.5531	582.7802	1163.5691	582.2882	P	720.4151	360.7112	703.3886	352.1979	702.4046	351.7059	6
13	1282.6274	641.8173	1265.6008	633.3040	1264.6168	632.8120	T	623.3624	312.1848	606.3358	303.6715	605.3518	303.1795	5
14	1419.6863	710.3468	1402.6597	701.8335	1401.6757	701.3415	H	522.3147	261.6610	505.2881	253.1477			4
15	1516.7390	**758.8732**	1499.7125	750.3599	1498.7285	749.8679	P	385.2558	193.1315	368.2292	184.6183			3
16	1629.8231	815.4152	1612.7966	806.9019	1611.8125	806.4099	I	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1

AT1G78300.1





NCBI **BLAST** search of SAQDIANAELAPTHPIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.6	1802.9275	-0.0019	SAQDIANAELAPTHPIR
16.8	1802.9308	-0.0052	TMSENSRNLEAGLLLR
14.5	1802.9283	-0.0027	ASLQMLQNWMQGKLR
5.7	1802.9275	-0.0019	AAQDIANSELAPTHPIR
5.1	1802.9275	-0.0019	VGENTLGSHPDIPQLAR
4.5	1802.9237	0.0019	GCSPLLSGVIPSGFGLDK
0.5	1802.9308	-0.0052	REAALSPLKNMDLSSR
0.3	1802.9210	0.0046	ERMRQSSPYPVRPGK

AT1G78340.1

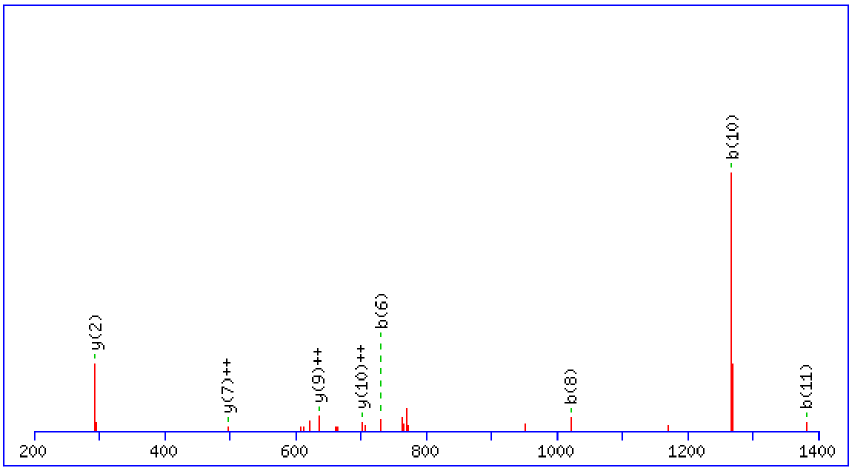
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVEFEYREENLR**
Found in **AT1G78340.1** in **TAIR_Arabidopsis**, Symbols: ATGSTU22 | ATGSTU22 (Arabidopsis thaliana Glutathione S-transferase (class tau) 22); glutathione transferase | chr1:29477939-29478690 REVERSE

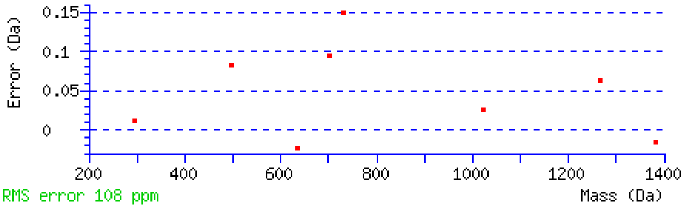
Match to Query 6534: 1558.676842 from(780.345697,2+) index(4100)
Title: Elution from: 37.490 to 37.490 scan no 5139 cid35.00 polarity:+
Data file D6h-3_3.mgf

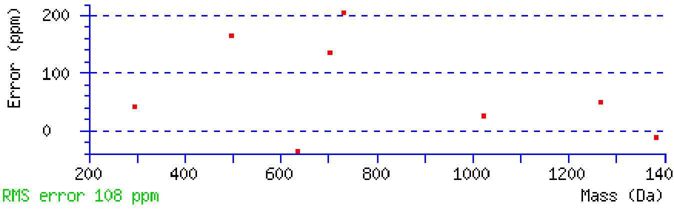
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1558.6754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.048
Matches : 8/110 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							12
2	159.0912	80.0492					V	1501.6642	751.3357	1483.6406	742.3240	1483.6536	742.3305	11
3	289.1309	145.0691			271.1203	136.0638	E	1401.5988	701.3030	1383.5752	692.2912	1383.5882	692.2977	10
4	437.1963	219.1018			419.1857	210.0965	F	1271.5591	636.2832	1253.5356	627.2714	1253.5486	627.2779	9
5	567.2359	284.1216			549.2254	275.1163	E	1123.4937	562.2505	1105.4701	553.2387	1105.4831	553.2452	8
6	***731.2963***	366.1518			713.2857	357.1465	Y	993.4541	497.2307	975.4305	488.2189	975.4435	488.2254	7
7	891.3855	446.1964	873.3620	437.1846	873.3750	437.1911	R	829.3937	415.2005	811.3701	406.1887	811.3831	406.1952	6
8	***1021.4252***	511.2162	1003.4016	502.2044	1003.4146	502.2109	E	669.3044	335.1559	651.2809	326.1441	651.2939	326.1506	5
9	1151.4648	576.2360	1133.4412	567.2242	1133.4542	567.2308	E	539.2648	270.1360	521.2412	261.1243	521.2543	261.1308	4
10	***1267.5018***	634.2545	1249.4782	625.2427	1249.4912	625.2493	N	409.2252	205.1162	391.2016	196.1044			3
11	***1381.5829***	691.2951	1363.5593	682.2833	1363.5723	682.2898	L	293.1882	147.0977	275.1646	138.0859			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GVEFEYREENLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G78340.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.7	1558.6754	0.0014	GVEFEYREENLR
10.9	1558.6810	-0.0042	GMLESGHYVTYLR
4.5	1558.6792	-0.0024	CESRATTQGVKSGR
3.6	1558.6767	0.0001	ASRGCAKAMWNLR
3.5	1558.6741	0.0028	CKYHVTKTMESR
3.5	1558.6784	-0.0015	EMDAFYILEELR
3.5	1558.6788	-0.0020	EMQERYSEISLR
3.5	1558.6788	-0.0020	LENHDMPLTDAIR
3.5	1558.6788	-0.0019	MVQSTGTANAEYLR

AT1G78360.1

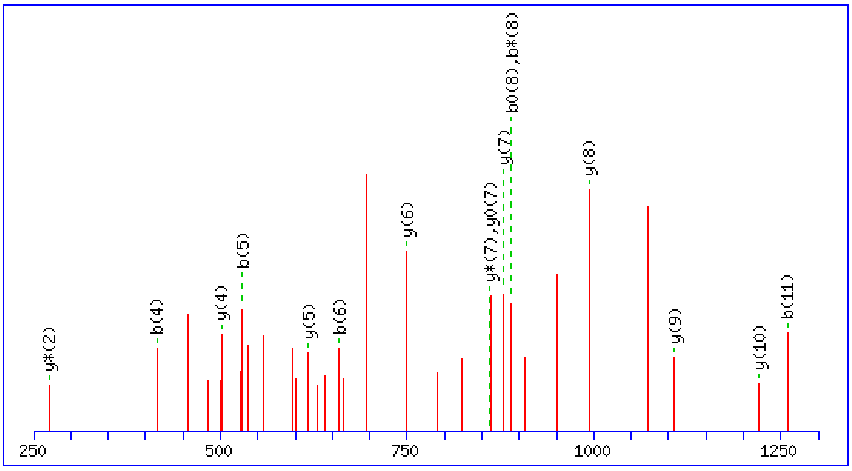
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPLLLEMNPIHK**
Found in **AT1G78360.1** in **TAIR_Arabidopsis**, Symbols: ATGSTU21 | ATGSTU21 (Arabidopsis thaliana Glutathione S-transferase (class tau) 21); glutathione transferase | chr1:29486963-29487859 REVERSE

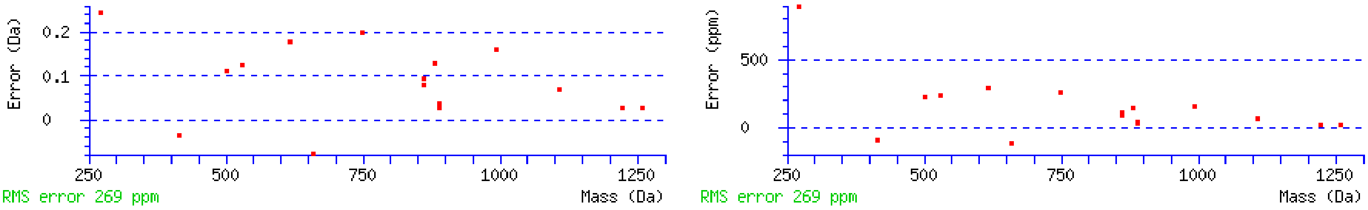
Match to Query 5016: 1406.715266 from(704.364909,2+) index(5841)
Title: Elution from: 55.173 to 55.173 scan no 7615 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1406.7168
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00014
Matches : 16/106 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	187.0861	94.0467			169.0756	85.0414	P	1319.6950	660.3512	1301.6714	651.3394	1301.6845	651.3459	11
3	301.1672	151.0873			283.1567	142.0820	L	***1221.6452***	611.3263	1203.6216	602.3145	1203.6347	602.3210	10
4	**415.2483**	208.1278			397.2378	199.1225	L	***1107.5641***	554.2857	1089.5405	545.2739	1089.5536	545.2804	9
5	**529.3294**	265.1684			511.3189	256.1631	L	***993.4830***	497.2452	975.4594	488.2334	975.4725	488.2399	8
6	**659.3691**	330.1882			641.3585	321.1829	E	***879.4019***	440.2046	861.3784	431.1928	861.3914	431.1993	7
7	791.4066	396.2069			773.3960	387.2016	M	***749.3623***	375.1848	731.3387	366.1730			6
8	907.4436	454.2254	889.4200	445.2136	889.4330	445.2201	N	***617.3248***	309.1660	599.3012	300.1542			5
9	1005.4934	503.2503	987.4698	494.2385	987.4828	494.2450	P	***501.2878***	251.1475	483.2642	242.1357			4
10	1119.5745	560.2909	1101.5509	551.2791	1101.5639	551.2856	I	403.2380	202.1226	385.2144	193.1108			3
11	**1259.6245**	630.3159	1241.6009	621.3041	1241.6139	621.3106	H	289.1569	145.0821	271.1333	136.0703			2
12							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of SPLLLEMNPIHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G78360.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.1	1406.7168	-0.0016	SPLLLEMNPIHK
9.1	1406.7183	-0.0031	FRFHKWLVEK
7.8	1406.7168	-0.0015	DMALILDVARFK
0.8	1406.7112	0.0041	LAVSGLLTDQAFR

AT1G78370.1

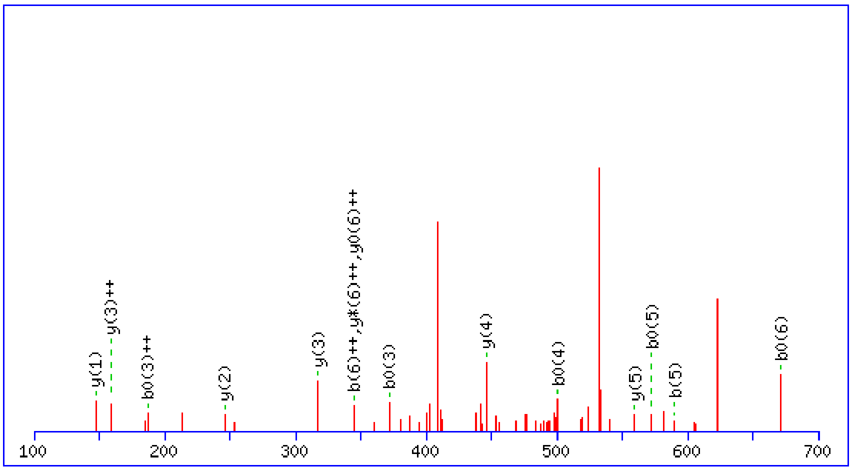
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFIEAVK**
Found in **AT1G78370.1** in **TAIR_Arabidopsis**, Symbols: ATGSTU20 | ATGSTU20 (Arabidopsis thaliana Glutathione S-transferase (class tau) 20); glutathione transferase | chr1:29489321-29490097 REVERSE

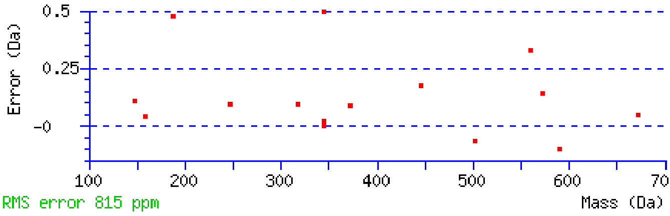
Match to Query 1020: 834.448776 from(418.231664,2+) index(2453)
Title: Elution from: 29.326 to 29.326 scan no 3194 cid35.00 polarity:+
Data file D1d-1_1.mgf

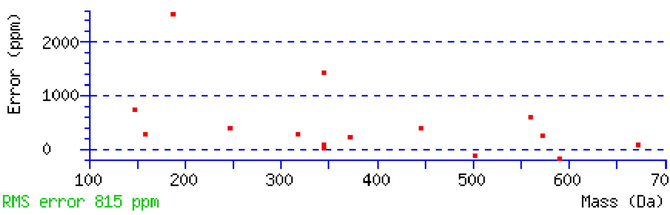
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 834.4487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.032
Matches : 15/54 fragment ions using 24 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	112.0393	56.5233	E							7
2	277.1183	139.0628	259.1077	130.0575	F	706.4134	353.7103	689.3869	345.1971	688.4028	344.7051	6
3	390.2023	195.6048	372.1918	186.5995	I	***559.3450***	280.1761	542.3184	271.6629	541.3344	271.1709	5
4	519.2449	260.1261	501.2344	251.1208	E	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
5	590.2821	295.6447	572.2715	286.6394	A	***317.2183***	159.1128	300.1918	150.5995			3
6	689.3505	345.1789	671.3399	336.1736	V	***246.1812***	123.5942	229.1547	115.0810			2
7					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EFIEAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.4	834.4487	0.0001	EFIEAVK
17.1	834.4487	0.0001	FIEEVAK

AT1G78370.1

5.4	834.4487	0.0001	ALEIFDK
1.9	834.4494	-0.0006	MARASKR
1.4	834.4494	-0.0006	SAMARKR
0.6	834.4487	0.0001	TTPELFK
0.3	834.4494	-0.0006	MRSAAKR
0.3	834.4487	0.0001	FLEAVEK
0.3	834.4500	-0.0013	WAKFQR

AT1G78380.1

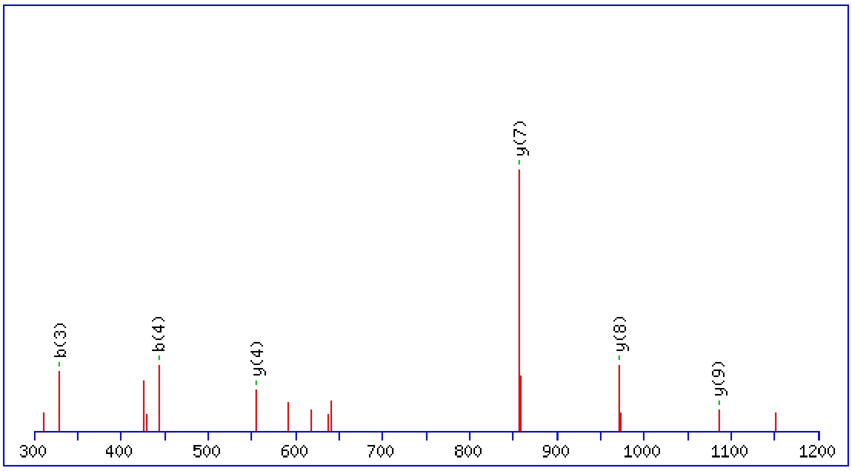
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPILPSDPYLR**
Found in **AT1G78380.1** in **TAIR_Arabidopsis**, Symbols: GST8, ATGSTU19 | ATGSTU19 (GLUTATHIONE TRANSFERASE 8); glutathione transferase | chr1:29491552-29492712 REVERSE

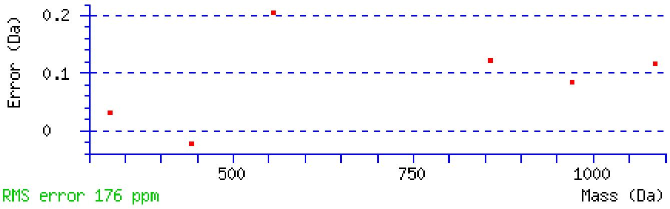
Match to Query 4546: 1298.642180 from(650.328366,2+) index(6081)
Title: Elution from: 53.933 to 53.933 scan no 7815 cid35.00 polarity:+
Data file D6h-2_3.mgf

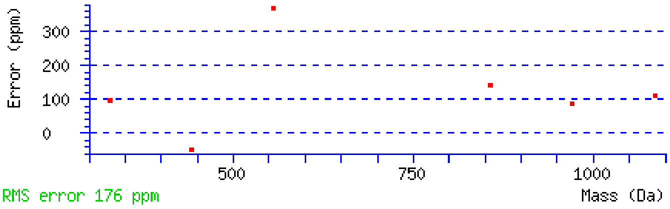
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1298.6429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0035
Matches : 6/102 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							11
2	215.0941	108.0507	197.0705	99.0389			P	1183.6132	592.3102	1165.5896	583.2984	1165.6026	583.3050	10
3	**329.1752**	165.0912	311.1516	156.0794			I	***1085.5634***	543.2853	1067.5398	534.2735	1067.5528	534.2801	9
4	**443.2563**	222.1318	425.2327	213.1200			L	***971.4823***	486.2448	953.4587	477.2330	953.4717	477.2395	8
5	541.3061	271.1567	523.2825	262.1449			P	***857.4012***	429.2042	839.3776	420.1924	839.3906	420.1990	7
6	629.3351	315.1712	611.3115	306.1594	611.3246	306.1659	S	759.3514	380.1793	741.3278	371.1675	741.3408	371.1741	6
7	745.3591	373.1832	727.3355	364.1714	727.3485	364.1779	D	671.3223	336.1648	653.2987	327.1530	653.3118	327.1595	5
8	843.4089	422.2081	825.3853	413.1963	825.3983	413.2028	P	***555.2984***	278.1528	537.2748	269.1410			4
9	1007.4693	504.2383	989.4457	495.2265	989.4587	495.2330	Y	457.2486	229.1279	439.2250	220.1161			3
10	1121.5504	561.2788	1103.5268	552.2670	1103.5398	552.2735	L	293.1882	147.0977	275.1646	138.0859			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NPILPSDPYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G78380.1

Score	Mr(calc)	Delta	Sequence
32.1	1298.6429	-0.0007	NPILPSDPYLR

Mascot: http://www.matrixscience.com/

AT1G78530.1

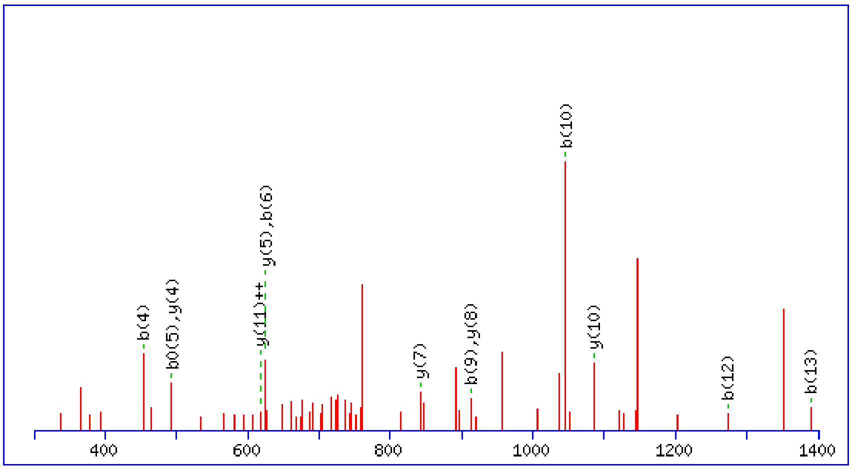
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSDFGLATLMEPDK**
Found in **AT1G78530.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr1:29544167-29545574 REVERSE

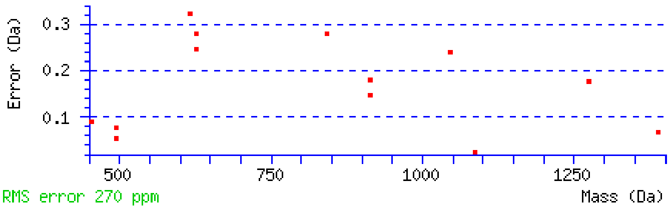
Match to Query 6388: 1536.694516 from(769.354534,2+) index(6548)
Title: Elution from: 60.909 to 60.909 scan no 8551 cid35.00 polarity:+
Data file D1d-1_1.mgf

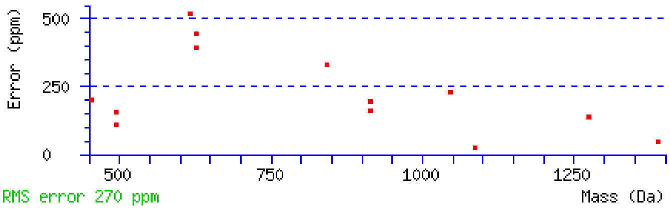
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1536.6940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.042
Matches : 13/126 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							14
2	189.1018	95.0545	171.0912	86.0492	S	1437.6358	719.3216	1419.6123	710.3098	1419.6253	710.3163	13
3	305.1258	153.0665	287.1152	144.0612	D	1349.6068	675.3070	1331.5832	666.2952	1331.5962	666.3017	12
4	***453.1912***	227.0992	435.1807	218.0940	F	1233.5828	617.2950	1215.5592	608.2832	1215.5722	608.2898	11
5	511.2097	256.1085	493.1991	247.1032	G	***1085.5174***	543.2623	1067.4938	534.2505	1067.5068	534.2570	10
6	***625.2908***	313.1490	607.2802	304.1438	L	1027.4989	514.2531	1009.4753	505.2413	1009.4883	505.2478	9
7	697.3250	349.1661	679.3144	340.1608	A	***913.4178***	457.2125	895.3942	448.2007	895.4072	448.2072	8
8	799.3697	400.1885	781.3591	391.1832	T	***841.3836***	421.1954	823.3600	412.1837	823.3730	412.1902	7
9	***913.4508***	457.2290	895.4402	448.2237	L	739.3389	370.1731	721.3153	361.1613	721.3283	361.1678	6
10	***1045.4883***	523.2478	1027.4777	514.2425	M	***625.2578***	313.1325	607.2342	304.1207	607.2472	304.1273	5
11	1175.5279	588.2676	1157.5174	579.2623	E	***493.2203***	247.1138	475.1967	238.1020	475.2097	238.1085	4
12	***1273.5777***	637.2925	1255.5672	628.2872	P	363.1807	182.0940	345.1571	173.0822	345.1701	173.0887	3
13	***1389.6017***	695.3045	1371.5911	686.2992	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
14					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VSDFGLATLMEPDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G78530.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.8	1536.6940	0.0005	VSDFGLATLMEPDK
8.7	1536.6940	0.0005	MFEIEGELSPKDK
1.5	1536.6967	-0.0022	SLYCSVDHANLLK
0.0	1536.6967	-0.0022	MDELVQFGKTHSK

AT1G78570.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPISSDLNNPR**
Found in **AT1G78570.1** in **TAIR_Arabidopsis**, Symbols: RHM1, ROL1 | RHM1/ROL1 (RHAMNOSE BIOSYNTHESIS1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic | chr1:29555003-29557100 FORWARD

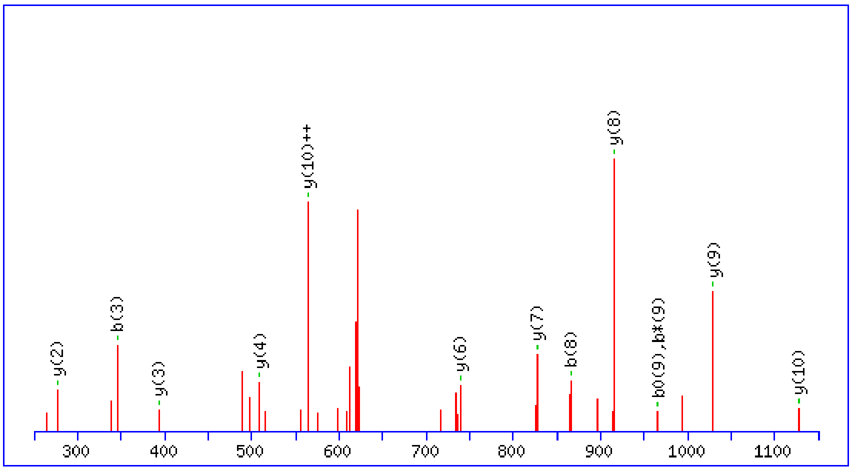
Match to Query 4698: 1258.554588 from(630.284570,2+) index(2941)
Title: Elution from: 30.182 to 30.182 scan no 3663 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1150 Da Full range

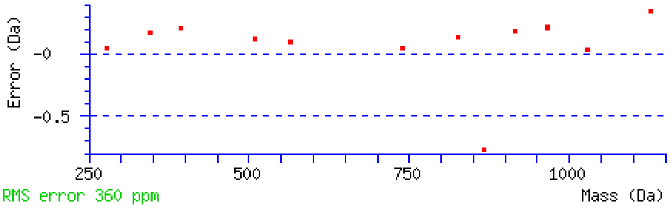
Label all possible matches ○ Label matches used for scoring ●

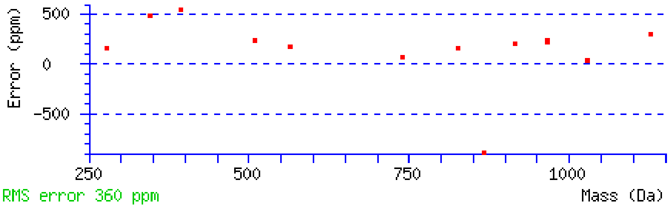
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1258.5553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 6.7e-006
Matches : 13/90 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	133.0448	67.0260					M							11
2	231.0946	116.0509					P	**1127.5250**	**564.2661**	1109.5014	555.2543	1109.5144	555.2608	10
3	**345.1757**	173.0915					I	**1029.4752**	515.2412	1011.4516	506.2294	1011.4646	506.2359	9
4	433.2048	217.1060			415.1942	208.1007	S	**915.3941**	458.2007	897.3705	449.1889	897.3835	449.1954	8
5	521.2338	261.1205			503.2233	252.1153	S	**827.3650**	414.1862	809.3414	405.1744	809.3545	405.1809	7
6	637.2578	319.1325			619.2472	310.1273	D	**739.3360**	370.1716	721.3124	361.1598	721.3254	361.1663	6
7	751.3389	376.1731			733.3283	367.1678	L	623.3120	312.1596	605.2884	303.1478			5
8	**867.3759**	434.1916	849.3523	425.1798	849.3653	425.1863	N	**509.2309**	255.1191	491.2073	246.1073			4
9	983.4129	492.2101	**965.3893**	483.1983	**965.4023**	483.2048	N	**393.1939**	197.1006	375.1703	188.0888			3
10	1081.4627	541.2350	1063.4391	532.2232	1063.4521	532.2297	P	**277.1569**	139.0821	259.1333	130.0703			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MPISSDLNNPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G78570.1

Score	Mr(calc)	Delta	Sequence
58.7	1258.5553	-0.0007	MPISSDLNNPR
1.0	1258.5526	0.0020	MPESDDLSPKK

Mascot: http://www.matrixscience.com/

AT1G78820.1

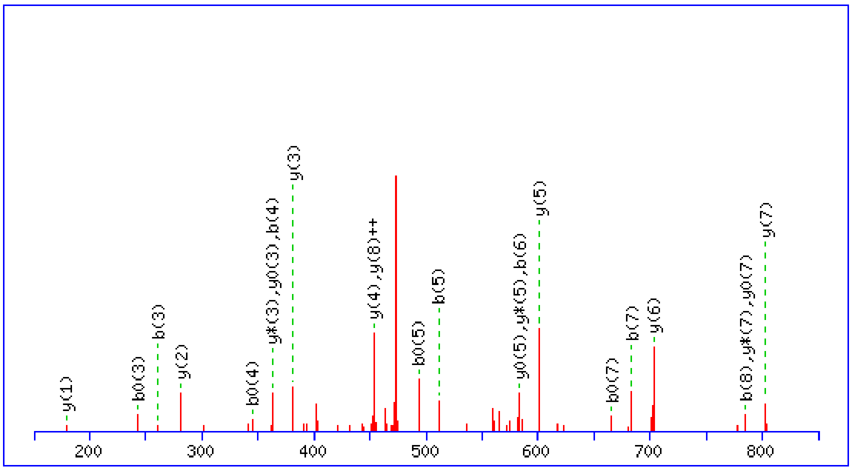
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTVTFAVTR**
Found in **AT1G78820.1** in **TAIR_Arabidopsis**, Symbols: | curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein | chr1:29639294-29640661 REVERSE

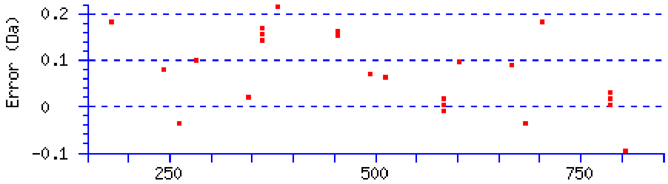
Match to Query 1912: 962.480636 from(482.247594,2+) index(2753)
Title: Elution from: 31.280 to 31.280 scan no 3570 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

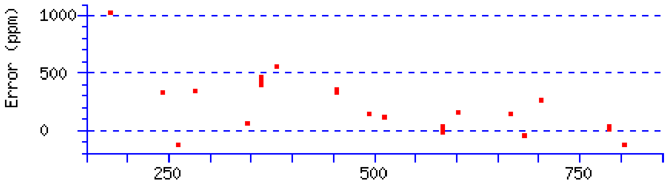


Monoisotopic mass of neutral peptide Mr(calc): 962.4829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.7e-007
Matches : 24/76 fragment ions using 21 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	59.0258	30.0165			G							9
2	161.0705	81.0389	143.0599	72.0336	T	905.4717	453.2395	887.4481	444.2277	887.4612	444.2342	8
3	**261.1359**	131.0716	243.1254	122.0663	V	***803.4270***	402.2171	785.4034	393.2054	785.4164	393.2119	7
4	**363.1806**	182.0940	345.1701	173.0887	T	***703.3616***	352.1844	685.3380	343.1726	685.3510	343.1791	6
5	**511.2461**	256.1267	493.2355	247.1214	F	***601.3169***	301.1621	583.2933	292.1503	583.3063	292.1568	5
6	**583.2802**	292.1438	565.2697	283.1385	A	***453.2514***	227.1293	435.2278	218.1175	435.2408	218.1241	4
7	**683.3457**	342.1765	665.3351	333.1712	V	***381.2173***	191.1123	363.1937	182.1005	363.2067	182.1070	3
8	**785.3904**	393.1988	767.3798	384.1936	T	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	2
9					R	***179.1071***	90.0572	161.0835	81.0454			1



RMS error 327 ppm



RMS error 327 ppm

NCBI **BLAST** search of GTVTFAVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G78820.1

76.0	962.4829	-0.0023	GTVTFAVTR
19.1	962.4829	-0.0023	ISGAAYLTR
13.1	962.4782	0.0024	GCRAFLVK
11.1	962.4782	0.0024	LFVEMRR
10.3	962.4786	0.0020	MRSAIGRR
9.6	962.4789	0.0017	KMTSMIVK
9.0	962.4834	-0.0027	RKLSGGSSR
7.2	962.4829	-0.0023	LSRFSDVK
6.2	962.4816	-0.0009	MLVRIMR
3.5	962.4816	-0.0009	AKRVAMMK

AT1G78830.1

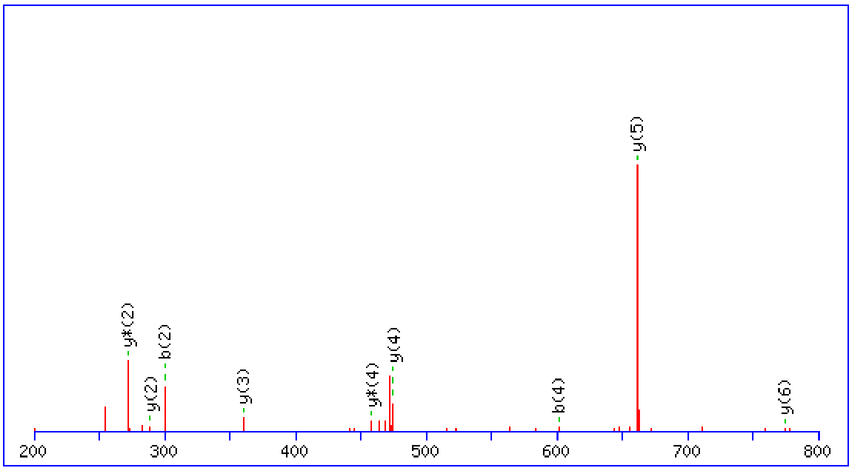
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WIWDANR**
Found in **AT1G78830.1** in **TAIR_Arabidopsis**, Symbols: | curculin-like (mannose-binding) lectin family protein | chr1:29642034-29643401 REVERSE

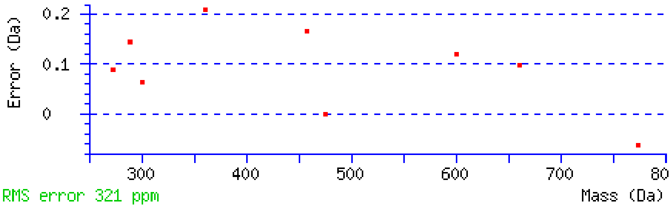
Match to Query 2170: 959.461126 from(480.737839,2+) index(6472)
Title: Elution from: 55.937 to 55.937 scan no 8305 cid35.00 polarity:+
Data file D1d-3_3.mgf

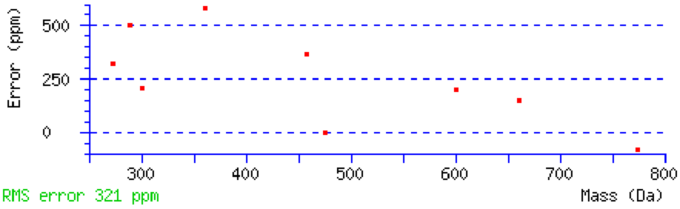
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 959.4613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0027
Matches : 9/50 fragment ions using 22 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							7
2	**300.1707**	150.5890					I	***774.3893***	387.6983	757.3628	379.1850	756.3787	378.6930	6
3	486.2500	243.6286					W	***661.3052***	331.1563	644.2787	322.6430	643.2947	322.1510	5
4	**601.2769**	301.1421			583.2663	292.1368	D	***475.2259***	238.1166	458.1994	229.6033	457.2154	229.1113	4
5	672.3140	336.6606			654.3035	327.6554	A	***360.1990***	180.6031	343.1724	172.0899			3
6	786.3569	393.6821	769.3304	385.1688	768.3464	384.6768	N	***289.1619***	145.0846	272.1353	136.5713			2
7							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of WIWDANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.5	959.4613	-0.0002	WIWDANR
5.6	959.4613	-0.0002	WVWEANR

AT1G78850.1

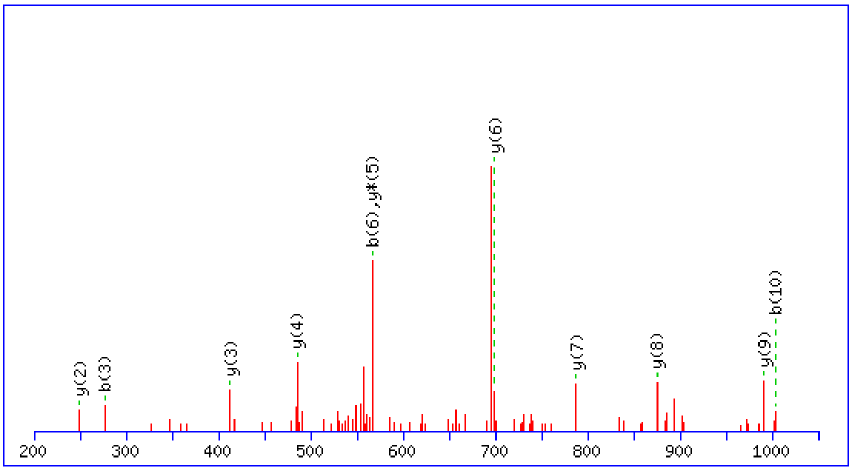
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGDSSLVAYVK**
Found in **AT1G78850.1** in **TAIR_Arabidopsis**, Symbols: | curculin-like (mannose-binding) lectin family protein | chr1:29646965-29648290 REVERSE

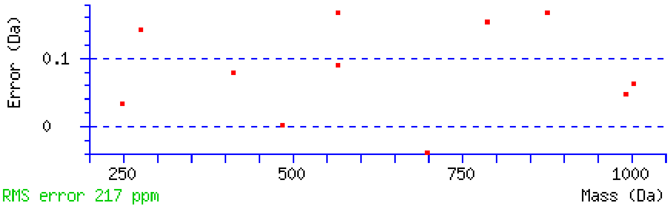
Match to Query 3751: 1150.551034 from(576.282793,2+) index(3983)
Title: Elution from: 37.223 to 37.223 scan no 4987 cid35.00 polarity:+
Data file D6h-3_2.mgf

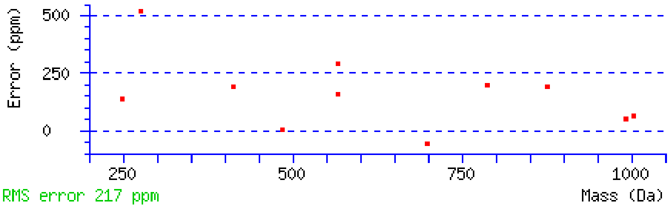
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1150.5514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 2.9e-005
Matches : 11/88 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							11
2	161.0705	81.0389	143.0599	72.0336	G	1049.5140	525.2606	1031.4904	516.2488	1031.5034	516.2553	10
3	**277.0945**	139.0509	259.0839	130.0456	D	***991.4955***	496.2514	973.4719	487.2396	973.4849	487.2461	9
4	365.1235	183.0654	347.1130	174.0601	S	***875.4715***	438.2394	857.4479	429.2276	857.4609	429.2341	8
5	453.1526	227.0799	435.1420	218.0747	S	***787.4424***	394.2249	769.4189	385.2131	769.4319	385.2196	7
6	**567.2337**	284.1205	549.2231	275.1152	L	***699.4134***	350.2103	681.3898	341.1985			6
7	667.2991	334.1532	649.2886	325.1479	V	585.3323	293.1698	567.3087	284.1580			5
8	739.3333	370.1703	721.3227	361.1650	A	***485.2668***	243.1371	467.2433	234.1253			4
9	903.3937	452.2005	885.3831	443.1952	Y	***413.2327***	207.1200	395.2091	198.1082			3
10	**1003.4591**	502.2332	985.4485	493.2279	V	***249.1723***	125.0898	231.1487	116.0780			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TGDSSLVAYVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G78850.1

Score	Mr(calc)	Delta	Sequence
54.4	1150.5514	-0.0004	TGDSSLVAYVK
11.8	1150.5486	0.0024	RNHGFFARK
6.0	1150.5523	-0.0013	MDYPMKKVK
6.0	1150.5514	-0.0004	TAEKTTFDVK
5.9	1150.5519	-0.0008	RSVEKQSSSK
5.3	1150.5541	-0.0030	RFATTVADGAK
2.9	1150.5541	-0.0031	ASSTVANLAFR
2.7	1150.5527	-0.0017	MKQLRAMNK
0.9	1150.5500	0.0010	LLETTMMRK

AT1G78900.1

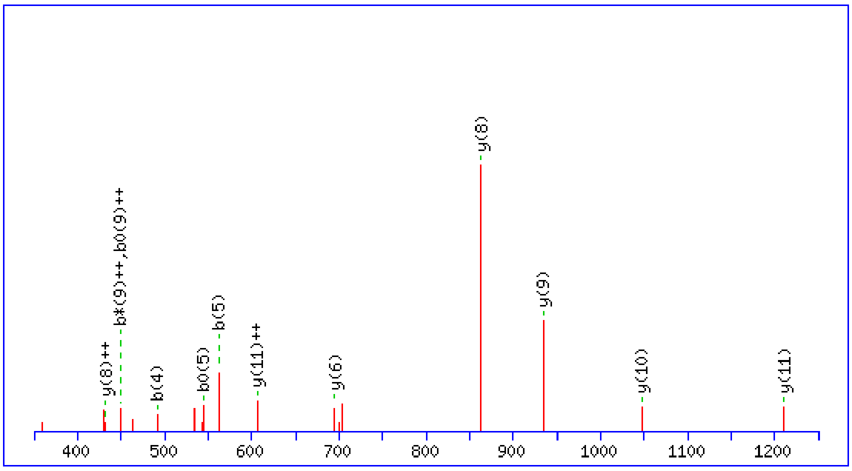
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITYIAPAGQYSLK**
Found in **AT1G78900.1** in **TAIR_Arabidopsis**, Symbols: VHA-A | VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism | chr1:29665356-29669468 FORWARD

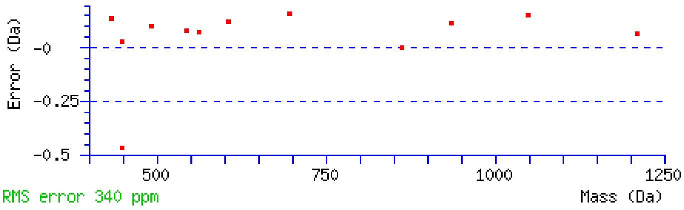
Match to Query 5697: 1423.768854 from(712.891703,2+) index(5422)
Title: Elution from: 47.549 to 47.549 scan no 6799 cid35.00 polarity:+
Data file C7-3_2.mgf

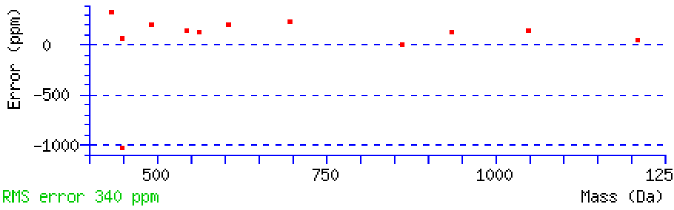
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1423.7711
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00032
Matches : 12/122 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	215.1390	108.0731			197.1285	99.0679	T	1311.6943	656.3508	1294.6678	647.8375	1293.6838	647.3455	12
3	378.2023	189.6048			360.1918	180.5995	Y	***1210.6467***	605.8270	1193.6201	597.3137	1192.6361	596.8217	11
4	**491.2864**	246.1468			473.2758	237.1416	I	***1047.5833***	524.2953	1030.5568	515.7820	1029.5728	515.2900	10
5	**562.3235**	281.6654			544.3130	272.6601	A	***934.4993***	467.7533	917.4727	459.2400	916.4887	458.7480	9
6	659.3763	330.1918			641.3657	321.1865	P	***863.4621***	432.2347	846.4356	423.7214	845.4516	423.2294	8
7	730.4134	365.7103			712.4028	356.7051	A	766.4094	383.7083	749.3828	375.1951	748.3988	374.7030	7
8	787.4349	394.2211			769.4243	385.2158	G	***695.3723***	348.1898	678.3457	339.6765	677.3617	339.1845	6
9	915.4934	458.2504	898.4669	449.7371	897.4829	449.2451	Q	638.3508	319.6790	621.3243	311.1658	620.3402	310.6738	5
10	1078.5568	539.7820	1061.5302	531.2688	1060.5462	530.7767	Y	510.2922	255.6498	493.2657	247.1365	492.2817	246.6445	4
11	1165.5888	583.2980	1148.5623	574.7848	1147.5782	574.2928	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	1278.6729	639.8401	1261.6463	631.3268	1260.6623	630.8348	L	260.1969	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ITYIAPAGQYSLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT1G78900.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.5	1423.7711	-0.0022	ITYIAPAGQYSLK

AT1G79040.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGANVDGYSPIYNENEWSASGDVYK**
Found in **AT1G79040.1** in **TAIR_Arabidopsis**, Symbols: PSBR | PSBR (photosystem II subunit R) | chr1:29740978-29741674 FORWARD

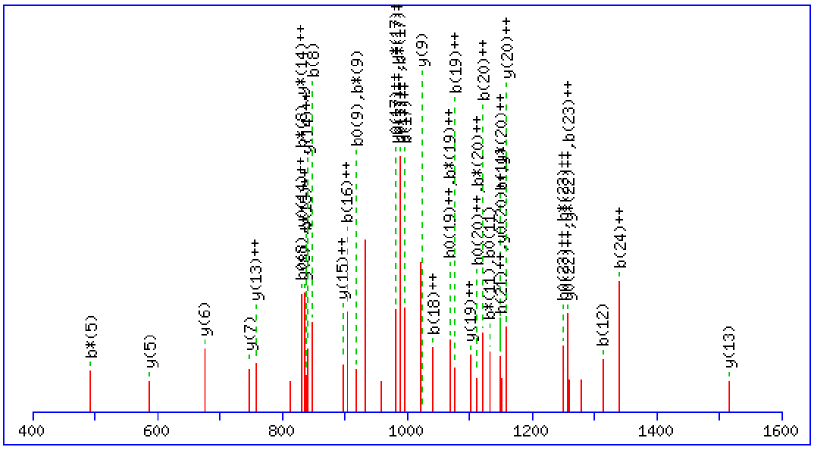
Match to Query 10278: 2827.126539 from(943.382789,3+) index(7433)
Title: Elution from: 67.920 to 67.920 scan no 9857 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

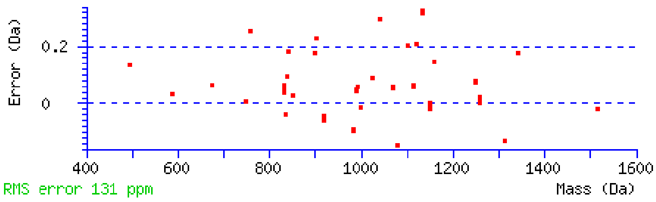
Show Y-axis ☐

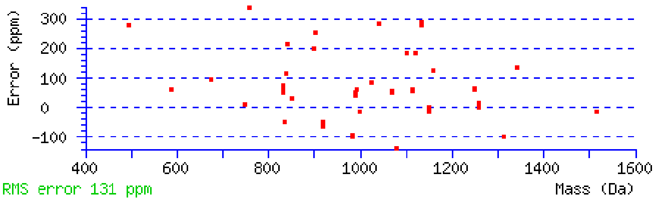


Monoisotopic mass of neutral peptide Mr(calc): 2827.1254
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90 **Expect:** 1.4e-009
Matches : 47/266 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	165.0676	83.0375					**Y**							**25**
2	223.0861	112.0467					**G**	2664.0723	1332.5398	2646.0487	1323.5280	2646.0618	1323.5345	**24**
3	295.1203	148.0638					**A**	2606.0538	1303.5306	2588.0302	1294.5188	2588.0433	1294.5253	**23**
4	411.1573	206.0823	393.1337	197.0705			**N**	2534.0197	1267.5135	2515.9961	1258.5017	2516.0091	1258.5082	**22**
5	511.2227	256.1150	493.1991	247.1032			**V**	2417.9827	1209.4950	2399.9591	1200.4832	2399.9721	1200.4897	**21**
6	627.2467	314.1270	609.2231	305.1152	609.2361	305.1217	**D**	2317.9172	1159.4623	2299.8937	1150.4505	2299.9067	1150.4570	**20**
7	685.2652	343.1362	667.2416	334.1245	667.2546	334.1310	**G**	2201.8933	1101.4503	2183.8697	1092.4385	2183.8827	1092.4450	**19**
8	**849.3256**	425.1664	831.3020	416.1546	831.3150	416.1611	**Y**	2143.8748	1072.4410	2125.8512	1063.4292	2125.8642	1063.4357	**18**
9	937.3546	469.1810	919.3311	460.1692	919.3441	460.1757	**S**	1979.8144	990.4108	1961.7908	981.3990	1961.8038	981.4056	**17**
10	1035.4044	518.2059	1017.3809	509.1941	1017.3939	509.2006	**P**	1891.7853	946.3963	1873.7617	937.3845	1873.7748	937.3910	**16**
11	**1149.4855**	575.2464	1131.4620	566.2346	1131.4750	566.2411	**I**	1793.7355	897.3714	1775.7120	888.3596	1775.7250	888.3661	**15**
12	**1313.5459**	657.2766	1295.5223	648.2648	1295.5353	648.2713	**Y**	1679.6544	840.3309	1661.6309	831.3191	1661.6439	831.3256	**14**
13	1429.5829	715.2951	1411.5593	706.2833	1411.5723	706.2898	**N**	**1515.5941**	758.3007	1497.5705	749.2889	1497.5835	749.2954	**13**
14	1559.6225	780.3149	1541.5989	771.3031	1541.6120	771.3096	**E**	1399.5571	700.2822	1381.5335	691.2704	1381.5465	691.2769	**12**
15	1675.6595	***838.3334***	1657.6359	829.3216	1657.6490	829.3281	**N**	1269.5174	635.2624	1251.4939	626.2506	1251.5069	626.2571	**11**
16	1805.6991	***903.3532***	1787.6756	894.3414	1787.6886	894.3479	**E**	1153.4805	577.2439	1135.4569	568.2321	1135.4699	568.2386	**10**
17	1993.7725	***997.3899***	1975.7489	988.3781	1975.7620	988.3846	**W**	**1023.4408**	512.2240	1005.4172	503.2123	1005.4303	503.2188	**9**
18	2081.8016	***1041.4044***	2063.7780	1032.3926	2063.7910	1032.3992	**S**	**835.3674**	418.1874	817.3439	409.1756	817.3569	409.1821	**8**
19	2153.8357	***1077.4215***	2135.8122	1068.4097	2135.8252	1068.4162	**A**	**747.3384**	374.1728	729.3148	365.1610	729.3278	365.1675	**7**
20	2241.8648	***1121.4360***	2223.8412	1112.4242	2223.8542	1112.4308	**S**	**675.3042**	338.1558	657.2806	329.1440	657.2937	329.1505	**6**
21	2299.8833	***1150.4453***	2281.8597	1141.4335	2281.8727	1141.4400	**G**	**587.2752**	294.1412	569.2516	285.1294	569.2646	285.1359	**5**
22	2415.9073	1208.4573	2397.8837	1199.4455	2397.8967	1199.4520	**D**	529.2567	265.1320	511.2331	256.1202	511.2461	256.1267	**4**
23	2515.9727	***1258.4900***	2497.9491	1249.4782	2497.9622	1249.4847	**V**	413.2327	207.1200	395.2091	198.1082			**3**
24	2680.0331	***1340.5202***	2662.0095	1331.5084	2662.0225	1331.5149	**Y**	313.1672	157.0873	295.1437	148.0755			**2**
25							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT1G79040.1





NCBI **BLAST** search of YGANVDGYSPIYNENEWSASGDVYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.3	2827.1254	0.0011	YGANVDGYSPIYNENEWSASGDVYK

Mascot: http://www.matrixscience.com/

AT1G79230.1

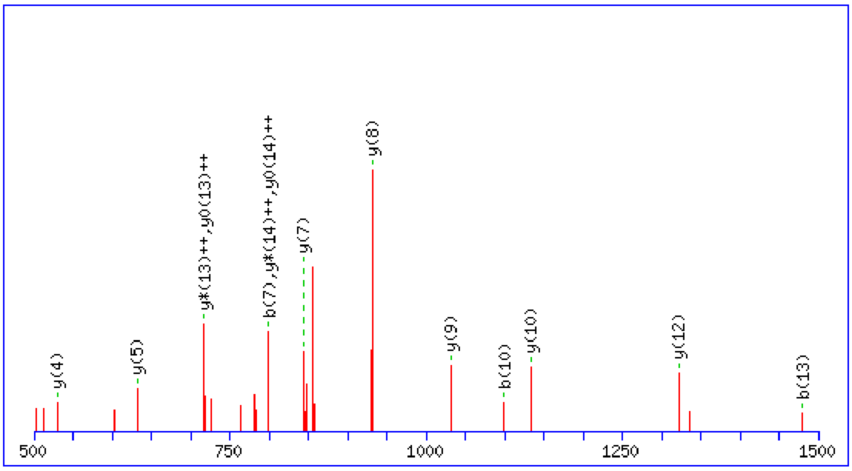
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYQGQTVSPITFQTK**
Found in **AT1G79230.1** in **TAIR_Arabidopsis**, Symbols: ATMST1, MST1, ATRDH1, ST1 | ST1 (MERCAPTOPYRUVATE SULFURTRANSFERASE 1); thiosulfate sulfurtransferase | chr1:29805717-29808572 FORWARD

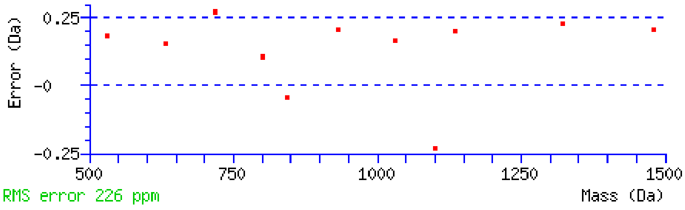
Match to Query 8383: 1728.841234 from(865.427893,2+) index(5619)
Title: Elution from: 50.886 to 50.886 scan no 7113 cid35.00 polarity:+
Data file 0-3_1.mgf

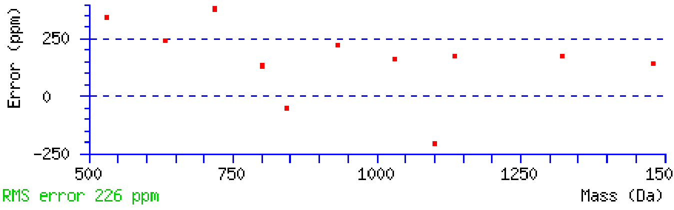
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1728.8425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 3.5e-005
Matches : 14/152 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							15
2	279.1487	140.0780					Y	1615.7687	808.3880	1597.7451	799.3762	1597.7581	799.3827	14
3	409.2014	205.1043	391.1778	196.0925			Q	1451.7083	726.3578	1433.6847	717.3460	1433.6977	717.3525	13
4	467.2199	234.1136	449.1963	225.1018			G	***1321.6557***	661.3315	1303.6321	652.3197	1303.6451	652.3262	12
5	597.2725	299.1399	579.2489	290.1281			Q	1263.6372	632.3222	1245.6136	623.3104	1245.6266	623.3169	11
6	699.3172	350.1623	681.2937	341.1505	681.3067	341.1570	T	***1133.5845***	567.2959	1115.5609	558.2841	1115.5740	558.2906	10
7	**799.3827**	400.1950	781.3591	391.1832	781.3721	391.1897	V	***1031.5398***	516.2735	1013.5162	507.2617	1013.5292	507.2683	9
8	887.4118	444.2095	869.3882	435.1977	869.4012	435.2042	S	***931.4744***	466.2408	913.4508	457.2290	913.4638	457.2355	8
9	985.4616	493.2344	967.4380	484.2226	967.4510	484.2291	P	***843.4453***	422.2263	825.4217	413.2145	825.4347	413.2210	7
10	**1099.5427**	550.2750	1081.5191	541.2632	1081.5321	541.2697	I	745.3955	373.2014	727.3719	364.1896	727.3849	364.1961	6
11	1201.5874	601.2973	1183.5638	592.2855	1183.5768	592.2920	T	***631.3144***	316.1608	613.2908	307.1490	613.3038	307.1556	5
12	1349.6528	675.3300	1331.6292	666.3183	1331.6423	666.3248	F	***529.2697***	265.1385	511.2461	256.1267	511.2591	256.1332	4
13	**1479.7055**	740.3564	1461.6819	731.3446	1461.6949	731.3511	Q	381.2042	191.1058	363.1806	182.0940	363.1937	182.1005	3
14	1581.7502	791.3787	1563.7266	782.3669	1563.7396	782.3734	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT1G79230.1

NCBI **BLAST** search of IYQGQTVSPITFQTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.9	1728.8425	-0.0012	IYQGQTVSPITFQTK
6.0	1728.8429	-0.0017	AVEHIRVLAEEIDGR

AT1G79330.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESGGSSGLGIK**
Found in **AT1G79330.1** in **TAIR_Arabidopsis**, Symbols: AMC6, ATMCP2B, ATMC5 | AMC6/ATMC5/ATMCP2B (TYPE-II METACASPASES); caspase/ cysteine-type endopeptidase | chr1:29843615-29845030 FORWARD

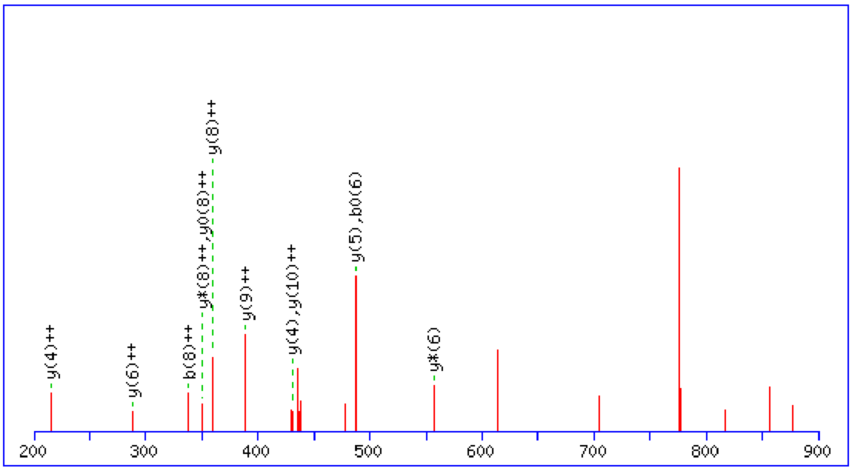
Match to Query 2570: 990.498754 from(496.256653,2+) index(4173)
Title: Elution from: 37.775 to 37.775 scan no 5179 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

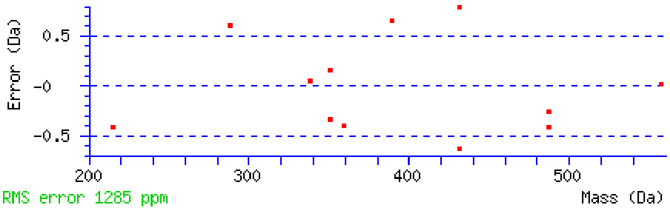
Label all possible matches ○ Label matches used for scoring ●

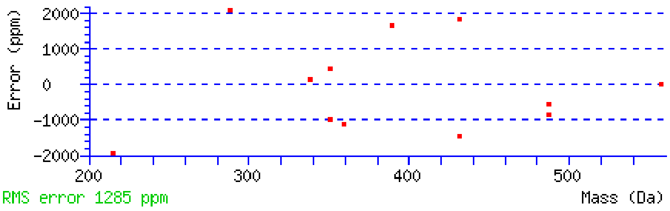
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 990.4982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.018
Matches : 12/90 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							11
2	217.0819	109.0446	199.0713	100.0393	S	862.4629	431.7351	845.4363	423.2218	844.4523	422.7298	10
3	274.1034	137.5553	256.0928	128.5500	G	775.4308	388.2191	758.4043	379.7058	757.4203	379.2138	9
4	331.1248	166.0661	313.1143	157.0608	G	718.4094	359.7083	701.3828	351.1951	700.3988	350.7030	8
5	418.1569	209.5821	400.1463	200.5768	S	661.3879	331.1976	644.3614	322.6843	643.3774	322.1923	7
6	505.1889	253.0981	487.1783	244.0928	S	574.3559	287.6816	557.3293	279.1683	556.3453	278.6763	6
7	562.2103	281.6088	544.1998	272.6035	G	**487.3239**	244.1656	470.2973	235.6523			5
8	675.2944	338.1508	657.2838	329.1456	L	**430.3024**	215.6548	413.2758	207.1416			4
9	732.3159	366.6616	714.3053	357.6563	G	317.2183	159.1128	300.1918	150.5995			3
10	845.3999	423.2036	827.3894	414.1983	I	260.1969	130.6021	243.1703	122.0888			2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ESGGSSGLGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G79330.1

Score	Mr(calc)	Delta	Sequence
22.2	990.4982	0.0006	ESGGSSGLGIK
3.8	990.4982	0.0006	SKEEELTR
3.7	990.4991	-0.0003	MVPMQTIR
3.7	990.4991	-0.0003	MVPMQTIR
1.4	990.4982	0.0006	ASETSLIDR

AT1G79350.1

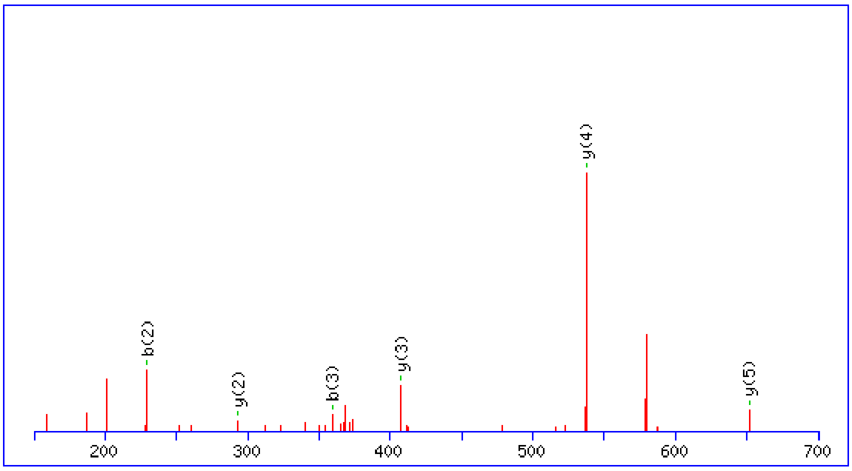
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIEIIR**
Found in **AT1G79350.1** in **TAIR_Arabidopsis**, Symbols: EMB1135 | EMB1135 (EMBRYO DEFECTIVE 1135); DNA binding | chr1:29849722-29858108 REVERSE

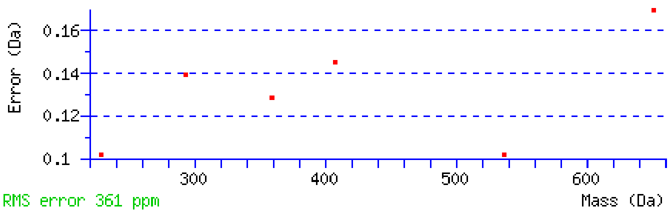
Match to Query 871: 764.464056 from(383.239304,2+) index(5122)
Title: Elution from: 45.560 to 45.560 scan no 6391 cid35.00 polarity:+
Data file D6h-1_1.mgf

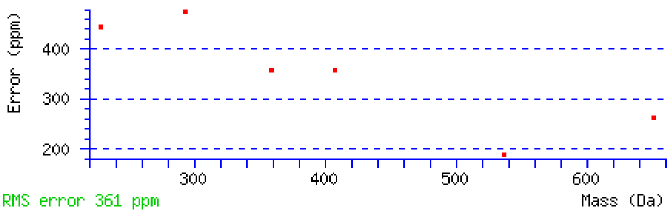
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 764.4638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.03
Matches : 6/40 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							6
2	**229.1695**	115.0884			I	***651.3900***	326.1986	633.3664	317.1869	633.3795	317.1934	5
3	**359.2091**	180.1082	341.1985	171.1029	E	***537.3089***	269.1581	519.2853	260.1463	519.2984	260.1528	4
4	473.2902	237.1487	455.2796	228.1435	I	***407.2693***	204.1383	389.2457	195.1265			3
5	587.3713	294.1893	569.3607	285.1840	I	***293.1882***	147.0977	275.1646	138.0859			2
6					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IIEIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.6	764.4638	0.0002	IIEIIR
20.6	764.4638	0.0002	LIELIR
9.7	764.4638	0.0002	LILELR

AT1G79350.1

9.7	764.4638	0.0002	LLLELR
4.5	764.4638	0.0002	LELILR
0.5	764.4638	0.0002	EIIILR
0.5	764.4638	0.0002	EILILR
0.5	764.4638	0.0002	ELLLLR

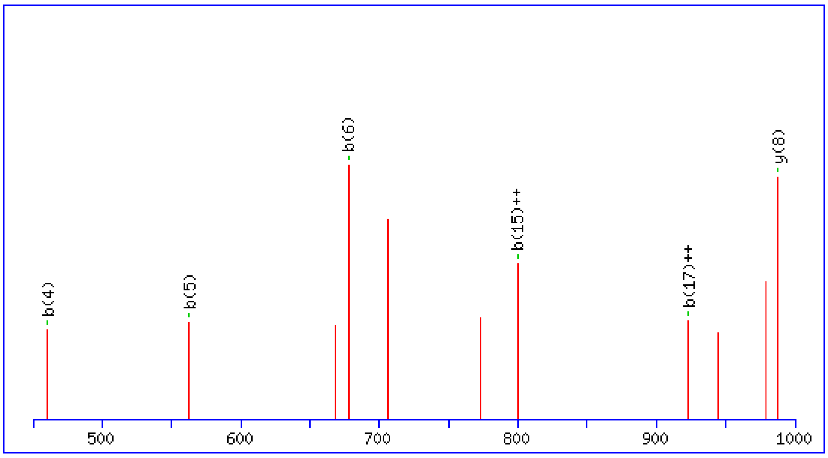
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLNLTIPLGSEVVDDMIRK**
Found in **AT1G79460.1** in **TAIR_Arabidopsis**, Symbols: KS, ATKS, GA2 | GA2 (GA REQUIRING 2); ent-kaurene synthase | chr1:29895461-29899329 FORWARD

Match to Query 9865: 2151.055113 from(718.025647,3+) index(10224)
Title: Elution from: 94.286 to 94.286 scan no 14140 cid35.00 polarity:+
Data file C7-3_1.mgf

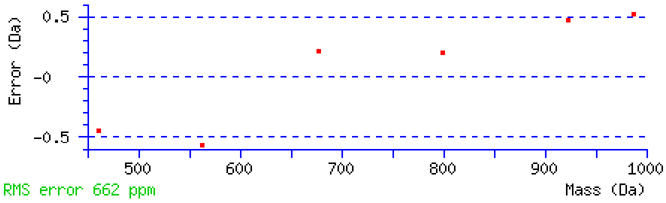
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

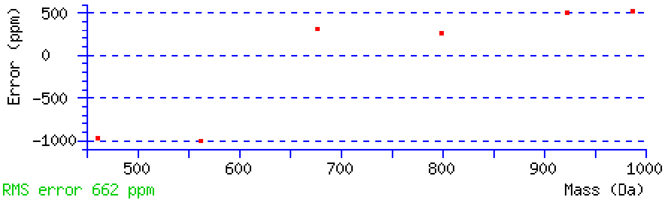


Monoisotopic mass of neutral peptide Mr(calc): 2151.0534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.025
Matches : 6/204 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							19
2	231.1124	116.0598			213.1018	107.0545	L	2036.0367	1018.5220	2018.0131	1009.5102	2018.0261	1009.5167	18
3	347.1493	174.0783	329.1258	165.0665	329.1388	165.0730	N	1921.9556	961.4814	1903.9320	952.4696	1903.9450	952.4762	17
4	***461.2304***	231.1189	443.2069	222.1071	443.2199	222.1136	L	1805.9186	903.4629	1787.8950	894.4511	1787.9080	894.4577	16
5	***563.2752***	282.1412	545.2516	273.1294	545.2646	273.1359	T	1691.8375	846.4224	1673.8139	837.4106	1673.8269	837.4171	15
6	***677.3563***	339.1818	659.3327	330.1700	659.3457	330.1765	I	1589.7928	795.4000	1571.7692	786.3882	1571.7822	786.3947	14
7	775.4061	388.2067	757.3825	379.1949	757.3955	379.2014	P	1475.7117	738.3595	1457.6881	729.3477	1457.7011	729.3542	13
8	889.4872	445.2472	871.4636	436.2354	871.4766	436.2419	L	1377.6619	689.3346	1359.6383	680.3228	1359.6513	680.3293	12
9	947.5057	474.2565	929.4821	465.2447	929.4951	465.2512	G	1263.5808	632.2940	1245.5572	623.2822	1245.5702	623.2887	11
10	1035.5347	518.2710	1017.5111	509.2592	1017.5242	509.2657	S	1205.5623	603.2848	1187.5387	594.2730	1187.5517	594.2795	10
11	1165.5743	583.2908	1147.5508	574.2790	1147.5638	574.2855	E	1117.5332	559.2703	1099.5096	550.2585	1099.5227	550.2650	9
12	1265.6398	633.3235	1247.6162	624.3117	1247.6292	624.3183	V	987.4936	494.2504	969.4700	485.2386	969.4830	485.2452	8
13	1365.7052	683.3563	1347.6817	674.3445	1347.6947	674.3510	V	887.4281	444.2177	869.4046	435.2059	869.4176	435.2124	7
14	1481.7292	741.3683	1463.7056	732.3565	1463.7187	732.3630	D	787.3627	394.1850	769.3391	385.1732	769.3521	385.1797	6
15	1597.7532	***799.3802***	1579.7296	790.3684	1579.7426	790.3750	D	671.3387	336.1730	653.3151	327.1612	653.3282	327.1677	5
16	1729.7907	865.3990	1711.7671	856.3872	1711.7802	856.3937	M	555.3147	278.1610	537.2912	269.1492			4
17	1843.8718	***922.4395***	1825.8482	913.4278	1825.8613	913.4343	I	423.2772	212.1423	405.2536	203.1305			3
18	2003.9611	1002.4842	1985.9375	993.4724	1985.9505	993.4789	R	309.1961	155.1017	291.1725	146.0899			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT1G79460.1





NCBI **BLAST** search of DLNLTIPLGSEVVDDMIRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	2151.0534	0.0017	DLNLTIPLGSEVVDDMIRK
13.3	2151.0531	0.0020	QNANAVLNVIANLQQQNLR
13.1	2151.0561	-0.0010	VLQMIANGKSSLSEIHLER
8.0	2151.0610	-0.0059	RNPDLDPVGPPPPPMIRVR
7.3	2151.0556	-0.0005	KISLGGWEPVDAVAAVEMIK
5.7	2151.0560	-0.0009	QISGPAKTLIDTLQAAGMGPR
4.4	2151.0583	-0.0032	LMNVEGLTIYHVKSHLQK
3.6	2151.0527	0.0024	GFSLLADPERHLITAESLR
2.5	2151.0505	0.0046	KETNPQKNTSLPTSNVLPR
1.5	2151.0576	-0.0025	EKLTHLRVYWHDIVTGR

AT1G79550.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAALADVYVNDAFGTAHR**
Found in **AT1G79550.1** in **TAIR_Arabidopsis**, Symbols: PGK | PGK (PHOSPHOGLYCERATE KINASE) | chr1:29929240-29931188 REVERSE

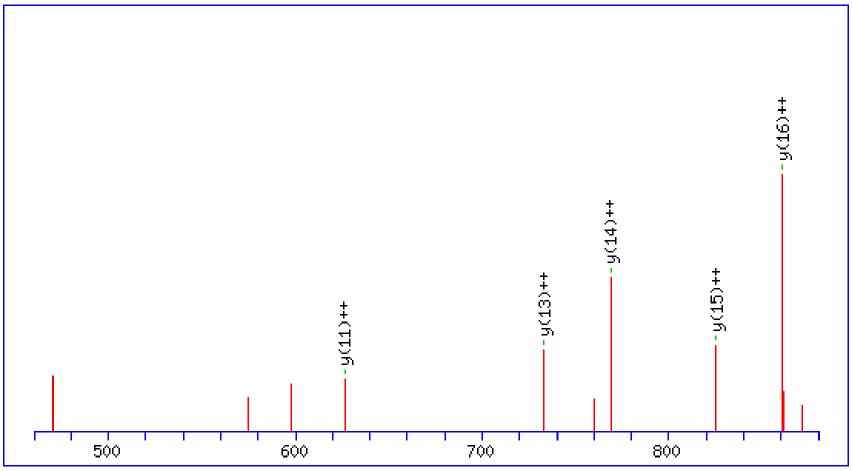
Match to Query 9123: 1902.958785 from(635.326871,3+) index(8058)
Title: Elution from: 73.598 to 73.598 scan no 10662 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 460 to 880 Da Full range

Label all possible matches ○ Label matches used for scoring ●

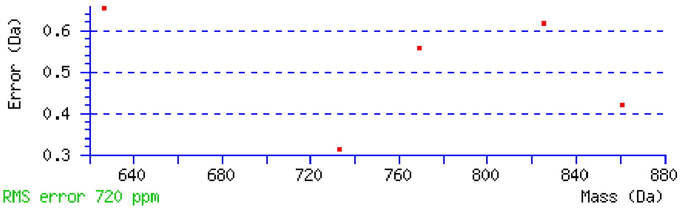
Show Y-axis ☐

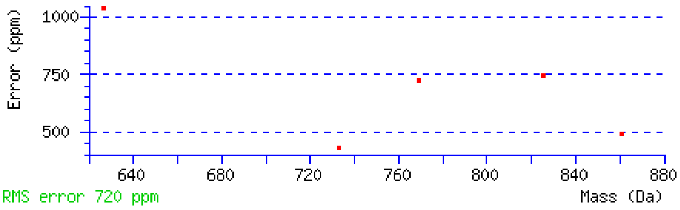


Monoisotopic mass of neutral peptide Mr(calc): 1902.9588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0036
Matches : 5/170 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							18
2	185.1285	93.0679					A	1790.8820	895.9447	1773.8555	887.4314	1772.8715	886.9394	17
3	256.1656	128.5864					A	1719.8449	860.4261	1702.8184	851.9128	1701.8343	851.4208	16
4	369.2496	185.1285					L	1648.8078	824.9075	1631.7812	816.3943	1630.7972	815.9023	15
5	440.2867	220.6470					A	1535.7237	768.3655	1518.6972	759.8522	1517.7132	759.3602	14
6	555.3137	278.1605			537.3031	269.1552	D	1464.6866	732.8469	1447.6601	724.3337	1446.6761	723.8417	13
7	654.3821	327.6947			636.3715	318.6894	V	1349.6597	675.3335	1332.6331	666.8202	1331.6491	666.3282	12
8	817.4454	409.2264			799.4349	400.2211	Y	1250.5913	625.7993	1233.5647	617.2860	1232.5807	616.7940	11
9	916.5138	458.7606			898.5033	449.7553	V	1087.5279	544.2676	1070.5014	535.7543	1069.5174	535.2623	10
10	1030.5568	515.7820	1013.5302	507.2688	1012.5462	506.7767	N	988.4595	494.7334	971.4330	486.2201	970.4490	485.7281	9
11	1145.5837	573.2955	1128.5572	564.7822	1127.5732	564.2902	D	874.4166	437.7119	857.3900	429.1987	856.4060	428.7067	8
12	1216.6208	608.8141	1199.5943	600.3008	1198.6103	599.8088	A	759.3896	380.1985	742.3631	371.6852	741.3791	371.1932	7
13	1363.6892	682.3483	1346.6627	673.8350	1345.6787	673.3430	F	688.3525	344.6799	671.3260	336.1666	670.3420	335.6746	6
14	1420.7107	710.8590	1403.6842	702.3457	1402.7001	701.8537	G	541.2841	271.1457	524.2576	262.6324	523.2736	262.1404	5
15	1521.7584	761.3828	1504.7318	752.8696	1503.7478	752.3775	T	484.2627	242.6350	467.2361	234.1217	466.2521	233.6297	4
16	1592.7955	796.9014	1575.7690	788.3881	1574.7849	787.8961	A	383.2150	192.1111	366.1884	183.5979			3
17	1729.8544	865.4308	1712.8279	856.9176	1711.8438	856.4256	H	312.1779	156.5926	295.1513	148.0793			2
18							R	175.1190	88.0631	158.0924	79.5498			1

AT1G79550.1





NCBI **BLAST** search of LAALADVYVNDAFGTAHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.9	1902.9588	-0.0000	LAALADVYVNDAFGTAHR
0.4	1902.9581	0.0006	QDGNDSLDMLIRRAVGK
0.2	1902.9548	0.0040	SPDRVDSFDVSSPIRAR
0.0	1902.9588	-0.0000	SVFDDQTSKALKNWHK

Mascot: http://www.matrixscience.com/

AT1G79560.1

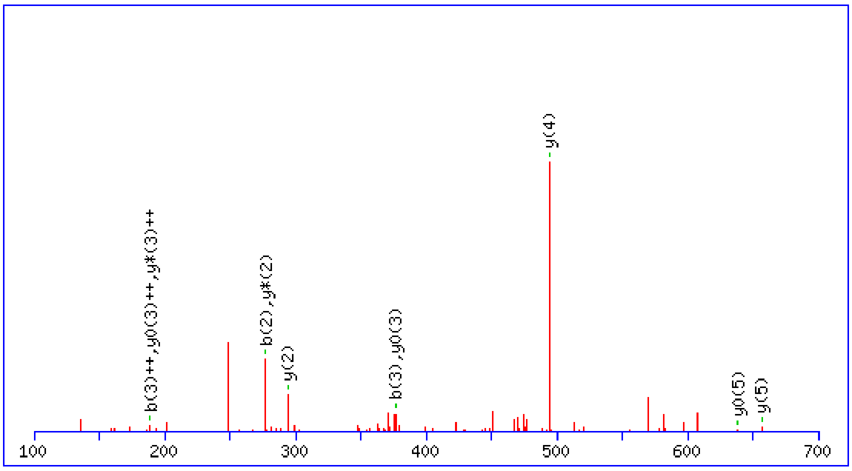
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYVTMK**
Found in **AT1G79560.1** in **TAIR_Arabidopsis**, Symbols: EMB1047, FTSH12 | EMB1047/FTSH12 (EMBRYO DEFECTIVE 1047); ATP-dependent peptidase/ ATPase/ metallopeptidase | chr1:29931869-29937201 FORWARD

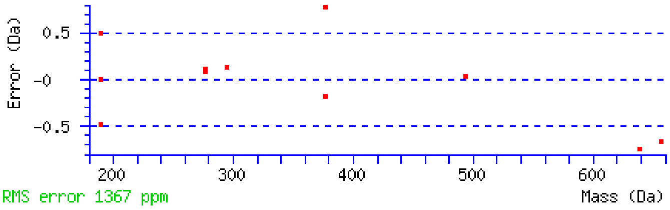
Match to Query 825: 769.404274 from(385.709413,2+) index(2579)
Title: Elution from: 26.805 to 26.805 scan no 3207 cid35.00 polarity:+
Data file D12h-1_3.mgf

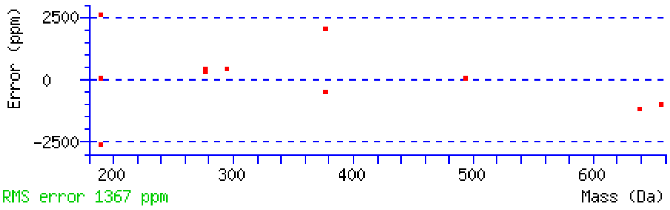
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 769.4044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 15 **Expect:** 0.033
Matches : 11/66 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							6
2	*277.1547*	139.0810			Y	*657.3276*	329.1675	640.3011	320.6542	639.3171	320.1622	5
3	*376.2231*	188.6152			V	*494.2643*	247.6358	477.2377	239.1225	476.2537	238.6305	4
4	477.2708	239.1390	459.2602	230.1337	T	395.1959	198.1016	378.1693	189.5883	377.1853	189.0963	3
5	624.3062	312.6567	606.2956	303.6514	M	*294.1482*	147.5777	277.1217	139.0645			2
6					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LYVTMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.8	769.4044	-0.0001	LYVTMK

AT1G79740.1

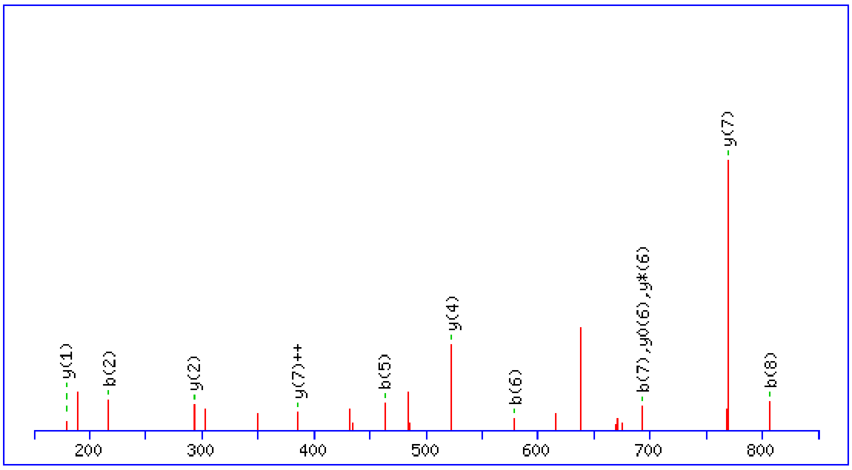
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTGGQDIIR**
Found in **AT1G79740.1** in **TAIR_Arabidopsis**, Symbols: | hAT dimerisation domain-containing protein | chr1:30009260-30011122 REVERSE

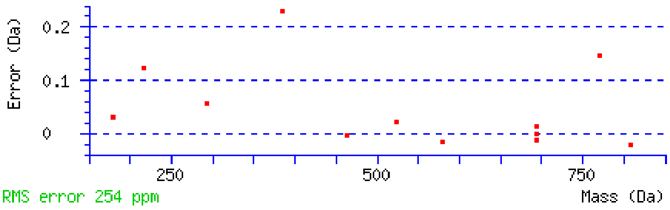
Match to Query 2271: 984.503668 from(493.259110,2+) index(8703)
Title: Elution from: 77.643 to 77.643 scan no 11648 cid35.00 polarity:+
Data file 0-3_2.mgf

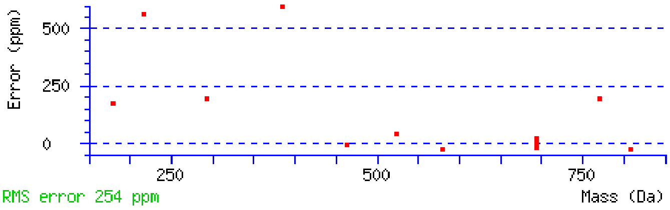
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.5014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.01
Matches : 12/80 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							9
2	***217.1331***	109.0702			199.1225	100.0649	T	871.4276	436.2175	853.4040	427.2057	853.4171	427.2122	8
3	275.1516	138.0794			257.1410	129.0741	G	**769.3829**	385.1951	751.3593	376.1833	751.3723	376.1898	7
4	333.1701	167.0887			315.1595	158.0834	G	711.3644	356.1858	693.3408	347.1741	693.3538	347.1806	6
5	***463.2227***	232.1150	445.1991	223.1032	445.2122	223.1097	Q	653.3459	327.1766	635.3223	318.1648	635.3353	318.1713	5
6	***579.2467***	290.1270	561.2231	281.1152	561.2361	281.1217	D	**523.2933**	262.1503	505.2697	253.1385	505.2827	253.1450	4
7	***693.3278***	347.1675	675.3042	338.1558	675.3172	338.1623	I	407.2693	204.1383	389.2457	195.1265			3
8	***807.4089***	404.2081	789.3853	395.1963	789.3983	395.2028	I	**293.1882**	147.0977	275.1646	138.0859			2
9							R	**179.1071**	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LTGGQDIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.4	984.5014	0.0022	LTGGQDIIR

AT1G79740.1

15.0	984.5014	0.0022	LQTDNIIR
12.6	984.5037	-0.0000	WIEIAVSR
9.2	984.5037	-0.0000	VPNDLFIR
8.7	984.5041	-0.0004	TLRTVHSR
7.7	984.5063	-0.0027	NVFKGLHR
6.7	984.5041	-0.0004	TVRNVGPAR
5.3	984.5063	-0.0027	QWKKGPAR
5.2	984.5014	0.0022	TKVKDEPR
4.7	984.5014	0.0022	EGVNITALR

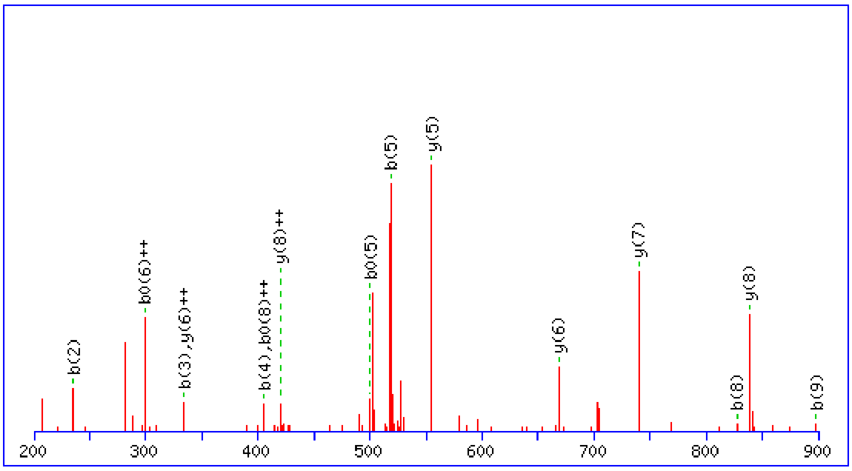
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFVALPVIAR**
Found in **AT1G79850.1** in **TAIR_Arabidopsis**, Symbols: ORE4, CS17, PRPS17, RPS17 | RPS17 (ribosomal protein S17); structural constituent of ribosome | chr1:30046366-30046815 REVERSE

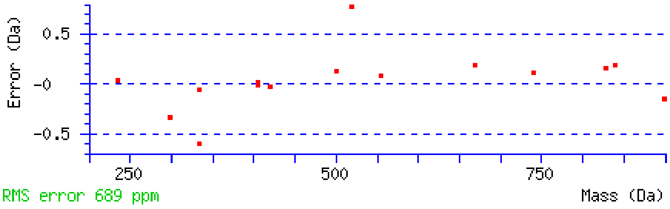
Match to Query 2909: 1071.644784 from(536.829668,2+) index(7140)
Title: Elution from: 62.307 to 62.307 scan no 9300 cid35.00 polarity:+
Data file D6h-3_3.mgf

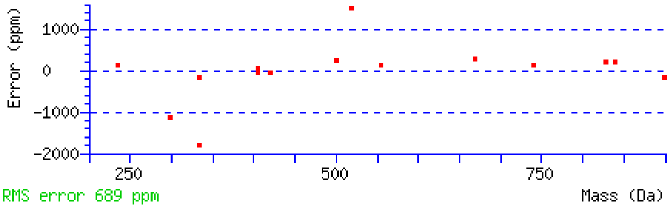
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1071.6441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00022
Matches : 15/72 fragment ions using 26 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	88.0393	44.5233	70.0287	35.5180	S					10
2	***235.1077***	118.0575	217.0972	109.0522	F	985.6193	493.3133	968.5928	484.8000	9
3	***334.1761***	167.5917	316.1656	158.5864	V	**838.5509**	419.7791	821.5244	411.2658	8
4	***405.2132***	203.1103	387.2027	194.1050	A	**739.4825**	370.2449	722.4559	361.7316	7
5	***518.2973***	259.6523	500.2867	250.6470	L	**668.4454**	334.7263	651.4188	326.2130	6
6	615.3501	308.1787	597.3395	299.1734	P	**555.3613**	278.1843	538.3348	269.6710	5
7	714.4185	357.7129	696.4079	348.7076	V	458.3085	229.6579	441.2820	221.1446	4
8	***827.5026***	414.2549	809.4920	405.2496	I	359.2401	180.1237	342.2136	171.6104	3
9	***898.5397***	449.7735	880.5291	440.7682	A	246.1561	123.5817	229.1295	115.0684	2
10					R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of SFVALPVIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G79850.1

Score	Mr(calc)	Delta	Sequence
38.3	1071.6441	0.0007	SFVALPVIAR
0.1	1071.6441	0.0007	LAPSGFVLLR

Mascot: http://www.matrixscience.com/

AT1G79920.1

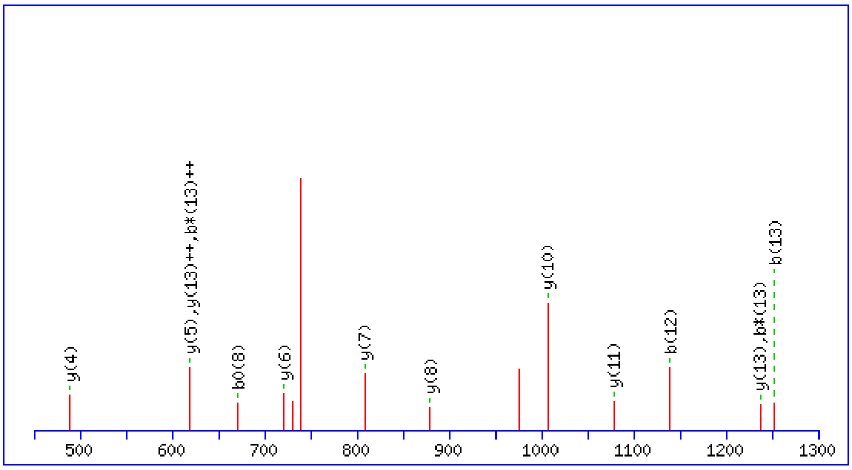
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FIGTAGAASTMMNPK**
Found in **AT1G79920.1** in **TAIR_Arabidopsis**, Symbols: | heat shock protein 70, putative / HSP70, putative | chr1:30064195-30067117 REVERSE

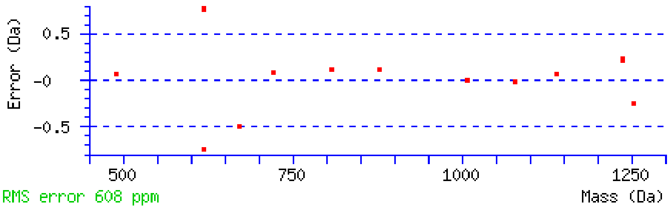
Match to Query 5859: 1495.716876 from(748.865714,2+) index(4294)
Title: Elution from: 42.650 to 42.650 scan no 5514 cid35.00 polarity:+
Data file D1d-2_2.mgf

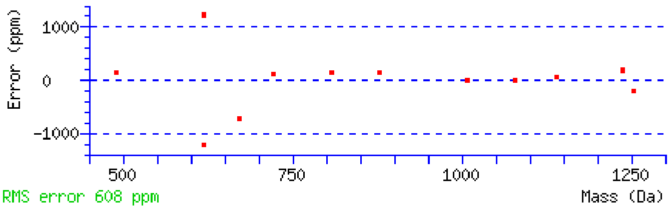
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1495.7163
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 8.9e-008
Matches : 14/128 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							15
2	261.1598	131.0835					I	1349.6552	675.3312	1332.6286	666.8180	1331.6446	666.3259	14
3	318.1812	159.5942					G	***1236.5711***	618.7892	1219.5446	610.2759	1218.5606	609.7839	13
4	419.2289	210.1181			401.2183	201.1128	T	1179.5497	590.2785	1162.5231	581.7652	1161.5391	581.2732	12
5	490.2660	245.6366			472.2554	236.6314	A	***1078.5020***	539.7546	1061.4754	531.2414	1060.4914	530.7493	11
6	547.2875	274.1474			529.2769	265.1421	G	***1007.4649***	504.2361	990.4383	495.7228	989.4543	495.2308	10
7	618.3246	309.6659			600.3140	300.6607	A	950.4434	475.7253	933.4169	467.2121	932.4328	466.7201	9
8	689.3617	345.1845			671.3511	336.1792	A	***879.4063***	440.2068	862.3797	431.6935	861.3957	431.2015	8
9	776.3937	388.7005			758.3832	379.6952	S	***808.3692***	404.6882	791.3426	396.1749	790.3586	395.6829	7
10	877.4414	439.2243			859.4308	430.2191	T	***721.3371***	361.1722	704.3106	352.6589	703.3266	352.1669	6
11	1008.4819	504.7446			990.4713	495.7393	M	***620.2895***	310.6484	603.2629	302.1351			5
12	**1139.5224**	570.2648			1121.5118	561.2595	M	***489.2490***	245.1281	472.2224	236.6149			4
13	**1253.5653**	627.2863	1236.5388	618.7730	1235.5547	618.2810	N	358.2085	179.6079	341.1819	171.0946			3
14	1350.6181	675.8127	1333.5915	667.2994	1332.6075	666.8074	P	244.1656	122.5864	227.1390	114.0731			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FIGTAGAASTMMNPK

AT1G79920.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
77.9	1495.7163	0.0006	FIGTAGAASTMMNPK
3.8	1495.7163	0.0006	NEACKQMLVYPK
3.6	1495.7168	0.0001	SWDTRSFQQVSR
3.4	1495.7154	0.0015	EHIEALETESNPK
1.5	1495.7163	0.0006	MLDMGFEPQIRK
1.2	1495.7130	0.0039	YPSDVVPCEFRK
1.2	1495.7163	0.0006	QQMTFNDMQLLK
1.0	1495.7197	-0.0028	KCVSDMLKDCLK
0.8	1495.7188	-0.0019	IMTSTVDIKDDSR

AT1G79930.1

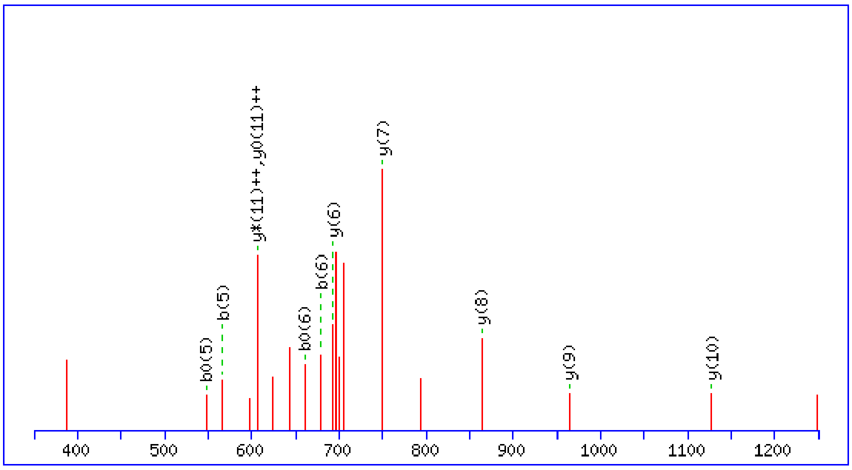
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISTYTIGPFQSSK**
Found in **AT1G79930.1** in **TAIR_Arabidopsis**, Symbols: HSP91 | HSP91 (Heat shock protein 91) | chr1:30068674-30071960 REVERSE

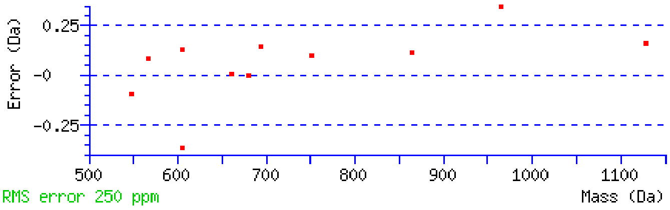
Match to Query 5421: 1427.726858 from(714.870705,2+) index(5485)
Title: Elution from: 48.892 to 48.892 scan no 7069 cid35.00 polarity:+
Data file D12h-3_3.mgf

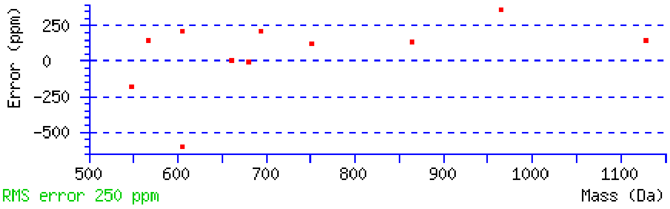
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1427.7296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0015
Matches : 11/122 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	201.1234	101.0653			183.1128	92.0600	S	1315.6529	658.3301	1298.6263	649.8168	1297.6423	649.3248	12
3	302.1710	151.5892			284.1605	142.5839	T	1228.6208	614.8141	1211.5943	606.3008	1210.6103	605.8088	11
4	465.2344	233.1208			447.2238	224.1155	Y	***1127.5732***	564.2902	1110.5466	555.7769	1109.5626	555.2849	10
5	**566.2821**	283.6447			548.2715	274.6394	T	***964.5098***	482.7585	947.4833	474.2453	946.4993	473.7533	9
6	**679.3661**	340.1867			661.3556	331.1814	I	***863.4621***	432.2347	846.4356	423.7214	845.4516	423.2294	8
7	736.3876	368.6974			718.3770	359.6921	G	***750.3781***	375.6927	733.3515	367.1794	732.3675	366.6874	7
8	833.4403	417.2238			815.4298	408.2185	P	***693.3566***	347.1819	676.3301	338.6687	675.3461	338.1767	6
9	980.5088	490.7580			962.4982	481.7527	F	596.3039	298.6556	579.2773	290.1423	578.2933	289.6503	5
10	1108.5673	554.7873	1091.5408	546.2740	1090.5568	545.7820	Q	449.2354	225.1214	432.2089	216.6081	431.2249	216.1161	4
11	1195.5994	598.3033	1178.5728	589.7900	1177.5888	589.2980	S	321.1769	161.0921	304.1503	152.5788	303.1663	152.0868	3
12	1282.6314	641.8193	1265.6048	633.3061	1264.6208	632.8141	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ISTYTIGPFQSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT1G79930.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.5	1427.7296	-0.0028	ISTYTIGPFQSSK

Mascot: http://www.matrixscience.com/

AT1G80380.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVDPQLEVVNK**
Found in **AT1G80380.1** in **TAIR_Arabidopsis**, Symbols: | phosphoribulokinase/uridine kinase-related | chr1:30222224-30224676 FORWARD

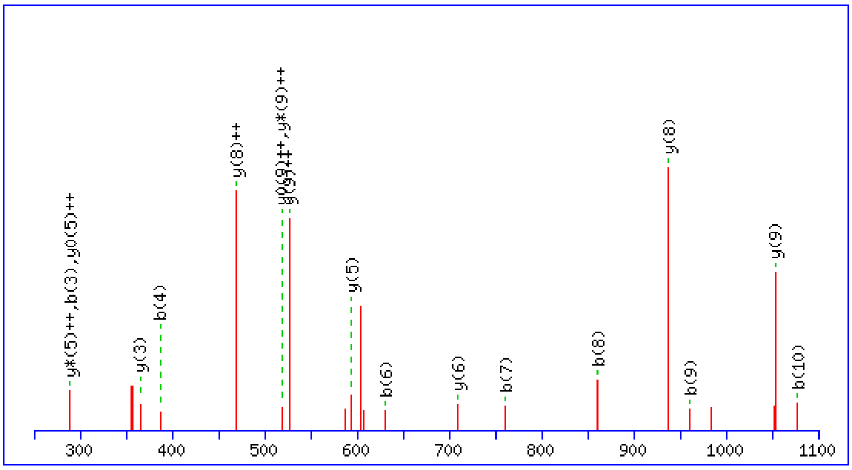
Match to Query 4155: 1224.614698 from(613.314625,2+) index(3065)
Title: Elution from: 30.492 to 30.492 scan no 3806 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1100 Da Full range

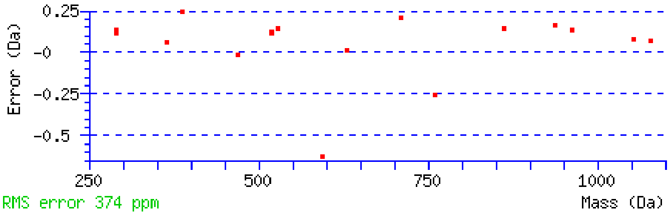
Label all possible matches ○ Label matches used for scoring ●

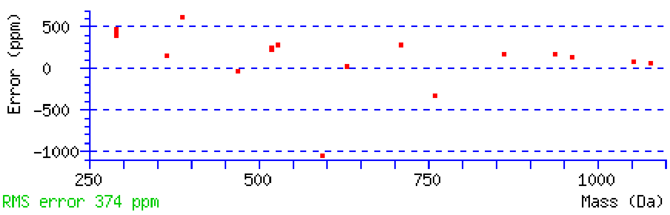
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1224.6142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1e-005
Matches : 18/100 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							11
2	173.1069	87.0571					V	1153.5874	577.2973	1135.5638	568.2855	1135.5768	568.2920	10
3	***289.1309***	145.0691			271.1203	136.0638	D	***1053.5219***	527.2646	1035.4983	518.2528	1035.5114	518.2593	9
4	***387.1807***	194.0940			369.1701	185.0887	P	***937.4979***	469.2526	919.4744	460.2408	919.4874	460.2473	8
5	517.2333	259.1203	499.2097	250.1085	499.2227	250.1150	Q	839.4481	420.2277	821.4246	411.2159	821.4376	411.2224	7
6	***631.3144***	316.1608	613.2908	307.1490	613.3038	307.1556	L	***709.3955***	355.2014	691.3719	346.1896	691.3849	346.1961	6
7	***761.3540***	381.1807	743.3304	372.1689	743.3435	372.1754	E	***595.3144***	298.1608	577.2908	289.1490	577.3038	289.1556	5
8	***861.4195***	431.2134	843.3959	422.2016	843.4089	422.2081	V	465.2748	233.1410	447.2512	224.1292			4
9	***961.4849***	481.2461	943.4613	472.2343	943.4744	472.2408	V	***365.2093***	183.1083	347.1857	174.0965			3
10	***1077.5219***	539.2646	1059.4983	530.2528	1059.5114	530.2593	N	265.1439	133.0756	247.1203	124.0638			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AVDPQLEVVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G80380.1

Score	Mr(calc)	Delta	Sequence
56.9	1224.6142	0.0005	AVDPQLEVVNK
4.2	1224.6169	-0.0022	VSKRTGGYVNK
3.6	1224.6169	-0.0022	AVYESLSRRK
2.7	1224.6169	-0.0022	AREVLATPSHK
1.1	1224.6122	0.0025	RICPGVGLAHK

AT1G80600.1

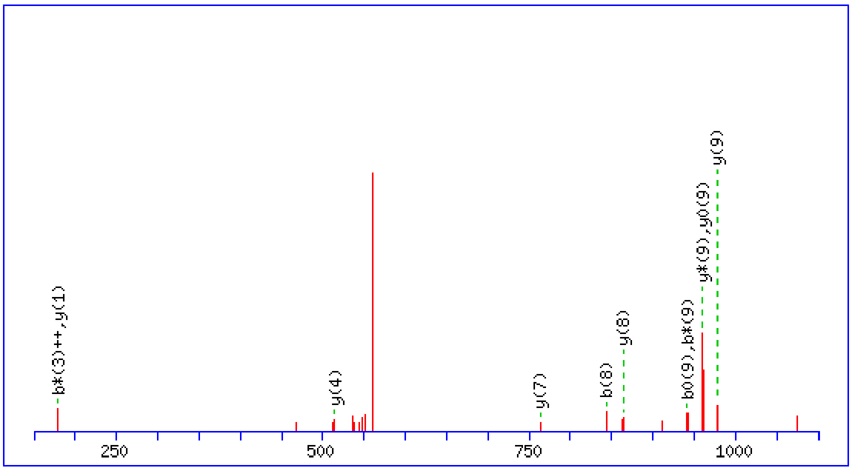
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RLVASSFADR**
Found in **AT1G80600.1** in **TAIR_Arabidopsis**, Symbols: | acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOTA, putative / ACOAT, putative | chr1:30303567-30305405 REVERSE

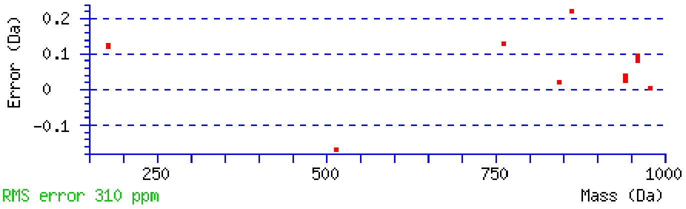
Match to Query 3521: 1136.548736 from(569.281644,2+) index(1807)
Title: Elution from: 21.491 to 21.491 scan no 2336 cid35.00 polarity:+
Data file 0-3_3.mgf

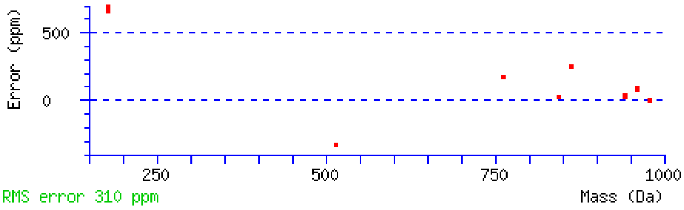
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1136.5515
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0097
Matches : 12/98 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							10
2	275.1776	138.0925	257.1540	129.0807			L	***977.4695***	489.2384	959.4459	480.2266	959.4589	480.2331	9
3	375.2431	188.1252	357.2195	179.1134			V	***863.3884***	432.1978	845.3648	423.1860	845.3778	423.1926	8
4	447.2772	224.1422	429.2536	215.1305			A	***763.3229***	382.1651	745.2994	373.1533	745.3124	373.1598	7
5	535.3063	268.1568	517.2827	259.1450	517.2957	259.1515	S	691.2888	346.1480	673.2652	337.1362	673.2782	337.1428	6
6	623.3353	312.1713	605.3118	303.1595	605.3248	303.1660	S	603.2597	302.1335	585.2361	293.1217	585.2492	293.1282	5
7	771.4008	386.2040	753.3772	377.1922	753.3902	377.1988	F	***515.2307***	258.1190	497.2071	249.1072	497.2201	249.1137	4
8	**843.4349**	422.2211	825.4114	413.2093	825.4244	413.2158	A	367.1652	184.0862	349.1416	175.0745	349.1547	175.0810	3
9	**959.4589**	480.2331	941.4353	471.2213	941.4484	471.2278	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
10							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RLVASSFADR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT1G80600.1

Score	Mr(calc)	Delta	Sequence
28.8	1136.5515	-0.0027	RLVASSFADR
14.5	1136.5515	-0.0027	IRVNYATER
11.8	1136.5515	-0.0027	RDFLQSLSR
6.0	1136.5488	-0.0001	LEEYKSISR
4.6	1136.5515	-0.0027	ALSSSPRFTR
4.6	1136.5515	-0.0027	IASQLDRYR
4.6	1136.5515	-0.0027	EYEKLQRR
4.5	1136.5515	-0.0027	FSREAAATIR
4.5	1136.5515	-0.0027	IKEEYQRR
4.5	1136.5515	-0.0027	LQQSKNTFR

AT1G80660.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALDLGVNVK**
Found in **AT1G80660.1** in **TAIR_Arabidopsis**, Symbols: AHA9 | AHA9 (Arabidopsis H(+)-ATPase 9); hydrogen-exporting ATPase, phosphorylative mechanism | chr1:30321119-30324840 REVERSE

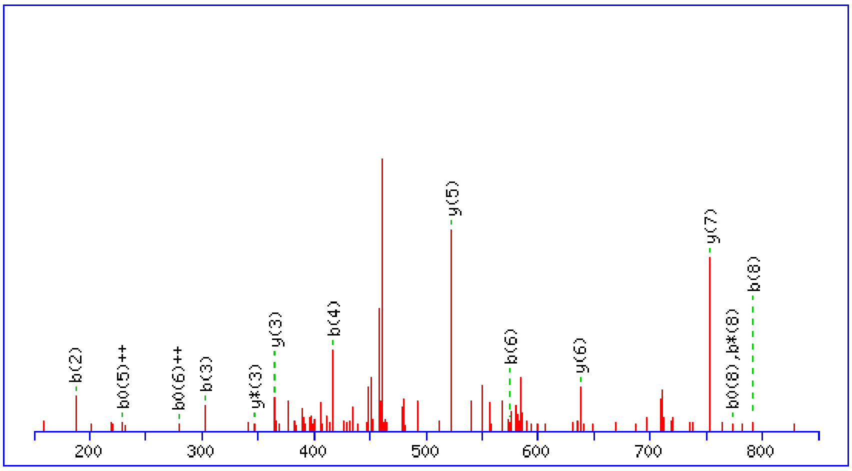
Match to Query 1645: 938.506878 from(470.260715,2+) index(3476)
Title: Elution from: 34.457 to 34.457 scan no 4416 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

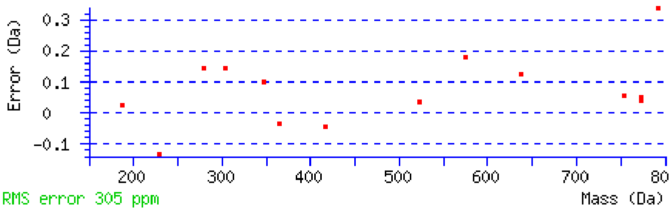
Label all possible matches ○ Label matches used for scoring ●

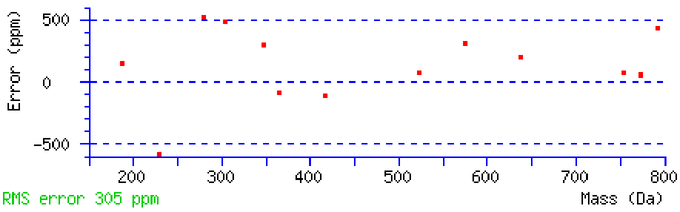
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 938.5063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.022
Matches : 14/68 fragment ions using 34 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244					A							9
2	***187.1225***	94.0649					L	867.4794	434.2434	849.4559	425.2316	849.4689	425.2381	8
3	***303.1465***	152.0769			285.1359	143.0716	D	**753.3983**	377.2028	735.3748	368.1910	735.3878	368.1975	7
4	***417.2276***	209.1174			399.2170	200.1122	L	**637.3744**	319.1908	619.3508	310.1790			6
5	475.2461	238.1267			457.2355	229.1214	G	**523.2933**	262.1503	505.2697	253.1385			5
6	***575.3115***	288.1594			557.3010	279.1541	V	465.2748	233.1410	447.2512	224.1292			4
7	691.3485	346.1779	673.3250	337.1661	673.3380	337.1726	N	**365.2093**	183.1083	347.1857	174.0965			3
8	***791.4140***	396.2106	773.3904	387.1988	773.4034	387.2054	V	249.1723	125.0898	231.1487	116.0780			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ALDLGVNVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT1G80660.1

24.4	938.5063	0.0006	ALDLGVNVK
4.8	938.5063	0.0006	EVGIGIGVGK

AT2G01140.1

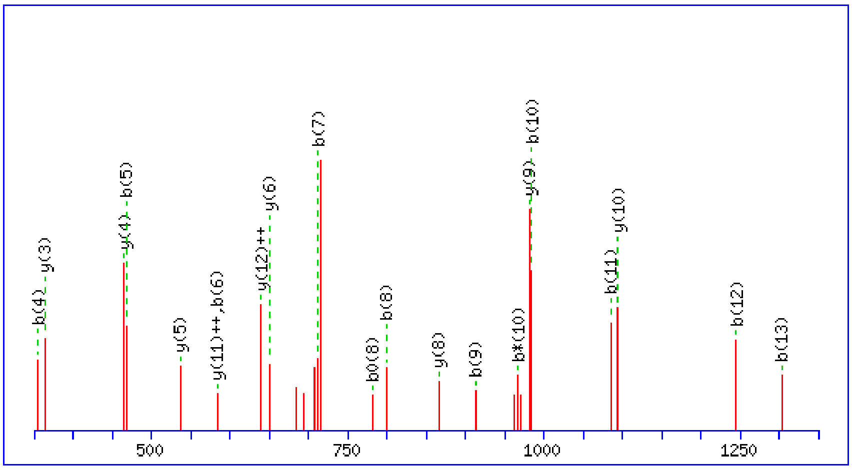
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GILAIDESNATCGK**
Found in **AT2G01140.1** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr2:95005-96490 REVERSE

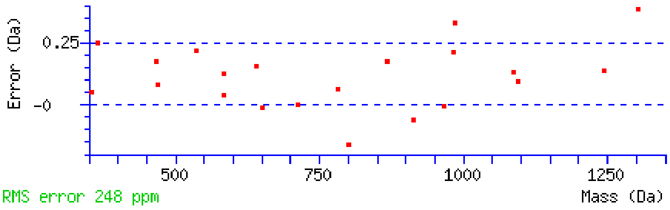
Match to Query 5727: 1447.696320 from(724.855436,2+) index(4066)
Title: Elution from: 41.163 to 41.163 scan no 5256 cid35.00 polarity:+
Data file D12h-2_1.mgf

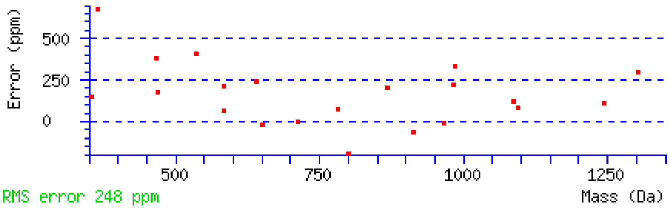
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1447.6977
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 113  Expect: 2e-011
Matches : 21/124 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							14
2	171.1128	86.0600					I	1391.6835	696.3454	1374.6570	687.8321	1373.6729	687.3401	13
3	284.1969	142.6021					L	1278.5994	639.8034	1261.5729	631.2901	1260.5889	630.7981	12
4	***355.2340***	178.1206					A	1165.5154	583.2613	1148.4888	574.7481	1147.5048	574.2560	11
5	***468.3180***	234.6627					I	**1094.4783**	547.7428	1077.4517	539.2295	1076.4677	538.7375	10
6	***583.3450***	292.1761			565.3344	283.1709	D	**981.3942**	491.2007	964.3677	482.6875	963.3836	482.1955	9
7	***712.3876***	356.6974			694.3770	347.6921	E	**866.3673**	433.6873	849.3407	425.1740	848.3567	424.6820	8
8	***799.4196***	400.2134			781.4090	391.2082	S	737.3247	369.1660	720.2981	360.6527	719.3141	360.1607	7
9	***913.4625***	457.2349	896.4360	448.7216	895.4520	448.2296	N	**650.2926**	325.6500	633.2661	317.1367	632.2821	316.6447	6
10	***984.4997***	492.7535	967.4731	484.2402	966.4891	483.7482	A	**536.2497**	268.6285	519.2232	260.1152	518.2391	259.6232	5
11	***1085.5473***	543.2773	1068.5208	534.7640	1067.5368	534.2720	T	**465.2126**	233.1099	448.1860	224.5967	447.2020	224.1047	4
12	***1245.5780***	623.2926	1228.5514	614.7794	1227.5674	614.2873	C	**364.1649**	182.5861	347.1384	174.0728			3
13	***1302.5994***	651.8034	1285.5729	643.2901	1284.5889	642.7981	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GILAIDESNATCGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G01140.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
113.4	1447.6977	-0.0014	GILAIDESNATCGK
8.1	1447.6943	0.0020	ATYEDSSQVHAIK
5.6	1447.6952	0.0011	MYLVGGNMIDAHK
1.1	1447.6977	-0.0014	LGNNPTSDDKMLK

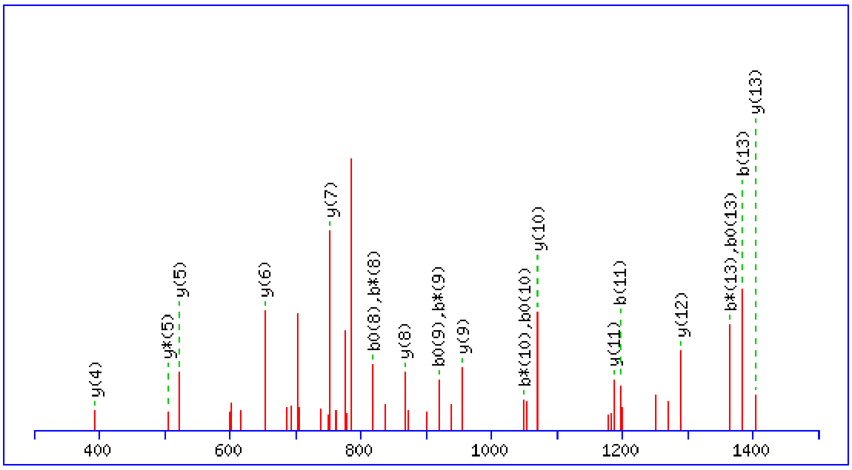
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IALTDNSIVEQALGK**
Found in **AT2G01250.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L7 (RPL7B) | chr2:132942-134263 REVERSE

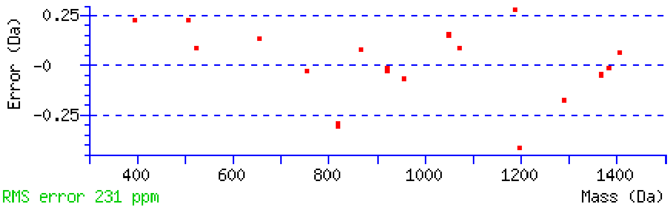
Match to Query 6966: 1588.798616 from(795.406584,2+) index(8327)
Title: Elution from: 73.289 to 73.289 scan no 11093 cid35.00 polarity:+
Data file C7-2_3.mgf

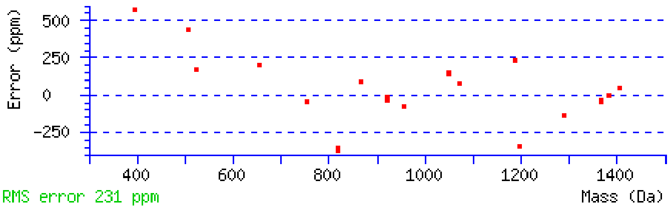
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1588.8033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 104 **Expect:** 1.7e-010
Matches : 21/142 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							15
2	187.1225	94.0649					A	1475.7294	738.3684	1457.7059	729.3566	1457.7189	729.3631	14
3	301.2036	151.1054					L	***1403.6953***	702.3513	1385.6717	693.3395	1385.6847	693.3460	13
4	403.2483	202.1278			385.2378	193.1225	T	***1289.6142***	645.3107	1271.5906	636.2989	1271.6036	636.3055	12
5	519.2723	260.1398			501.2617	251.1345	D	***1187.5695***	594.2884	1169.5459	585.2766	1169.5589	585.2831	11
6	635.3093	318.1583	617.2857	309.1465	617.2987	309.1530	N	***1071.5455***	536.2764	1053.5219	527.2646	1053.5349	527.2711	10
7	723.3384	362.1728	705.3148	353.1610	705.3278	353.1675	S	***955.5085***	478.2579	937.4849	469.2461	937.4979	469.2526	9
8	837.4195	419.2134	819.3959	410.2016	819.4089	410.2081	I	***867.4794***	434.2434	849.4559	425.2316	849.4689	425.2381	8
9	937.4849	469.2461	919.4613	460.2343	919.4744	460.2408	V	***753.3983***	377.2028	735.3748	368.1910	735.3878	368.1975	7
10	1067.5246	534.2659	1049.5010	525.2541	1049.5140	525.2606	E	***653.3329***	327.1701	635.3093	318.1583	635.3223	318.1648	6
11	**1197.5772**	599.2922	1179.5536	590.2804	1179.5666	590.2870	Q	***523.2933***	262.1503	505.2697	253.1385			5
12	1269.6113	635.3093	1251.5878	626.2975	1251.6008	626.3040	A	***393.2406***	197.1239	375.2170	188.1122			4
13	**1383.6924**	692.3499	1365.6689	683.3381	1365.6819	683.3446	L	321.2065	161.1069	303.1829	152.0951			3
14	1441.7109	721.3591	1423.6874	712.3473	1423.7004	712.3538	G	207.1254	104.0663	189.1018	95.0545			2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IALTDNSIVEQALGK

AT2G01250.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
103.6	1588.8033	-0.0046	IALTDNSIVEQALGK
2.6	1588.8033	-0.0047	NELEIGKAAEEKLK
1.1	1588.8008	-0.0021	TKRFVFGSLMIEK
0.5	1588.7974	0.0012	RTFKLPNSIYYVA

AT2G01810.1

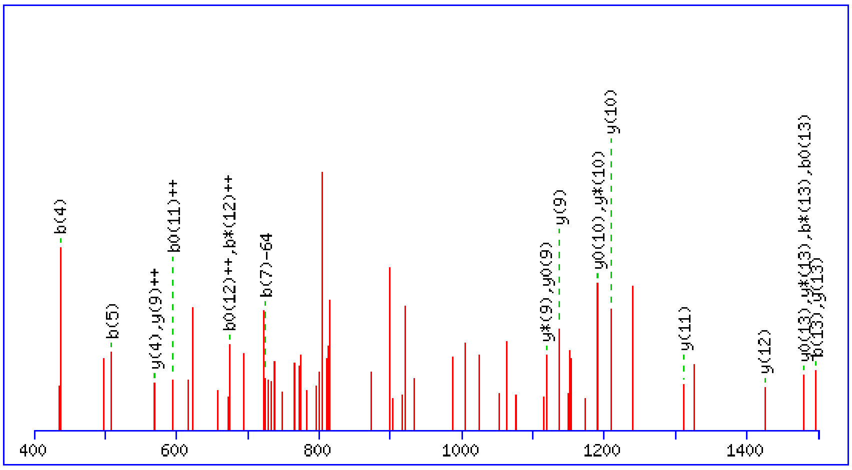
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAITAYDALTERQK**
Found in **AT2G01810.1** in **TAIR_Arabidopsis**, Symbols: | PHD finger family protein | chr2:347536-349951 FORWARD

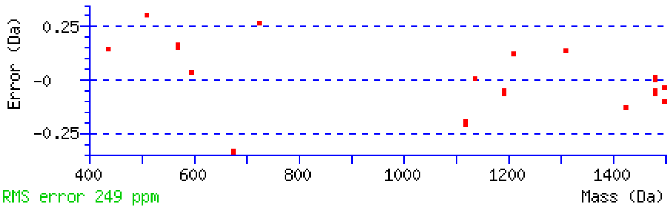
Match to Query 7543: 1644.747312 from(823.380932,2+) index(7317)
Title: Elution from: 65.191 to 65.191 scan no 9616 cid35.00 polarity:+
Data file 0-2_2.mgf

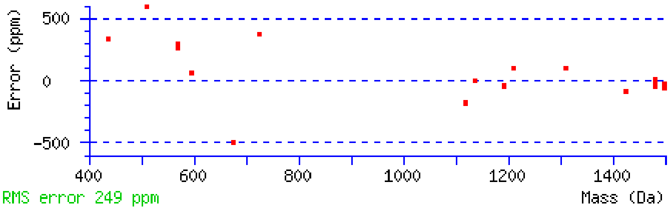
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1644.7520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.031
Matches : 22/172 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							14
2	221.0739	111.0406					A	***1497.7268***	749.3670	1479.7032	740.3553	1479.7162	740.3618	13
3	335.1550	168.0811					I	***1425.6927***	713.3500	1407.6691	704.3382	1407.6821	704.3447	12
4	**437.1997**	219.1035			419.1891	210.0982	T	***1311.6116***	656.3094	1293.5880	647.2976	1293.6010	647.3041	11
5	**509.2338**	255.1205			491.2233	246.1153	A	***1209.5669***	605.2871	1191.5433	596.2753	1191.5563	596.2818	10
6	673.2942	337.1507			655.2836	328.1454	Y	***1137.5327***	569.2700	1119.5091	560.2582	1119.5221	560.2647	9
7	789.3182	395.1627			771.3076	386.1574	D	973.4723	487.2398	955.4488	478.2280	955.4618	478.2345	8
8	861.3523	431.1798			843.3417	422.1745	A	857.4484	429.2278	839.4248	420.2160	839.4378	420.2225	7
9	975.4334	488.2203			957.4228	479.2151	L	785.4142	393.2107	767.3906	384.1990	767.4036	384.2055	6
10	1077.4781	539.2427			1059.4676	530.2374	T	671.3331	336.1702	653.3095	327.1584	653.3225	327.1649	5
11	1207.5178	604.2625			1189.5072	595.2572	E	***569.2884***	285.1478	551.2648	276.1360	551.2778	276.1426	4
12	1367.6070	684.3071	1349.5834	675.2953	1349.5964	675.3019	R	439.2488	220.1280	421.2252	211.1162			3
13	**1497.6596**	749.3335	1479.6361	740.3217	1479.6491	740.3282	Q	279.1595	140.0834	261.1359	131.0716			2
14							K	149.1069	75.0571	131.0833	66.0453			1





AT2G01810.1

NCBI **BLAST** search of MAITAYDALTERQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.6	1644.7520	-0.0046	MAITAYDALTERQK
18.6	1644.7465	0.0008	FHHMLSGRPQDVAK
16.7	1644.7479	-0.0006	MTMLSMGKTLVEQK
16.7	1644.7479	-0.0006	MTMLSMGKTLVEQK
11.2	1644.7479	-0.0006	MTMLSMGKTLVEQK
0.8	1644.7472	0.0001	EVGRAQGMYALTAMK
0.6	1644.7464	0.0009	ENNSSANLKIYSSAK
0.2	1644.7520	-0.0046	MATATATSERFELAK

AT2G02010.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFEVELK**
Found in **AT2G02010.1** in **TAIR_Arabidopsis**, Symbols: GAD4 | GAD4 (GLUTAMATE DECARBOXYLASE 4); calmodulin binding | chr2:474374-476494 REVERSE

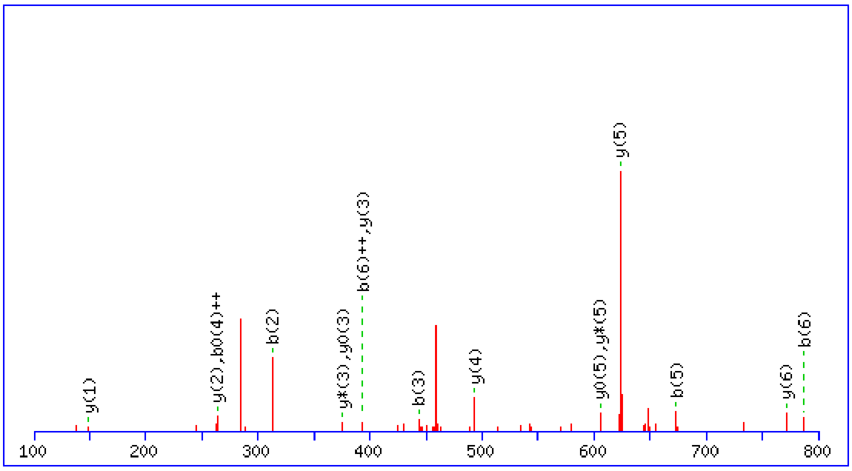
Match to Query 1878: 934.451896 from(468.233224,2+) index(4995)
Title: Elution from: 44.990 to 44.990 scan no 6268 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

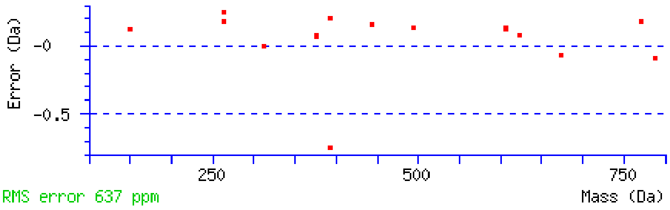
Label all possible matches ○ Label matches used for scoring ●

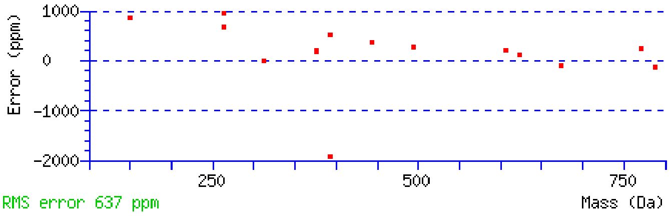
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 934.4512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00021
Matches : 16/52 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375			Y							7
2	**313.1331**	157.0702			F	***771.3981***	386.2027	753.3745	377.1909	753.3876	377.1974	6
3	**443.1727**	222.0900	425.1622	213.0847	E	***623.3327***	312.1700	605.3091	303.1582	605.3221	303.1647	5
4	543.2382	272.1227	525.2276	263.1174	V	***493.2930***	247.1502	475.2695	238.1384	475.2825	238.1449	4
5	**673.2778**	337.1425	655.2672	328.1373	E	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
6	**787.3589**	394.1831	769.3483	385.1778	L	***263.1880***	132.0976	245.1644	123.0858			2
7					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YFEVELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.9	934.4512	0.0007	YFEVELK
31.7	934.4512	0.0007	YFLDELK

AT2G02010.1

11.7	934.4512	0.0007	FLEYLDK
9.7	934.4532	-0.0013	KIMMMIK
9.7	934.4532	-0.0013	KIMMMIK
6.8	934.4539	-0.0020	FINLDFR
5.5	934.4516	0.0003	KAASQYQK
5.3	934.4503	0.0016	KMCLRSK
4.6	934.4516	0.0003	TVERYQK
4.5	934.4516	0.0003	FREESKK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLMEILK**
Found in **AT2G02560.1** in **TAIR_Arabidopsis**, Symbols: ATCAND1, ETA2, TIP120, HVE, CAND1 | CAND1 (CULLIN-ASSOCIATED AND NEDDYLATION DISSOCIATED); binding | chr2:690344-697341 FORWARD

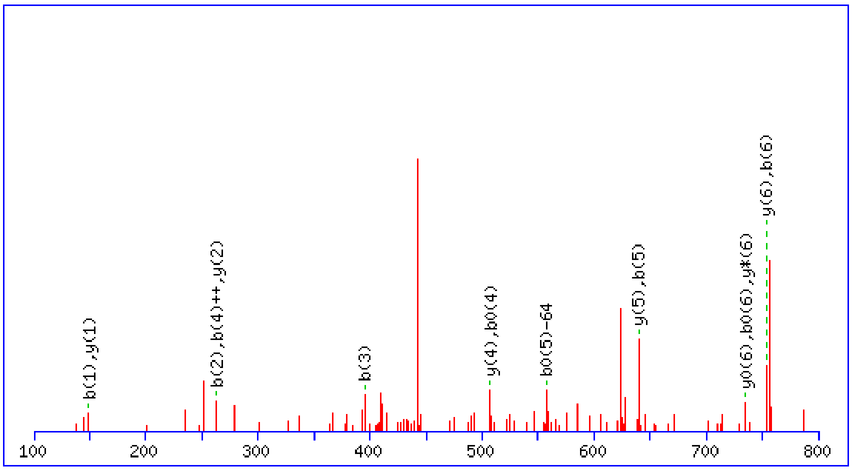
Match to Query 1573: 900.451406 from(451.232979,2+) index(2595)
Title: Elution from: 28.214 to 28.214 scan no 3308 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

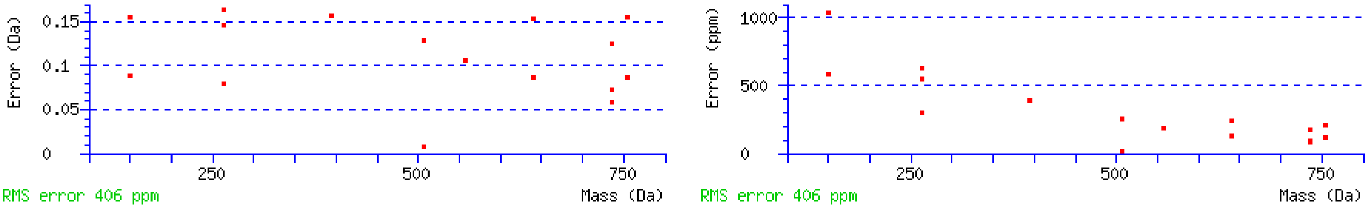
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 900.4525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.005
Matches : 16/66 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	***149.0397***	75.0235			M							7
2	***263.1208***	132.0640			L	**753.4273**	377.2173	735.4037	368.2055	735.4168	368.2120	6
3	***395.1583***	198.0828			M	**639.3462**	320.1767	621.3226	311.1650	621.3357	311.1715	5
4	525.1980	263.1026	507.1874	254.0973	E	**507.3087**	254.1580	489.2851	245.1462	489.2981	245.1527	4
5	***639.2791***	320.1432	621.2685	311.1379	I	377.2691	189.1382	359.2455	180.1264			3
6	***753.3602***	377.1837	735.3496	368.1784	L	**263.1880**	132.0976	245.1644	123.0858			2
7					K	**149.1069**	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of MLMEILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
31.2	900.4525	-0.0011	MLMEILK	Oxidation M1 98.14%

AT2G02560.1

25.6	900.4495	0.0019	CNGGIKIK	
19.9	900.4491	0.0023	MLPFLEK	
19.4	900.4496	0.0019	NCKNILK	
17.7	900.4491	0.0023	IFLEMPK	
17.6	900.4495	0.0019	CVKNIQK	
14.9	900.4495	0.0019	TCAGKPKK	
14.0	900.4525	-0.0011	MLMEILK	Oxidation M3 1.86%
14.0	900.4495	0.0019	NAKQGMLK	
12.1	900.4495	0.0019	EMKLNVR	

Mascot: http://www.matrixscience.com/

AT2G02930.1

Mascot Search Results

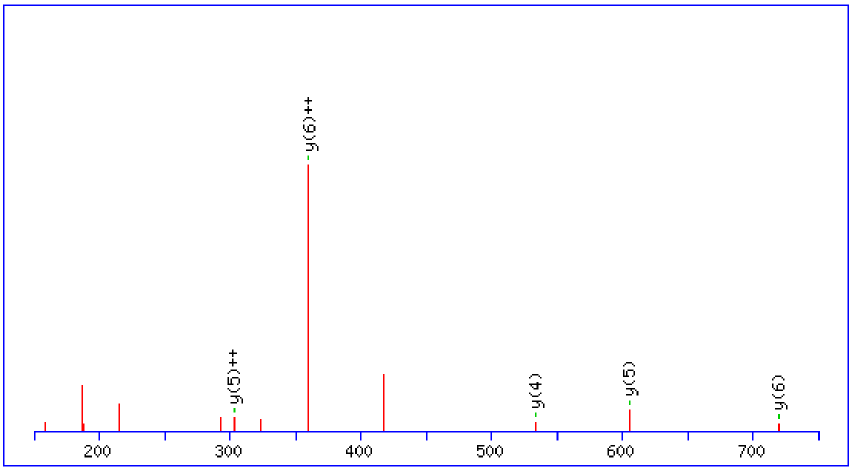
Peptide View

MS/MS Fragmentation of **VLIALHEK**
Found in **AT2G02930.1** in **TAIR_Arabidopsis**, Symbols: GST16, ATGSTF3 | ATGSTF3 (GLUTATHIONE S-TRANSFERASE 16); glutathione transferase | chr2:851347-852105 REVERSE

Match to Query 1937: 932.531544 from(311.851124,3+) index(2184)
Title: Elution from: 23.859 to 23.859 scan no 2760 cid35.00 polarity:+
Data file C7-3_2.mgf

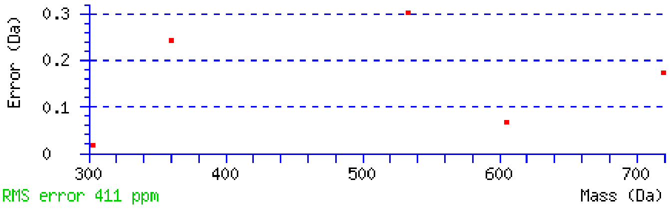
Click mouse within plot area to zoom in by factor of two about that point

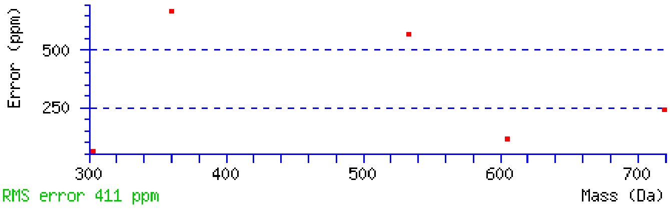
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 932.5321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.0067
Matches : 5/56 fragment ions using 6 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400			V							8
2	215.1538	108.0805			L	833.4740	417.2406	815.4504	408.2288	815.4634	408.2353	7
3	329.2349	165.1211			I	***719.3929***	360.2001	701.3693	351.1883	701.3823	351.1948	6
4	401.2691	201.1382			A	***605.3118***	303.1595	587.2882	294.1477	587.3012	294.1542	5
5	515.3502	258.1787			L	***533.2776***	267.1424	515.2540	258.1307	515.2671	258.1372	4
6	655.4002	328.2037			H	419.1965	210.1019	401.1729	201.0901	401.1860	201.0966	3
7	785.4398	393.2235	767.4293	384.2183	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VLIALHEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	932.5321	-0.0006	VLIALHEK

AT2G02930.1

20.0	932.5321	-0.0006	LVLELHAK

Mascot: http://www.matrixscience.com/

AT2G03070.1

Mascot Search Results

Peptide View

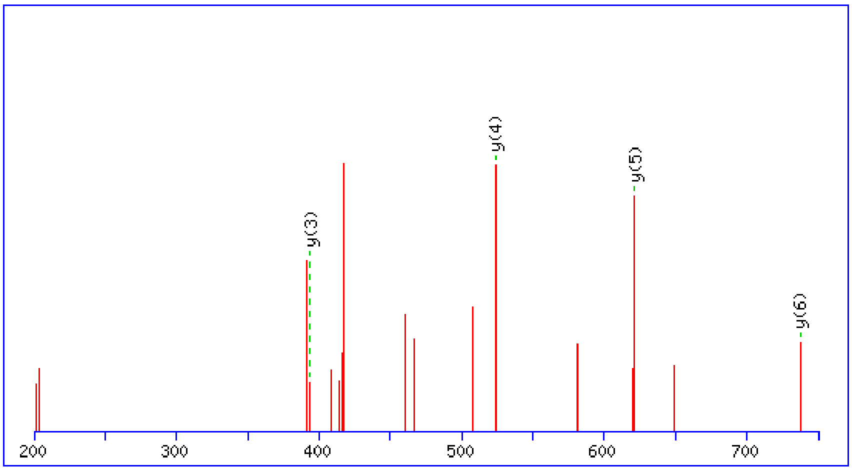
MS/MS Fragmentation of **LNPKLEK**
Found in **AT2G03070.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO41701.1) | chr2:905977-908791 FORWARD

Match to Query 1357: 850.475942 from(426.245247,2+) index(4162)
Title: Elution from: 38.439 to 38.439 scan no 5184 cid35.00 polarity:+
Data file C7-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

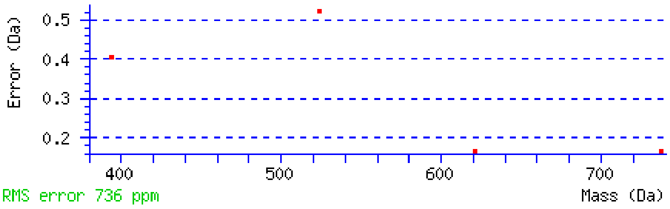
Or, Plot from 200 to 750 Da Full range

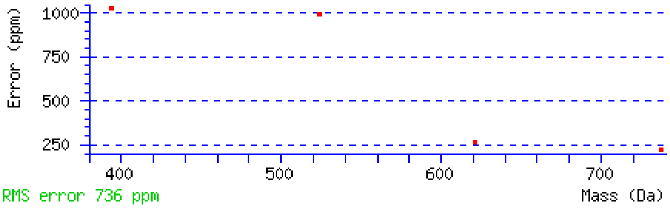
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 850.4773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.017
Matches : 4/58 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							7
2	231.1254	116.0663	213.1018	107.0545			N	*737.4034*	369.2054	719.3798	360.1936	719.3929	360.2001	6
3	329.1752	165.0912	311.1516	156.0794			P	*621.3664*	311.1869	603.3428	302.1751	603.3559	302.1816	5
4	459.2642	230.1357	441.2406	221.1239			K	*523.3166*	262.1620	505.2930	253.1502	505.3061	253.1567	4
5	573.3453	287.1763	555.3217	278.1645			L	*393.2276*	197.1174	375.2040	188.1056	375.2170	188.1122	3
6	703.3849	352.1961	685.3613	343.1843	685.3744	343.1908	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LNPKLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.0	850.4773	-0.0013	LNPKLEK
10.8	850.4773	-0.0013	NLPISIGK

AT2G03070.1

6.4	850.4772	-0.0013	ITELPIR
6.1	850.4772	-0.0013	LAAAQVVVA
1.7	850.4773	-0.0013	IPLNEKK
0.8	850.4772	-0.0013	KLVDPAAK

AT2G03140.1

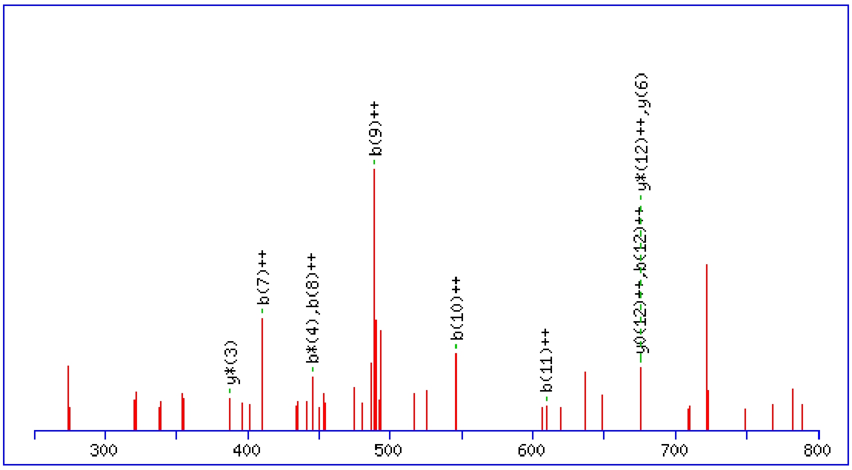
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYGLDLKASNKEK**
Found in **AT2G03140.1** in **TAIR_Arabidopsis**, Symbols: | CAAX amino terminal protease family protein | chr2:941997-949334 FORWARD

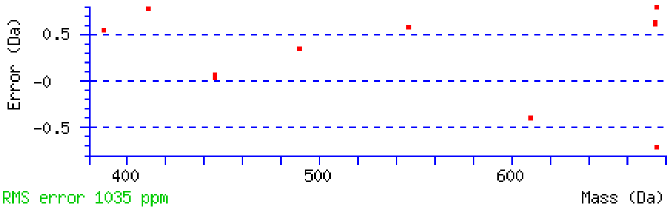
Match to Query 6185: 1492.787793 from(498.603207,3+) index(1130)
Title: Elution from: 19.584 to 19.584 scan no 1681 cid35.00 polarity:+
Data file D1d-2_1.mgf

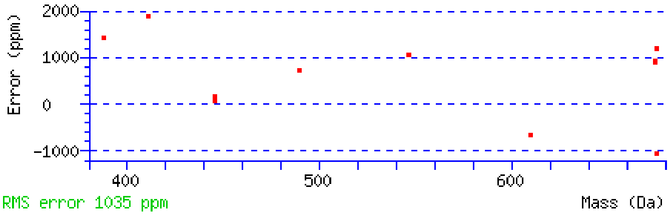
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1492.7885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.048
Matches : 11/134 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							13
2	292.1292	146.5682	275.1026	138.0550			Y	1365.7373	683.3723	1348.7107	674.8590	1347.7267	674.3670	12
3	349.1506	175.0790	332.1241	166.5657			G	1202.6739	601.8406	1185.6474	593.3273	1184.6634	592.8353	11
4	462.2347	231.6210	445.2082	223.1077			L	1145.6525	573.3299	1128.6259	564.8166	1127.6419	564.3246	10
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	D	1032.5684	516.7878	1015.5419	508.2746	1014.5578	507.7826	9
6	690.3457	345.6765	673.3192	337.1632	672.3352	336.6712	L	917.5415	459.2744	900.5149	450.7611	899.5309	450.2691	8
7	818.4407	***409.7240***	801.4141	401.2107	800.4301	400.7187	K	804.4574	402.7323	787.4308	394.2191	786.4468	393.7271	7
8	889.4778	***445.2425***	872.4512	436.7293	871.4672	436.2373	A	676.3624	338.6849	659.3359	330.1716	658.3519	329.6796	6
9	976.5098	***488.7585***	959.4833	480.2453	958.4993	479.7533	S	605.3253	303.1663	588.2988	294.6530	587.3148	294.1610	5
10	1090.5528	***545.7800***	1073.5262	537.2667	1072.5422	536.7747	N	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
11	1218.6477	***609.8275***	1201.6212	601.3142	1200.6371	600.8222	K	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	3
12	1347.6903	***674.3488***	1330.6638	665.8355	1329.6797	665.3435	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of QYGLDLKASNKEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G03140.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.8	1492.7885	-0.0007	QYGLDLKASNKEK
8.9	1492.7885	-0.0007	YRKEELETLQGK
7.9	1492.7886	-0.0008	GESHLLLIGDPGTGK
3.6	1492.7858	0.0019	SHHRRLSSEISGK
1.9	1492.7885	-0.0007	SRATPYTEAEIKK

AT2G03280.1

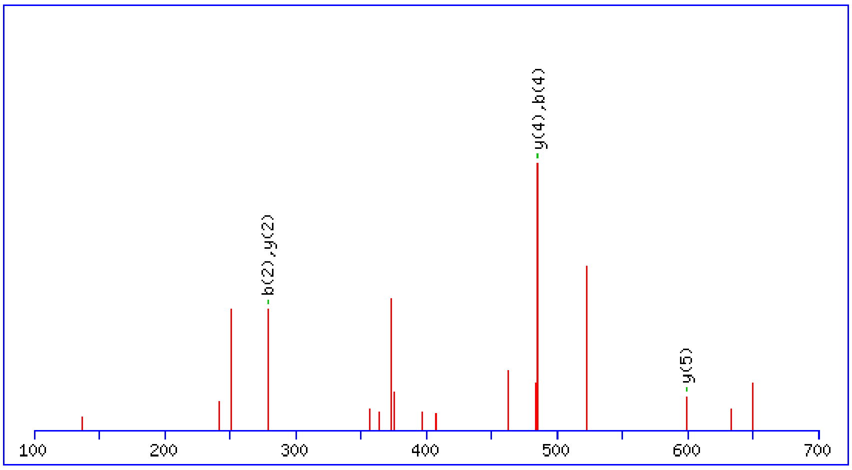
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLGFKK**
Found in **AT2G03280.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G14020.1); similar to hypothetical protein OsJ_000519 [Oryza sativa (japonica cultivar-group)] (GB:EAZ10694.1); similar to hypothetical protein OsI_000541 [Oryza sativa (indica

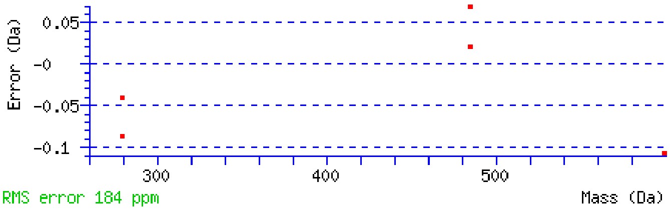
Match to Query 688: 762.413550 from(382.214051,2+) index(3336)
Title: Elution from: 35.478 to 35.478 scan no 4294 cid35.00 polarity:+
Data file D1d-2_2.mgf

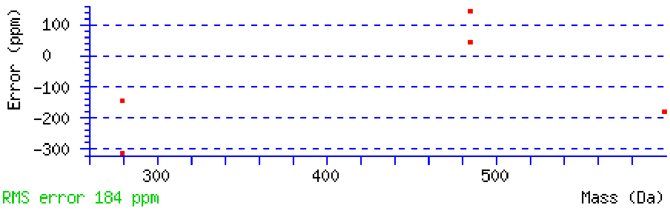
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 762.4140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.024
Matches : 5/32 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	165.0676	83.0375			Y					6
2	**279.1487**	140.0780			L	***599.3610***	300.1841	581.3374	291.1723	5
3	337.1672	169.0873			G	***485.2799***	243.1436	467.2563	234.1318	4
4	**485.2327**	243.1200			F	427.2614	214.1343	409.2378	205.1225	3
5	615.3217	308.1645	597.2981	299.1527	K	***279.1959***	140.1016	261.1723	131.0898	2
6					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of YLGFKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.5	762.4140	-0.0005	YLGFKK
9.0	762.4140	-0.0005	YFGIKK

AT2G03280.1

7.1	762.4140	-0.0005	KFYVAK
4.8	762.4118	0.0017	YSKKTK
1.2	762.4140	-0.0005	VFFSKK

AT2G03440.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGVGQYLEK**
Found in **AT2G03440.1** in **TAIR_Arabidopsis**, Symbols: | nodulin-related | chr2:1039406-1039969 REVERSE

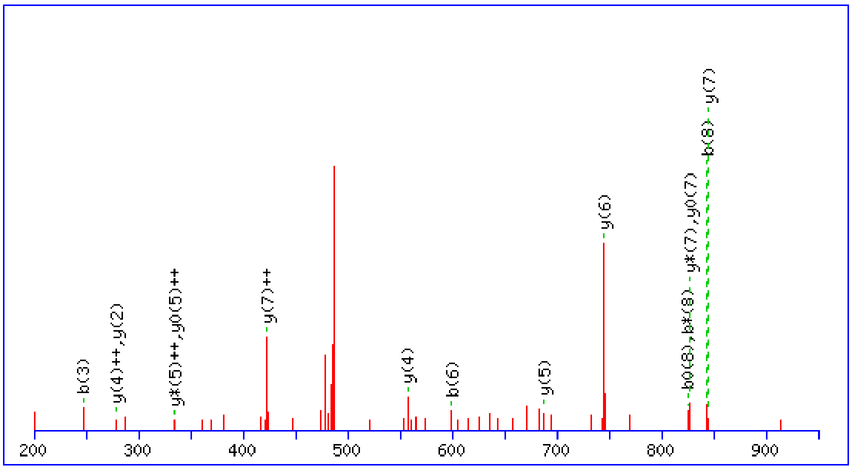
Match to Query 2593: 990.462580 from(496.238566,2+) index(2541)
Title: Elution from: 26.694 to 26.694 scan no 3200 cid35.00 polarity:+
Data file D1d-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

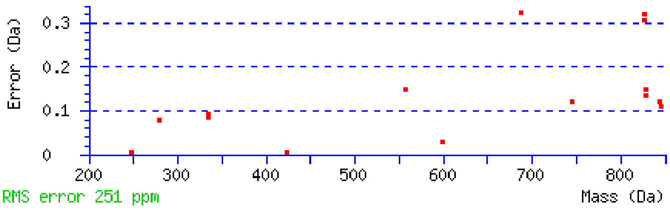
Label all possible matches ○ Label matches used for scoring ●

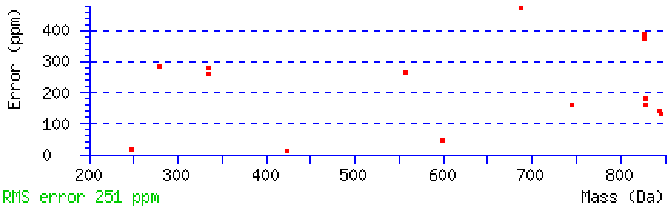
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 990.4648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.012
Matches : 16/86 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							9
2	147.0548	74.0311			129.0443	65.0258	G	903.4431	452.2252	885.4195	443.2134	885.4325	443.2199	8
3	***247.1203***	124.0638			229.1097	115.0585	V	***845.4246***	423.2159	827.4010	414.2041	827.4140	414.2106	7
4	305.1388	153.0730			287.1282	144.0677	G	***745.3591***	373.1832	727.3355	364.1714	727.3485	364.1779	6
5	435.1914	218.0994	417.1678	209.0876	417.1809	209.0941	Q	***687.3406***	344.1739	669.3170	335.1622	669.3300	335.1687	5
6	***599.2518***	300.1295	581.2282	291.1177	581.2412	291.1243	Y	***557.2880***	279.1476	539.2644	270.1358	539.2774	270.1423	4
7	713.3329	357.1701	695.3093	348.1583	695.3223	348.1648	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
8	***843.3725***	422.1899	825.3489	413.1781	825.3620	413.1846	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SGVGQYLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.0	990.4648	-0.0022	SGVGQYLEK

AT2G03440.1

16.0	990.4648	-0.0023	ENGEKYIK
12.5	990.4648	-0.0023	NEKGYIEK
12.0	990.4648	-0.0023	EFAAEASKK
8.5	990.4648	-0.0023	SFAEEAAKK
7.5	990.4648	-0.0022	KDSLQDFK
7.3	990.4626	-0.0000	ATKSTGGTEK
6.4	990.4648	-0.0022	YGDNIITGK
5.5	990.4648	-0.0022	DKDAIGFSK
5.5	990.4648	-0.0023	ASAFQSELK

AT2G04030.1

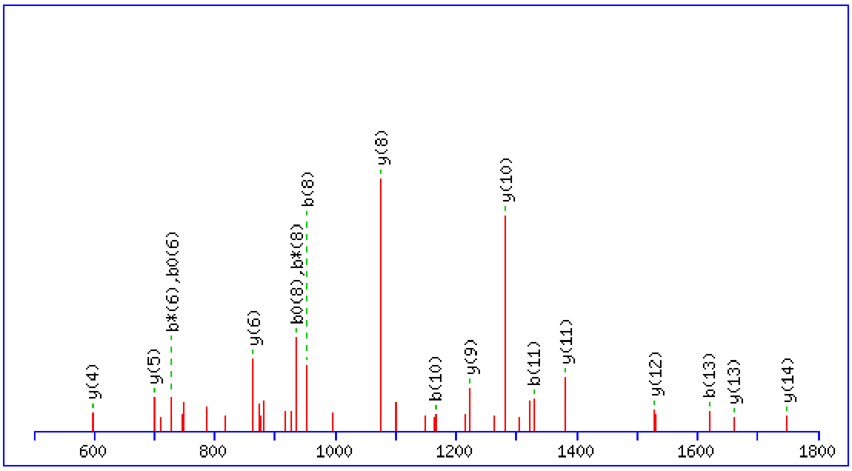
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NYSQFVGFPIYTWQEK**
Found in **AT2G04030.1** in **TAIR_Arabidopsis**, Symbols: EMB1956, CR88 | CR88 (EMBRYO DEFECTIVE 1956); ATP binding | chr2:1281980-1285906 FORWARD

Match to Query 9533: 2026.891380 from(1014.452966,2+) index(10083)
Title: Elution from: 93.056 to 93.056 scan no 13969 cid35.00 polarity:+
Data file D12h-3_1.mgf

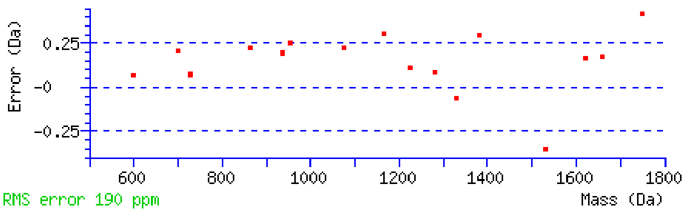
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

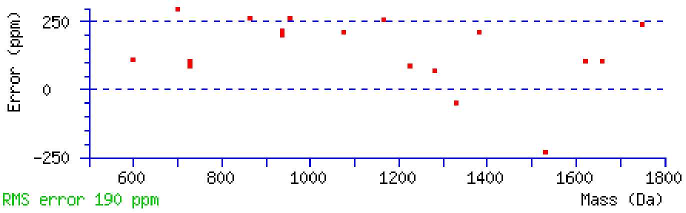


Monoisotopic mass of neutral peptide Mr(calc): 2026.8951
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 4.6e-009
Matches : 18/174 fragment ions using 20 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0443	59.0258	99.0207	50.0140			N							16
2	281.1046	141.0560	263.0811	132.0442			Y	1911.8654	956.4364	1893.8418	947.4246	1893.8549	947.4311	15
3	369.1337	185.0705	351.1101	176.0587	351.1231	176.0652	S	***1747.8051***	874.4062	1729.7815	865.3944	1729.7945	865.4009	14
4	499.1863	250.0968	481.1628	241.0850	481.1758	241.0915	Q	***1659.7760***	830.3916	1641.7524	821.3798	1641.7654	821.3864	13
5	647.2518	324.1295	629.2282	315.1177	629.2412	315.1243	F	***1529.7234***	765.3653	1511.6998	756.3535	1511.7128	756.3600	12
6	747.3172	374.1623	729.2937	365.1505	729.3067	365.1570	V	***1381.6579***	691.3326	1363.6343	682.3208	1363.6473	682.3273	11
7	805.3357	403.1715	787.3122	394.1597	787.3252	394.1662	G	***1281.5925***	641.2999	1263.5689	632.2881	1263.5819	632.2946	10
8	**953.4012**	477.2042	935.3776	468.1924	935.3906	468.1990	F	***1223.5740***	612.2906	1205.5504	603.2788	1205.5634	603.2853	9
9	1051.4510	526.2291	1033.4274	517.2173	1033.4404	517.2239	P	***1075.5085***	538.2579	1057.4849	529.2461	1057.4979	529.2526	8
10	**1165.5321**	583.2697	1147.5085	574.2579	1147.5215	574.2644	I	977.4587	489.2330	959.4351	480.2212	959.4481	480.2277	7
11	**1329.5925**	665.2999	1311.5689	656.2881	1311.5819	656.2946	Y	***863.3776***	432.1924	845.3540	423.1807	845.3670	423.1872	6
12	1431.6372	716.3222	1413.6136	707.3104	1413.6266	707.3169	T	***699.3172***	350.1623	681.2937	341.1505	681.3067	341.1570	5
13	**1619.7106**	810.3589	1601.6870	801.3471	1601.7000	801.3536	W	***597.2725***	299.1399	579.2489	290.1281	579.2620	290.1346	4
14	1749.7632	875.3852	1731.7396	866.3734	1731.7526	866.3800	Q	409.1991	205.1032	391.1756	196.0914	391.1886	196.0979	3
15	1879.8028	940.4051	1861.7792	931.3933	1861.7923	931.3998	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT2G04030.1





NCBI **BLAST** search of NYSQFVGFPIYTWQEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
92.0	2026.8951	-0.0037	NYSQFVGFPIYTWQEK
0.8	2026.8891	0.0023	GVLSPDEVMTESETIDLR

Mascot: http://www.matrixscience.com/

AT2G04170.1

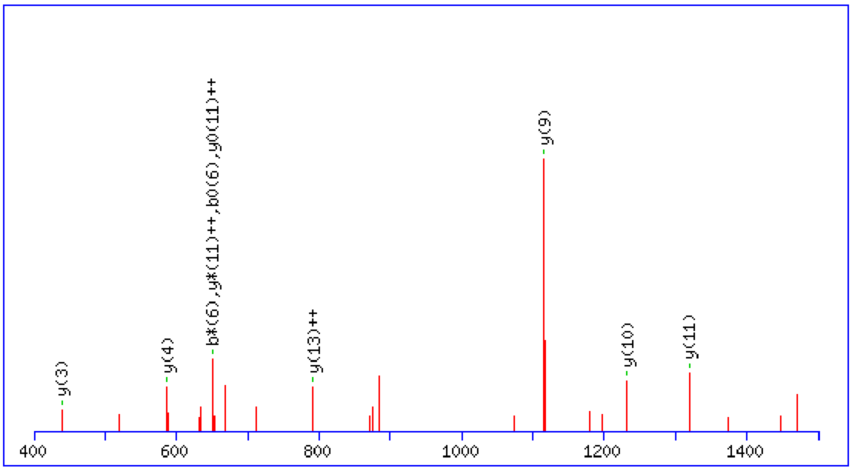
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTFISNPPNNVFTWK**
Found in **AT2G04170.1** in **TAIR_Arabidopsis**, Symbols: | meprin and TRAF homology domain-containing protein / MATH domain-containing protein | chr2:1417401-1419153 REVERSE

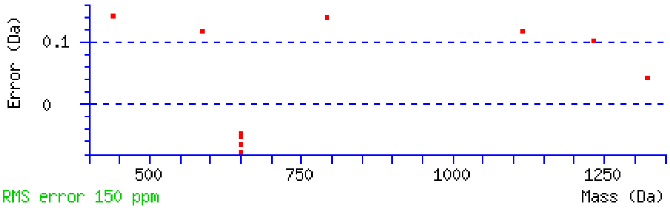
Match to Query 8306: 1782.844482 from(892.429517,2+) index(8667)
Title: Elution from: 77.688 to 77.688 scan no 11652 cid35.00 polarity:+
Data file D12h-3_2.mgf

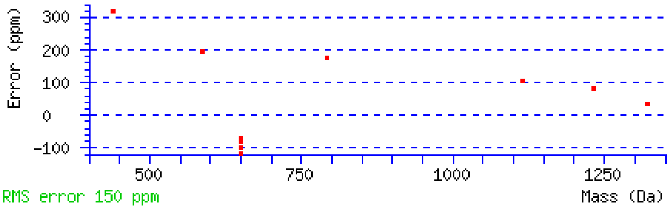
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1782.8450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0056
Matches : 10/152 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							15
2	203.1174	102.0624			185.1069	93.0571	T	1683.7868	842.3970	1665.7632	833.3852	1665.7762	833.3917	14
3	351.1829	176.0951			333.1723	167.0898	F	1581.7421	791.3747	1563.7185	782.3629	1563.7315	782.3694	13
4	465.2640	233.1356			447.2534	224.1303	I	1433.6766	717.3419	1415.6530	708.3302	1415.6661	708.3367	12
5	553.2930	277.1502			535.2825	268.1449	S	***1319.5955***	660.3014	1301.5719	651.2896	1301.5850	651.2961	11
6	669.3300	335.1687	651.3065	326.1569	651.3195	326.1634	N	***1231.5665***	616.2869	1213.5429	607.2751	1213.5559	607.2816	10
7	767.3798	384.1936	749.3563	375.1818	749.3693	375.1883	P	***1115.5295***	558.2684	1097.5059	549.2566	1097.5189	549.2631	9
8	865.4296	433.2185	847.4061	424.2067	847.4191	424.2132	P	1017.4797	509.2435	999.4561	500.2317	999.4691	500.2382	8
9	981.4666	491.2370	963.4431	482.2252	963.4561	482.2317	N	919.4299	460.2186	901.4063	451.2068	901.4193	451.2133	7
10	1097.5036	549.2555	1079.4801	540.2437	1079.4931	540.2502	N	803.3929	402.2001	785.3693	393.1883	785.3823	393.1948	6
11	1197.5691	599.2882	1179.5455	590.2764	1179.5585	590.2829	V	687.3559	344.1816	669.3323	335.1698	669.3453	335.1763	5
12	1345.6345	673.3209	1327.6110	664.3091	1327.6240	664.3156	F	***587.2904***	294.1488	569.2668	285.1371	569.2799	285.1436	4
13	1447.6792	724.3433	1429.6557	715.3315	1429.6687	715.3380	T	***439.2250***	220.1161	421.2014	211.1043	421.2144	211.1108	3
14	1635.7526	818.3800	1617.7290	809.3682	1617.7421	809.3747	W	337.1803	169.0938	319.1567	160.0820			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT2G04170.1

NCBI **BLAST** search of VTFISNPPNNVFTWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1782.8450	-0.0005	VTFISNPPNNVFTWK
4.5	1782.8439	0.0006	TIMPNAGSERAASLSLK
3.0	1782.8409	0.0036	KAAQAAGASSGGAAGGKGAAAK
2.6	1782.8461	-0.0016	MRKPFLSEPEQSVSK
2.6	1782.8432	0.0013	EKPVTALRSSSFHGSR
2.0	1782.8432	0.0013	NIPHVVSVGTPAPNSNR
1.3	1782.8449	-0.0005	IQYAANWFVPGEAVAK
0.5	1782.8404	0.0040	LDVRDALDGFEDRLK
0.1	1782.8461	-0.0016	GSPNLQVLDIFEMKR

AT2G04380.1

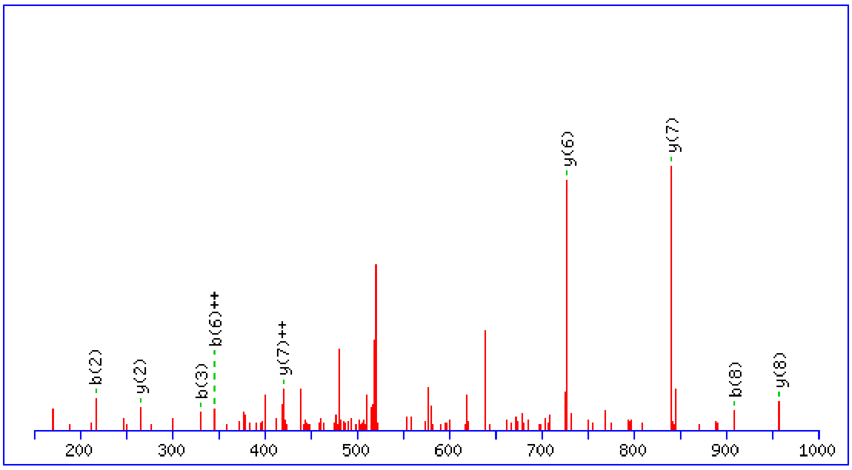
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNILKDTDK**
Found in **AT2G04380.1** in **TAIR_Arabidopsis**, Symbols: | unknown protein | chr2:1525639-1526499 FORWARD

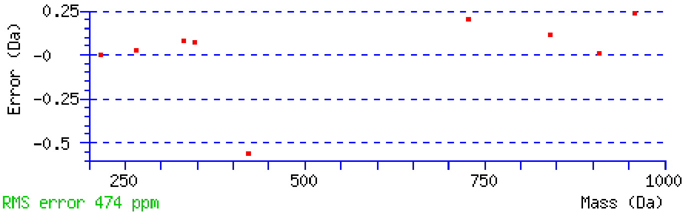
Match to Query 3165: 1056.542880 from(529.278716,2+) index(4725)
Title: Elution from: 42.689 to 42.689 scan no 5902 cid35.00 polarity:+
Data file D6h-1_1.mgf

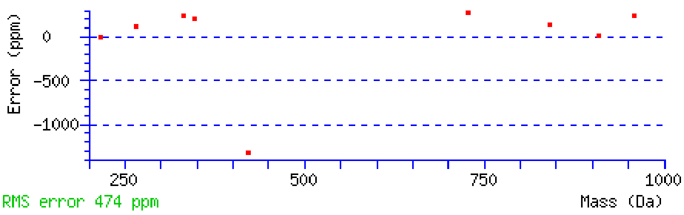
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.5459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.016
Matches : 9/82 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							9
2	***217.1097***	109.0585	199.0861	100.0467			N	***957.4878***	479.2475	939.4642	470.2357	939.4772	470.2422	8
3	***331.1908***	166.0990	313.1672	157.0873			I	***841.4508***	421.2290	823.4272	412.2172	823.4402	412.2237	7
4	445.2719	223.1396	427.2483	214.1278			L	***727.3697***	364.1885	709.3461	355.1767	709.3591	355.1832	6
5	575.3610	288.1841	557.3374	279.1723			K	613.2886	307.1479	595.2650	298.1361	595.2780	298.1426	5
6	691.3849	346.1961	673.3613	337.1843	673.3744	337.1908	D	483.1995	242.1034	465.1760	233.0916	465.1890	233.0981	4
7	793.4296	397.2185	775.4061	388.2067	775.4191	388.2132	T	367.1756	184.0914	349.1520	175.0796	349.1650	175.0861	3
8	***909.4536***	455.2304	891.4300	446.2187	891.4431	446.2252	D	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VNILKDTDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.2	1056.5459	-0.0030	VNILKDTDK

AT2G04380.1

9.7	1056.5459	-0.0030	VEVGKKEEK
7.5	1056.5412	0.0017	VVKCIPNSK
7.2	1056.5459	-0.0030	DVSLEKQVK
5.9	1056.5459	-0.0030	DQAVVLATTK
4.0	1056.5459	-0.0030	LTLETLEAR
2.1	1056.5459	-0.0031	TIDPSKEKK
1.6	1056.5439	-0.0010	HRKMVNLK

AT2G04390.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILEEVAIIPSK**
Found in **AT2G04390.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S17 (RPS17A) | chr2:1527908-1528333 FORWARD

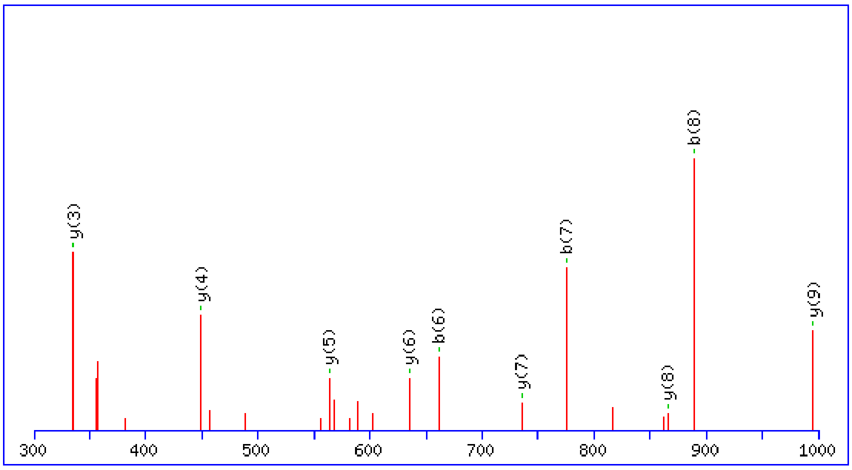
Match to Query 4431: 1222.680738 from(612.347645,2+) index(6652)
Title: Elution from: 58.728 to 58.728 scan no 8509 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1000 Da Full range

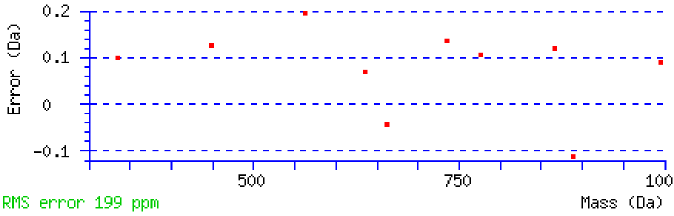
Label all possible matches ○ Label matches used for scoring ●

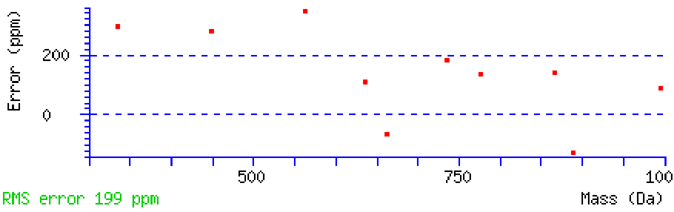
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1222.6817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 1.1e-006
Matches : 10/94 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			I							11
2	229.1695	115.0884			L	1109.6079	555.3076	1091.5843	546.2958	1091.5973	546.3023	10
3	359.2091	180.1082	341.1985	171.1029	E	***995.5268***	498.2670	977.5032	489.2552	977.5162	489.2617	9
4	489.2487	245.1280	471.2382	236.1227	E	***865.4872***	433.2472	847.4636	424.2354	847.4766	424.2419	8
5	589.3142	295.1607	571.3036	286.1554	V	***735.4475***	368.2274	717.4239	359.2156	717.4370	359.2221	7
6	**661.3483**	331.1778	643.3378	322.1725	A	***635.3821***	318.1947	617.3585	309.1829	617.3715	309.1894	6
7	**775.4294**	388.2184	757.4189	379.2131	I	***563.3479***	282.1776	545.3243	273.1658	545.3374	273.1723	5
8	**889.5105**	445.2589	871.5000	436.2536	I	***449.2668***	225.1371	431.2433	216.1253	431.2563	216.1318	4
9	987.5603	494.2838	969.5498	485.2785	P	***335.1857***	168.0965	317.1622	159.0847	317.1752	159.0912	3
10	1075.5894	538.2983	1057.5788	529.2930	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ILEEVAIIPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G04390.1

Score	Mr(calc)	Delta	Sequence
60.9	1222.6817	-0.0010	ILEEVAIIPSK

Mascot: http://www.matrixscience.com/

AT2G04780.1

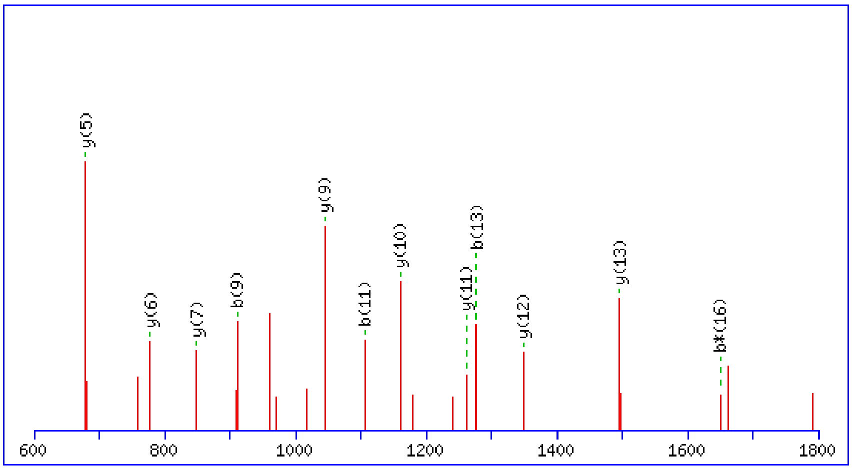
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSSVFSTDPVAVYQVNR**
Found in **AT2G04780.1** in **TAIR_Arabidopsis**, Symbols: FLA7 | FLA7 | chr2:1677485-1678249 FORWARD

Match to Query 8740: 1953.979226 from(977.996889,2+) index(6886)
Title: Elution from: 64.849 to 64.849 scan no 9131 cid35.00 polarity:+
Data file D1d-1-2.mgf

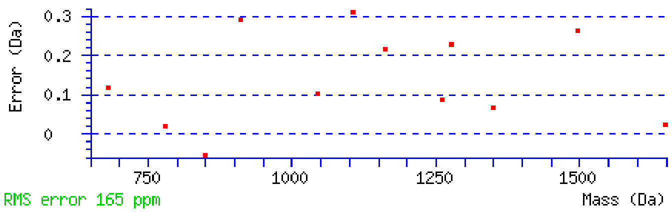
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

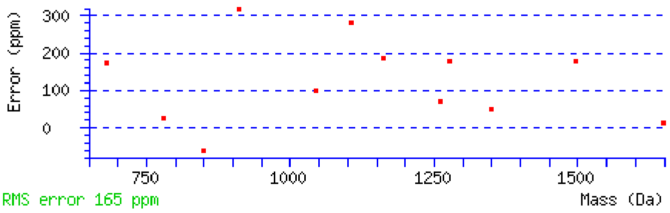


Monoisotopic mass of neutral peptide Mr(calc): 1953.9796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 5.2e-006
Matches : 12/156 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							18
2	187.1077	94.0575			169.0972	85.0522	S	1855.9185	928.4629	1838.8919	919.9496	1837.9079	919.4576	17
3	274.1397	137.5735			256.1292	128.5682	S	1768.8864	884.9469	1751.8599	876.4336	1750.8759	875.9416	16
4	361.1718	181.0895			343.1612	172.0842	S	1681.8544	841.4308	1664.8279	832.9176	1663.8438	832.4256	15
5	460.2402	230.6237			442.2296	221.6184	V	1594.8224	797.9148	1577.7958	789.4016	1576.8118	788.9095	14
6	607.3086	304.1579			589.2980	295.1527	F	***1495.7540***	748.3806	1478.7274	739.8673	1477.7434	739.3753	13
7	694.3406	347.6740			676.3301	338.6687	S	***1348.6856***	674.8464	1331.6590	666.3331	1330.6750	665.8411	12
8	795.3883	398.1978			777.3777	389.1925	T	***1261.6535***	631.3304	1244.6270	622.8171	1243.6430	622.3251	11
9	**910.4153**	455.7113			892.4047	446.7060	D	***1160.6058***	580.8066	1143.5793	572.2933	1142.5953	571.8013	10
10	1007.4680	504.2376			989.4575	495.2324	P	***1045.5789***	523.2931	1028.5524	514.7798			9
11	**1106.5364**	553.7719			1088.5259	544.7666	V	948.5261	474.7667	931.4996	466.2534			8
12	1177.5735	589.2904			1159.5630	580.2851	A	***849.4577***	425.2325	832.4312	416.7192			7
13	**1276.6420**	638.8246			1258.6314	629.8193	V	***778.4206***	389.7139	761.3941	381.2007			6
14	1439.7053	720.3563			1421.6947	711.3510	Y	***679.3522***	340.1797	662.3257	331.6665			5
15	1567.7639	784.3856	1550.7373	775.8723	1549.7533	775.3803	Q	516.2889	258.6481	499.2623	250.1348			4
16	1666.8323	833.9198	1649.8057	825.4065	1648.8217	824.9145	V	388.2303	194.6188	371.2037	186.1055			3
17	1780.8752	890.9412	1763.8487	882.4280	1762.8646	881.9360	N	289.1619	145.0846	272.1353	136.5713			2
18							R	175.1190	88.0631	158.0924	79.5498			1

AT2G04780.1





NCBI **BLAST** search of VSSSVFSTDPVAVYQVNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.1	1953.9796	-0.0004	VSSSVFSTDPVAVYQVNR
3.0	1953.9756	0.0037	RVPTKPDDPNESENTKK
0.8	1953.9829	-0.0037	ATKMAYEDTVAKITEQR
0.5	1953.9782	0.0010	YEEELVEAITTATTEKK

Mascot: http://www.matrixscience.com/

AT2G05070.1

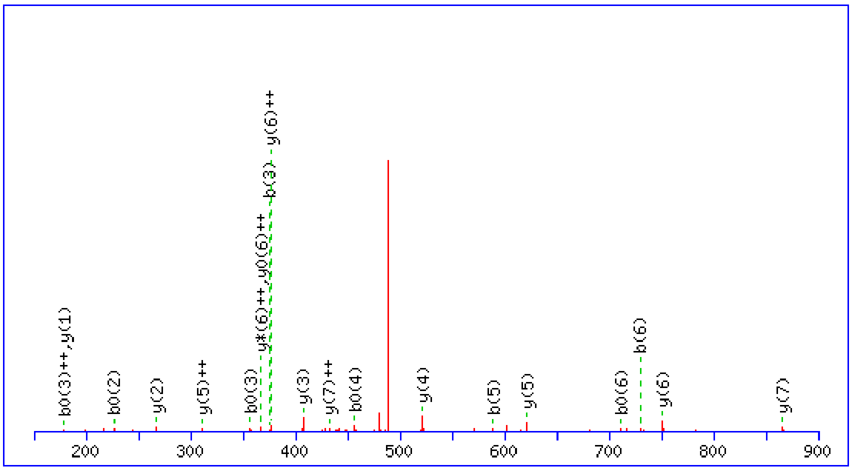
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELEVIHSR**
Found in **AT2G05070.1** in **TAIR_Arabidopsis**, Symbols: LHCB2, LHCB2.2 | LHCB2.2 (Photosystem II light harvesting complex gene 2.2); chlorophyll binding | chr2:1799433-1800326 REVERSE

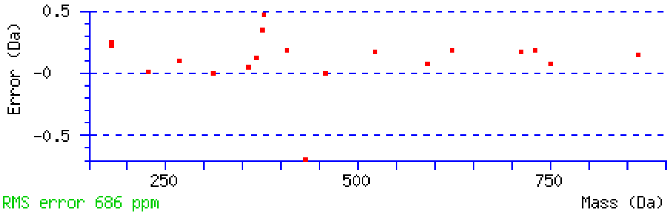
Match to Query 2055: 994.486722 from(498.250637,2+) index(964)
Title: Elution from: 19.169 to 19.169 scan no 1504 cid35.00 polarity:+
Data file D1d-1_1.mgf

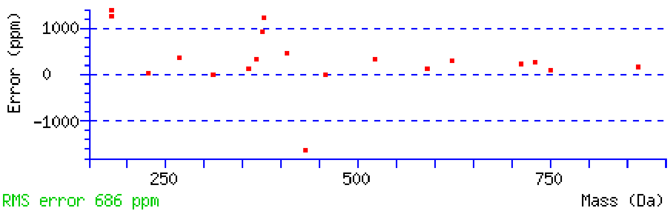
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.4858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 1.6e-005
Matches : 20/68 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							8
2	245.1280	123.0676	227.1174	114.0624	L	***865.4534***	433.2304	847.4299	424.2186	847.4429	424.2251	7
3	**375.1676**	188.0875	357.1571	179.0822	E	***751.3723***	376.1898	733.3488	367.1780	733.3618	367.1845	6
4	475.2331	238.1202	457.2225	229.1149	V	***621.3327***	311.1700	603.3091	302.1582	603.3222	302.1647	5
5	**589.3142**	295.1607	571.3036	286.1554	I	***521.2673***	261.1373	503.2437	252.1255	503.2567	252.1320	4
6	**729.3642**	365.1857	711.3536	356.1805	H	***407.1862***	204.0967	389.1626	195.0849	389.1756	195.0914	3
7	817.3933	409.2003	799.3827	400.1950	S	***267.1362***	134.0717	249.1126	125.0599	249.1256	125.0664	2
8					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ELEVIHSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.0	994.4858	0.0009	ELEVIHSR

AT2G05070.1

20.6	994.4858	0.0009	ELLDLSHR
10.7	994.4858	0.0009	QPADPISVR
10.7	994.4858	0.0009	HLEELVSR
5.8	994.4858	0.0009	ELTVHIDR
5.7	994.4858	0.0009	KVDSKYSR
5.2	994.4858	0.0009	IQDTIHQK
3.3	994.4858	0.0009	LPPIQSGDR
3.2	994.4880	-0.0013	SFALGFVSR
3.1	994.4858	0.0009	EKHIAEQK

AT2G05710.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNFSFDGQPAELK**
Found in **AT2G05710.1** in **TAIR_Arabidopsis**, Symbols: | aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr2:2141588-2146347 FORWARD

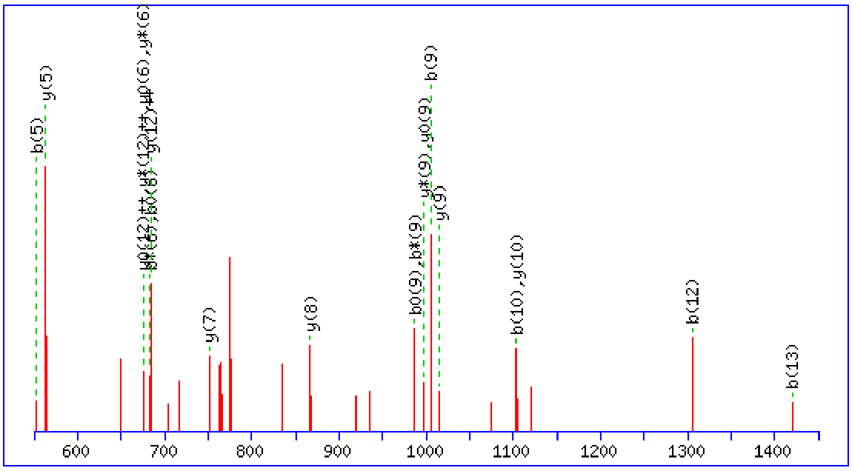
Match to Query 6499: 1566.725646 from(784.370099,2+) index(6538)
Title: Elution from: 58.248 to 58.248 scan no 8504 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1450 Da Full range

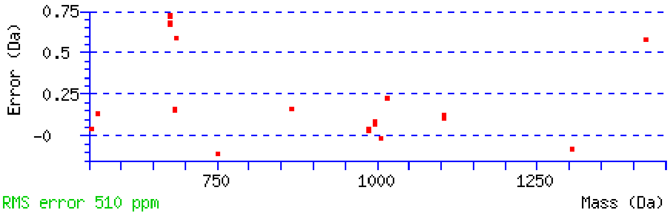
Label all possible matches ○ Label matches used for scoring ●

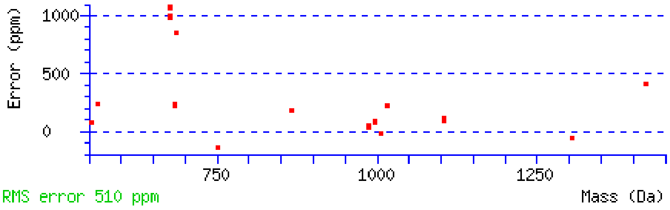
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1566.7272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.003
Matches : 21/140 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							14
2	201.1382	101.0727					V	1467.6691	734.3382	1449.6455	725.3264	1449.6585	725.3329	13
3	317.1752	159.0912	299.1516	150.0794			N	1367.6036	684.3055	1349.5800	675.2937	1349.5931	675.3002	12
4	465.2406	233.1239	447.2170	224.1122			F	1251.5666	626.2870	1233.5430	617.2752	1233.5561	617.2817	11
5	***553.2697***	277.1385	535.2461	268.1267	535.2591	268.1332	S	***1103.5012***	552.2542	1085.4776	543.2424	1085.4906	543.2489	10
6	701.3351	351.1712	683.3115	342.1594	683.3246	342.1659	F	***1015.4721***	508.2397	997.4485	499.2279	997.4616	499.2344	9
7	817.3591	409.1832	799.3355	400.1714	799.3485	400.1779	D	***867.4067***	434.2070	849.3831	425.1952	849.3961	425.2017	8
8	875.3776	438.1924	857.3540	429.1807	857.3670	429.1872	G	***751.3827***	376.1950	733.3591	367.1832	733.3721	367.1897	7
9	***1005.4303***	503.2188	987.4067	494.2070	987.4197	494.2135	Q	693.3642	347.1857	675.3406	338.1739	675.3536	338.1805	6
10	***1103.4801***	552.2437	1085.4565	543.2319	1085.4695	543.2384	P	***563.3115***	282.1594	545.2880	273.1476	545.3010	273.1541	5
11	1175.5142	588.2607	1157.4906	579.2489	1157.5036	579.2555	A	465.2618	233.1345	447.2382	224.1227	447.2512	224.1292	4
12	***1305.5538***	653.2806	1287.5302	644.2688	1287.5433	644.2753	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
13	***1419.6349***	710.3211	1401.6113	701.3093	1401.6244	701.3158	L	263.1880	132.0976	245.1644	123.0858			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VVNFSFDGQPAELK

AT2G05710.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.9	1566.7272	-0.0016	VVNFSFDGQPAELK
11.4	1566.7229	0.0027	LMFRQDGHKELR
10.9	1566.7272	-0.0016	SVDSAPLGNYTIWK
4.8	1566.7250	0.0006	FLSSEASGSPKPNTK
3.8	1566.7229	0.0027	RFDQKMSAHGAGIK
1.8	1566.7280	-0.0023	LEYLEMQEELIK
1.1	1566.7284	-0.0027	VSGTDANSLMTNVLK
0.9	1566.7259	-0.0002	LMVKHQIMEFNK
0.8	1566.7299	-0.0043	AINYSAQVFVNGHK
0.8	1566.7250	0.0006	QGLLGSESDFSGPKK

AT2G05840.1

Mascot Search Results

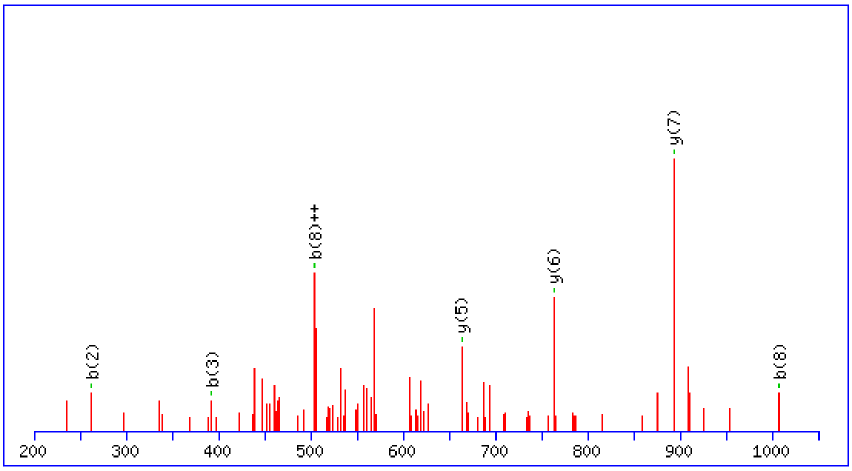
Peptide View

MS/MS Fragmentation of **LFQVEYAFK**
Found in **AT2G05840.1** in **TAIR_Arabidopsis**, Symbols: PAA2 | PAA2 (20S PROTEASOME SUBUNIT PAA2); peptidase | chr2:2234223-2236050 FORWARD

Match to Query 3308: 1154.562250 from(578.288401,2+) index(6752)
Title: Elution from: 63.716 to 63.716 scan no 8945 cid35.00 polarity:+
Data file D1d-1-2.mgf

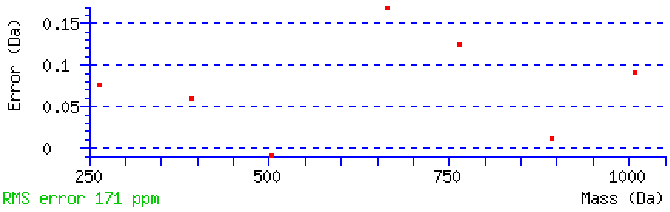
Click mouse within plot area to zoom in by factor of two about that point

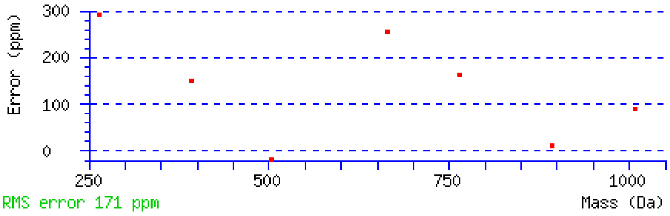
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.5638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.015
Matches : 7/76 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							9
2	***263.1538***	132.0805					F	1041.4900	521.2486	1023.4664	512.2369	1023.4794	512.2434	8
3	***393.2065***	197.1069	375.1829	188.0951			Q	***893.4246***	447.2159	875.4010	438.2041	875.4140	438.2106	7
4	493.2719	247.1396	475.2483	238.1278			V	***763.3719***	382.1896	745.3483	373.1778	745.3613	373.1843	6
5	623.3115	312.1594	605.2880	303.1476	605.3010	303.1541	E	***663.3065***	332.1569	645.2829	323.1451	645.2959	323.1516	5
6	787.3719	394.1896	769.3483	385.1778	769.3613	385.1843	Y	533.2668	267.1371	515.2433	258.1253			4
7	859.4061	430.2067	841.3825	421.1949	841.3955	421.2014	A	369.2065	185.1069	351.1829	176.0951			3
8	***1007.4715***	504.2394	989.4479	495.2276	989.4609	495.2341	F	297.1723	149.0898	279.1487	140.0780			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LFQVEYAFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G05840.1

25.9	1154.5638	-0.0016	LFQVEYAFK
23.2	1154.5591	0.0032	FGWFSMKLK
12.4	1154.5650	-0.0027	KMQEDGLLPL
10.0	1154.5620	0.0002	DSLGDRHVLK
4.0	1154.5616	0.0007	FATKFSDSIK
1.5	1154.5593	0.0029	GGDDSAPAIVLK
0.8	1154.5650	-0.0027	SKMSYASILK
0.6	1154.5638	-0.0016	APSFYYVGLK
0.4	1154.5620	0.0002	DAHESRAILK
0.4	1154.5650	-0.0027	MKVSTYLSSK

AT2G05990.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFIAGIADDNGYGWAIAK**
Found in **AT2G05990.1** in **TAIR_Arabidopsis**, Symbols: ENR1, MOD1 | MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase | chr2:2322873-2324864 FORWARD

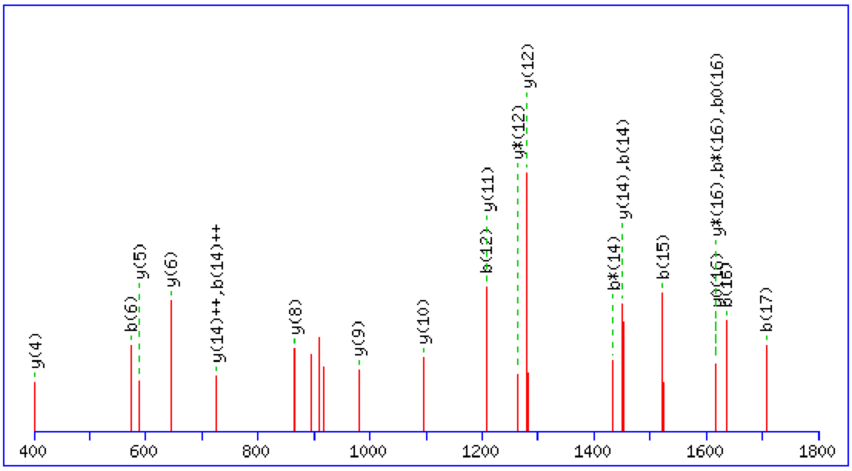
Match to Query 8748: 1851.916680 from(926.965616,2+) index(9086)
Title: Elution from: 81.404 to 81.404 scan no 12259 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

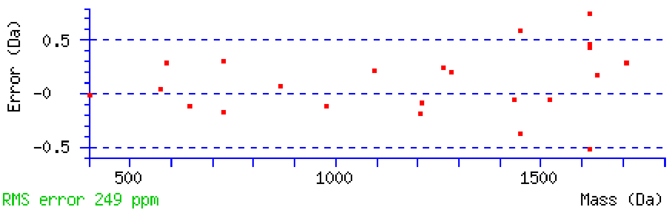
Show Y-axis ☐

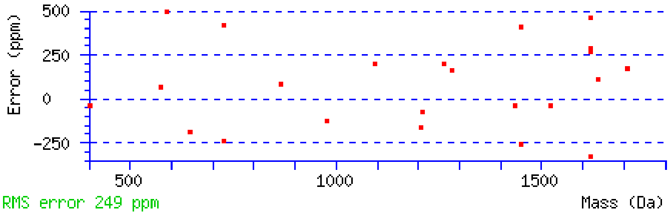


Monoisotopic mass of neutral peptide Mr(calc): 1851.9155
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.5e-007
Matches : 23/154 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							18
2	219.1128	110.0600					F	1781.8857	891.4465	1764.8592	882.9332	1763.8751	882.4412	17
3	332.1969	166.6021					I	1634.8173	817.9123	1617.7907	809.3990	1616.8067	808.9070	16
4	403.2340	202.1206					A	1521.7332	761.3703	1504.7067	752.8570	1503.7227	752.3650	15
5	460.2554	230.6314					G	***1450.6961***	725.8517	1433.6696	717.3384	1432.6856	716.8464	14
6	***573.3395***	287.1734					I	1393.6747	697.3410	1376.6481	688.8277	1375.6641	688.3357	13
7	644.3766	322.6920					A	***1280.5906***	640.7989	1263.5640	632.2857	1262.5800	631.7937	12
8	759.4036	380.2054			741.3930	371.2001	D	***1209.5535***	605.2804	1192.5269	596.7671	1191.5429	596.2751	11
9	874.4305	437.7189			856.4199	428.7136	D	***1094.5265***	547.7669	1077.5000	539.2536	1076.5160	538.7616	10
10	988.4734	494.7404	971.4469	486.2271	970.4629	485.7351	N	***979.4996***	490.2534	962.4730	481.7402			9
11	1045.4949	523.2511	1028.4684	514.7378	1027.4843	514.2458	G	***865.4567***	433.2320	848.4301	424.7187			8
12	***1208.5582***	604.7828	1191.5317	596.2695	1190.5477	595.7775	Y	808.4352	404.7212	791.4087	396.2080			7
13	1265.5797	633.2935	1248.5531	624.7802	1247.5691	624.2882	G	***645.3719***	323.1896	628.3453	314.6763			6
14	***1451.6590***	726.3331	1434.6325	717.8199	1433.6484	717.3279	W	***588.3504***	294.6788	571.3239	286.1656			5
15	***1522.6961***	761.8517	1505.6696	753.3384	1504.6856	752.8464	A	***402.2711***	201.6392	385.2445	193.1259			4
16	***1635.7802***	818.3937	1618.7536	809.8805	1617.7696	809.3884	I	331.2340	166.1206	314.2074	157.6074			3
17	***1706.8173***	853.9123	1689.7907	845.3990	1688.8067	844.9070	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT2G05990.1





NCBI **BLAST** search of AFIAGIADDNGYGWAIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.0	1851.9155	0.0012	AFIAGIADDNGYGWAIAK
2.4	1851.9149	0.0018	EVERDQHISPPSLMAK

Mascot: http://www.matrixscience.com/

AT2G06025.1

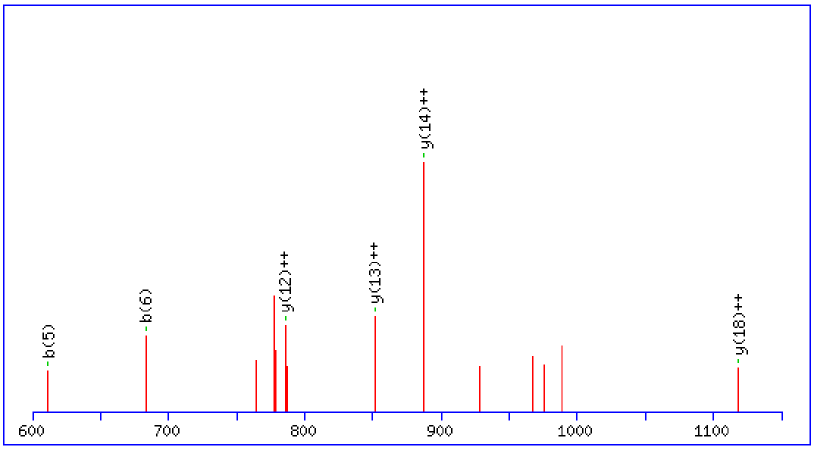
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVAREAMLDEEYWTAAWLR**
Found in **AT2G06025.1** in **TAIR_Arabidopsis**, Symbols: | GCN5-related N-acetyltransferase (GNAT) family protein | chr2:2350228-2351895 FORWARD

Match to Query 10004: 2383.054851 from(795.358893,3+) index(9181)
Title: Elution from: 86.574 to 86.574 scan no 12697 cid35.00 polarity:+
Data file D12h-2_2.mgf

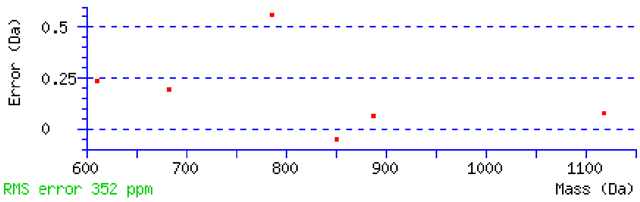
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

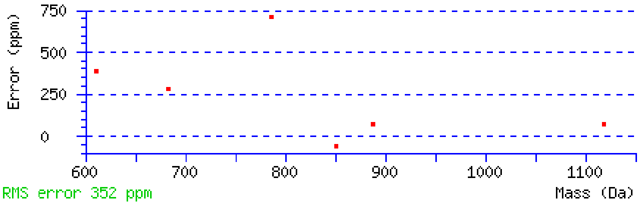


Monoisotopic mass of neutral peptide Mr(calc): 2383.0509
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.048
Matches : 6/192 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							19
2	249.1382	125.0727					V	2235.9928	1118.5000	2217.9692	1109.4883	2217.9822	1109.4948	18
3	321.1723	161.0898					A	2135.9274	1068.4673	2117.9038	1059.4555	2117.9168	1059.4620	17
4	481.2616	241.1344	463.2380	232.1226			R	2063.8932	1032.4502	2045.8696	1023.4385	2045.8826	1023.4450	16
5	**611.3012**	306.1542	593.2776	297.1424	593.2906	297.1490	E	1903.8040	952.4056	1885.7804	943.3938	1885.7934	943.4003	15
6	**683.3354**	342.1713	665.3118	333.1595	665.3248	333.1660	A	1773.7643	887.3858	1755.7407	878.3740	1755.7538	878.3805	14
7	815.3729	408.1901	797.3493	399.1783	797.3623	399.1848	M	1701.7302	851.3687	1683.7066	842.3569	1683.7196	842.3634	13
8	929.4540	465.2306	911.4304	456.2188	911.4434	456.2253	L	1569.6927	785.3500	1551.6691	776.3382	1551.6821	776.3447	12
9	1045.4779	523.2426	1027.4544	514.2308	1027.4674	514.2373	D	1455.6116	728.3094	1437.5880	719.2976	1437.6010	719.3041	11
10	1175.5176	588.2624	1157.4940	579.2506	1157.5070	579.2571	E	1339.5876	670.2974	1321.5640	661.2856	1321.5770	661.2921	10
11	1305.5572	653.2822	1287.5336	644.2704	1287.5466	644.2770	E	1209.5480	605.2776	1191.5244	596.2658	1191.5374	596.2723	9
12	1469.6176	735.3124	1451.5940	726.3006	1451.6070	726.3071	Y	1079.5083	540.2578	1061.4847	531.2460	1061.4978	531.2525	8
13	1657.6910	829.3491	1639.6674	820.3373	1639.6804	820.3438	W	915.4480	458.2276	897.4244	449.2158	897.4374	449.2223	7
14	1759.7357	880.3715	1741.7121	871.3597	1741.7251	871.3662	T	727.3746	364.1909	709.3510	355.1791	709.3640	355.1856	6
15	1831.7698	916.3885	1813.7462	907.3768	1813.7592	907.3833	A	625.3299	313.1686	607.3063	304.1568			5
16	1903.8040	952.4056	1885.7804	943.3938	1885.7934	943.4003	A	553.2957	277.1515	535.2721	268.1397			4
17	2091.8773	1046.4423	2073.8538	1037.4305	2073.8668	1037.4370	W	481.2616	241.1344	463.2380	232.1226			3
18	2205.9584	1103.4829	2187.9349	1094.4711	2187.9479	1094.4776	L	293.1882	147.0977	275.1646	138.0859			2
19							R	179.1071	90.0572	161.0835	81.0454			1

AT2G06025.1





NCBI **BLAST** search of FVAREAMLDEEYWTAAWLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.4	2383.0509	0.0039	FVAREAMLDEEYWTAAWLR
18.2	2383.0573	-0.0024	GFAVSNQKRNTNGSSISDPVMK
14.1	2383.0490	0.0059	NSDIDPQEAQQTLEIAEANLR
13.6	2383.0573	-0.0024	LYLKRMQGLSSGGGAGSDPATDR
10.9	2383.0606	-0.0058	NSTDASVMTTAMSGVERGVRVGK
7.9	2383.0542	0.0007	DEASSMLKATDFGVSVFIEEGK
5.6	2383.0510	0.0039	MEYNWGSDAALFKPERWLK
5.6	2383.0593	-0.0045	VVPTVDEKQVSEEEEGRPSDK
5.3	2383.0546	0.0002	LSPSSSVVLTQESSNCNYKQK
4.8	2383.0487	0.0061	GVVSMANSGPHTNGSQFFVLYK

Mascot: http://www.matrixscience.com/

AT2G06850.1

Mascot Search Results

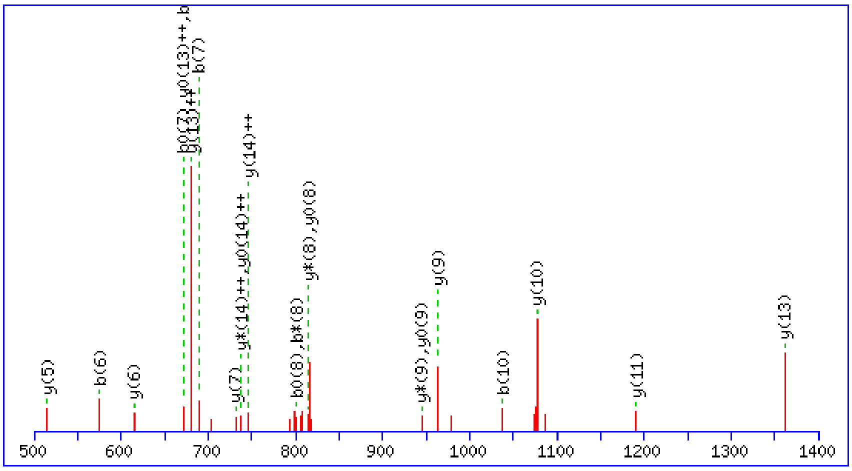
Peptide View

MS/MS Fragmentation of **TGQPAILQTNVFTGGK**
Found in **AT2G06850.1** in **TAIR_Arabidopsis**, Symbols: EXT, EXGT-A1 | EXGT-A1 (ENDOXYLOGLUCAN TRANSFERASE); hydrolase, acting on glycosyl bonds | chr2:2763616-2765487 FORWARD

Match to Query 7452: 1650.810198 from(826.412375,2+) index(6648)
Title: Elution from: 58.482 to 58.482 scan no 8577 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

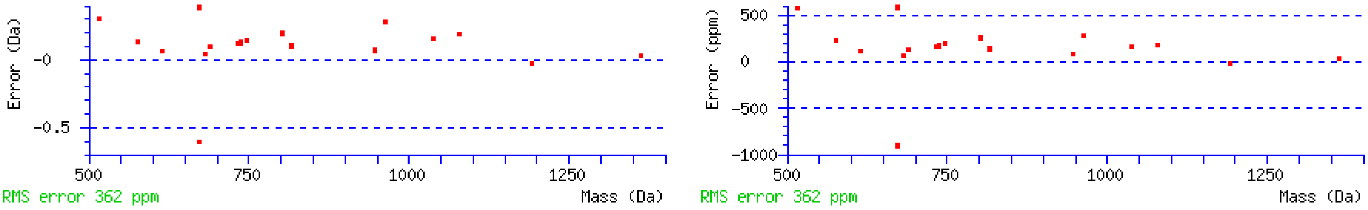
Or, Plot from 500 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1650.8085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.0004
Matches : 24/170 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							16
2	161.0705	81.0389			143.0599	72.0336	G	1549.7711	775.3892	1531.7475	766.3774	1531.7606	766.3839	15
3	291.1231	146.0652	273.0996	137.0534	273.1126	137.0599	Q	1491.7526	746.3800	1473.7290	737.3682	1473.7421	737.3747	14
4	389.1729	195.0901	371.1494	186.0783	371.1624	186.0848	P	***1361.7000***	681.3536	1343.6764	672.3418	1343.6894	672.3483	13
5	461.2071	231.1072	443.1835	222.0954	443.1965	222.1019	A	1263.6502	632.3287	1245.6266	623.3169	1245.6396	623.3234	12
6	**575.2882**	288.1477	557.2646	279.1359	557.2776	279.1424	I	***1191.6160***	596.3117	1173.5925	587.2999	1173.6055	587.3064	11
7	**689.3693**	345.1883	671.3457	336.1765	671.3587	336.1830	L	***1077.5349***	539.2711	1059.5114	530.2593	1059.5244	530.2658	10
8	819.4219	410.2146	801.3983	401.2028	801.4114	401.2093	Q	***963.4538***	482.2306	945.4303	473.2188	945.4433	473.2253	9
9	921.4666	461.2370	903.4431	452.2252	903.4561	452.2317	T	833.4012	417.2042	815.3776	408.1924	815.3906	408.1990	8
10	**1037.5036**	519.2555	1019.4801	510.2437	1019.4931	510.2502	N	***731.3565***	366.1819	713.3329	357.1701	713.3459	357.1766	7
11	1137.5691	569.2882	1119.5455	560.2764	1119.5585	560.2829	V	***615.3195***	308.1634	597.2959	299.1516	597.3089	299.1581	6
12	1285.6345	643.3209	1267.6110	634.3091	1267.6240	634.3156	F	***515.2540***	258.1307	497.2305	249.1189	497.2435	249.1254	5
13	1387.6792	694.3433	1369.6557	685.3315	1369.6687	685.3380	T	367.1886	184.0979	349.1650	175.0861	349.1780	175.0926	4
14	1445.6977	723.3525	1427.6742	714.3407	1427.6872	714.3472	G	265.1439	133.0756	247.1203	124.0638			3
15	1503.7162	752.3618	1485.6927	743.3500	1485.7057	743.3565	G	207.1254	104.0663	189.1018	95.0545			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT2G06850.1



NCBI **BLAST** search of TGQPAILQTNVFTGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.0	1650.8085	0.0017	TGQPAILQTNVFTGGK
2.7	1650.8068	0.0034	GTQPGLMIYMLPLGK
0.5	1650.8093	0.0009	SSLLVDDLGSMLKEK

Mascot: http://www.matrixscience.com/

AT2G10940.1

{MATRIX SCIENCE} Mascot Search Results

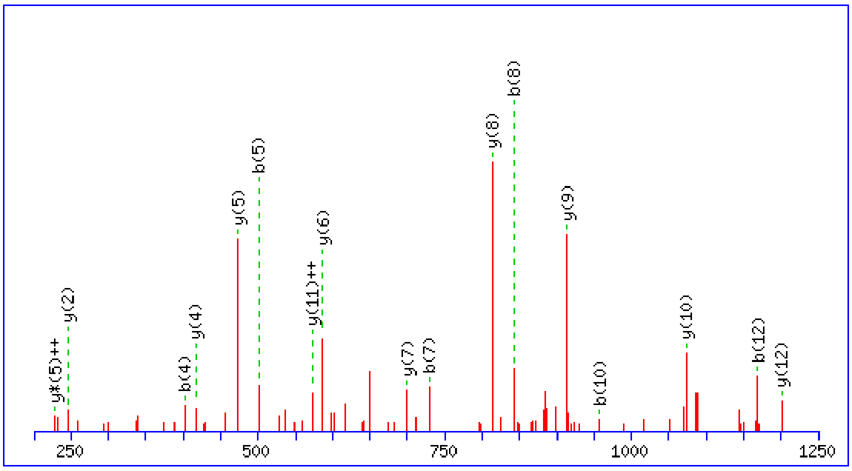
Peptide View

MS/MS Fragmentation of **LGACVDLLGGLVK**
Found in **AT2G10940.1** in **TAIR_Arabidopsis**, Symbols: | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | chr2:4318242-4319117 REVERSE

Match to Query 4513: 1313.737100 from(657.875826,2+) index(8943)
Title: Elution from: 82.485 to 82.485 scan no 12070 cid35.00 polarity:+
Data file D1d-1_1.mgf

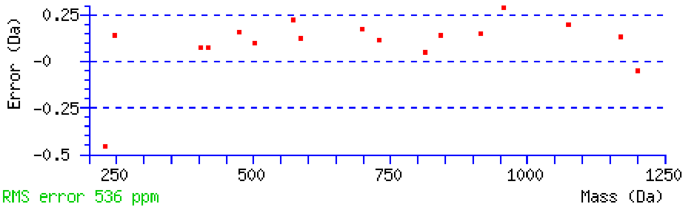
Click mouse within plot area to zoom in by factor of two about that point

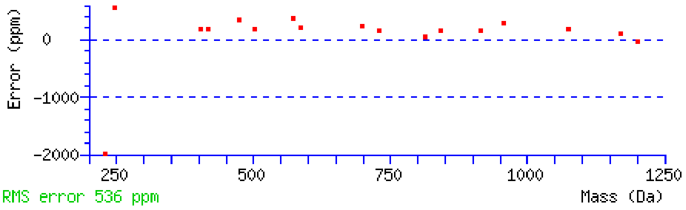
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1313.7377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 5.1e-009
Matches : 17/96 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							13
2	171.1128	86.0600			G	***1201.6609***	601.3341	1184.6344	592.8208	1183.6504	592.3288	12
3	242.1499	121.5786			A	1144.6395	572.8234	1127.6129	564.3101	1126.6289	563.8181	11
4	***402.1806***	201.5939			C	***1073.6023***	537.3048	1056.5758	528.7915	1055.5918	528.2995	10
5	***501.2490***	251.1281			V	***913.5717***	457.2895	896.5451	448.7762	895.5611	448.2842	9
6	616.2759	308.6416	598.2654	299.6363	D	***814.5033***	407.7553	797.4767	399.2420	796.4927	398.7500	8
7	***729.3600***	365.1836	711.3494	356.1783	L	***699.4763***	350.2418	682.4498	341.7285			7
8	***842.4441***	421.7257	824.4335	412.7204	L	***586.3923***	293.6998	569.3657	285.1865			6
9	899.4655	450.2364	881.4550	441.2311	G	***473.3082***	237.1577	456.2817	228.6445			5
10	***956.4870***	478.7471	938.4764	469.7418	G	***416.2867***	208.6470	399.2602	200.1337			4
11	1069.5710	535.2892	1051.5605	526.2839	L	359.2653	180.1363	342.2387	171.6230			3
12	***1168.6395***	584.8234	1150.6289	575.8181	V	***246.1812***	123.5942	229.1547	115.0810			2
13					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LGACVDLLGGLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G10940.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.8	1313.7377	-0.0006	LGACVDLLGGLVK
1.1	1313.7343	0.0028	QVQEFLNIPVK

Mascot: http://www.matrixscience.com/

AT2G13360.1

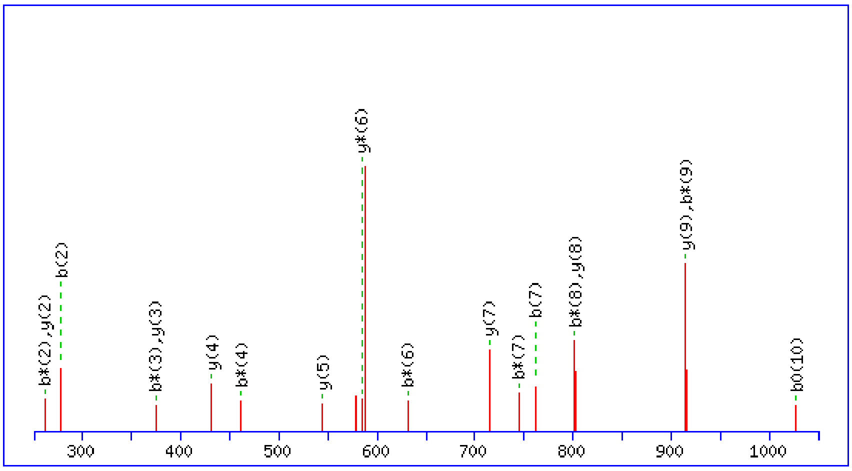
Mascot Search Results

Peptide View

MS/MS Fragmentation of YNLSLGLGLNK
Found in AT2G13360.1 in TAIR_Arabidopsis, Symbols: AGT1, AGT | AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE) | chr2:5546499-5547984 REVERSE

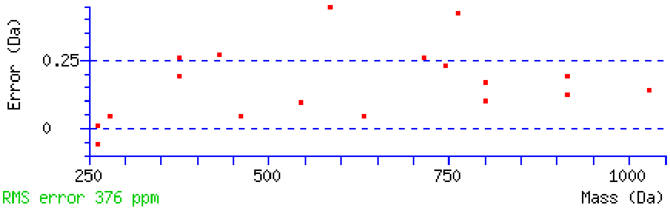
Match to Query 3640: 1190.666044 from(596.340298,2+) index(7011)
Title: Elution from: 65.035 to 65.035 scan no 9227 cid35.00 polarity:+
Data file D1d-1_1.mgf

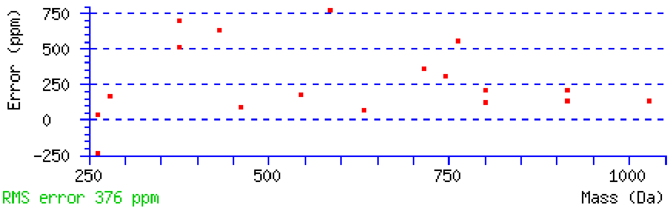
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1190.6659
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.3e-006
Matches : 18/98 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							11
2	**278.1135**	139.5604	261.0870	131.0471			N	1028.6099	514.8086	1011.5833	506.2953	1010.5993	505.8033	10
3	391.1976	196.1024	374.1710	187.5892			L	***914.5669***	457.7871	897.5404	449.2738	896.5564	448.7818	9
4	478.2296	239.6185	461.2031	231.1052	460.2191	230.6132	S	***801.4829***	401.2451	784.4563	392.7318	783.4723	392.2398	8
5	591.3137	296.1605	574.2871	287.6472	573.3031	287.1552	L	***714.4509***	357.7291	697.4243	349.2158			7
6	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	G	601.3668	301.1870	584.3402	292.6738			6
7	**761.4192**	381.2132	744.3927	372.7000	743.4087	372.2080	L	***544.3453***	272.6763	527.3188	264.1630			5
8	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	G	***431.2613***	216.1343	414.2347	207.6210			4
9	931.5247	466.2660	914.4982	457.7527	913.5142	457.2607	L	***374.2398***	187.6235	357.2132	179.1103			3
10	1045.5677	523.2875	1028.5411	514.7742	1027.5571	514.2822	N	***261.1557***	131.0815	244.1292	122.5682			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YNLSLGLGLNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G13360.1

Score	Mr(calc)	Delta	Sequence
64.7	1190.6659	0.0001	YNLSLGLGLNK
10.3	1190.6659	0.0001	YLNGVAGKEIK
8.3	1190.6693	-0.0032	SKITSMLNAVK
8.2	1190.6659	0.0002	LYNLINEKGK
2.5	1190.6659	0.0001	ASGKGVLTSPFK
2.3	1190.6693	-0.0032	TKMALAEKGVK
0.7	1190.6659	0.0001	YRSVVPTIEK
0.5	1190.6659	0.0001	YLPISVKTDR
0.4	1190.6659	0.0002	QGLAYAAKLEK

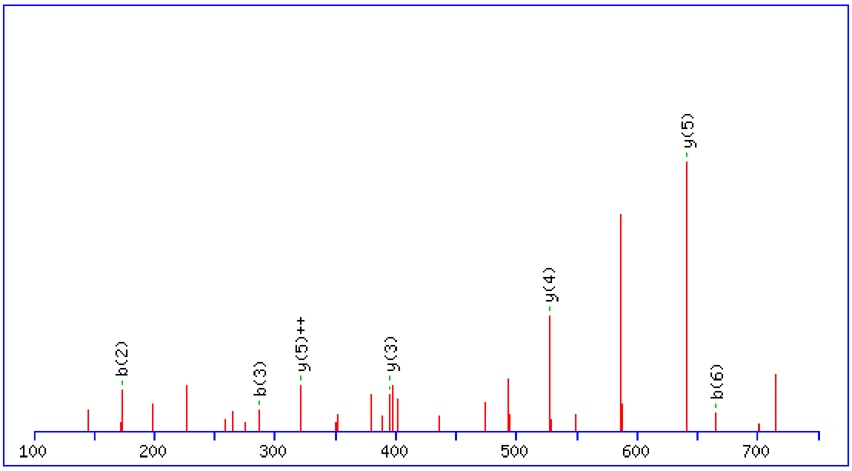
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GILMMLK**
Found in **AT2G14050.1** in **TAIR_Arabidopsis**, Symbols: MCM9 | MCM9; ATP binding / DNA binding / DNA-dependent ATPase | chr2:5916322-5920899 FORWARD

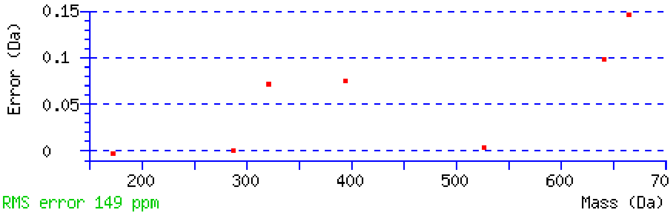
Match to Query 906: 812.435366 from(407.224959,2+) index(5914)
Title: Elution from: 54.731 to 54.731 scan no 7626 cid35.00 polarity:+
Data file D1d-2_1.mgf

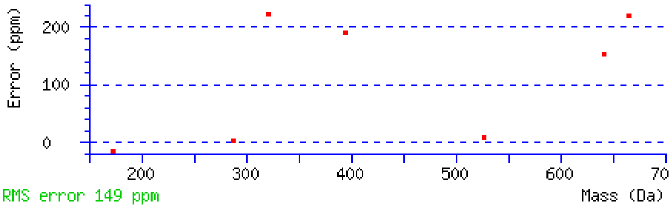
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 812.4364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.011
Matches : 7/36 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	59.0258	30.0165	G					7
2	*173.1069*	87.0571	I	755.4252	378.2162	737.4016	369.2045	6
3	*287.1880*	144.0976	L	*641.3441*	321.1757	623.3205	312.1639	5
4	419.2255	210.1164	M	*527.2630*	264.1351	509.2394	255.1234	4
5	551.2630	276.1351	M	*395.2255*	198.1164	377.2019	189.1046	3
6	*665.3441*	333.1757	L	263.1880	132.0976	245.1644	123.0858	2
7			K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of GILMMLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.6	812.4364	-0.0011	GILMMLK

Mascot: http://www.matrixscience.com/

AT2G14720.1

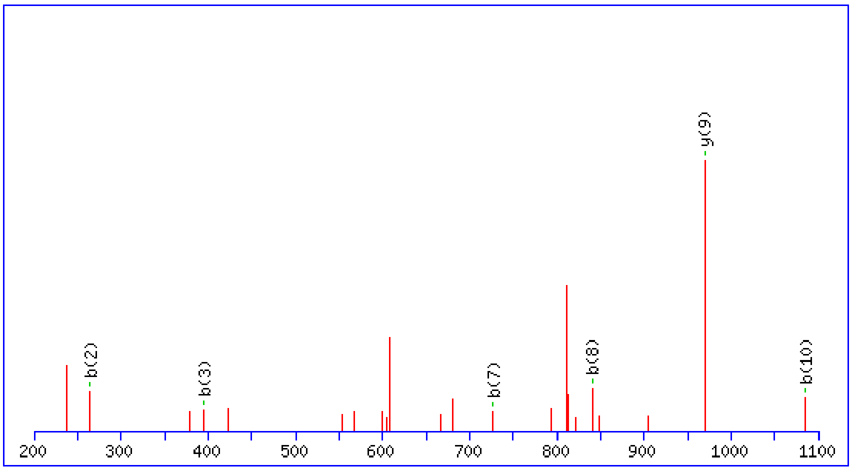
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFKGAAQILEK**
Found in **AT2G14720.1** in **TAIR_Arabidopsis**, Symbols: VSR-2 | VSR-2 (Vacuolar sorting receptor 2); calcium ion binding | chr2:6307960-6311238 REVERSE

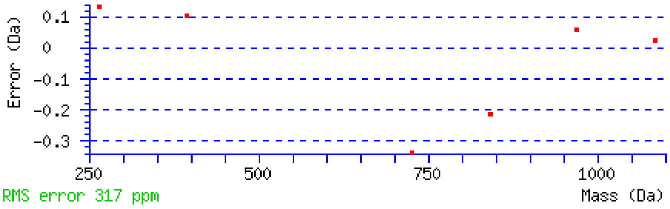
Match to Query 4484: 1232.617518 from(617.316035,2+) index(7785)
Title: Elution from: 67.305 to 67.305 scan no 10050 cid35.00 polarity:+
Data file C7-1_1.mgf

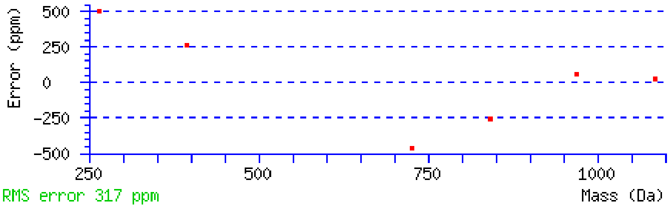
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1232.6193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.039
Matches : 6/114 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							11
2	***265.0967***	133.0520			247.0861	124.0467	F	1117.6026	559.3050	1099.5790	550.2932	1099.5921	550.2997	10
3	***395.1857***	198.0965	377.1622	189.0847	377.1752	189.0912	K	969.5372	485.2722	951.5136	476.2604	951.5266	476.2669	9
4	453.2042	227.1058	435.1807	218.0940	435.1937	218.1005	G	839.4481	420.2277	821.4246	411.2159	821.4376	411.2224	8
5	525.2384	263.1228	507.2148	254.1110	507.2278	254.1175	A	781.4296	391.2185	763.4061	382.2067	763.4191	382.2132	7
6	597.2725	299.1399	579.2489	290.1281	579.2620	290.1346	A	709.3955	355.2014	691.3719	346.1896	691.3849	346.1961	6
7	***727.3252***	364.1662	709.3016	355.1544	709.3146	355.1609	Q	637.3613	319.1843	619.3378	310.1725	619.3508	310.1790	5
8	***841.4063***	421.2068	823.3827	412.1950	823.3957	412.2015	I	507.3087	254.1580	489.2851	245.1462	489.2981	245.1527	4
9	955.4874	478.2473	937.4638	469.2355	937.4768	469.2420	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
10	***1085.5270***	543.2671	1067.5034	534.2553	1067.5164	534.2619	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DFKGAAQILEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G14720.1

Score	Mr(calc)	Delta	Sequence
23.3	1232.6193	-0.0018	DFKGAAQILEK
14.4	1232.6193	-0.0018	LGEDFLERIK
12.8	1232.6193	-0.0018	DVYILGAANVGK
9.9	1232.6171	0.0004	ESQSKLASALGK
7.8	1232.6171	0.0004	LKSSEERLEK
7.8	1232.6171	0.0004	SLKESERLEK
7.1	1232.6171	0.0005	GGAVTKSETLQK
6.5	1232.6193	-0.0018	VSGSSWIEVKK
6.2	1232.6198	-0.0022	AREVVQSGKNK
4.9	1232.6198	-0.0022	EAQKASARINK

AT2G14960.1

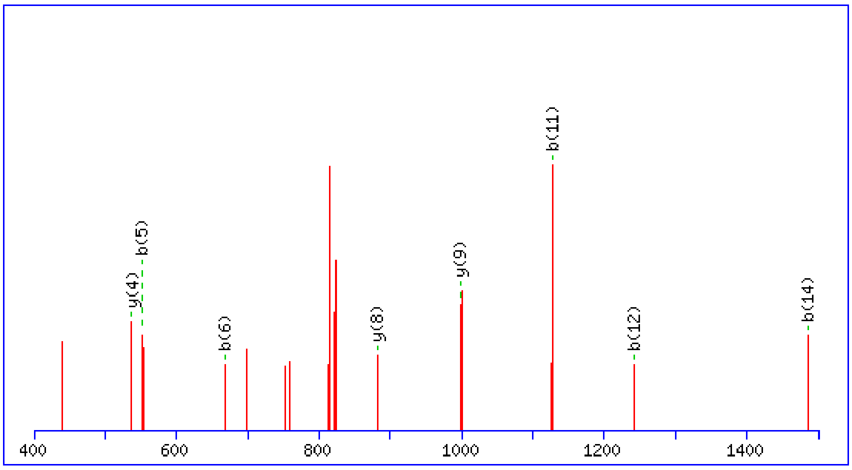
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSRVADNSVGPLEIR**
Found in **AT2G14960.1** in **TAIR_Arabidopsis**, Symbols: GH3.1 | GH3.1 | chr2:6458741-6460752 REVERSE

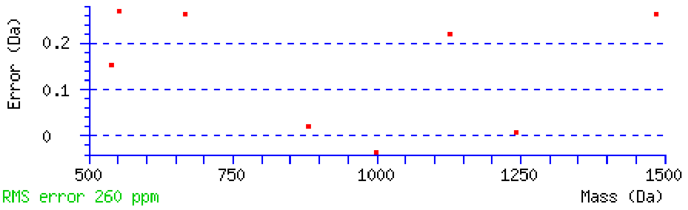
Match to Query 8087: 1662.798268 from(832.406410,2+) index(11076)
Title: Elution from: 107.339 to 107.339 scan no 15879 cid35.00 polarity:+
Data file C7-2_1.mgf

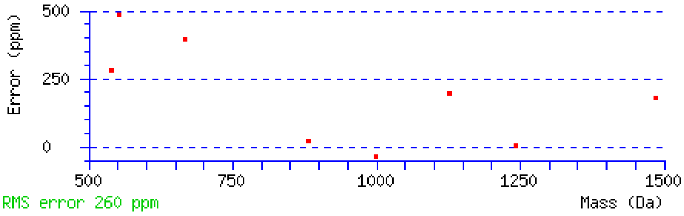
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1662.7960
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0068
Matches : 8/162 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							15
2	219.0890	110.0481	201.0654	101.0363	201.0784	101.0428	S	1533.7506	767.3789	1515.7270	758.3672	1515.7401	758.3737	14
3	379.1782	190.0928	361.1547	181.0810	361.1677	181.0875	R	1445.7216	723.3644	1427.6980	714.3526	1427.7110	714.3591	13
4	479.2437	240.1255	461.2201	231.1137	461.2331	231.1202	V	1285.6323	643.3198	1267.6087	634.3080	1267.6217	634.3145	12
5	*551.2778*	276.1426	533.2543	267.1308	533.2673	267.1373	A	1185.5669	593.2871	1167.5433	584.2753	1167.5563	584.2818	11
6	*667.3018*	334.1545	649.2782	325.1428	649.2912	325.1493	D	1113.5327	557.2700	1095.5091	548.2582	1095.5221	548.2647	10
7	783.3388	392.1730	765.3152	383.1613	765.3282	383.1678	N	**997.5087**	499.2580	979.4851	490.2462	979.4982	490.2527	9
8	871.3679	436.1876	853.3443	427.1758	853.3573	427.1823	S	**881.4717**	441.2395	863.4481	432.2277	863.4612	432.2342	8
9	971.4333	486.2203	953.4097	477.2085	953.4228	477.2150	V	793.4427	397.2250	775.4191	388.2132	775.4321	388.2197	7
10	1029.4518	515.2295	1011.4282	506.2178	1011.4413	506.2243	G	693.3772	347.1922	675.3536	338.1805	675.3667	338.1870	6
11	*1127.5016*	564.2544	1109.4780	555.2427	1109.4911	555.2492	P	635.3587	318.1830	617.3351	309.1712	617.3482	309.1777	5
12	*1241.5827*	621.2950	1223.5591	612.2832	1223.5722	612.2897	L	**537.3089**	269.1581	519.2853	260.1463	519.2984	260.1528	4
13	1371.6223	686.3148	1353.5988	677.3030	1353.6118	677.3095	E	423.2278	212.1175	405.2042	203.1058	405.2173	203.1123	3
14	*1485.7034*	743.3554	1467.6799	734.3436	1467.6929	734.3501	I	293.1882	147.0977	275.1646	138.0859			2
15							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of QSRVADNSVGPLEIR

AT2G14960.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.7	1662.7960	0.0023	QSRVADNSVGPLEIR
30.7	1662.7955	0.0027	NSTNIDQVIDWLVK
19.7	1662.7933	0.0050	DQVESVINTIIEGAR
13.7	1662.7935	0.0048	MHEFNITLRPVQR
7.2	1662.8016	-0.0033	IHSDTTVARMLVGNK
4.8	1662.8009	-0.0026	FDHLPRNTKNQLR
3.0	1662.7933	0.0050	DSVNQLSLAIAELDR
2.3	1662.7982	0.0001	DHEGAYAQLIRLQK
1.8	1662.7955	0.0027	DGVYASLVQLHLTAAS
0.8	1662.7964	0.0019	NLEMTFSMKFLKR

AT2G15090.1

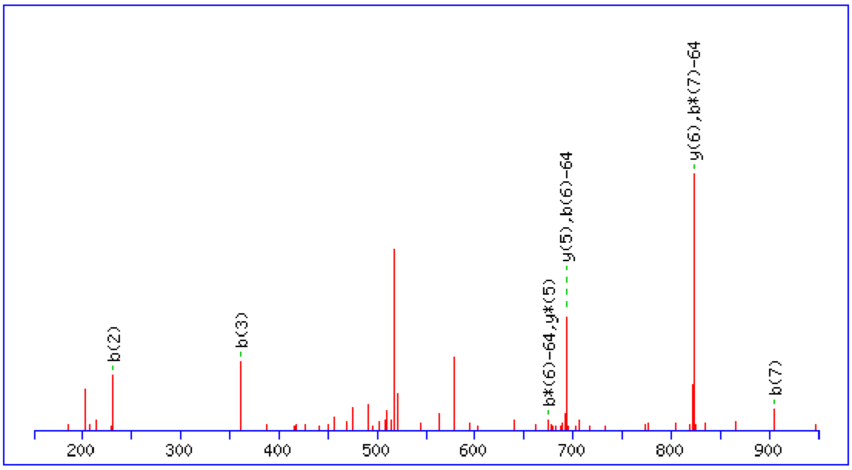
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLKMVFFK**
Found in **AT2G15090.1** in **TAIR_Arabidopsis**, Symbols: | fatty acid elongase, putative | chr2:6549418-6550863 FORWARD

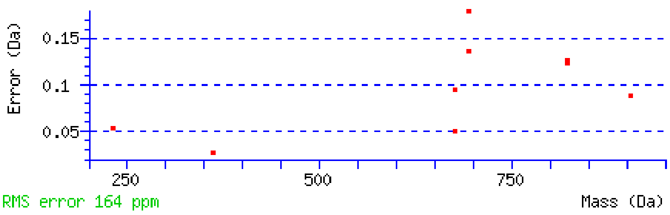
Match to Query 3104: 1052.533582 from(527.274067,2+) index(4064)
Title: Elution from: 38.150 to 38.150 scan no 5059 cid35.00 polarity:+
Data file C7-3_1.mgf

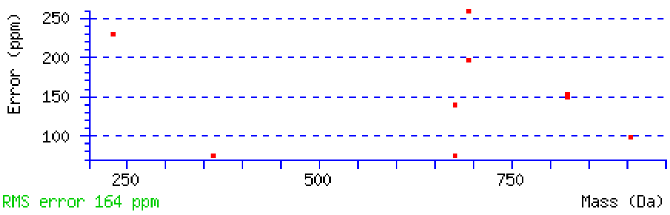
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1052.5355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.012
Matches : 9/84 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	117.0443	59.0258	99.0207	50.0140	N					8
2	***231.1254***	116.0663	213.1018	107.0545	L	937.5058	469.2565	919.4822	460.2447	7
3	***361.2144***	181.1108	343.1908	172.0990	K	**823.4247**	412.2160	805.4011	403.2042	6
4	509.2468	255.1271	491.2233	246.1153	M	**693.3357**	347.1715	675.3121	338.1597	5
5	609.3123	305.1598	591.2887	296.1480	V	545.3032	273.1552	527.2796	264.1435	4
6	757.3777	379.1925	739.3542	370.1807	F	445.2378	223.1225	427.2142	214.1107	3
7	***905.4432***	453.2252	887.4196	444.2134	F	297.1723	149.0898	279.1487	140.0780	2
8					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of NLKMVFFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.6	1052.5355	-0.0019	NLKMVFFK

AT2G15090.1

Mascot: http://www.matrixscience.com/

AT2G15320.1

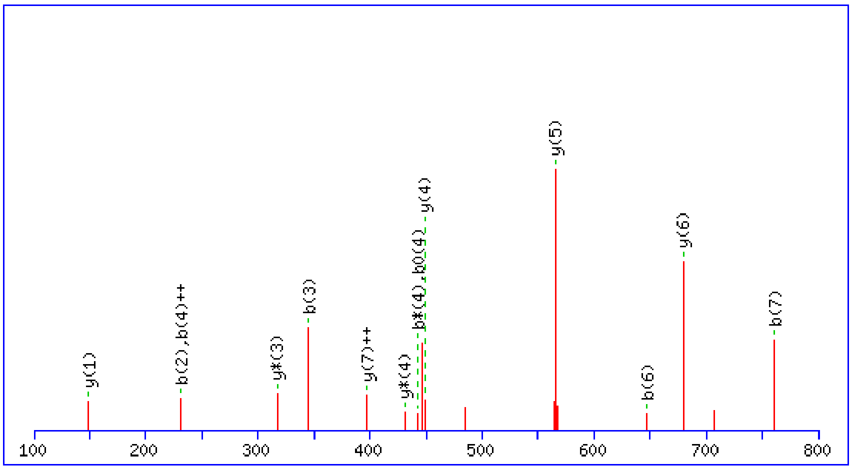
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLIDLALK**
Found in **AT2G15320.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat family protein | chr2:6673609-6674757 REVERSE

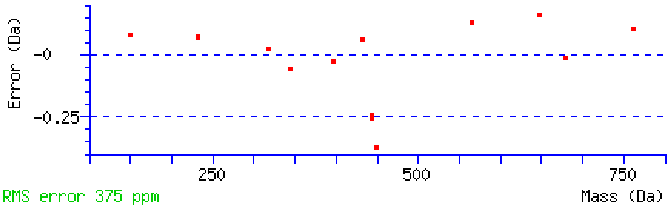
Match to Query 1715: 908.519586 from(455.267069,2+) index(6259)
Title: Elution from: 54.610 to 54.610 scan no 7977 cid35.00 polarity:+
Data file C7-3_2.mgf

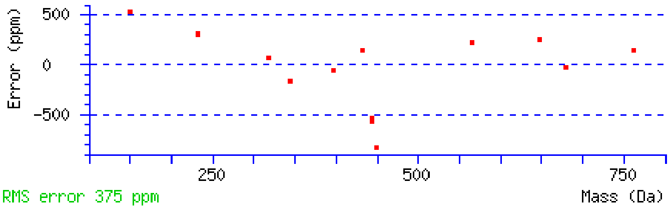
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 908.5191
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0013
Matches : 14/70 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							8
2	***231.1254***	116.0663	213.1018	107.0545			L	793.4894	397.2483	775.4658	388.2365	775.4788	388.2431	7
3	***345.2065***	173.1069	327.1829	164.0951			I	***679.4083***	340.2078	661.3847	331.1960	661.3977	331.2025	6
4	461.2304	231.1189	443.2069	222.1071	443.2199	222.1136	D	***565.3272***	283.1672	547.3036	274.1554	547.3166	274.1620	5
5	575.3115	288.1594	557.2880	279.1476	557.3010	279.1541	L	***449.3032***	225.1552	431.2796	216.1435			4
6	***647.3457***	324.1765	629.3221	315.1647	629.3351	315.1712	A	335.2221	168.1147	317.1985	159.1029			3
7	***761.4268***	381.2170	743.4032	372.2052	743.4162	372.2118	L	263.1880	132.0976	245.1644	123.0858			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NLIDLALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.2	908.5191	0.0005	NLIDLALK
32.9	908.5191	0.0005	VKIDPSIK

AT2G15320.1

26.5	908.5191	0.0005	DLILNAIK
26.5	908.5191	0.0005	GGLLIDAIK
24.5	908.5213	-0.0018	EVLLWLK
24.5	908.5191	0.0005	INLGEILK
16.2	908.5218	-0.0022	KVLGQPVR
12.6	908.5191	0.0005	NVVIDVIK
10.2	908.5214	-0.0018	SLPPLVFK
9.3	908.5218	-0.0022	IPKPARSK

AT2G15620.1

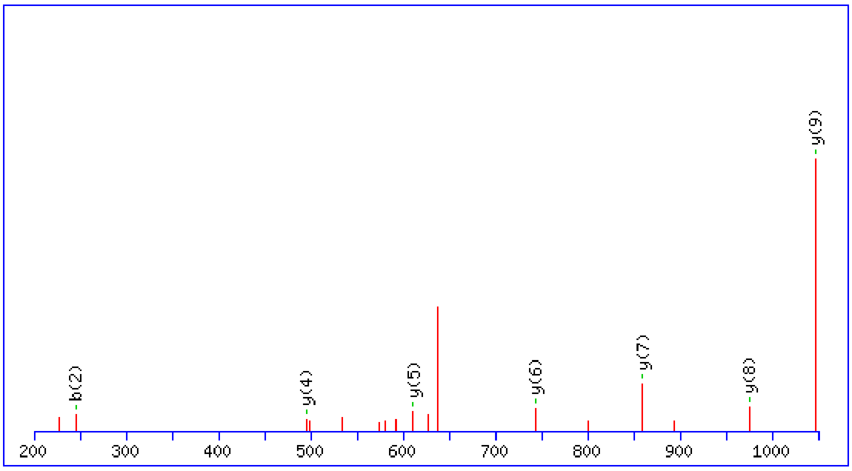
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQADDMDELAR**
Found in **AT2G15620.1** in **TAIR_Arabidopsis**, Symbols: NIR, ATHNIR, NIR1 | NIR1 (NITRITE REDUCTASE); ferredoxin-nitrate reductase | chr2:6817634-6819748 FORWARD

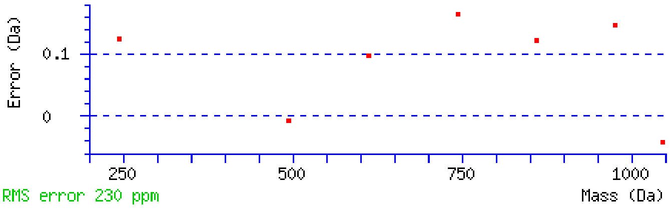
Match to Query 4479: 1290.532732 from(646.273642,2+) index(3881)
Title: Elution from: 36.982 to 36.982 scan no 4851 cid35.00 polarity:+
Data file C7-1_3.mgf

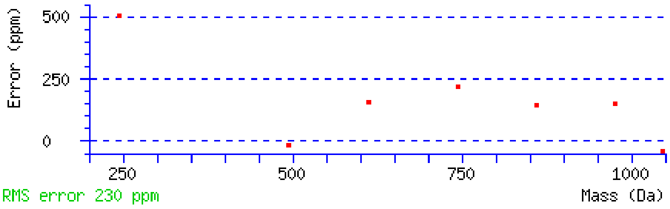
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1290.5320
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 7.2e-006
Matches : 7/106 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							11
2	245.1410	123.0741	227.1174	114.0624			Q	1177.4582	589.2327	1159.4346	580.2210	1159.4477	580.2275	10
3	317.1752	159.0912	299.1516	150.0794			A	***1047.4056***	524.2064	1029.3820	515.1946	1029.3950	515.2011	9
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	D	***975.3714***	488.1893	957.3478	479.1776	957.3609	479.1841	8
5	549.2231	275.1152	531.1995	266.1034	531.2126	266.1099	D	***859.3474***	430.1774	841.3239	421.1656	841.3369	421.1721	7
6	681.2606	341.1340	663.2371	332.1222	663.2501	332.1287	M	***743.3235***	372.1654	725.2999	363.1536	725.3129	363.1601	6
7	797.2846	399.1460	779.2610	390.1342	779.2741	390.1407	D	***611.2859***	306.1466	593.2624	297.1348	593.2754	297.1413	5
8	927.3243	464.1658	909.3007	455.1540	909.3137	455.1605	E	***495.2620***	248.1346	477.2384	239.1228	477.2514	239.1293	4
9	1041.4054	521.2063	1023.3818	512.1945	1023.3948	512.2010	L	365.2223	183.1148	347.1988	174.1030			3
10	1113.4395	557.2234	1095.4159	548.2116	1095.4289	548.2181	A	251.1412	126.0743	233.1177	117.0625			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LQADDMDELAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G15620.1

Score	Mr(calc)	Delta	Sequence
56.4	1290.5320	0.0007	LQADDMDELAR
1.7	1290.5347	-0.0020	HSQRCDTELK

Mascot: http://www.matrixscience.com/

AT2G16360.1

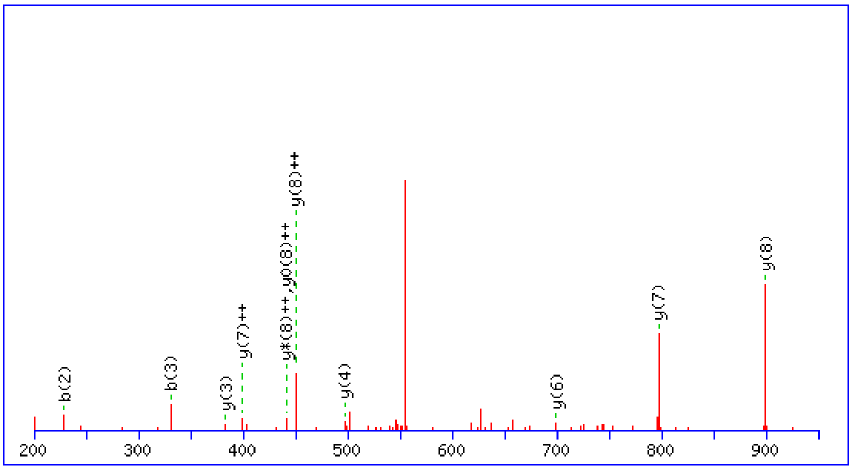
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LITPSILSDR**
Found in **AT2G16360.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S25 (RPS25A) | chr2:7083795-7084448 REVERSE

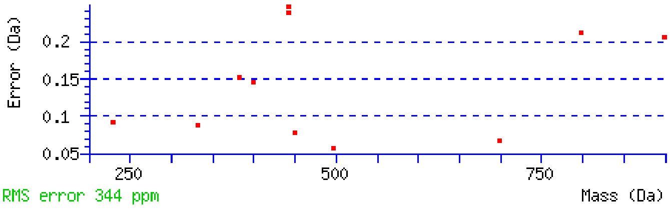
Match to Query 3540: 1126.598468 from(564.306510,2+) index(6099)
Title: Elution from: 53.895 to 53.895 scan no 7779 cid35.00 polarity:+
Data file C7-1_2.mgf

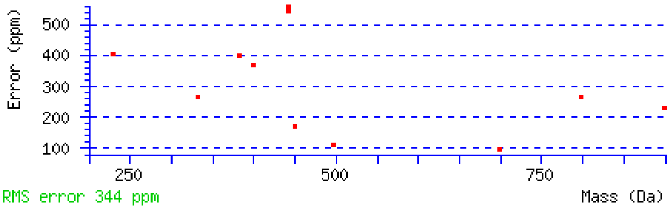
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1126.6008
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0059
Matches : 11/84 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			L							10
2	**229.1695**	115.0884			I	1013.5270	507.2671	995.5034	498.2553	995.5164	498.2619	9
3	**331.2142**	166.1107	313.2036	157.1054	T	***899.4459***	450.2266	881.4223	441.2148	881.4353	441.2213	8
4	429.2640	215.1356	411.2534	206.1303	P	***797.4012***	399.2042	779.3776	390.1924	779.3906	390.1990	7
5	517.2930	259.1502	499.2825	250.1449	S	***699.3514***	350.1793	681.3278	341.1675	681.3408	341.1741	6
6	631.3741	316.1907	613.3636	307.1854	I	611.3223	306.1648	593.2987	297.1530	593.3118	297.1595	5
7	745.4552	373.2313	727.4447	364.2260	L	***497.2412***	249.1243	479.2176	240.1125	479.2307	240.1190	4
8	833.4843	417.2458	815.4737	408.2405	S	***383.1601***	192.0837	365.1365	183.0719	365.1496	183.0784	3
9	949.5083	475.2578	931.4977	466.2525	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
10					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LITPSILSDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G16360.1

29.7	1126.6008	-0.0024	LITPSILSDR
3.5	1126.6008	-0.0024	QPVVSISSAVK
2.2	1126.6008	-0.0023	VVQVGEKVEK
1.4	1126.6008	-0.0024	IISLNLAENK

AT2G16600.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVVFGQVVEGLNVVR**
Found in **AT2G16600.1** in **TAIR_Arabidopsis**, Symbols: ROC3 | ROC3 (rotamase CyP 3); peptidyl-prolyl cis-trans isomerase | chr2:7207944-7208465 FORWARD

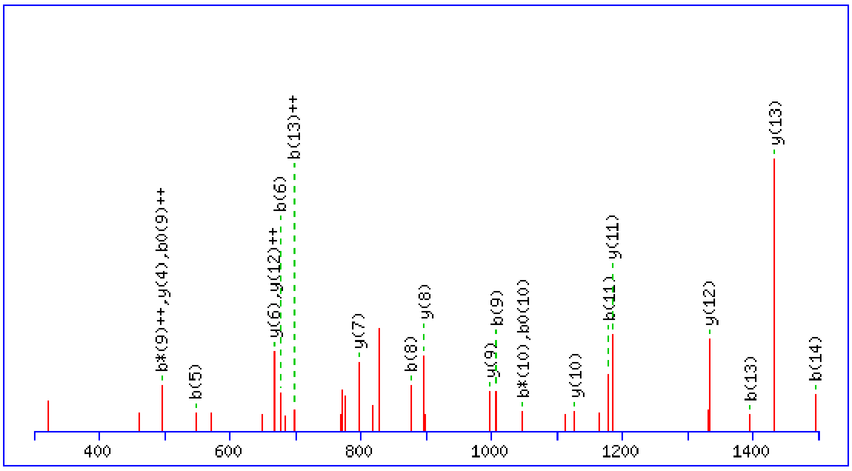
Match to Query 7891: 1672.852378 from(837.433465,2+) index(7292)
Title: Elution from: 64.460 to 64.460 scan no 9526 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

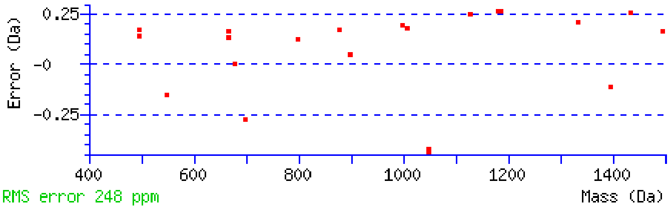
Label all possible matches ○ Label matches used for scoring ●

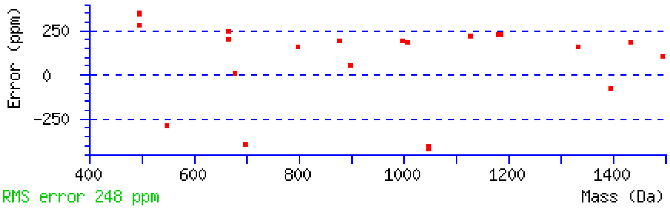
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1672.8553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 1.2e-007
Matches : 22/130 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	141.0573	71.0323					H							15
2	241.1227	121.0650					V	1533.8126	767.4099	1515.7890	758.3981	1515.8020	758.4047	14
3	341.1882	171.0977					V	***1433.7472***	717.3772	1415.7236	708.3654	1415.7366	708.3719	13
4	489.2536	245.1305					F	***1333.6817***	667.3445	1315.6581	658.3327	1315.6711	658.3392	12
5	***547.2721***	274.1397					G	***1185.6163***	593.3118	1167.5927	584.3000	1167.6057	584.3065	11
6	***677.3248***	339.1660	659.3012	330.1542			Q	***1127.5978***	564.3025	1109.5742	555.2907	1109.5872	555.2972	10
7	777.3902	389.1988	759.3667	380.1870			V	***997.5451***	499.2762	979.5215	490.2644	979.5345	490.2709	9
8	***877.4557***	439.2315	859.4321	430.2197			V	***897.4797***	449.2435	879.4561	440.2317	879.4691	440.2382	8
9	***1007.4953***	504.2513	989.4717	495.2395	989.4847	495.2460	E	***797.4142***	399.2107	779.3906	390.1990	779.4036	390.2055	7
10	1065.5138	533.2605	1047.4902	524.2488	1047.5032	524.2553	G	***667.3746***	334.1909	649.3510	325.1791			6
11	***1179.5949***	590.3011	1161.5713	581.2893	1161.5843	581.2958	L	609.3561	305.1817	591.3325	296.1699			5
12	1295.6319	648.3196	1277.6083	639.3078	1277.6213	639.3143	N	***495.2750***	248.1411	477.2514	239.1293			4
13	***1395.6974***	698.3523	1377.6738	689.3405	1377.6868	689.3470	V	379.2380	190.1226	361.2144	181.1108			3
14	***1495.7628***	748.3850	1477.7392	739.3732	1477.7522	739.3798	V	279.1725	140.0899	261.1490	131.0781			2
15							R	179.1071	90.0572	161.0835	81.0454			1





AT2G16600.1

NCBI **BLAST** search of HVVFGQVVEGLNVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.9	1672.8553	-0.0029	HVVFGQVVEGLNVVR
3.3	1672.8553	-0.0029	GGFGEVYRGKLLLSR

MATRIX SCIENCE

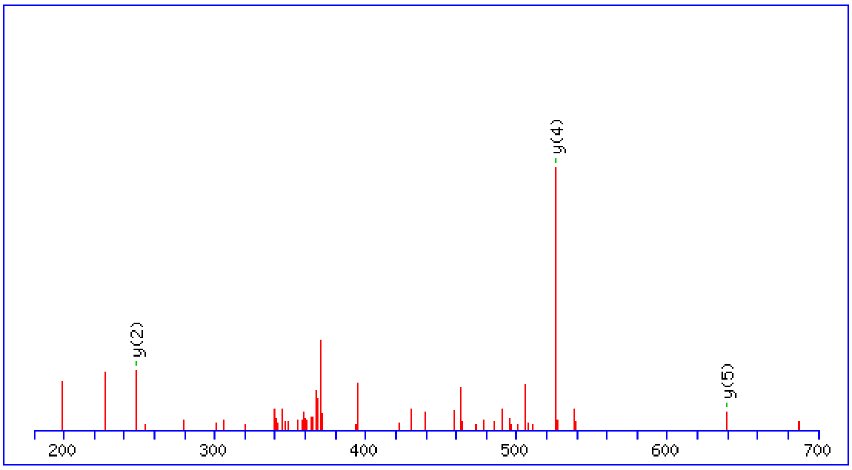
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLYDTK**
Found in **AT2G17360.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S4 (RPS4A) | chr2:7553680-7555220 FORWARD

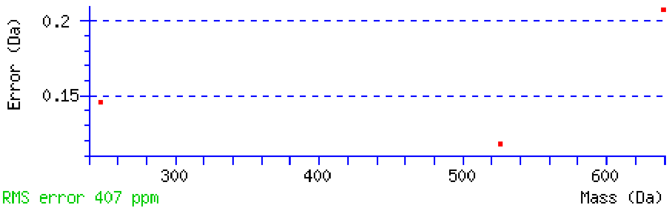
Match to Query 883: 751.411424 from(376.712988,2+) index(1673)
Title: Elution from: 21.882 to 21.882 scan no 2253 cid35.00 polarity:+
Data file D12h-1_1.mgf

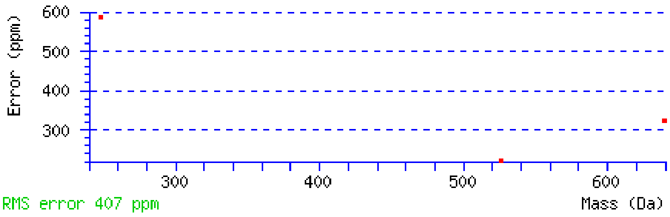
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 180 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 751.4116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.03
Matches : 3/42 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			**L**							**6**
2	227.1754	114.0913			**L**	***639.3348***	320.1710	622.3083	311.6578	621.3243	311.1658	**5**
3	390.2387	195.6230			**Y**	***526.2508***	263.6290	509.2242	255.1157	508.2402	254.6237	**4**
4	505.2657	253.1365	487.2551	244.1312	**D**	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	**3**
5	606.3134	303.6603	588.3028	294.6550	**T**	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
6					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LLYDTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.6	751.4116	-0.0002	LLYDTK

Mascot: http://www.matrixscience.com/

AT2G17440.1

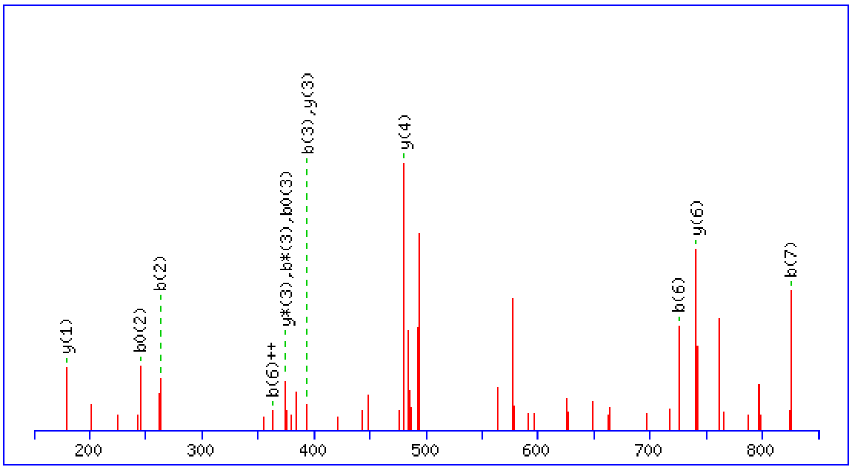
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EMKKSLVR**
Found in **AT2G17440.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat family protein | chr2:7578413-7580488 FORWARD

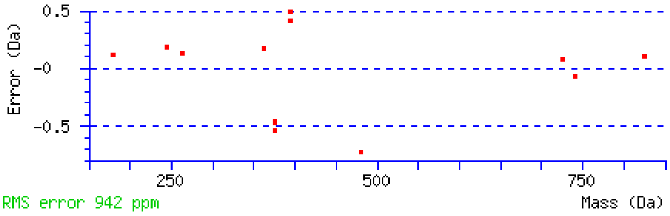
Match to Query 2050: 1002.532454 from(502.273503,2+) index(943)
Title: Elution from: 18.412 to 18.412 scan no 1458 cid35.00 polarity:+
Data file D12h-2_2.mgf

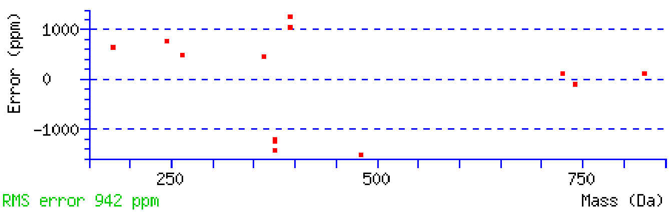
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1002.5306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.034
Matches : 13/74 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0469	66.0271			113.0363	57.0218	E							8
2	***263.0844***	132.0458			245.0739	123.0406	M	873.4983	437.2528	855.4747	428.2410	855.4877	428.2475	7
3	***393.1735***	197.0904	375.1499	188.0786	375.1629	188.0851	K	***741.4608***	371.2340	723.4372	362.2222	723.4502	362.2287	6
4	523.2625	262.1349	505.2389	253.1231	505.2519	253.1296	K	611.3717	306.1895	593.3482	297.1777	593.3612	297.1842	5
5	611.2916	306.1494	593.2680	297.1376	593.2810	297.1441	S	***481.2827***	241.1450	463.2591	232.1332	463.2721	232.1397	4
6	***725.3727***	363.1900	707.3491	354.1782	707.3621	354.1847	L	***393.2536***	197.1305	375.2301	188.1187			3
7	***825.4381***	413.2227	807.4145	404.2109	807.4275	404.2174	V	279.1725	140.0899	261.1490	131.0781			2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EMKKSLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.8	1002.5306	0.0018	EMKKSLVR
16.8	1002.5354	-0.0029	STSQISKLK

AT2G17440.1

13.7	1002.5306	0.0018	QMLSRVLK
8.7	1002.5306	0.0018	VKMRSELK
8.2	1002.5302	0.0023	LVFDMLLK
7.2	1002.5295	0.0030	IKEWLFR
3.5	1002.5354	-0.0029	SKTAESLKK
2.5	1002.5306	0.0018	LGELKMKR
1.9	1002.5306	0.0018	KEVAIKMR

AT2G17520.1

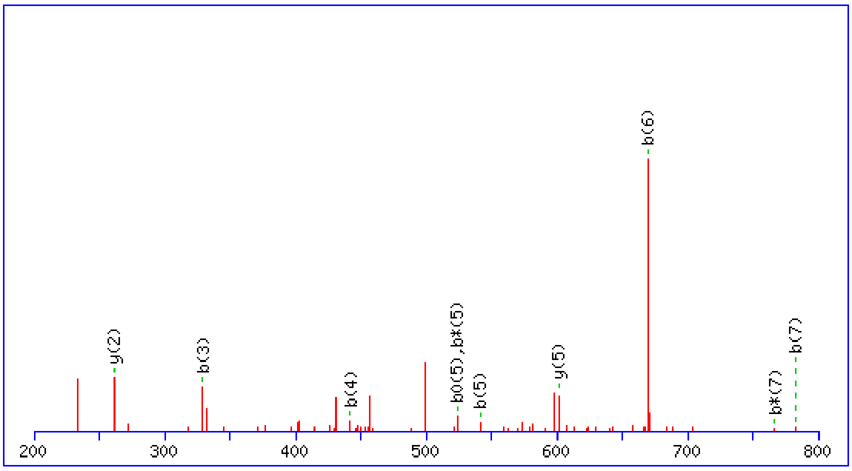
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVNIVKNK**
Found in **AT2G17520.1** in **TAIR_Arabidopsis**, Symbols: IRE1A | IRE1A (Yeast endoribonuclease/protein kinase IRE1-like gene); kinase | chr2:7624586-7628011 FORWARD

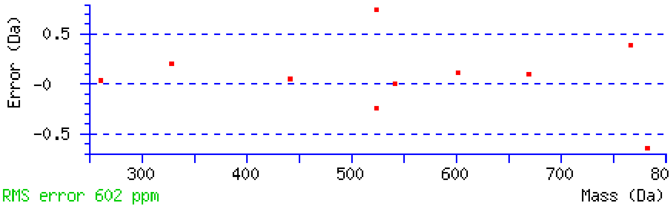
Match to Query 1877: 928.534890 from(465.274721,2+) index(5306)
Title: Elution from: 46.759 to 46.759 scan no 6619 cid35.00 polarity:+
Data file C7-1_1.mgf

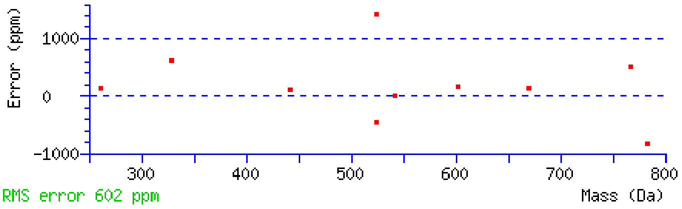
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 928.5342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.017
Matches : 10/66 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	116.0342	58.5207			98.0237	49.5155	D					8
2	215.1026	108.0550			197.0921	99.0497	V	814.5145	407.7609	797.4880	399.2476	7
3	***329.1456***	165.0764	312.1190	156.5631	311.1350	156.0711	N	715.4461	358.2267	698.4195	349.7134	6
4	***442.2296***	221.6185	425.2031	213.1052	424.2191	212.6132	I	**601.4032**	301.2052	584.3766	292.6919	5
5	***541.2980***	271.1527	524.2715	262.6394	523.2875	262.1474	V	488.3191	244.6632	471.2926	236.1499	4
6	***669.3930***	335.2001	652.3665	326.6869	651.3824	326.1949	K	389.2507	195.1290	372.2241	186.6157	3
7	***783.4359***	392.2216	766.4094	383.7083	765.4254	383.2163	N	**261.1557**	131.0815	244.1292	122.5682	2
8							K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of DVNIVKNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.1	928.5342	0.0007	DVNIVKNK

AT2G17520.1

8.4	928.5342	0.0007	KLEGIGQGK
6.9	928.5342	0.0007	IEAIGGKGGK
5.9	928.5341	0.0008	EAALREIK
4.6	928.5341	0.0007	LKELNQGK
3.7	928.5341	0.0007	AVEALNGKK
3.3	928.5341	0.0007	LALDQKNK
3.3	928.5342	0.0007	LVKGVDGNK
2.1	928.5342	0.0007	DEIVGRIK
1.4	928.5342	0.0007	KLDLGEVR

Mascot: http://www.matrixscience.com/

AT2G17540.1

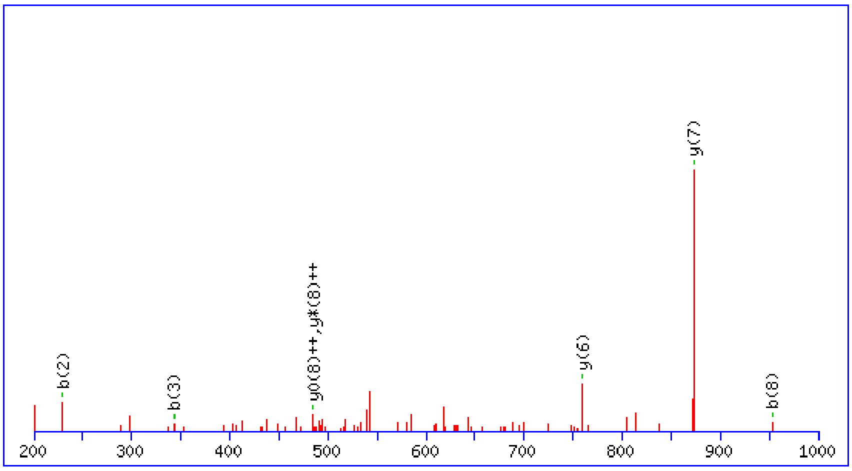
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLCDNTLK**
Found in **AT2G17540.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35510.1) | chr2:7637744-7638571 REVERSE

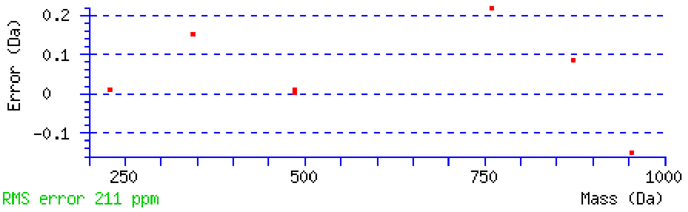
Match to Query 3444: 1100.556936 from(551.285744,2+) index(7745)
Title: Elution from: 67.541 to 67.541 scan no 10211 cid35.00 polarity:+
Data file D1d-3_3.mgf

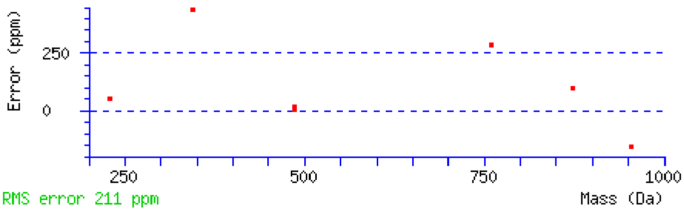
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1100.5544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.047
Matches : 7/74 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							9
2	***229.1695***	115.0884					L	987.4806	494.2439	969.4570	485.2321	969.4700	485.2386	8
3	***343.2506***	172.1289					L	**873.3995**	437.2034	855.3759	428.1916	855.3889	428.1981	7
4	505.2753	253.1413					C	**759.3184**	380.1628	741.2948	371.1510	741.3078	371.1575	6
5	621.2993	311.1533			603.2887	302.1480	D	597.2937	299.1505	579.2701	290.1387	579.2831	290.1452	5
6	737.3363	369.1718	719.3127	360.1600	719.3257	360.1665	N	481.2697	241.1385	463.2461	232.1267	463.2591	232.1332	4
7	839.3810	420.1941	821.3574	411.1823	821.3704	411.1888	T	365.2327	183.1200	347.2091	174.1082	347.2221	174.1147	3
8	***953.4621***	477.2347	935.4385	468.2229	935.4515	468.2294	L	263.1880	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LLLCDNTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G17540.1

22.2	1100.5544	0.0025	LLLCDNTLK
10.3	1100.5544	0.0025	LISVNPTSMK
7.8	1100.5544	0.0025	LGDIMGLLNK
6.8	1100.5544	0.0025	LLCLGSVAEK
2.6	1100.5544	0.0026	ILMVGLDGSGK
2.3	1100.5544	0.0026	VVMLGLDAAGK

Mascot: http://www.matrixscience.com/

AT2G17550.1

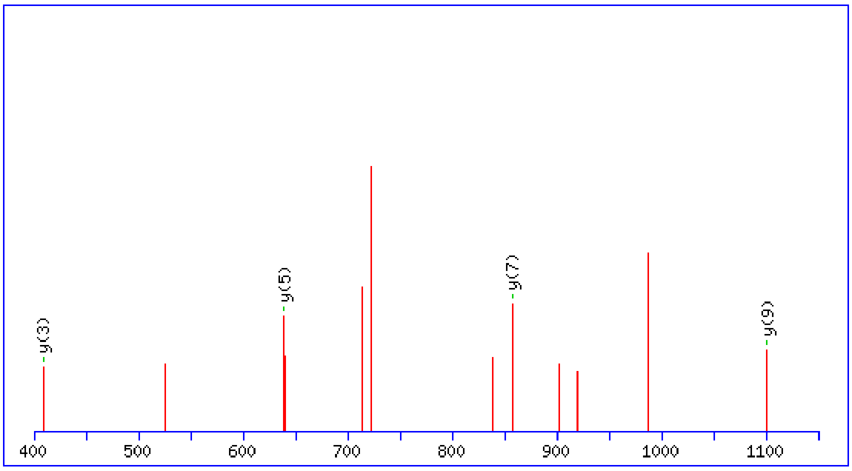
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QINELESEVQVR**
Found in **AT2G17550.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G02390.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14481.1) | chr2:7641577-7644294 REVERSE

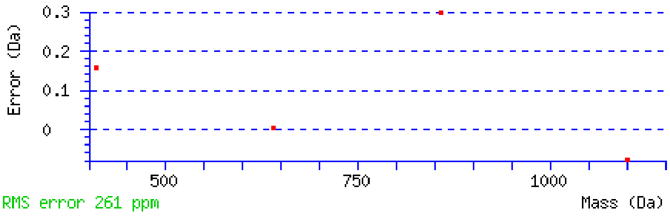
Match to Query 6389: 1460.682130 from(731.348341,2+) index(7424)
Title: Elution from: 64.424 to 64.424 scan no 9417 cid35.00 polarity:+
Data file 0-1_1.mgf

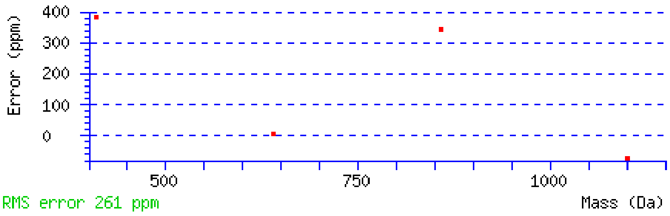
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1460.6831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.015
Matches : 4/118 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							12
2	245.1410	123.0741	227.1174	114.0624			I	1331.6378	666.3225	1313.6142	657.3107	1313.6272	657.3172	11
3	361.1780	181.0926	343.1544	172.0809			N	1217.5567	609.2820	1199.5331	600.2702	1199.5461	600.2767	10
4	491.2176	246.1125	473.1941	237.1007	473.2071	237.1072	E	***1101.5197***	551.2635	1083.4961	542.2517	1083.5091	542.2582	9
5	605.2987	303.1530	587.2752	294.1412	587.2882	294.1477	L	971.4801	486.2437	953.4565	477.2319	953.4695	477.2384	8
6	735.3384	368.1728	717.3148	359.1610	717.3278	359.1675	E	***857.3990***	429.2031	839.3754	420.1913	839.3884	420.1978	7
7	823.3674	412.1874	805.3439	403.1756	805.3569	403.1821	S	727.3593	364.1833	709.3357	355.1715	709.3488	355.1780	6
8	953.4071	477.2072	935.3835	468.1954	935.3965	468.2019	E	***639.3303***	320.1688	621.3067	311.1570	621.3197	311.1635	5
9	1053.4725	527.2399	1035.4489	518.2281	1035.4619	518.2346	V	509.2906	255.1490	491.2671	246.1372			4
10	1183.5252	592.2662	1165.5016	583.2544	1165.5146	583.2609	Q	***409.2252***	205.1162	391.2016	196.1044			3
11	1283.5906	642.2989	1265.5670	633.2872	1265.5800	633.2937	V	279.1725	140.0899	261.1490	131.0781			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of QINELESEVQVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G17550.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.4	1460.6831	-0.0010	QINELESEVQVR
14.1	1460.6831	-0.0010	KTHASDTAIDKEK
2.7	1460.6840	-0.0019	LGAMERHLMIEK
1.7	1460.6840	-0.0019	VGVKTMKMYTNR
0.9	1460.6831	-0.0010	SLEGTEPTKQTPR
0.3	1460.6831	-0.0010	LGTDDNAQLLDIR

AT2G17670.1

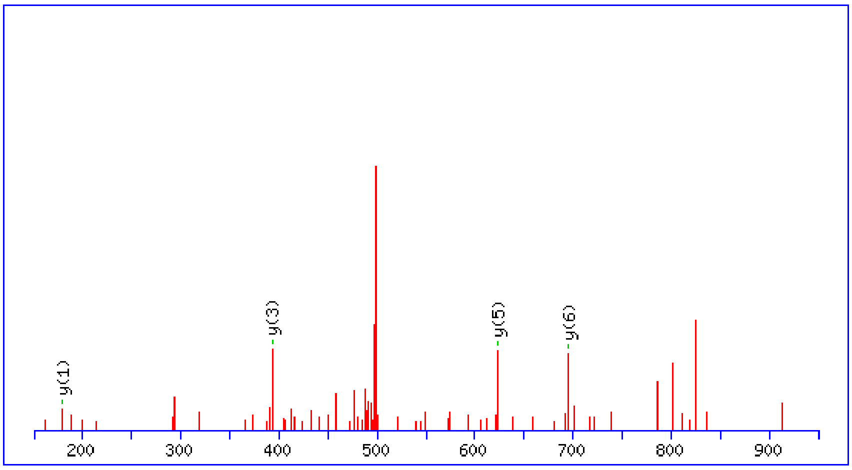
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMPANLLVR**
Found in **AT2G17670.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:7681502-7682893 FORWARD

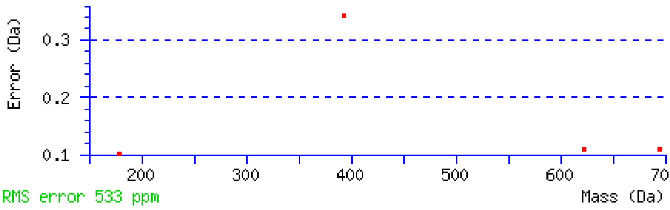
Match to Query 2611: 1012.513498 from(507.264025,2+) index(4944)
Title: Elution from: 43.956 to 43.956 scan no 6142 cid35.00 polarity:+
Data file C7-1_1.mgf

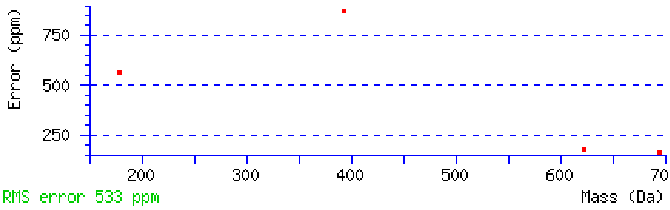
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1012.5150
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.025
Matches : 4/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	89.0363	45.0218			71.0258	36.0165	S					9
2	221.0739	111.0406			203.0633	102.0353	M	925.4932	463.2502	907.4696	454.2384	8
3	319.1237	160.0655			301.1131	151.0602	P	793.4557	397.2315	775.4321	388.2197	7
4	391.1578	196.0825			373.1472	187.0773	A	***695.4059***	348.2066	677.3823	339.1948	6
5	507.1948	254.1010	489.1712	245.0892	489.1842	245.0958	N	***623.3717***	312.1895	605.3482	303.1777	5
6	621.2759	311.1416	603.2523	302.1298	603.2653	302.1363	L	507.3347	254.1710	489.3112	245.1592	4
7	735.3570	368.1821	717.3334	359.1703	717.3464	359.1769	L	***393.2536***	197.1305	375.2301	188.1187	3
8	835.4225	418.2149	817.3989	409.2031	817.4119	409.2096	V	279.1725	140.0899	261.1490	131.0781	2
9							R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of SMPANLLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.3	1012.5150	-0.0015	SMPANLLVR

AT2G17670.1

24.2	1012.5138	-0.0003	WWIEVIR
14.9	1012.5150	-0.0015	VTMPALAAAR
12.5	1012.5121	0.0014	KGSINKHGR
12.5	1012.5116	0.0019	WEVIGGIAR
8.8	1012.5150	-0.0015	IPSVNAIMR
6.7	1012.5138	-0.0003	FYKLFQR
5.1	1012.5120	0.0015	DTKARLHR
2.3	1012.5139	-0.0004	WEPWKKK
2.3	1012.5116	0.0019	WESPVVRK

AT2G18020.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASGDYAIVIAHNPDSDTTR**
Found in **AT2G18020.1** in **TAIR_Arabidopsis**, Symbols: EMB2296 | EMB2296 (EMBRYO DEFECTIVE 2296); structural constituent of ribosome | chr2:7844233-7845242 FORWARD

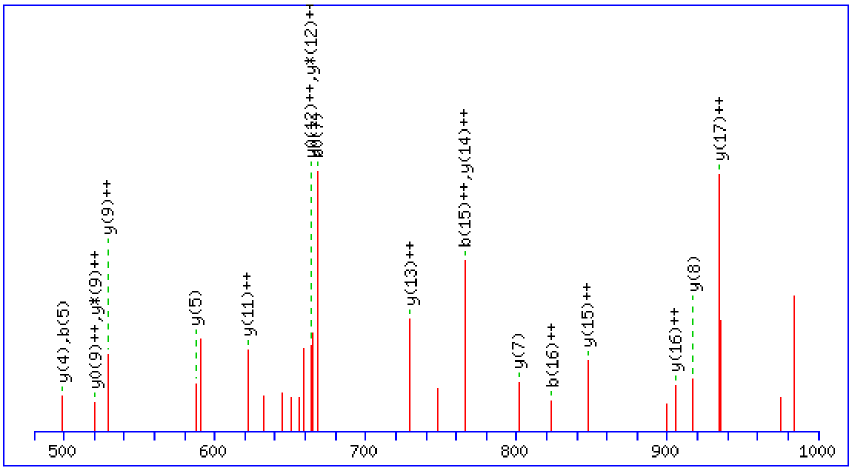
Match to Query 8741: 2026.866090 from(676.629306,3+) index(3764)
Title: Elution from: 35.683 to 35.683 scan no 4722 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 480 to 1000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

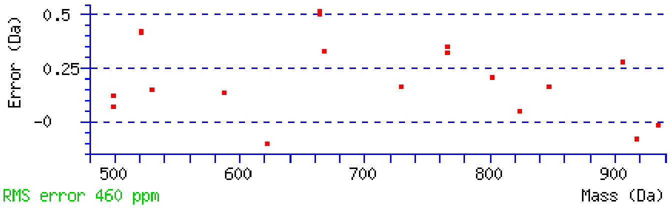
Show Y-axis ☐

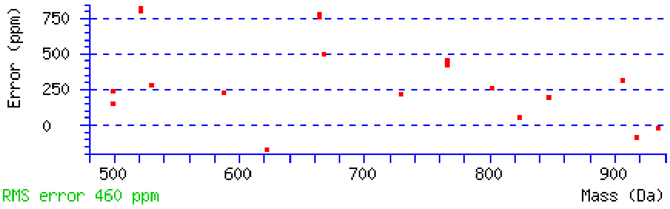


Monoisotopic mass of neutral peptide Mr(calc): 2026.8651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 7.1e-005
Matches : 20/190 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							19
2	161.0705	81.0389			143.0599	72.0336	S	1955.8382	978.4227	1937.8146	969.4109	1937.8276	969.4175	18
3	219.0890	110.0481			201.0784	101.0428	G	1867.8091	934.4082	1849.7856	925.3964	1849.7986	925.4029	17
4	335.1130	168.0601			317.1024	159.0548	D	1809.7906	905.3990	1791.7671	896.3872	1791.7801	896.3937	16
5	499.1733	250.0903			481.1628	241.0850	Y	1693.7667	847.3870	1675.7431	838.3752	1675.7561	838.3817	15
6	571.2075	286.1074			553.1969	277.1021	A	1529.7063	765.3568	1511.6827	756.3450	1511.6957	756.3515	14
7	685.2886	343.1479			667.2780	334.1426	I	1457.6721	729.3397	1439.6486	720.3279	1439.6616	720.3344	13
8	785.3540	393.1807			767.3435	384.1754	V	1343.5910	672.2992	1325.5675	663.2874	1325.5805	663.2939	12
9	899.4351	450.2212			881.4246	441.2159	I	1243.5256	622.2664	1225.5020	613.2546	1225.5150	613.2612	11
10	971.4693	486.2383			953.4587	477.2330	A	1129.4445	565.2259	1111.4209	556.2141	1111.4339	556.2206	10
11	1111.5193	556.2633			1093.5087	547.2580	H	1057.4103	529.2088	1039.3868	520.1970	1039.3998	520.2035	9
12	1227.5563	614.2818	1209.5327	605.2700	1209.5457	605.2765	N	***917.3603***	459.1838	899.3367	450.1720	899.3498	450.1785	8
13	1325.6061	***663.3067***	1307.5825	654.2949	1307.5955	654.3014	P	***801.3233***	401.1653	783.2998	392.1535	783.3128	392.1600	7
14	1441.6301	721.3187	1423.6065	712.3069	1423.6195	712.3134	D	703.2735	352.1404	685.2500	343.1286	685.2630	343.1351	6
15	1529.6591	***765.3332***	1511.6355	756.3214	1511.6486	756.3279	S	***587.2496***	294.1284	569.2260	285.1166	569.2390	285.1231	5
16	1645.6831	***823.3452***	1627.6595	814.3334	1627.6725	814.3399	D	***499.2205***	250.1139	481.1969	241.1021	481.2099	241.1086	4
17	1747.7278	874.3675	1729.7042	865.3558	1729.7173	865.3623	T	383.1965	192.1019	365.1729	183.0901	365.1860	183.0966	3
18	1849.7725	925.3899	1831.7489	916.3781	1831.7620	916.3846	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
19							R	179.1071	90.0572	161.0835	81.0454			1

AT2G18020.1





NCBI **BLAST** search of ASGDYAIVIAHNPDSDTTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.7	2026.8651	0.0010	ASGDYAIVIAHNPDSDTTR

Mascot: http://www.matrixscience.com/

AT2G18110.1

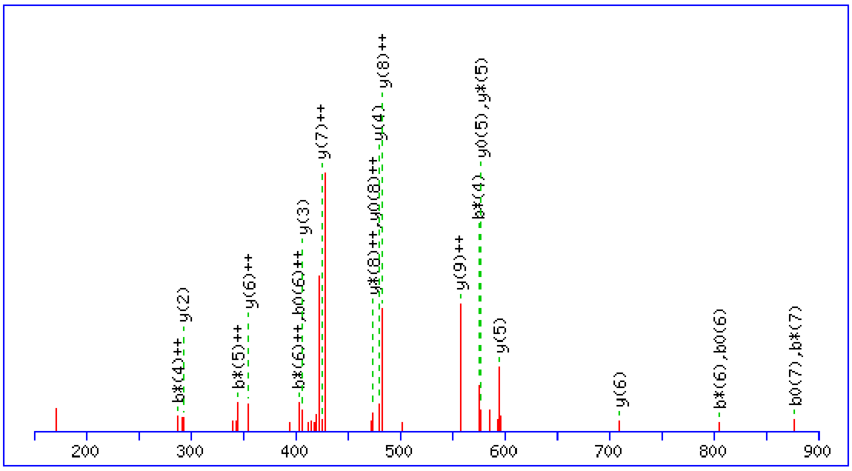
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WFNHIDALLR**
Found in **AT2G18110.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1-beta, putative / EF-1-beta, putative | chr2:7879718-7880795 FORWARD

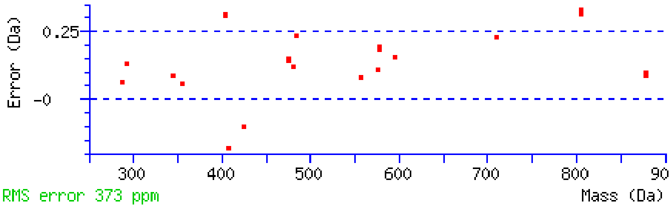
Match to Query 4224: 1300.625643 from(434.549157,3+) index(7269)
Title: Elution from: 68.065 to 68.065 scan no 9662 cid35.00 polarity:+
Data file D1d-1-2.mgf

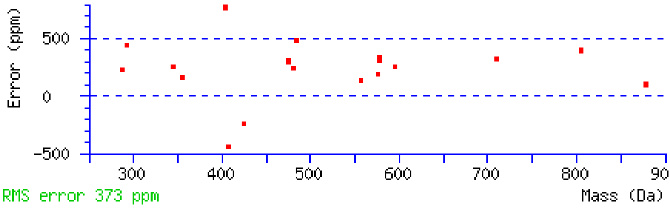
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1300.6271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.011
Matches : 22/86 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440					**W**							**10**
2	337.1461	169.0767					**F**	1113.5610	557.2841	1095.5374	548.2723	1095.5504	548.2788	**9**
3	453.1831	227.0952	435.1595	218.0834			**N**	965.4955	483.2514	947.4719	474.2396	947.4850	474.2461	**8**
4	593.2331	297.1202	575.2095	288.1084			**H**	849.4585	425.2329	831.4349	416.2211	831.4480	416.2276	**7**
5	707.3142	354.1607	689.2906	345.1490			**I**	***709.4085***	355.2079	691.3849	346.1961	691.3980	346.2026	**6**
6	823.3382	412.1727	805.3146	403.1609	805.3276	403.1675	**D**	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	**5**
7	895.3723	448.1898	877.3488	439.1780	877.3618	439.1845	**A**	***479.3034***	240.1554	461.2799	231.1436			**4**
8	1009.4534	505.2304	991.4299	496.2186	991.4429	496.2251	**L**	***407.2693***	204.1383	389.2457	195.1265			**3**
9	1123.5345	562.2709	1105.5110	553.2591	1105.5240	553.2656	**L**	***293.1882***	147.0977	275.1646	138.0859			**2**
10							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of WFNHIDALLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G18110.1

Score	Mr(calc)	Delta	Sequence
28.1	1300.6271	-0.0014	WFNHIDALLR
12.9	1300.6248	0.0008	FNRADYTKLR
9.2	1300.6248	0.0008	APPRGPATGFQGK
8.5	1300.6255	0.0001	SYSSVLKTMVR
0.2	1300.6256	0.0001	GPVSLPSQMNLK

AT2G18400.1

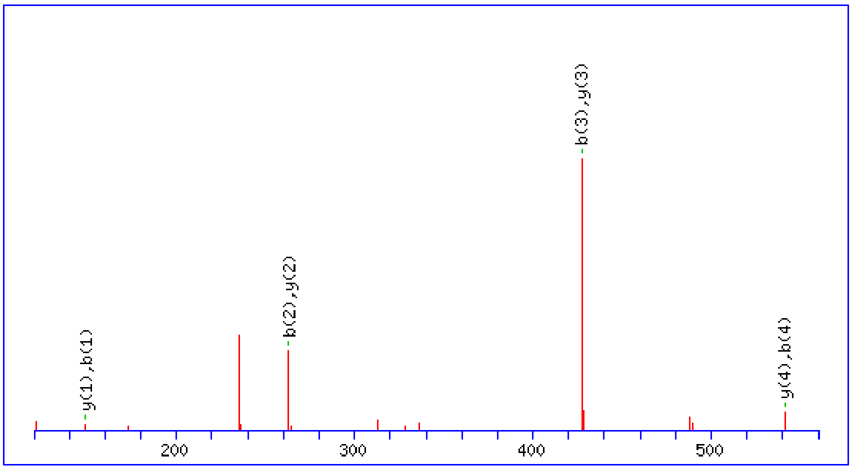
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLYLK**
Found in **AT2G18400.1** in **TAIR_Arabidopsis**

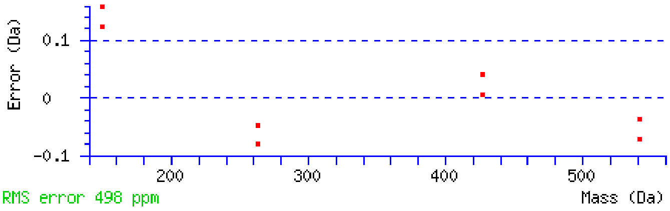
Match to Query 558: 688.387162 from(345.200857,2+) index(3050)
Title: Elution from: 30.834 to 30.834 scan no 3799 cid35.00 polarity:+
Data file C7-1_3.mgf

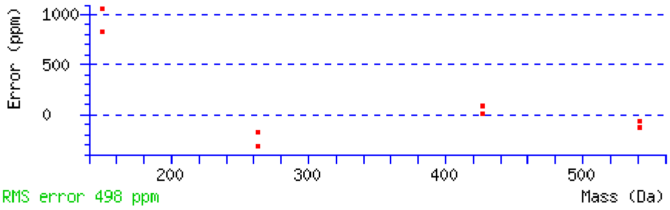
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 560 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 688.3876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0036
Matches : 8/24 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	*149.0727*	75.0400	F					5
2	*263.1538*	132.0805	L	*541.3294*	271.1684	523.3059	262.1566	4
3	*427.2142*	214.1107	Y	*427.2483*	214.1278	409.2248	205.1160	3
4	*541.2953*	271.1513	L	*263.1880*	132.0976	245.1644	123.0858	2
5			K	*149.1069*	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of FLYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.9	688.3876	-0.0004	FLYLK
25.9	688.3876	-0.0004	FIIYK
25.9	688.3876	-0.0004	FLIYK
25.9	688.3876	-0.0004	FLLYK
25.9	688.3876	-0.0004	FYIIK

16.8	688.3876	-0.0004	IFLYK
16.8	688.3876	-0.0004	YFIIK
11.4	688.3854	0.0018	IDPPIK
11.4	688.3880	-0.0009	RTFKK
11.4	688.3880	-0.0009	TRKFK

AT2G18450.1

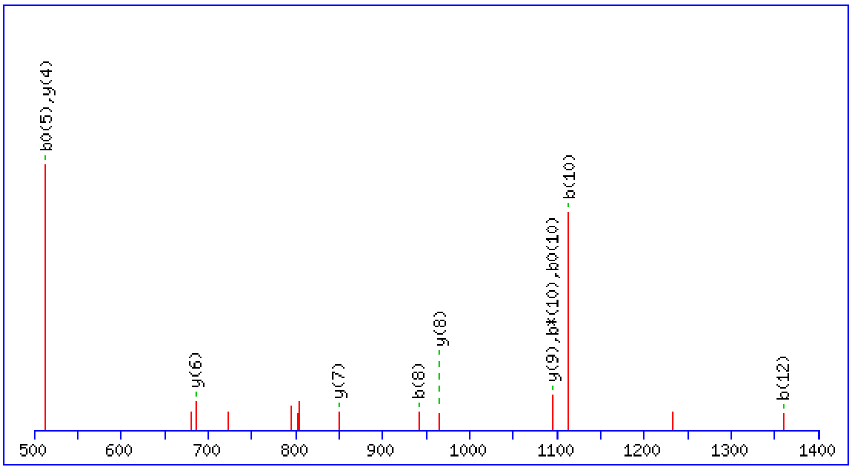
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVIELENYGLPFSR**
Found in **AT2G18450.1** in **TAIR_Arabidopsis**, Symbols: SDH1-2 | SDH1-2 (Succinate dehydrogenase 1-2) | chr2:8004592-8007883 REVERSE

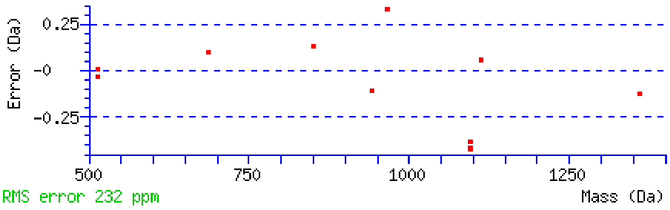
Match to Query 7093: 1624.786418 from(813.400485,2+) index(8871)
Title: Elution from: 79.977 to 79.977 scan no 12122 cid35.00 polarity:+
Data file 0-3_3.mgf

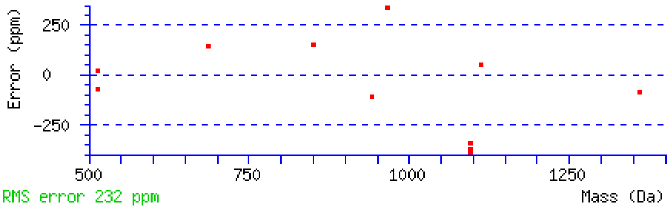
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1624.7821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0011
Matches : 11/136 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					**A**							**14**
2	173.1069	87.0571					**V**	1553.7553	777.3813	1535.7317	768.3695	1535.7447	768.3760	**13**
3	287.1880	144.0976					**I**	1453.6898	727.3485	1435.6662	718.3368	1435.6793	718.3433	**12**
4	417.2276	209.1174			399.2170	200.1122	**E**	1339.6087	670.3080	1321.5851	661.2962	1321.5982	661.3027	**11**
5	531.3087	266.1580			513.2981	257.1527	**L**	1209.5691	605.2882	1191.5455	596.2764	1191.5585	596.2829	**10**
6	661.3483	331.1778			643.3378	322.1725	**E**	***1095.4880***	548.2476	1077.4644	539.2358	1077.4774	539.2424	**9**
7	777.3853	389.1963	759.3617	380.1845	759.3748	380.1910	**N**	***965.4484***	483.2278	947.4248	474.2160	947.4378	474.2225	**8**
8	**941.4457**	471.2265	923.4221	462.2147	923.4351	462.2212	**Y**	***849.4114***	425.2093	831.3878	416.1975	831.4008	416.2040	**7**
9	999.4642	500.2357	981.4406	491.2239	981.4536	491.2304	**G**	***685.3510***	343.1791	667.3274	334.1673	667.3404	334.1739	**6**
10	**1113.5453**	557.2763	1095.5217	548.2645	1095.5347	548.2710	**L**	627.3325	314.1699	609.3089	305.1581	609.3219	305.1646	**5**
11	1211.5951	606.3012	1193.5715	597.2894	1193.5845	597.2959	**P**	***513.2514***	257.1293	495.2278	248.1175	495.2408	248.1241	**4**
12	**1359.6605**	680.3339	1341.6370	671.3221	1341.6500	671.3286	**F**	415.2016	208.1044	397.1780	199.0926	397.1910	199.0992	**3**
13	1447.6896	724.3484	1429.6660	715.3366	1429.6790	715.3432	**S**	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	**2**
14							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of AVIELENYGLPFSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G18450.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.5	1624.7821	0.0043	AVIELENYGLPFSR
4.7	1624.7906	-0.0042	SKDGQTVLGTLDSKR
0.5	1624.7904	-0.0040	HIYLEDLMRFLR

AT2G18570.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MRAMKPAVR**
Found in **AT2G18570.1** in **TAIR_Arabidopsis**, Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr2:8070511-8071923 FORWARD

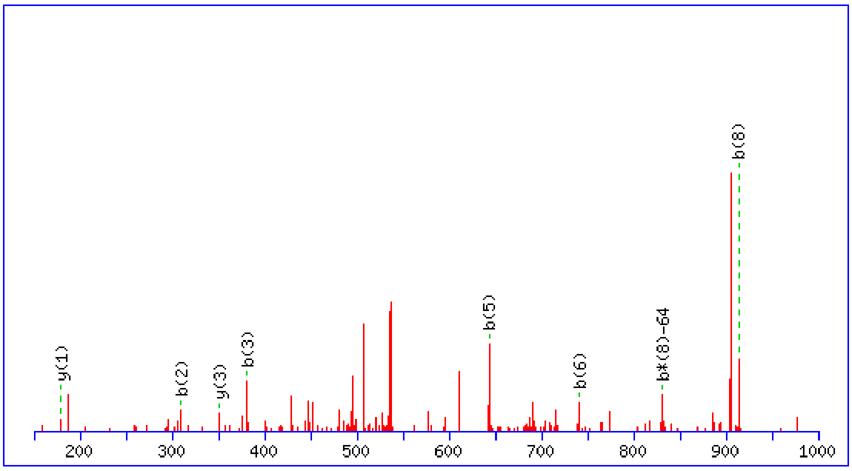
Match to Query 2878: 1090.531884 from(546.273218,2+) index(4189)
Title: Elution from: 42.248 to 42.248 scan no 5400 cid35.00 polarity:+
Data file D1d-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

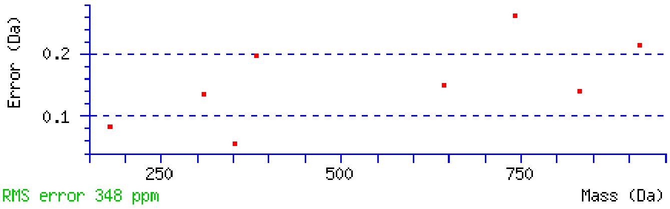
Label all possible matches ○ Label matches used for scoring ●

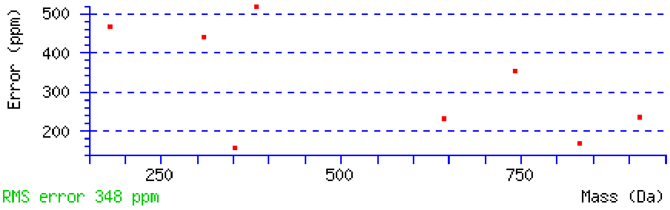
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1090.5316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.038
Matches : 8/92 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	149.0397	75.0235			M					9
2	*309.1290*	155.0681	291.1054	146.0563	R	943.5064	472.2569	925.4829	463.2451	8
3	*381.1631*	191.0852	363.1395	182.0734	A	783.4172	392.2122	765.3936	383.2004	7
4	513.2006	257.1040	495.1770	248.0922	M	711.3830	356.1952	693.3595	347.1834	6
5	*643.2897*	322.1485	625.2661	313.1367	K	579.3455	290.1764	561.3219	281.1646	5
6	*741.3395*	371.1734	723.3159	362.1616	P	449.2565	225.1319	431.2329	216.1201	4
7	813.3736	407.1904	795.3500	398.1787	A	351.2067	176.1070	333.1831	167.0952	3
8	*913.4391*	457.2232	895.4155	448.2114	V	279.1725	140.0899	261.1490	131.0781	2
9					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of MRAMKPAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G18570.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
24.9	1090.5316	0.0003	MRAMKPAVR	Oxidation M1 98.57%
10.9	1090.5325	-0.0006	IAFIGDGPYK	
10.4	1090.5330	-0.0011	IAEHALTGHK	
8.9	1090.5334	-0.0015	LARQSDRAR	
8.2	1090.5289	0.0030	MSMLKIAER	
7.9	1090.5329	-0.0011	AIRFVEGER	
7.2	1090.5330	-0.0011	QSIINFAQR	
6.5	1090.5330	-0.0011	FSLPDVSRR	
6.5	1090.5316	0.0003	MRAMKPAVR	Oxidation M4 1.43%
6.5	1090.5334	-0.0015	LGRNRSDVR	

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFLKNK**
Found in **AT2G18690.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18680.1); similar to hypothetical protein OsI_029427 [Oryza sativa (indica cultivar-group)] (GB:EAZ08195.1) | chr2:8104732-8105700 FORWARD

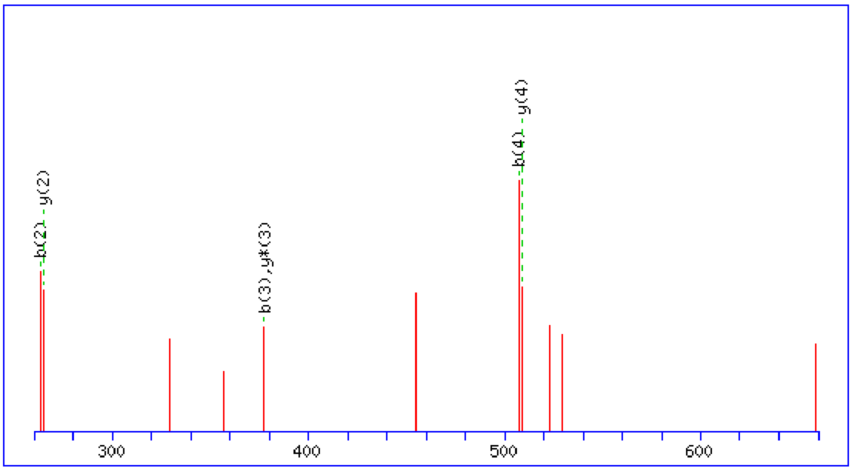
Match to Query 865: 770.454096 from(386.234324,2+) index(5206)
Title: Elution from: 46.771 to 46.771 scan no 6604 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 260 to 660 Da Full range

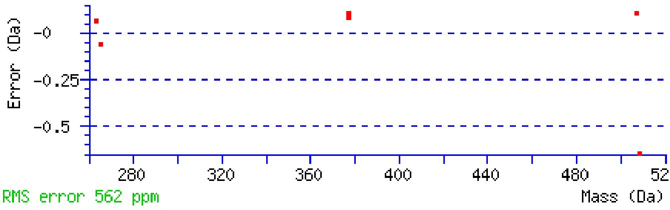
Label all possible matches ○ Label matches used for scoring ●

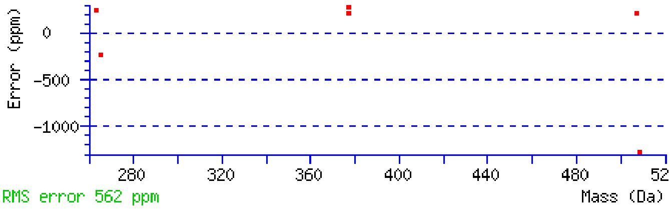
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.4533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.049
Matches : 6/34 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	115.0884	58.0478			L					6
2	***263.1538***	132.0805			F	657.3795	329.1934	639.3559	320.1816	5
3	***377.2349***	189.1211			L	**509.3140**	255.1606	491.2904	246.1488	4
4	***507.3240***	254.1656	489.3004	245.1538	K	395.2329	198.1201	377.2093	189.1083	3
5	623.3610	312.1841	605.3374	303.1723	N	**265.1439**	133.0756	247.1203	124.0638	2
6					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LFLKNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.7	770.4533	0.0008	FNKIIK
21.7	770.4533	0.0008	LFLKNK
13.2	770.4533	0.0008	LFKINK

AT2G18690.1

8.0	770.4533	0.0008	IFKNIK
7.8	770.4533	0.0008	NKFLIK
7.3	770.4533	0.0008	FIKGGIK
2.1	770.4533	0.0008	LFILTR
2.0	770.4533	0.0008	VYKPKK
1.4	770.4533	0.0008	FLLITR
1.4	770.4533	0.0008	FLLLTR

AT2G18915.1

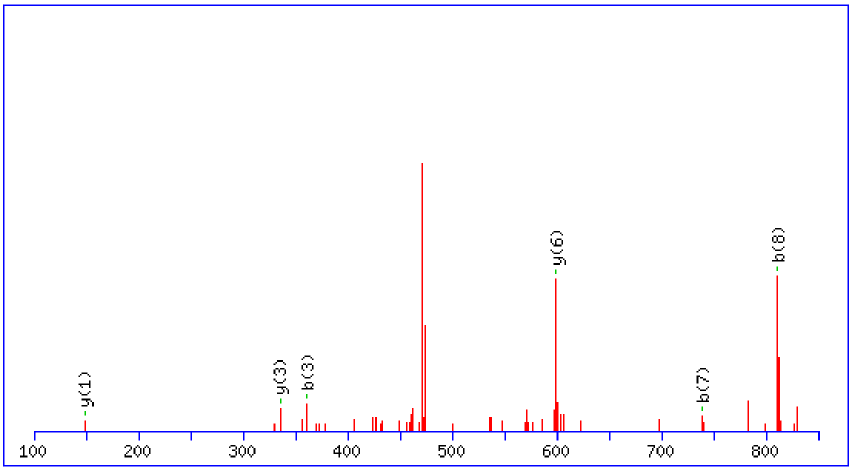
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILMFGGLAK**
Found in **AT2G18915.1** in **TAIR_Arabidopsis**, Symbols: ADO2, LKP2 | LKP2 (LOV KELCH PROTEIN 2); ubiquitin-protein ligase | chr2:8201874-8204337 REVERSE

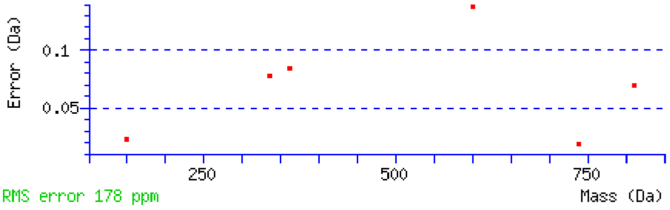
Match to Query 2200: 958.514444 from(480.264498,2+) index(1680)
Title: Elution from: 21.111 to 21.111 scan no 2211 cid35.00 polarity:+
Data file C7-2_2.mgf

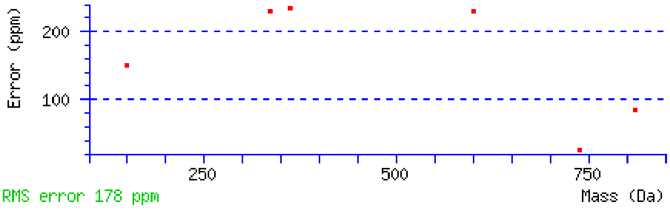
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 958.5170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.004
Matches : 6/48 fragment ions using 7 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	115.0884	58.0478	I					9
2	229.1695	115.0884	L	845.4432	423.2252	827.4196	414.2134	8
3	*361.2070*	181.1071	M	731.3621	366.1847	713.3385	357.1729	7
4	509.2724	255.1399	F	*599.3246*	300.1659	581.3010	291.1541	6
5	567.2909	284.1491	G	451.2591	226.1332	433.2355	217.1214	5
6	625.3094	313.1584	G	393.2406	197.1239	375.2170	188.1122	4
7	*739.3905*	370.1989	L	*335.2221*	168.1147	317.1985	159.1029	3
8	*811.4247*	406.2160	A	221.1410	111.0741	203.1174	102.0624	2
9			K	*149.1069*	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of ILMFGGLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G18915.1

33.2	958.5170	-0.0026	ILMFGGLAK
18.6	958.5148	-0.0003	MKIAIGTAK
18.0	958.5136	0.0008	VWAIGYIK
16.3	958.5118	0.0026	SRRDVIAK
14.0	958.5148	-0.0003	KAALMALSK
13.5	958.5148	-0.0003	ISSAKMLAK
12.8	958.5118	0.0026	QNRKASIK
12.2	958.5141	0.0004	FPIEKRR
8.4	958.5136	0.0008	FLKVWEK
8.4	958.5136	0.0008	FVWKELK

AT2G18950.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MESLLSSSSLVSAAGGFCWKKQNLK**
Found in **AT2G18950.1** in **TAIR_Arabidopsis**, Symbols: TPT1, ATHPT, HPT, VTE2, HPT1 | HPT1 (HOMOGENTISATE PHYTYLTRANSFERASE 1); prenyltransferase | chr2:8214573-8217129 FORWARD

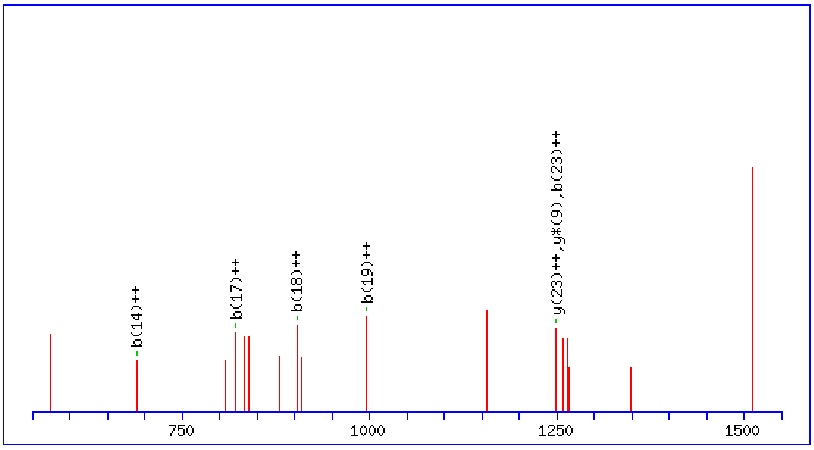
Match to Query 10257: 2759.269449 from(920.763759,3+) index(8710)
Title: Elution from: 82.300 to 82.300 scan no 11962 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1550 Da Full range

Label all possible matches ○ Label matches used for scoring ●

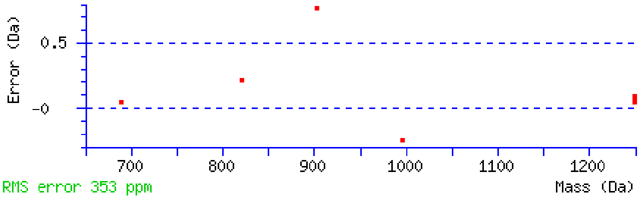
Show Y-axis ☐

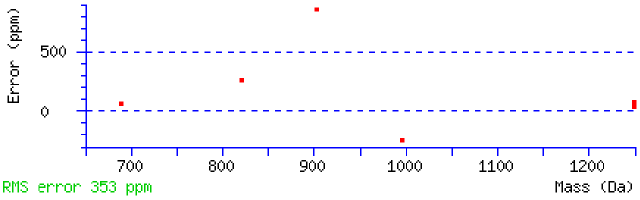


Monoisotopic mass of neutral peptide Mr(calc): 2759.2775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.04
Matches : 7/222 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	133.0448	67.0260					M							25
2	263.0844	132.0458			245.0739	123.0406	E	2628.2473	1314.6273	2610.2237	1305.6155	2610.2367	1305.6220	24
3	351.1135	176.0604			333.1029	167.0551	S	2498.2077	1249.6075	2480.1841	1240.5957	2480.1971	1240.6022	23
4	465.1946	233.1009			447.1840	224.0956	L	2410.1786	1205.5929	2392.1550	1196.5811	2392.1680	1196.5877	22
5	579.2757	290.1415			561.2651	281.1362	L	2296.0975	1148.5524	2278.0739	1139.5406	2278.0869	1139.5471	21
6	667.3047	334.1560			649.2942	325.1507	S	2182.0164	1091.5118	2163.9928	1082.5000	2164.0058	1082.5066	20
7	755.3338	378.1705			737.3232	369.1653	S	2093.9873	1047.4973	2075.9637	1038.4855	2075.9768	1038.4920	19
8	843.3629	422.1851			825.3523	413.1798	S	2005.9583	1003.4828	1987.9347	994.4710	1987.9477	994.4775	18
9	931.3919	466.1996			913.3814	457.1943	S	1917.9292	959.4682	1899.9056	950.4564	1899.9186	950.4630	17
10	1045.4730	523.2402			1027.4625	514.2349	L	1829.9001	915.4537	1811.8766	906.4419	1811.8896	906.4484	16
11	1145.5385	573.2729			1127.5279	564.2676	V	1715.8190	858.4132	1697.7955	849.4014	1697.8085	849.4079	15
12	1233.5675	617.2874			1215.5570	608.2821	S	1615.7536	808.3804	1597.7300	799.3686	1597.7430	799.3752	14
13	1305.6017	653.3045			1287.5911	644.2992	A	1527.7245	764.3659	1509.7009	755.3541			13
14	1377.6358	***689.3216***			1359.6253	680.3163	A	1455.6904	728.3488	1437.6668	719.3370			12
15	1435.6543	718.3308			1417.6438	709.3255	G	1383.6562	692.3318	1365.6326	683.3200			11
16	1493.6728	747.3401			1475.6623	738.3348	G	1325.6377	663.3225	1307.6141	654.3107			10
17	1641.7383	***821.3728***			1623.7277	812.3675	F	1267.6192	634.3133	1249.5956	625.3015			9
18	1803.7630	***902.3851***			1785.7524	893.3799	C	1119.5538	560.2805	1101.5302	551.2687			8
19	1991.8364	***996.4218***			1973.8258	987.4166	W	957.5291	479.2682	939.5055	470.2564			7
20	2121.9254	1061.4664	2103.9018	1052.4546	2103.9149	1052.4611	K	769.4557	385.2315	751.4321	376.2197			6
21	2252.0145	1126.5109	2233.9909	1117.4991	2234.0039	1117.5056	K	639.3667	320.1870	621.3431	311.1752			5
22	2382.0671	1191.5372	2364.0435	1182.5254	2364.0565	1182.5319	Q	509.2776	255.1424	491.2540	246.1307			4
23	2498.1041	***1249.5557***	2480.0805	1240.5439	2480.0935	1240.5504	N	379.2250	190.1161	361.2014	181.1043			3
24	2612.1852	1306.5962	2594.1616	1297.5844	2594.1746	1297.5910	L	263.1880	132.0976	245.1644	123.0858			2

25							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MESLLSSSSLVSAAGGFCWKKQNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.0	2759.2775	-0.0081	MESLLSSSSLVSAAGGFCWKKQNLK
1.6	2759.2670	0.0025	DIDASCSLVLYGKSSVETDTATRLK
1.5	2759.2645	0.0050	LAVIFNMGAGYCDVAVTATAGGVSQIK
1.3	2759.2701	-0.0007	SMLQVNACLGSLIDKSSMVFAWLK
1.3	2759.2692	0.0002	DLLTSYMNLDTTKYKLLNPSDER
0.9	2759.2645	0.0050	DILGNVLSGLSMQFSRPFSMGDTIK
0.4	2759.2692	0.0002	SSFLASADDSGDVKIIDLGQKCLYK

Mascot: http://www.matrixscience.com/

AT2G18960.1

{MATRIX SCIENCE} Mascot Search Results

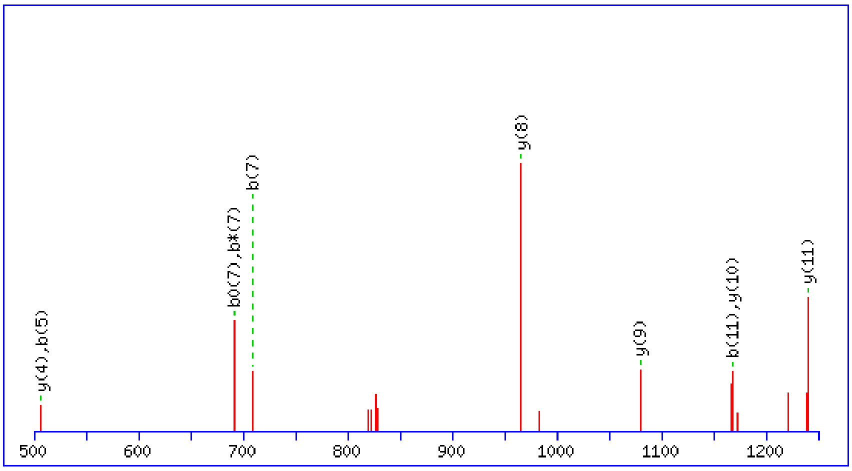
Peptide View

MS/MS Fragmentation of **DSNIASIPVEELIEK**
Found in **AT2G18960.1** in **TAIR_Arabidopsis**, Symbols: PMA, OST2, AHA1 | AHA1 (ARABIDOPSIS H+ ATPASE 1); ATPase | chr2:8228940-8234350 FORWARD

Match to Query 7854: 1672.808812 from(837.411682,2+) index(9206)
Title: Elution from: 83.920 to 83.920 scan no 12628 cid35.00 polarity:+
Data file 0-2_2.mgf

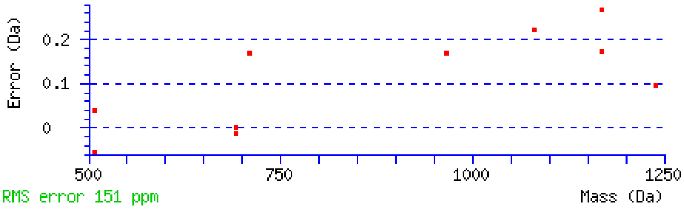
Click mouse within plot area to zoom in by factor of two about that point

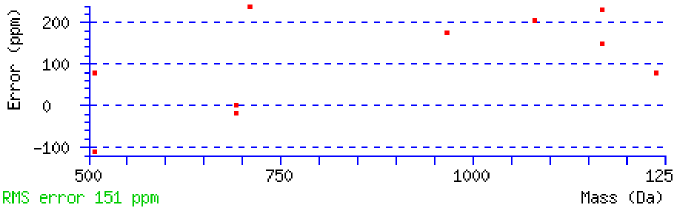
Or, Plot from 500 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1672.8114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00016
Matches : 10/162 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							15
2	205.0603	103.0338			187.0498	94.0285	S	1557.7947	779.4010	1539.7711	770.3892	1539.7841	770.3957	14
3	321.0973	161.0523	303.0737	152.0405	303.0867	152.0470	N	1469.7656	735.3864	1451.7420	726.3747	1451.7550	726.3812	13
4	435.1784	218.0928	417.1548	209.0811	417.1678	209.0876	I	1353.7286	677.3679	1335.7050	668.3562	1335.7180	668.3627	12
5	**507.2126**	254.1099	489.1890	245.0981	489.2020	245.1046	A	***1239.6475***	620.3274	1221.6239	611.3156	1221.6369	611.3221	11
6	595.2416	298.1245	577.2180	289.1127	577.2311	289.1192	S	***1167.6134***	584.3103	1149.5898	575.2985	1149.6028	575.3050	10
7	**709.3227**	355.1650	691.2991	346.1532	691.3122	346.1597	I	***1079.5843***	540.2958	1061.5607	531.2840	1061.5737	531.2905	9
8	807.3725	404.1899	789.3489	395.1781	789.3620	395.1846	P	***965.5032***	483.2552	947.4796	474.2434	947.4926	474.2500	8
9	907.4380	454.2226	889.4144	445.2108	889.4274	445.2173	V	867.4534	434.2303	849.4298	425.2185	849.4428	425.2251	7
10	1037.4776	519.2424	1019.4540	510.2306	1019.4670	510.2372	E	767.3880	384.1976	749.3644	375.1858	749.3774	375.1923	6
11	**1167.5172**	584.2623	1149.4936	575.2505	1149.5067	575.2570	E	637.3483	319.1778	619.3247	310.1660	619.3378	310.1725	5
12	1281.5983	641.3028	1263.5747	632.2910	1263.5878	632.2975	L	***507.3087***	254.1580	489.2851	245.1462	489.2981	245.1527	4
13	1395.6794	698.3434	1377.6558	689.3316	1377.6689	689.3381	I	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
14	1525.7191	763.3632	1507.6955	754.3514	1507.7085	754.3579	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT2G18960.1

NCBI **BLAST** search of DSNIASIPVEELIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.8	1672.8114	-0.0026	DSNIASIPVEELIEK
9.5	1672.8059	0.0029	ERVNKAFFGNLTEK
5.3	1672.8046	0.0042	MPQCSPLSPPILRR
2.1	1672.8082	0.0006	VLQRDSTPLFFPPH
1.9	1672.8082	0.0006	SHEIYAIEKWLHK

AT2G19050.1

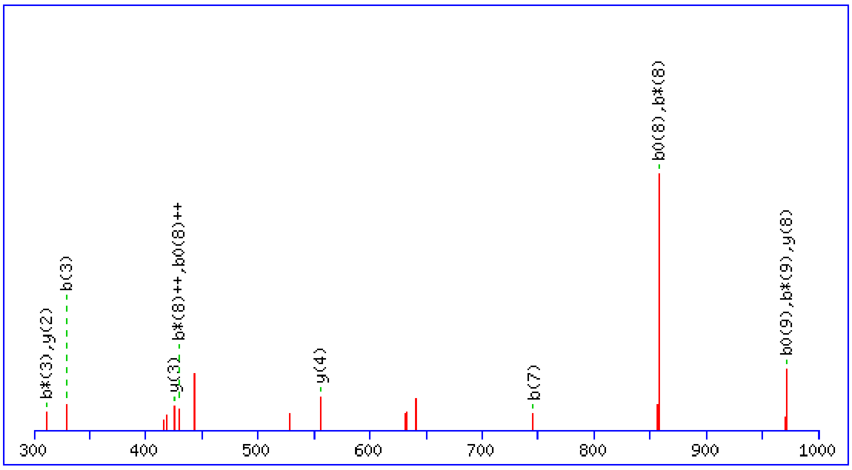
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIPDIIAELMR**
Found in **AT2G19050.1** in **TAIR_Arabidopsis**, Symbols: | GDSL-motif lipase/hydrolase family protein | chr2:8260498-8262616 FORWARD

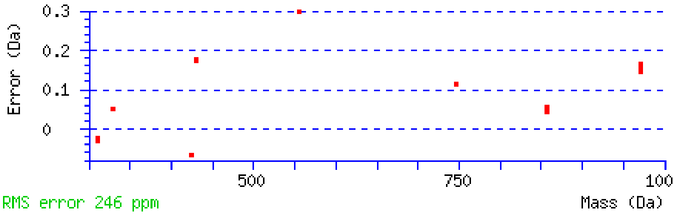
Match to Query 4893: 1298.647784 from(650.331168,2+) index(6375)
Title: Elution from: 55.317 to 55.317 scan no 8138 cid35.00 polarity:+
Data file D1d-3_2.mgf

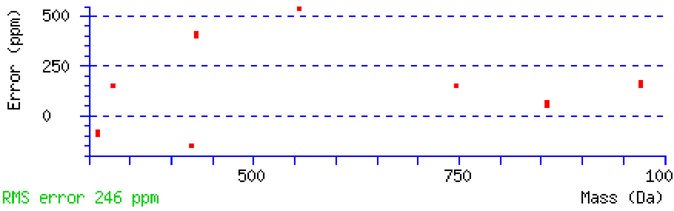
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1298.6463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0089
Matches : 13/108 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							11
2	231.1254	116.0663	213.1018	107.0545			I	1183.6166	592.3119	1165.5930	583.3001	1165.6060	583.3066	10
3	**329.1752**	165.0912	311.1516	156.0794			P	1069.5355	535.2714	1051.5119	526.2596	1051.5249	526.2661	9
4	445.1991	223.1032	427.1756	214.0914	427.1886	214.0979	D	***971.4857***	486.2465	953.4621	477.2347	953.4751	477.2412	8
5	559.2802	280.1438	541.2567	271.1320	541.2697	271.1385	I	855.4617	428.2345	837.4381	419.2227	837.4511	419.2292	7
6	673.3613	337.1843	655.3378	328.1725	655.3508	328.1790	I	741.3806	371.1939	723.3570	362.1821	723.3700	362.1886	6
7	**745.3955**	373.2014	727.3719	364.1896	727.3849	364.1961	A	627.2995	314.1534	609.2759	305.1416	609.2889	305.1481	5
8	875.4351	438.2212	857.4115	429.2094	857.4246	429.2159	E	***555.2653***	278.1363	537.2418	269.1245	537.2548	269.1310	4
9	989.5162	495.2617	971.4926	486.2500	971.5057	486.2565	L	***425.2257***	213.1165	407.2021	204.1047			3
10	1121.5537	561.2805	1103.5302	552.2687	1103.5432	552.2752	M	***311.1446***	156.0759	293.1210	147.0642			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NIPDIIAELMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G19050.1

Score	Mr(calc)	Delta	Sequence
26.6	1298.6463	0.0015	NIPDIIAELMR

Mascot: http://www.matrixscience.com/

AT2G19120.1

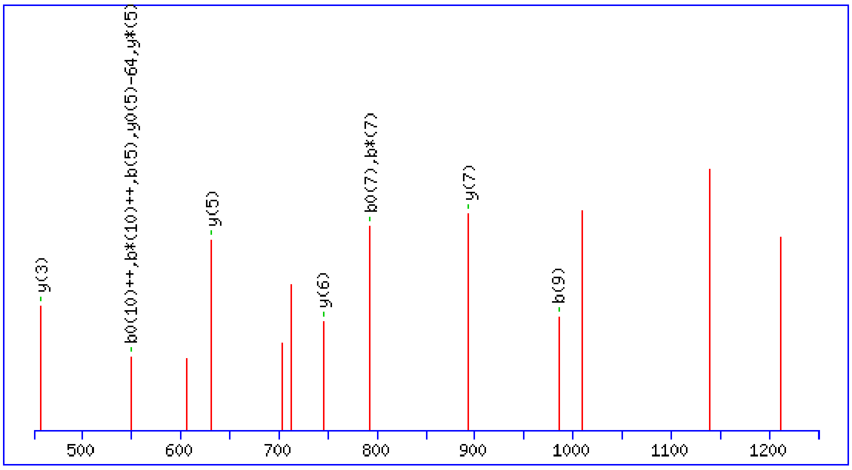
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLDRGFIDGEMR**
Found in **AT2G19120.1** in **TAIR_Arabidopsis**, Symbols: | tRNA-splicing endonuclease positive effector-related | chr2:8294118-8298884 REVERSE

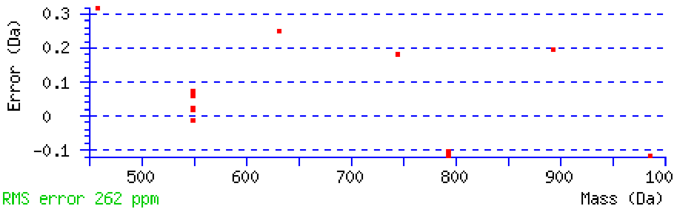
Match to Query 5694: 1440.640186 from(721.327369,2+) index(9962)
Title: Elution from: 92.600 to 92.600 scan no 13946 cid35.00 polarity:+
Data file D6h-1_2.mgf

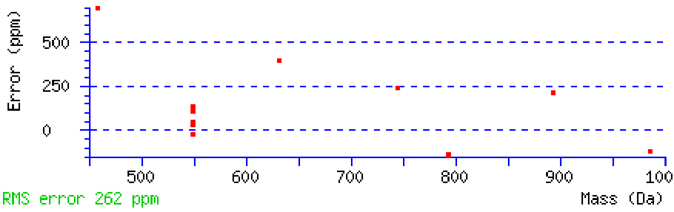
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1440.6391
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.029
Matches : 12/182 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							12
2	215.1538	108.0805					L	1341.5810	671.2941	1323.5574	662.2823	1323.5704	662.2889	11
3	331.1778	166.0925			313.1672	157.0873	D	1227.4999	614.2536	1209.4763	605.2418	1209.4893	605.2483	10
4	491.2671	246.1372	473.2435	237.1254	473.2565	237.1319	R	1111.4759	556.2416	1093.4523	547.2298	1093.4654	547.2363	9
5	**549.2856**	275.1464	531.2620	266.1346	531.2750	266.1411	G	951.3867	476.1970	933.3631	467.1852	933.3761	467.1917	8
6	697.3510	349.1791	679.3274	340.1673	679.3404	340.1739	F	***893.3682***	447.1877	875.3446	438.1759	875.3576	438.1824	7
7	811.4321	406.2197	793.4085	397.2079	793.4215	397.2144	I	***745.3027***	373.1550	727.2791	364.1432	727.2922	364.1497	6
8	927.4561	464.2317	909.4325	455.2199	909.4455	455.2264	D	***631.2216***	316.1145	613.1980	307.1027	613.2111	307.1092	5
9	**985.4746**	493.2409	967.4510	484.2291	967.4640	484.2356	G	515.1977	258.1025	497.1741	249.0907	497.1871	249.0972	4
10	1115.5142	558.2607	1097.4906	549.2489	1097.5036	549.2555	E	***457.1792***	229.0932	439.1556	220.0814	439.1686	220.0879	3
11	1263.5466	632.2770	1245.5231	623.2652	1245.5361	623.2717	M	327.1395	164.0734	309.1159	155.0616			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VLDRGFIDGEMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G19120.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.6	1440.6391	0.0010	VLDRGFIDGEMR
1.7	1440.6399	0.0003	EKSMQVETLMSK
1.2	1440.6392	0.0010	LNSIQAFMDVNR
0.8	1440.6367	0.0035	CMDAVLHFRFK
0.4	1440.6423	-0.0021	NLNINRSRNCR
0.3	1440.6369	0.0033	DTNLASQGVSKMR

AT2G19160.1

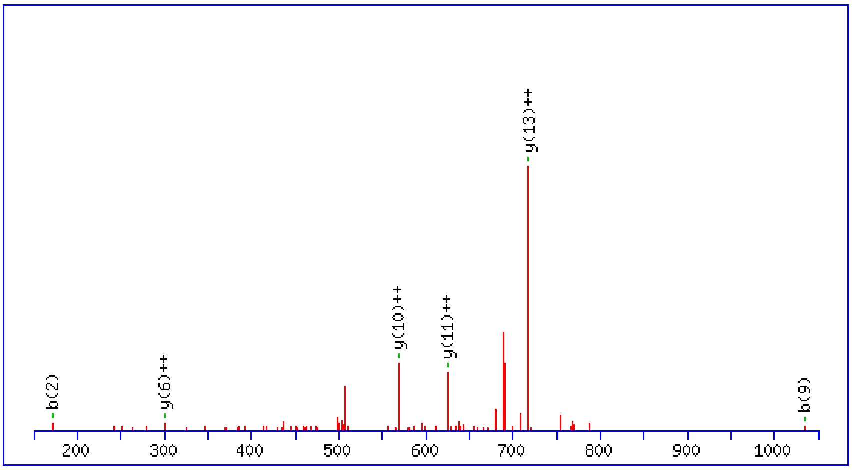
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGKINYMQSLPGAR**
Found in **AT2G19160.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G30060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64039.1); contains InterPro domain Protein of unknown function DUF266, plant (InterPro:IPR004949) | chr2:83

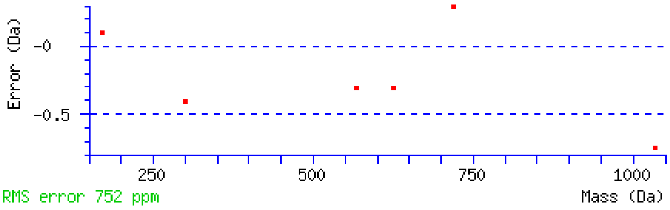
Match to Query 6669: 1546.824996 from(516.615608,3+) index(3991)
Title: Elution from: 37.326 to 37.326 scan no 4989 cid35.00 polarity:+
Data file 0-1_3.mgf

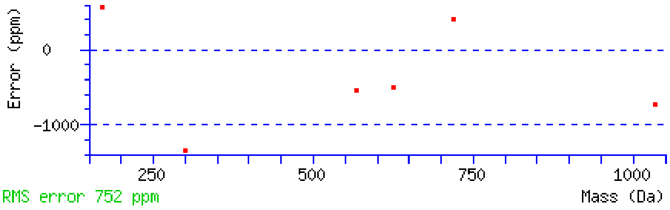
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1546.8289
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0069
Matches : 6/126 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							14
2	***171.1128***	86.0600					G	1434.7522	717.8797	1417.7256	709.3665	1416.7416	708.8745	13
3	299.2078	150.1075	282.1812	141.5942			K	1377.7307	689.3690	1360.7042	680.8557	1359.7202	680.3637	12
4	412.2918	206.6496	395.2653	198.1363			I	1249.6358	625.3215	1232.6092	616.8082	1231.6252	616.3162	11
5	526.3348	263.6710	509.3082	255.1577			N	1136.5517	568.7795	1119.5252	560.2662	1118.5411	559.7742	10
6	689.3981	345.2027	672.3715	336.6894			Y	1022.5088	511.7580	1005.4822	503.2448	1004.4982	502.7527	9
7	820.4386	410.7229	803.4120	402.2096			M	859.4454	430.2264	842.4189	421.7131	841.4349	421.2211	8
8	948.4972	474.7522	931.4706	466.2389			Q	728.4050	364.7061	711.3784	356.1928	710.3944	355.7008	7
9	***1035.5292***	518.2682	1018.5026	509.7550	1017.5186	509.2629	S	600.3464	300.6768	583.3198	292.1636	582.3358	291.6715	6
10	1148.6132	574.8103	1131.5867	566.2970	1130.6027	565.8050	L	513.3144	257.1608	496.2878	248.6475			5
11	1245.6660	623.3366	1228.6395	614.8234	1227.6554	614.3314	P	400.2303	200.6188	383.2037	192.1055			4
12	1302.6875	651.8474	1285.6609	643.3341	1284.6769	642.8421	G	303.1775	152.0924	286.1510	143.5791			3
13	1373.7246	687.3659	1356.6980	678.8527	1355.7140	678.3606	A	246.1561	123.5817	229.1295	115.0684			2
14							R	175.1190	88.0631	158.0924	79.5498			1





AT2G19160.1

NCBI **BLAST** search of LGKINYMQSLPGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.5	1546.8289	-0.0040	LGKINYMQSLPGAR
20.5	1546.8276	-0.0026	LGELEMDLLDKKK
10.5	1546.8211	0.0039	LGEAKQMLELMIR
8.9	1546.8211	0.0039	LGEAKQMLELMIR
7.3	1546.8256	-0.0006	GILQEAVKGQYWR
5.4	1546.8290	-0.0040	LAGMERVVSVFPSR
4.5	1546.8242	0.0008	VAADEILAAFSAIEK
3.9	1546.8216	0.0034	NSVFSNALSSPIRR
3.3	1546.8243	0.0007	IYSIGTIGLDGVDPK
2.8	1546.8215	0.0034	NNAASQQKKIFGNK

AT2G19200.1

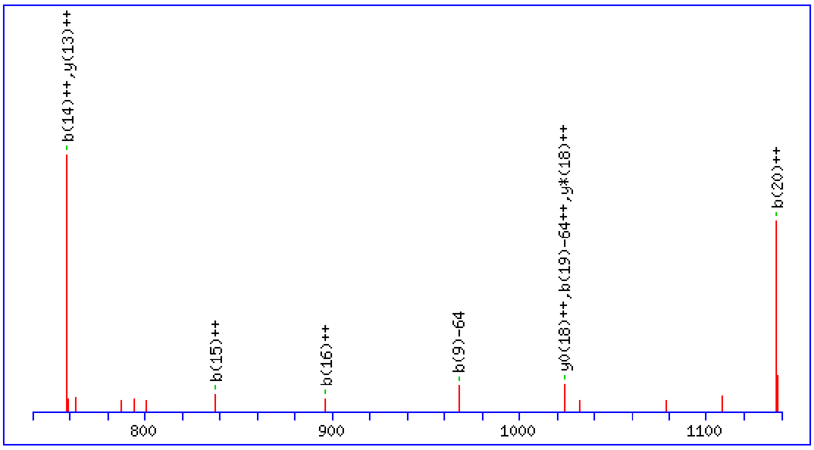
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILRVAMETTQDLGACDATFYVR**
Found in **AT2G19200.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11700.1); contains InterPro domain Protein of unknown function DUF626, Arabidopsis thaliana (InterPro:IPR006462) | chr2:8340300-8341703 FORWARD

Match to Query 10461: 2545.225023 from(849.415617,3+) index(8038)
Title: Elution from: 70.700 to 70.700 scan no 10525 cid35.00 polarity:+
Data file D12h-1_2.mgf

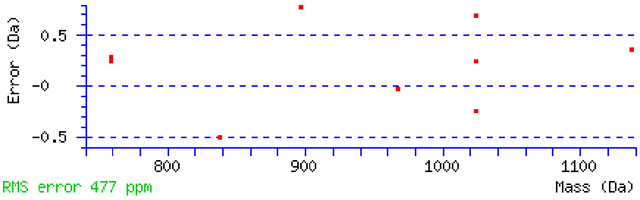
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 740 to 1140 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

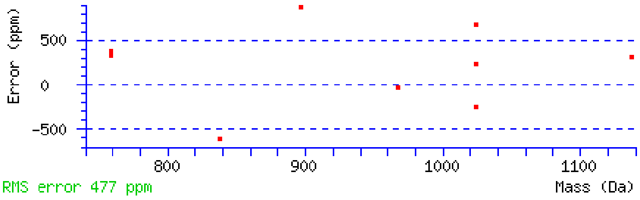


Monoisotopic mass of neutral peptide Mr(calc): 2545.2305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.026
Matches : 9/352 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							22
2	227.1754	114.0913					L	2433.1537	1217.0805	2416.1272	1208.5672	2415.1431	1208.0752	21
3	383.2765	192.1419	366.2500	183.6286			R	2320.0696	1160.5385	2303.0431	1152.0252	2302.0591	1151.5332	20
4	482.3449	241.6761	465.3184	233.1628			V	2163.9685	1082.4879	2146.9420	1073.9746	2145.9580	1073.4826	19
5	553.3820	277.1947	536.3555	268.6814			A	2064.9001	1032.9537	2047.8736	1024.4404	2046.8896	1023.9484	18
6	700.4174	350.7124	683.3909	342.1991			M	1993.8630	997.4351	1976.8365	988.9219	1975.8524	988.4299	17
7	829.4600	415.2337	812.4335	406.7204	811.4495	406.2284	E	1846.8276	923.9174	1829.8011	915.4042	1828.8170	914.9122	16
8	930.5077	465.7575	913.4812	457.2442	912.4972	456.7522	T	1717.7850	859.3961	1700.7585	850.8829	1699.7744	850.3909	15
9	1031.5554	516.2813	1014.5288	507.7681	1013.5448	507.2761	T	1616.7373	808.8723	1599.7108	800.3590	1598.7268	799.8670	14
10	1159.6140	580.3106	1142.5874	571.7973	1141.6034	571.3053	Q	1515.6897	758.3485	1498.6631	749.8352	1497.6791	749.3432	13
11	1274.6409	637.8241	1257.6144	629.3108	1256.6303	628.8188	D	1387.6311	694.3192	1370.6045	685.8059	1369.6205	685.3139	12
12	1387.7250	694.3661	1370.6984	685.8529	1369.7144	685.3608	L	1272.6041	636.8057	1255.5776	628.2924	1254.5936	627.8004	11
13	1444.7464	722.8769	1427.7199	714.3636	1426.7359	713.8716	G	1159.5201	580.2637	1142.4935	571.7504	1141.5095	571.2584	10
14	1515.7836	***758.3954***	1498.7570	749.8821	1497.7730	749.3901	A	1102.4986	551.7529	1085.4721	543.2397	1084.4880	542.7477	9
15	1675.8142	***838.4107***	1658.7877	829.8975	1657.8036	829.4055	C	1031.4615	516.2344	1014.4349	507.7211	1013.4509	507.2291	8
16	1790.8411	***895.9242***	1773.8146	887.4109	1772.8306	886.9189	D	871.4308	436.2191	854.4043	427.7058	853.4203	427.2138	7
17	1861.8783	931.4428	1844.8517	922.9295	1843.8677	922.4375	A	756.4039	378.7056	739.3774	370.1923	738.3933	369.7003	6
18	1962.9259	981.9666	1945.8994	973.4533	1944.9154	972.9613	T	685.3668	343.1870	668.3402	334.6738	667.3562	334.1817	5
19	2109.9944	1055.5008	2092.9678	1046.9875	2091.9838	1046.4955	F	584.3191	292.6632	567.2926	284.1499			4
20	2273.0577	***1137.0325***	2256.0311	1128.5192	2255.0471	1128.0272	Y	437.2507	219.1290	420.2241	210.6157			3
21	2372.1261	1186.5667	2355.0995	1178.0534	2354.1155	1177.5614	V	274.1874	137.5973	257.1608	129.0840			2
22							R	175.1190	88.0631	158.0924	79.5498			1

AT2G19200.1





NCBI **BLAST** search of ILRVAMETTQDLGACDATFYVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.9	2545.2305	-0.0055	ILRVAMETTQDLGACDATFYVR
6.2	2545.2266	-0.0016	LLGCCIEGEEKLLIYEFMANK
5.5	2545.2206	0.0045	SPWYEKIMNEMLGHLERQPR
3.1	2545.2240	0.0011	VKMHDVVREMALWISSGCGDQK
1.7	2545.2305	-0.0055	AHPDVFNMMLQILEDGRLTDSK
1.7	2545.2305	-0.0055	AHPDVFNMMLQILEDGRLTDSK

Mascot: http://www.matrixscience.com/

AT2G19480.1

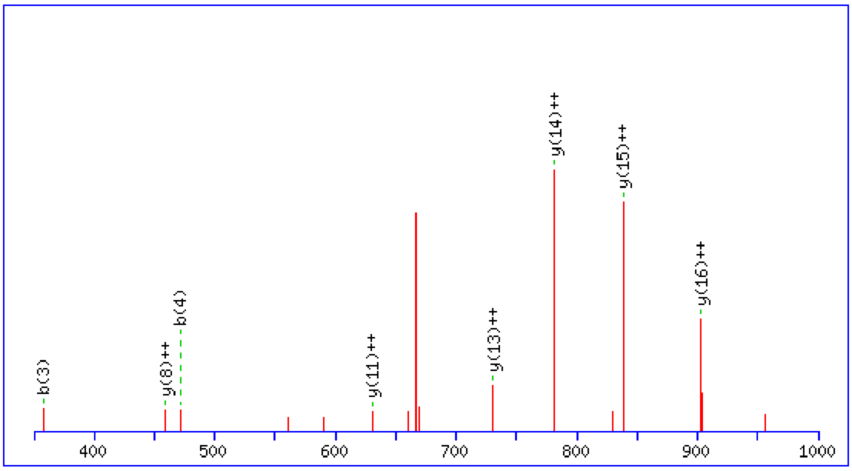
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNEITAEEITERDEGALK**
Found in **AT2G19480.1** in **TAIR_Arabidopsis**, Symbols: NAP1;2, NFA2 | NAP1;2/NFA2 (NUCLEOSOME ASSEMBLY PROTEIN1;2); DNA binding | chr2:8445683-8448122 FORWARD

Match to Query 9444: 2030.972763 from(677.998197,3+) index(4636)
Title: Elution from: 42.335 to 42.335 scan no 5831 cid35.00 polarity:+
Data file C7-1_2.mgf

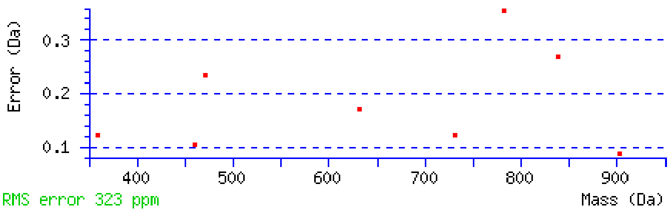
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

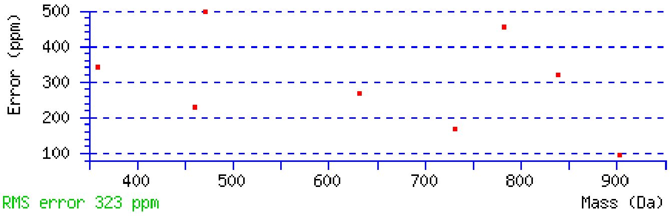


Monoisotopic mass of neutral peptide Mr(calc): 2030.9756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 9.5e-005
Matches : 8/192 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							18
2	229.0931	115.0502	212.0666	106.5369			N	1917.9400	959.4736	1900.9134	950.9604	1899.9294	950.4684	17
3	**358.1357**	179.5715	341.1092	171.0582	340.1252	170.5662	E	1803.8971	902.4522	1786.8705	893.9389	1785.8865	893.4469	16
4	**471.2198**	236.1135	454.1932	227.6003	453.2092	227.1082	I	1674.8545	837.9309	1657.8279	829.4176	1656.8439	828.9256	15
5	572.2675	286.6374	555.2409	278.1241	554.2569	277.6321	T	1561.7704	781.3888	1544.7439	772.8756	1543.7598	772.3836	14
6	643.3046	322.1559	626.2780	313.6427	625.2940	313.1506	A	1460.7227	730.8650	1443.6962	722.3517	1442.7122	721.8597	13
7	772.3472	386.6772	755.3206	378.1640	754.3366	377.6719	E	1389.6856	695.3464	1372.6591	686.8332	1371.6750	686.3412	12
8	901.3898	451.1985	884.3632	442.6852	883.3792	442.1932	E	1260.6430	630.8251	1243.6165	622.3119	1242.6325	621.8199	11
9	1014.4738	507.7406	997.4473	499.2273	996.4633	498.7353	I	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	10
10	1115.5215	558.2644	1098.4950	549.7511	1097.5109	549.2591	T	1018.5164	509.7618	1001.4898	501.2485	1000.5058	500.7565	9
11	1244.5641	622.7857	1227.5376	614.2724	1226.5535	613.7804	E	917.4687	459.2380	900.4421	450.7247	899.4581	450.2327	8
12	1400.6652	700.8362	1383.6387	692.3230	1382.6546	691.8310	R	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	7
13	1515.6922	758.3497	1498.6656	749.8364	1497.6816	749.3444	D	632.3250	316.6661	615.2984	308.1529	614.3144	307.6608	6
14	1644.7347	822.8710	1627.7082	814.3577	1626.7242	813.8657	E	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	5
15	1701.7562	851.3817	1684.7297	842.8685	1683.7456	842.3765	G	388.2554	194.6314	371.2289	186.1181			4
16	1772.7933	886.9003	1755.7668	878.3870	1754.7828	877.8950	A	331.2340	166.1206	314.2074	157.6074			3
17	1885.8774	943.4423	1868.8508	934.9291	1867.8668	934.4371	L	260.1969	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT2G19480.1





NCBI **BLAST** search of NNEITAEEITERDEGALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.5	2030.9756	-0.0028	NNEITAEEITERDEGALK
7.7	2030.9693	0.0035	VEEFLLMMNSLEFEIR
7.2	2030.9770	-0.0042	DIQQNIQHHLDNNSVEK
3.0	2030.9778	-0.0051	WRPERIDLSAMACPASR
1.6	2030.9691	0.0037	RKEGEDAVASCVISEPER
1.1	2030.9765	-0.0037	LDEAAKMVQDMRTEPGPK
1.1	2030.9765	-0.0037	LDEAAKMVQDMRTEPGPK
0.8	2030.9731	-0.0004	LNQADNMPSYEPPVALTR

Mascot: http://www.matrixscience.com/

AT2G19750.1

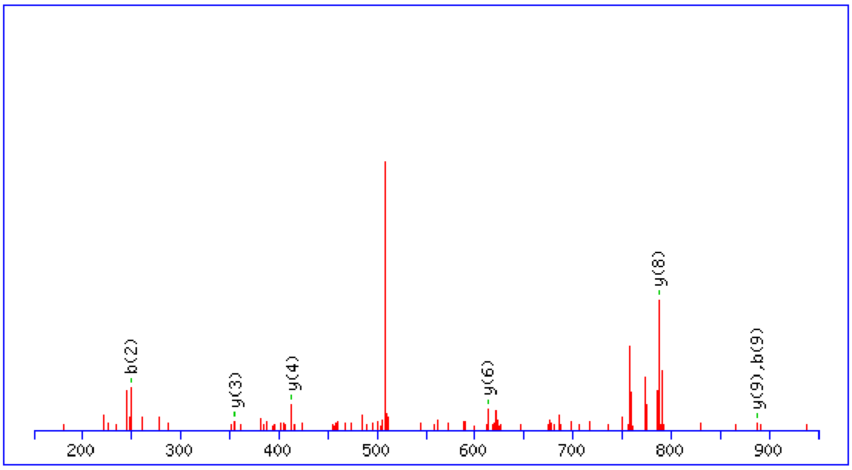
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVTAVVGFGK**
Found in **AT2G19750.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S30 (RPS30A) | chr2:8522119-8522888 FORWARD

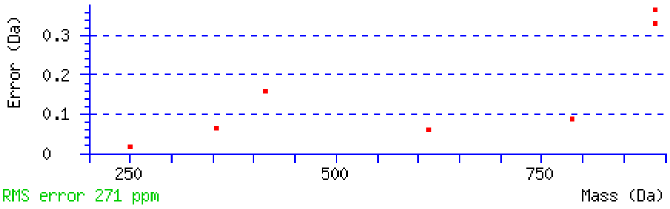
Match to Query 2817: 1034.545670 from(518.280111,2+) index(5772)
Title: Elution from: 51.043 to 51.043 scan no 7282 cid35.00 polarity:+
Data file D12h-1_2.mgf

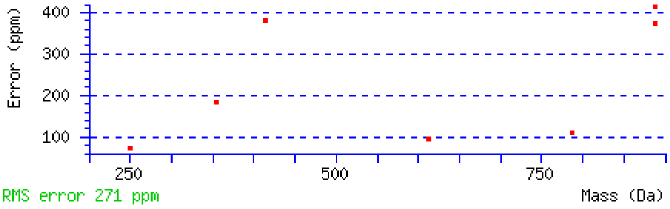
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1034.5427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00028
Matches : 7/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400			F							10
2	**249.1382**	125.0727			V	***887.4845***	444.2459	869.4609	435.2341	869.4740	435.2406	9
3	351.1829	176.0951	333.1723	167.0898	T	***787.4191***	394.2132	769.3955	385.2014	769.4085	385.2079	8
4	423.2170	212.1122	405.2065	203.1069	A	685.3744	343.1908	667.3508	334.1790			7
5	523.2825	262.1449	505.2719	253.1396	V	***613.3402***	307.1737	595.3166	298.1620			6
6	623.3479	312.1776	605.3374	303.1723	V	513.2748	257.1410	495.2512	248.1292			5
7	681.3664	341.1869	663.3559	332.1816	G	***413.2093***	207.1083	395.1857	198.0965			4
8	829.4319	415.2196	811.4213	406.2143	F	***355.1908***	178.0990	337.1672	169.0873			3
9	**887.4504**	444.2288	869.4398	435.2235	G	207.1254	104.0663	189.1018	95.0545			2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FVTAVVGFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G19750.1

43.4	1034.5427	0.0030	FVTAVVGFGK
7.4	1034.5487	-0.0031	FLRMLGLR
3.7	1034.5431	0.0025	VQKRTNFK
3.5	1034.5427	0.0030	GEPVWIPVK
1.6	1034.5431	0.0025	RSLRDVFK
1.6	1034.5465	-0.0008	SRLMRLTK
1.6	1034.5431	0.0025	TFNKRQVK
1.6	1034.5465	-0.0008	TTRMRLVK
1.3	1034.5487	-0.0031	CRGFLKLK
0.4	1034.5431	0.0025	AKNQYLRK

AT2G19900.1

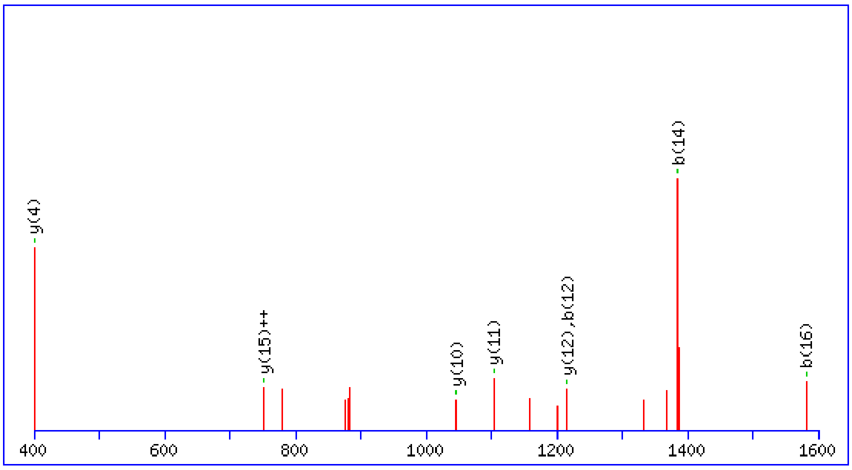
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILGLGDLGCQGMGIPVGK**
Found in **AT2G19900.1** in **TAIR_Arabidopsis**, Symbols: ATNADP-ME1 | ATNADP-ME1 (NADP-MALIC ENZYME 1); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr2:8599188-8602485 REVERSE

Match to Query 8651: 1783.932164 from(892.973358,2+) index(9529)
Title: Elution from: 87.370 to 87.370 scan no 12999 cid35.00 polarity:+
Data file D6h-2_1.mgf

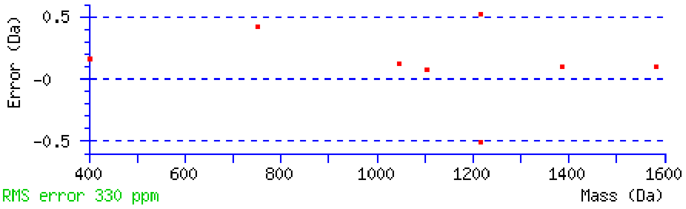
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

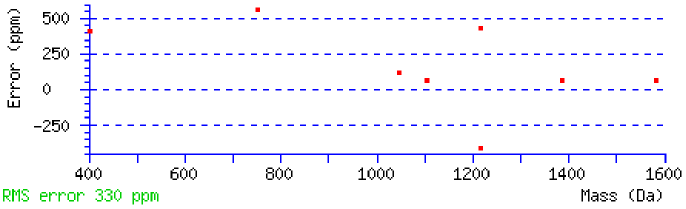


Monoisotopic mass of neutral peptide Mr(calc): 1783.9325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0019
Matches : 8/152 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							18
2	227.1754	114.0913					L	1671.8557	836.4315	1654.8291	827.9182	1653.8451	827.4262	17
3	284.1969	142.6021					G	1558.7716	779.8894	1541.7451	771.3762	1540.7610	770.8842	16
4	397.2809	199.1441					L	1501.7501	751.3787	1484.7236	742.8654	1483.7396	742.3734	15
5	454.3024	227.6548					G	1388.6661	694.8367	1371.6395	686.3234	1370.6555	685.8314	14
6	569.3293	285.1683			551.3188	276.1630	D	1331.6446	666.3259	1314.6181	657.8127	1313.6341	657.3207	13
7	682.4134	341.7103			664.4028	332.7051	L	***1216.6177***	608.8125	1199.5911	600.2992			12
8	739.4349	370.2211			721.4243	361.2158	G	***1103.5336***	552.2704	1086.5071	543.7572			11
9	899.4655	450.2364			881.4550	441.2311	C	***1046.5121***	523.7597	1029.4856	515.2464			10
10	1027.5241	514.2657	1010.4975	505.7524	1009.5135	505.2604	Q	886.4815	443.7444	869.4550	435.2311			9
11	1084.5456	542.7764	1067.5190	534.2631	1066.5350	533.7711	G	758.4229	379.7151	741.3964	371.2018			8
12	***1215.5860***	608.2967	1198.5595	599.7834	1197.5755	599.2914	M	701.4015	351.2044	684.3749	342.6911			7
13	1272.6075	636.8074	1255.5810	628.2941	1254.5969	627.8021	G	570.3610	285.6841	553.3344	277.1709			6
14	***1385.6916***	693.3494	1368.6650	684.8361	1367.6810	684.3441	I	513.3395	257.1734	496.3130	248.6601			5
15	1482.7443	741.8758	1465.7178	733.3625	1464.7338	732.8705	P	***400.2554***	200.6314	383.2289	192.1181			4
16	***1581.8127***	791.4100	1564.7862	782.8967	1563.8022	782.4047	V	303.2027	152.1050	286.1761	143.5917			3
17	1638.8342	819.9207	1621.8077	811.4075	1620.8236	810.9155	G	204.1343	102.5708	187.1077	94.0575			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT2G19900.1





NCBI **BLAST** search of ILGLGDLGCQGMGIPVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.2	1783.9325	-0.0003	ILGLGDLGCQGMGIPVGK
3.1	1783.9329	-0.0007	ETSQRWERVAAAVPGK
0.9	1783.9291	0.0031	MTLYRAFSGLVQTPGK

Mascot: http://www.matrixscience.com/

AT2G19940.1

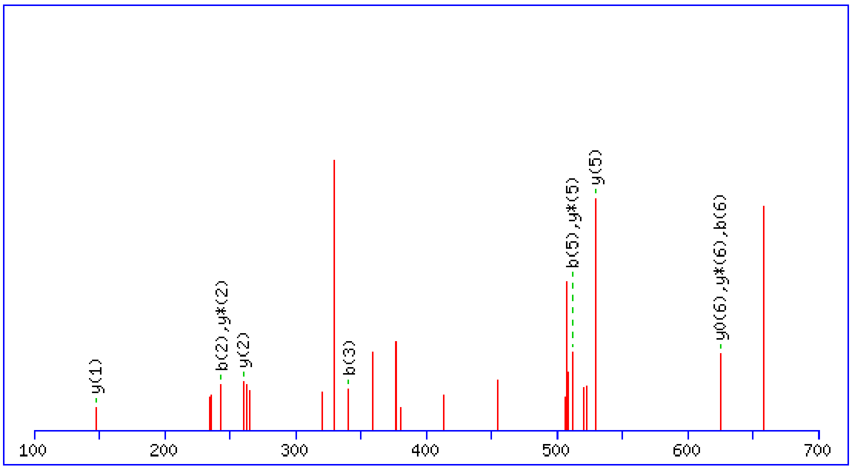
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELPTALK**
Found in **AT2G19940.1** in **TAIR_Arabidopsis**, Symbols: | semialdehyde dehydrogenase family protein | chr2:8620505-8622730 FORWARD

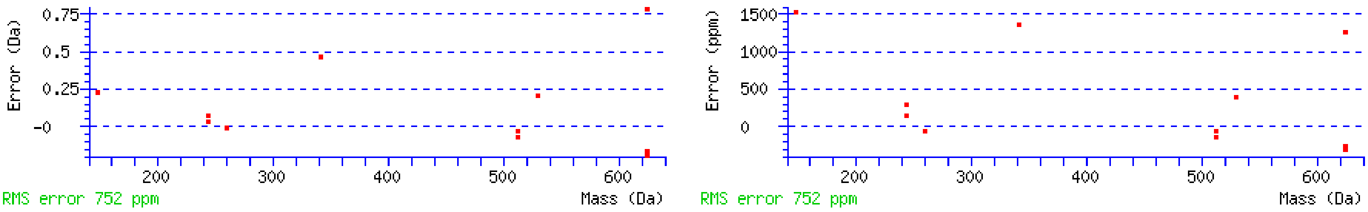
Match to Query 913: 770.453810 from(386.234181,2+) index(5545)
Title: Elution from: 49.579 to 49.579 scan no 6977 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.4538
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.031
Matches : 11/54 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							7
2	***243.1339***	122.0706	225.1234	113.0653	L	642.4185	321.7129	625.3919	313.1996	624.4079	312.7076	6
3	***340.1867***	170.5970	322.1761	161.5917	P	**529.3344**	265.1709	512.3079	256.6576	511.3239	256.1656	5
4	441.2344	221.1208	423.2238	212.1155	T	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
5	***512.2715***	256.6394	494.2609	247.6341	A	331.2340	166.1206	314.2074	157.6074			3
6	***625.3556***	313.1814	607.3450	304.1761	L	**260.1969**	130.6021	243.1703	122.0888			2
7					K	**147.1128**	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of ELPTALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	770.4538	0.0000	ELPTALK
15.5	770.4538	0.0000	LPETALK
11.4	770.4538	0.0000	DPLSVLK

AT2G19940.1

11.0	770.4538	0.0000	LSPVDLK
6.0	770.4551	-0.0013	IHFARK
5.9	770.4551	-0.0013	IARFHK
5.1	770.4538	0.0000	IPELATK
2.8	770.4551	-0.0013	HFRALK
2.0	770.4538	0.0000	ESVVPLK
1.8	770.4538	0.0000	APETLLK

AT2G19950.1

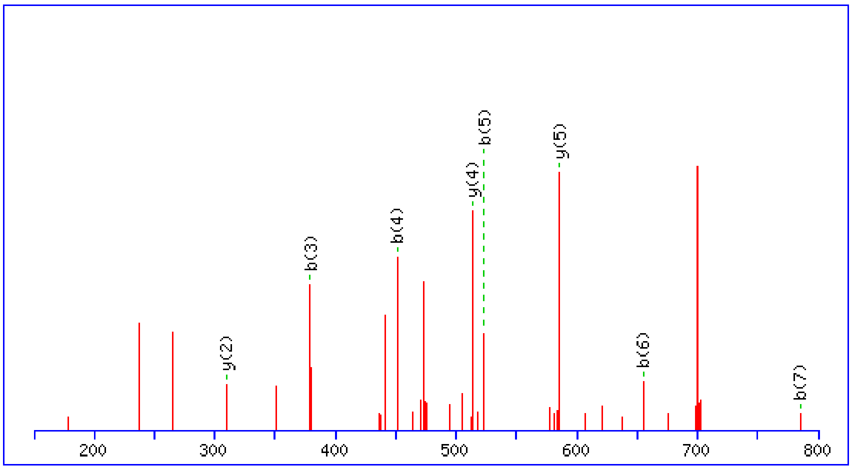
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEMAAMKR**
Found in **AT2G19950.1** in **TAIR_Arabidopsis**, Symbols: GC1 | This gene is predicted to encode a protein that functions as a Golgi apparatus structural component known as a golgin in mammals and yeast. A fluorescently-tagged version of GC1 co-localizes with Golgi markers, and this localization

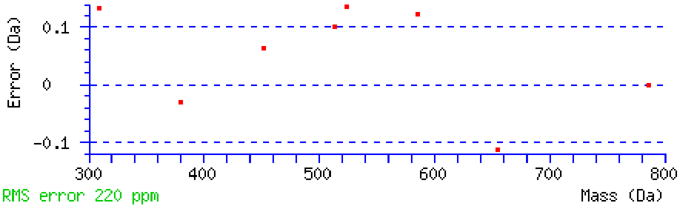
Match to Query 2091: 962.432452 from(482.223502,2+) index(5413)
Title: Elution from: 48.430 to 48.430 scan no 6878 cid35.00 polarity:+
Data file C7-3_3.mgf

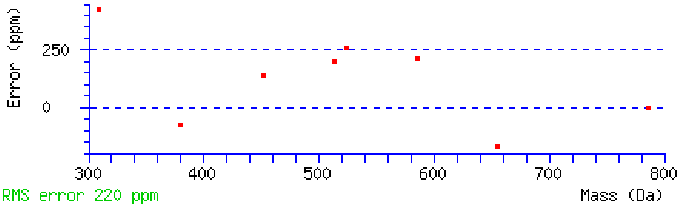
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 962.4322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37  Expect: 0.0011
Matches : 8/90 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							8
2	231.1124	116.0598			213.1018	107.0545	E	863.3740	432.1906	845.3504	423.1788	845.3634	423.1854	7
3	***379.1448***	190.0760			361.1342	181.0707	M	733.3344	367.1708	715.3108	358.1590			6
4	***451.1789***	226.0931			433.1684	217.0878	A	**585.3019**	293.1546	567.2784	284.1428			5
5	***523.2131***	262.1102			505.2025	253.1049	A	**513.2678**	257.1375	495.2442	248.1257			4
6	***655.2506***	328.1289			637.2400	319.1237	M	441.2336	221.1205	423.2101	212.1087			3
7	***785.3396***	393.1735	767.3161	384.1617	767.3291	384.1682	K	**309.1961**	155.1017	291.1725	146.0899			2
8							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VEMAAMKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G19950.1

Score	Mr(calc)	Delta	Sequence
37.3	962.4322	0.0003	VEMAAMKR
24.1	962.4313	0.0011	SSSALTTER
15.5	962.4322	0.0003	MKEEMKR
10.3	962.4322	0.0003	SMLAVVCR
8.3	962.4335	-0.0011	YGGVSLNDK
7.4	962.4315	0.0010	MLNGWRR
6.1	962.4340	-0.0015	STGRLSDGR
5.9	962.4322	0.0003	MEEKMRK
5.4	962.4348	-0.0024	MMVQQRR
5.1	962.4340	-0.0015	SVSESRQR

Mascot: http://www.matrixscience.com/

AT2G20020.1

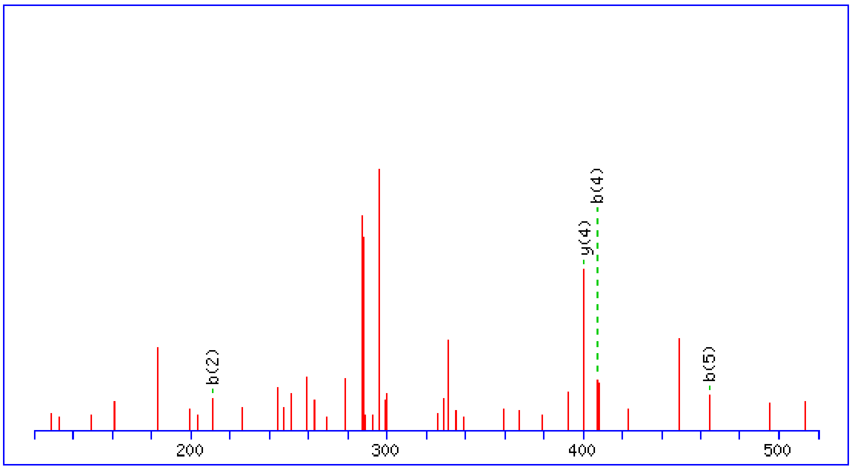
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPVGK**
Found in **AT2G20020.1** in **TAIR_Arabidopsis**, Symbols: | Identical to CRS2-associated factor 1, chloroplast precursor [Arabidopsis Thaliana] (GB:Q9SL79;GB:Q94AQ2); similar to ATCAF2/CAF2 (ARABIDOPSIS THALIANA HOMOLOG OF MAIZE CAF2) [Arabidopsis thaliana] (TAIR:AT1G23400.1); similar to unname

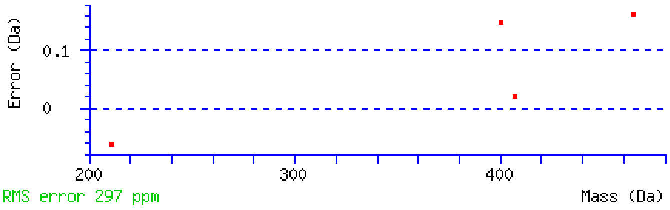
Match to Query 518: 609.384730 from(305.699641,2+) index(843)
Title: Elution from: 14.526 to 14.526 scan no 1224 cid35.00 polarity:+
Data file 0-2_1.mgf

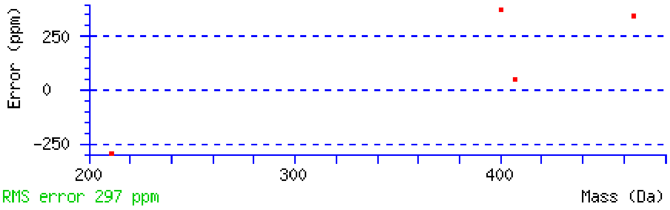
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 520 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 609.3850
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 0.035
Matches : 4/30 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.0913	57.5493	L					6
2	***211.1441***	106.0757	P	497.3082	249.1577	480.2817	240.6445	5
3	308.1969	154.6021	P	400.2554	200.6314	383.2289	192.1181	4
4	***407.2653***	204.1363	V	303.2027	152.1050	286.1761	143.5917	3
5	***464.2867***	232.6470	G	204.1343	102.5708	187.1077	94.0575	2
6			K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of LPPVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.6	609.3850	-0.0003	LPPVGK
12.6	609.3850	-0.0003	PIGVPK

AT2G20020.1

7.0	609.3850	-0.0003	IPGPVK
7.0	609.3850	-0.0003	LPGPVK

Mascot: http://www.matrixscience.com/

AT2G20140.1

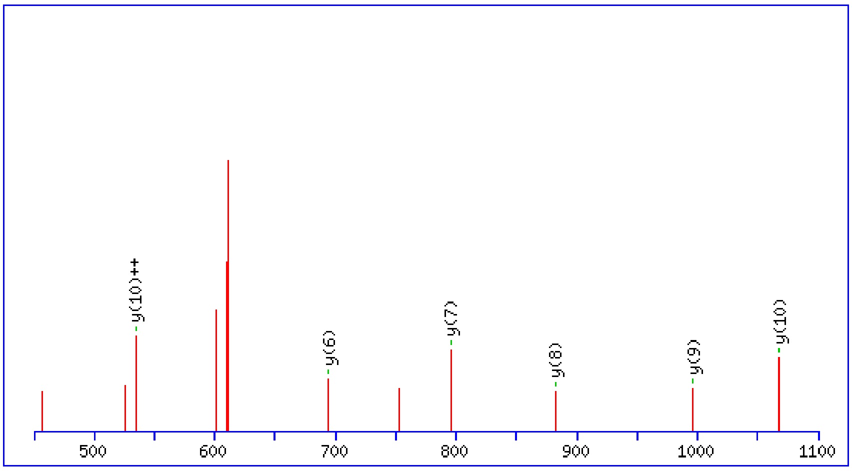
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVANSTSATFLR**
Found in **AT2G20140.1** in **TAIR_Arabidopsis**, Symbols: | 26S protease regulatory complex subunit 4, putative | chr2:8699817-8701918 FORWARD

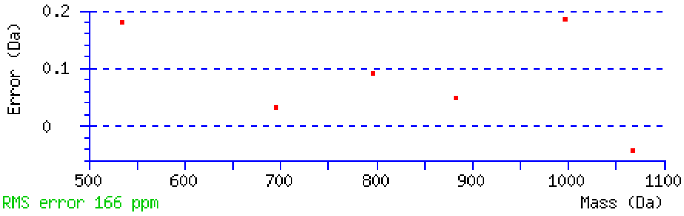
Match to Query 4226: 1236.647284 from(619.330918,2+) index(3023)
Title: Elution from: 31.664 to 31.664 scan no 3801 cid35.00 polarity:+
Data file D6h-2_2.mgf

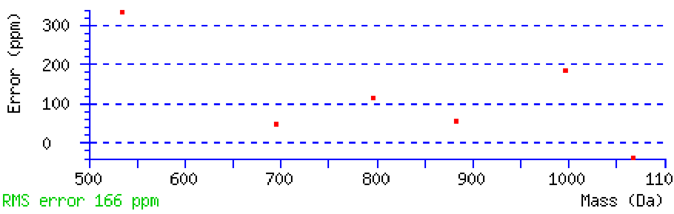
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1236.6462
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0002
Matches : 6/112 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							12
2	171.1128	86.0600					V	1166.6164	583.8118	1149.5899	575.2986	1148.6058	574.8066	11
3	242.1499	121.5786					A	***1067.5480***	534.2776	1050.5215	525.7644	1049.5374	525.2724	10
4	356.1928	178.6001	339.1663	170.0868			N	***996.5109***	498.7591	979.4843	490.2458	978.5003	489.7538	9
5	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	S	***882.4680***	441.7376	865.4414	433.2243	864.4574	432.7323	8
6	544.2726	272.6399	527.2460	264.1266	526.2620	263.6346	T	***795.4359***	398.2216	778.4094	389.7083	777.4254	389.2163	7
7	631.3046	316.1559	614.2780	307.6427	613.2940	307.1506	S	***694.3883***	347.6978	677.3617	339.1845	676.3777	338.6925	6
8	702.3417	351.6745	685.3151	343.1612	684.3311	342.6692	A	607.3562	304.1817	590.3297	295.6685	589.3457	295.1765	5
9	803.3894	402.1983	786.3628	393.6850	785.3788	393.1930	T	536.3191	268.6632	519.2926	260.1499	518.3085	259.6579	4
10	950.4578	475.7325	933.4312	467.2193	932.4472	466.7272	F	435.2714	218.1394	418.2449	209.6261			3
11	1063.5419	532.2746	1046.5153	523.7613	1045.5313	523.2693	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AVANSTSATFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G20140.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.0	1236.6462	0.0010	AVANSTSATFLR

Mascot: http://www.matrixscience.com/

AT2G20270.1

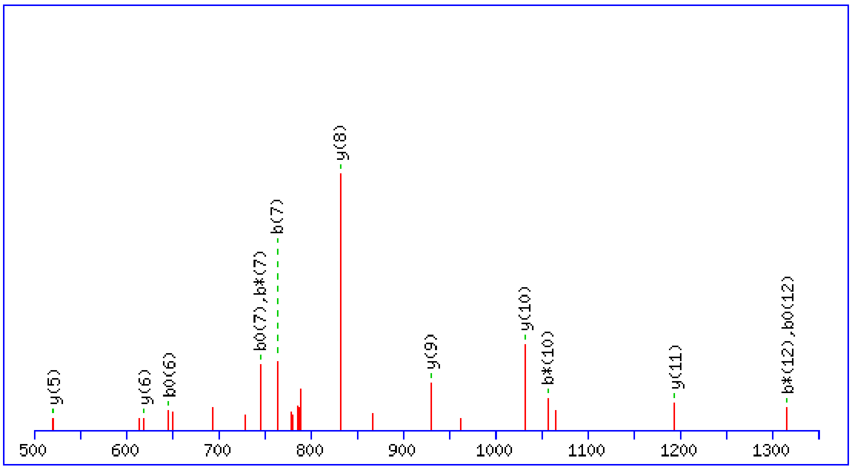
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITGQYTVPNVFIGGK**
Found in **AT2G20270.1** in **TAIR_Arabidopsis**, Symbols: | glutaredoxin family protein | chr2:8745082-8746698 REVERSE

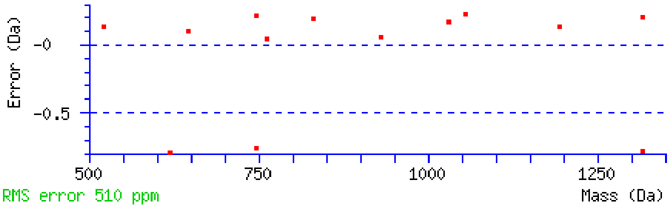
Match to Query 7596: 1592.855762 from(797.435157,2+) index(7741)
Title: Elution from: 67.402 to 67.402 scan no 10044 cid35.00 polarity:+
Data file D6h-1_1.mgf

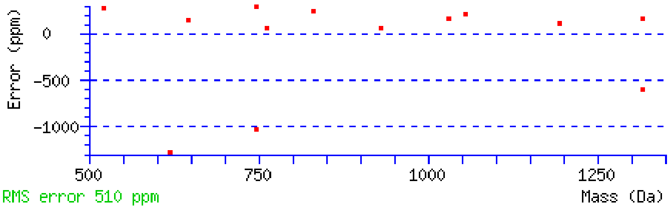
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1592.8563
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0064
Matches : 13/142 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							15
2	215.1390	108.0731			197.1285	99.0679	T	1480.7795	740.8934	1463.7529	732.3801	1462.7689	731.8881	14
3	272.1605	136.5839			254.1499	127.5786	G	1379.7318	690.3695	1362.7052	681.8563	1361.7212	681.3642	13
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	Q	1322.7103	661.8588	1305.6838	653.3455	1304.6997	652.8535	12
5	563.2824	282.1448	546.2558	273.6316	545.2718	273.1396	Y	***1194.6517***	597.8295	1177.6252	589.3162	1176.6412	588.8242	11
6	664.3301	332.6687	647.3035	324.1554	646.3195	323.6634	T	***1031.5884***	516.2978	1014.5619	507.7846	1013.5778	507.2926	10
7	763.3985	382.2029	746.3719	373.6896	745.3879	373.1976	V	***930.5407***	465.7740	913.5142	457.2607			9
8	860.4512	430.7293	843.4247	422.2160	842.4407	421.7240	P	***831.4723***	416.2398	814.4458	407.7265			8
9	974.4942	487.7507	957.4676	479.2375	956.4836	478.7454	N	734.4196	367.7134	717.3930	359.2001			7
10	1073.5626	537.2849	1056.5360	528.7717	1055.5520	528.2796	V	***620.3766***	310.6919	603.3501	302.1787			6
11	1220.6310	610.8191	1203.6045	602.3059	1202.6204	601.8139	F	***521.3082***	261.1577	504.2817	252.6445			5
12	1333.7151	667.3612	1316.6885	658.8479	1315.7045	658.3559	I	374.2398	187.6235	357.2132	179.1103			4
13	1390.7365	695.8719	1373.7100	687.3586	1372.7260	686.8666	G	261.1557	131.0815	244.1292	122.5682			3
14	1447.7580	724.3826	1430.7314	715.8694	1429.7474	715.3774	G	204.1343	102.5708	187.1077	94.0575			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ITGQYTVPNVFIGGK

AT2G20270.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.6	1592.8563	-0.0005	ITGQYTVPNVFIGGK
0.2	1592.8537	0.0020	VFADAKMWKWALK

AT2G20280.1

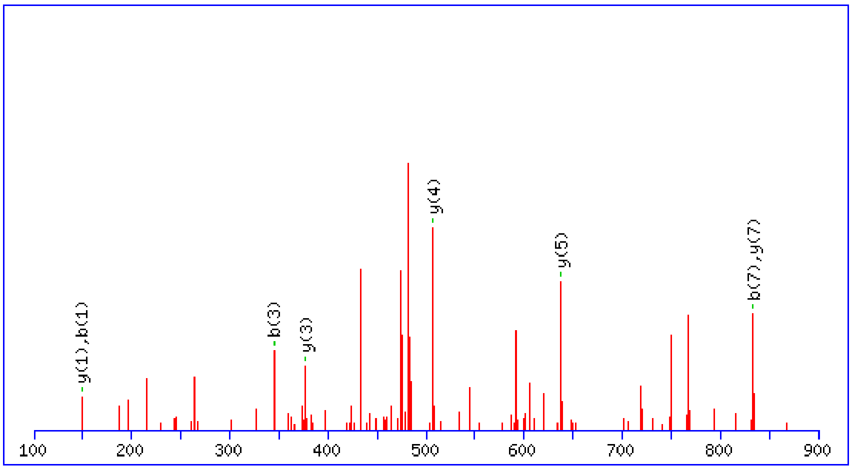
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPPKQQPK**
Found in **AT2G20280.1** in **TAIR_Arabidopsis**, Symbols: | zinc finger (CCCH-type) family protein | chr2:8747135-8749430 REVERSE

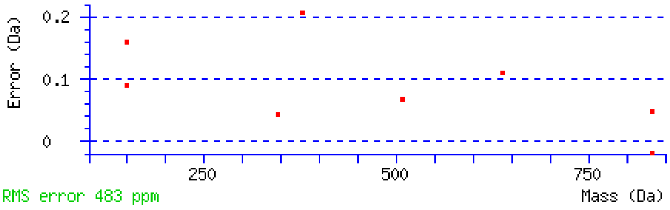
Match to Query 2305: 980.473084 from(491.243818,2+) index(2087)
Title: Elution from: 22.756 to 22.756 scan no 2616 cid35.00 polarity:+
Data file C7-2_3.mgf

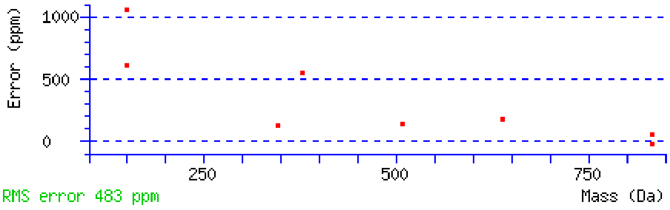
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 980.4758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.018
Matches : 8/72 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	**149.0397**	75.0235			M					8
2	247.0895	124.0484			P	***833.4506***	417.2289	815.4270	408.2171	7
3	**345.1393**	173.0733			P	735.4008	368.2040	717.3772	359.1922	6
4	475.2283	238.1178	457.2048	229.1060	K	***637.3510***	319.1791	619.3274	310.1673	5
5	605.2810	303.1441	587.2574	294.1323	Q	***507.2620***	254.1346	489.2384	245.1228	4
6	735.3336	368.1705	717.3101	359.1587	Q	***377.2093***	189.1083	359.1857	180.0965	3
7	**833.3834**	417.1954	815.3599	408.1836	P	247.1567	124.0820	229.1331	115.0702	2
8					K	***149.1069***	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MPPKQQPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	980.4758	-0.0027	MPPKQQPK

AT2G20280.1

22.3	980.4758	-0.0027	AIHCDILK
22.1	980.4702	0.0029	SHNQIELK
9.3	980.4758	-0.0027	MSTARFIK
8.9	980.4758	-0.0027	NHPTLMIK
6.8	980.4724	0.0007	IFDHPNVK
6.2	980.4702	0.0029	RDNLPEPK
6.0	980.4728	0.0003	RLTSHSHK
4.7	980.4758	-0.0027	MAIFSRTK
4.2	980.4701	0.0029	DDVHLKNK

AT2G20420.1

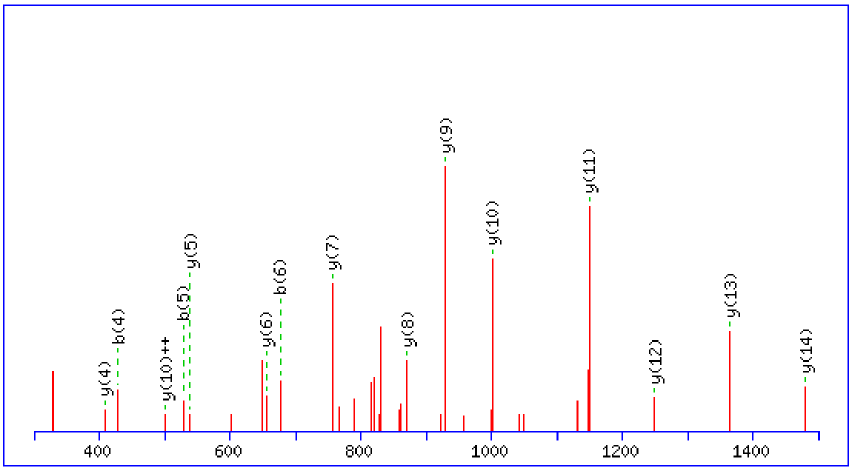
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPIDVFAGITDEDAAK**
Found in **AT2G20420.1** in **TAIR_Arabidopsis**, Symbols: | succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative | chr2:8812655-8814939 FORWARD

Match to Query 7781: 1676.784952 from(839.399752,2+) index(8623)
Title: Elution from: 79.565 to 79.565 scan no 11595 cid35.00 polarity:+
Data file D1d-1_1.mgf

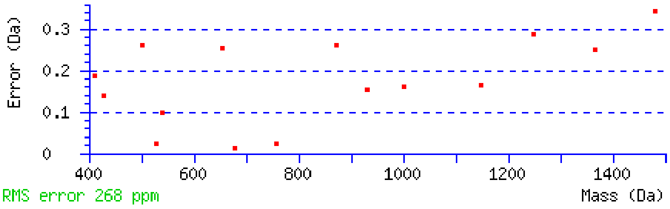
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

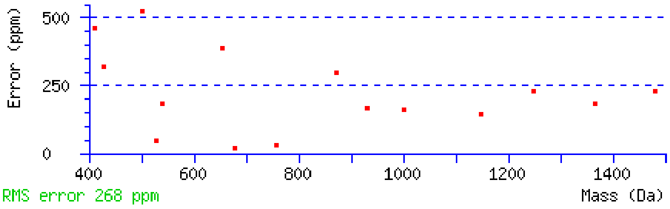


Monoisotopic mass of neutral peptide Mr(calc): 1676.7851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 1.2e-008
Matches : 15/138 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							16
2	199.1225	100.0649			P	1577.7270	789.3671	1559.7034	780.3553	1559.7164	780.3619	15
3	313.2036	157.1054			I	***1479.6772***	740.3422	1461.6536	731.3304	1461.6666	731.3370	14
4	**429.2276**	215.1174	411.2170	206.1122	D	***1365.5961***	683.3017	1347.5725	674.2899	1347.5855	674.2964	13
5	**529.2930**	265.1502	511.2825	256.1449	V	***1249.5721***	625.2897	1231.5485	616.2779	1231.5615	616.2844	12
6	**677.3585**	339.1829	659.3479	330.1776	F	***1149.5067***	575.2570	1131.4831	566.2452	1131.4961	566.2517	11
7	749.3926	375.2000	731.3821	366.1947	A	***1001.4412***	501.2242	983.4176	492.2125	983.4307	492.2190	10
8	807.4111	404.2092	789.4006	395.2039	G	***929.4071***	465.2072	911.3835	456.1954	911.3965	456.2019	9
9	921.4922	461.2498	903.4817	452.2445	I	***871.3886***	436.1979	853.3650	427.1861	853.3780	427.1926	8
10	1023.5370	512.2721	1005.5264	503.2668	T	***757.3075***	379.1574	739.2839	370.1456	739.2969	370.1521	7
11	1139.5609	570.2841	1121.5504	561.2788	D	***655.2628***	328.1350	637.2392	319.1232	637.2522	319.1297	6
12	1269.6006	635.3039	1251.5900	626.2986	E	***539.2388***	270.1230	521.2152	261.1112	521.2282	261.1177	5
13	1385.6245	693.3159	1367.6140	684.3106	D	***409.1992***	205.1032	391.1756	196.0914	391.1886	196.0979	4
14	1457.6587	729.3330	1439.6481	720.3277	A	293.1752	147.0912	275.1516	138.0794			3
15	1529.6928	765.3501	1511.6823	756.3448	A	221.1410	111.0741	203.1174	102.0624			2
16					K	149.1069	75.0571	131.0833	66.0453			1

AT2G20420.1





NCBI **BLAST** search of VPIDVFAGITDEDAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.3	1676.7851	-0.0002	VPIDVFAGITDEDAAK
3.0	1676.7804	0.0046	VFTLVTSQNAGKTMF
0.5	1676.7838	0.0012	VDEAHLMLEKMLSK

Mascot: http://www.matrixscience.com/

AT2G20450.1

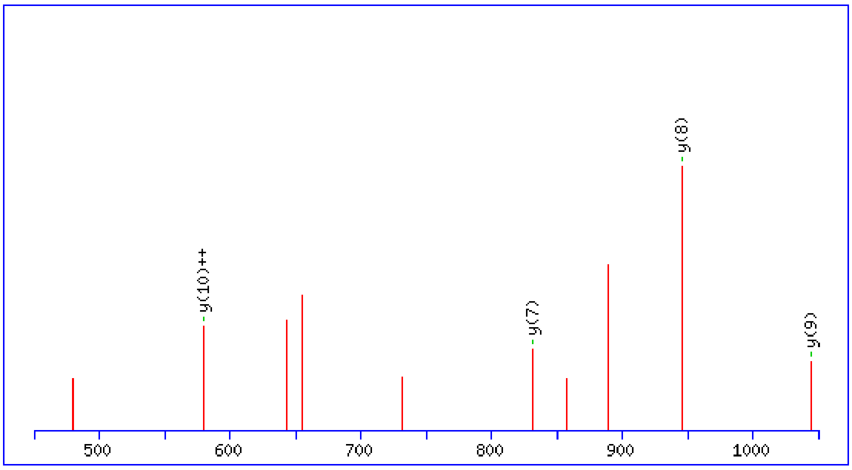
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VALVNYGEDYGK**
Found in **AT2G20450.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L14 (RPL14A) | chr2:8821004-8822152 FORWARD

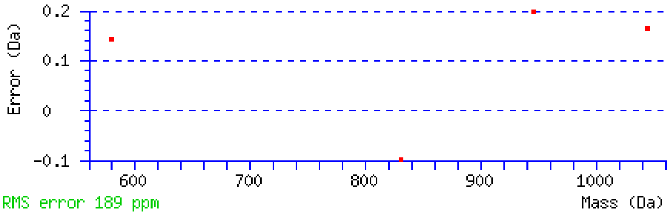
Match to Query 4845: 1326.644214 from(664.329383,2+) index(4270)
Title: Elution from: 40.169 to 40.169 scan no 5389 cid35.00 polarity:+
Data file D6h-1_2.mgf

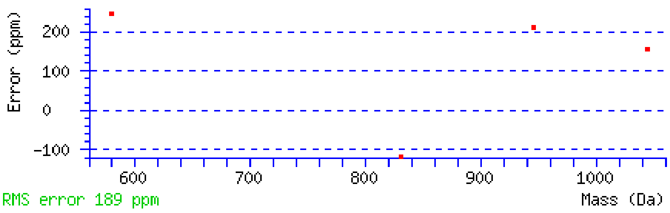
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1326.6456
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.023
Matches : 4/104 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							12
2	171.1128	86.0600					A	1228.5844	614.7959	1211.5579	606.2826	1210.5739	605.7906	11
3	284.1969	142.6021					L	1157.5473	579.2773	1140.5208	570.7640	1139.5368	570.2720	10
4	383.2653	192.1363					V	***1044.4633***	522.7353	1027.4367	514.2220	1026.4527	513.7300	9
5	497.3082	249.1577	480.2817	240.6445			N	***945.3949***	473.2011	928.3683	464.6878	927.3843	464.1958	8
6	660.3715	330.6894	643.3450	322.1761			Y	***831.3519***	416.1796	814.3254	407.6663	813.3414	407.1743	7
7	717.3930	359.2001	700.3665	350.6869			G	668.2886	334.6479	651.2620	326.1347	650.2780	325.6427	6
8	846.4356	423.7214	829.4090	415.2082	828.4250	414.7162	E	611.2671	306.1372	594.2406	297.6239	593.2566	297.1319	5
9	961.4625	481.2349	944.4360	472.7216	943.4520	472.2296	D	482.2245	241.6159	465.1980	233.1026	464.2140	232.6106	4
10	1124.5259	562.7666	1107.4993	554.2533	1106.5153	553.7613	Y	367.1976	184.1024	350.1710	175.5892			3
11	1181.5473	591.2773	1164.5208	582.7640	1163.5368	582.2720	G	204.1343	102.5708	187.1077	94.0575			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VALVNYGEDYGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G20450.1

Score	Mr(calc)	Delta	Sequence
18.8	1326.6456	-0.0014	VALVNYGEDYGK

Mascot: http://www.matrixscience.com/

AT2G20890.1

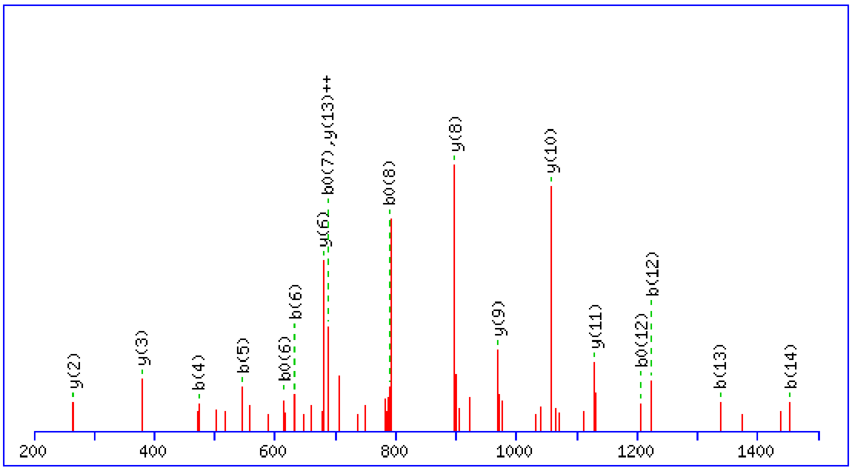
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLELASATDPTVLDK**
Found in **AT2G20890.1** in **TAIR_Arabidopsis**, Symbols: THF1, PSB29 | PSB29 (THYLAKOID FORMATION1) | chr2:8994864-8996266 FORWARD

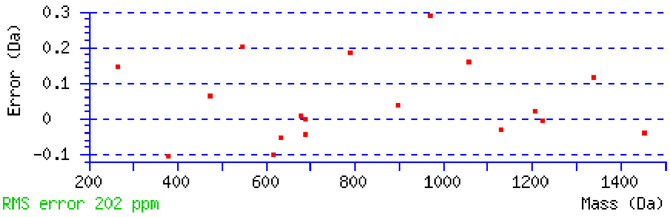
Match to Query 6774: 1600.812370 from(801.413461,2+) index(6950)
Title: Elution from: 62.035 to 62.035 scan no 9127 cid35.00 polarity:+
Data file C7-3_3.mgf

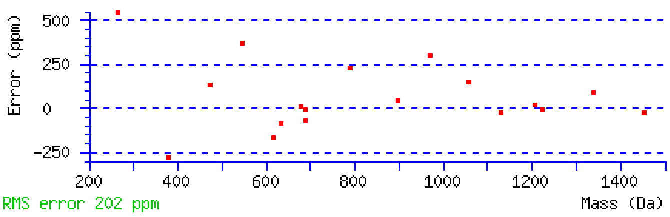
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1600.8136
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 8.7e-006
Matches : 18/134 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			**L**							**15**
2	229.1695	115.0884			**L**	1487.7398	744.3735	1469.7162	735.3617	1469.7292	735.3683	**14**
3	359.2091	180.1082	341.1985	171.1029	**E**	1373.6587	687.3330	1355.6351	678.3212	1355.6481	678.3277	**13**
4	***473.2902***	237.1487	455.2796	228.1435	**L**	1243.6191	622.3132	1225.5955	613.3014	1225.6085	613.3079	**12**
5	***545.3243***	273.1658	527.3138	264.1605	**A**	***1129.5380***	565.2726	1111.5144	556.2608	1111.5274	556.2673	**11**
6	***633.3534***	317.1803	615.3428	308.1751	**S**	***1057.5038***	529.2555	1039.4802	520.2438	1039.4932	520.2503	**10**
7	705.3876	353.1974	687.3770	344.1921	**A**	***969.4748***	485.2410	951.4512	476.2292	951.4642	476.2357	**9**
8	807.4323	404.2198	789.4217	395.2145	**T**	***897.4406***	449.2239	879.4170	440.2121	879.4300	440.2187	**8**
9	923.4563	462.2318	905.4457	453.2265	**D**	795.3959	398.2016	777.3723	389.1898	777.3853	389.1963	**7**
10	1021.5061	511.2567	1003.4955	502.2514	**P**	***679.3719***	340.1896	661.3483	331.1778	661.3613	331.1843	**6**
11	1123.5508	562.2790	1105.5402	553.2737	**T**	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	**5**
12	***1223.6162***	612.3117	1205.6056	603.3065	**V**	479.2774	240.1423	461.2538	231.1305	461.2668	231.1371	**4**
13	***1337.6973***	669.3523	1319.6867	660.3470	**L**	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	**3**
14	***1453.7213***	727.3643	1435.7107	718.3590	**D**	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	**2**
15					**K**	149.1069	75.0571	131.0833	66.0453			**1**





AT2G20890.1

NCBI **BLAST** search of LLELASATDPTVLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.0	1600.8136	-0.0012	LLELASATDPTVLDK
10.7	1600.8136	-0.0012	ELLETITSNLPLDK
7.8	1600.8126	-0.0003	YVLQPFWTRFVK
2.6	1600.8115	0.0008	MKVQRSTFLAVTGK

Mascot: http://www.matrixscience.com/

AT2G20900.1

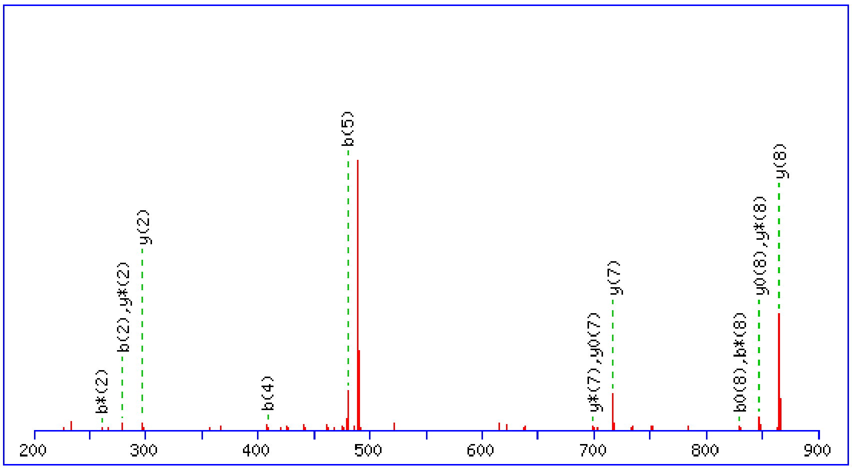
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFGAADTFK**
Found in **AT2G20900.1** in **TAIR_Arabidopsis**, Symbols: | diacylglycerol kinase, putative | chr2:8996493-8999879 REVERSE

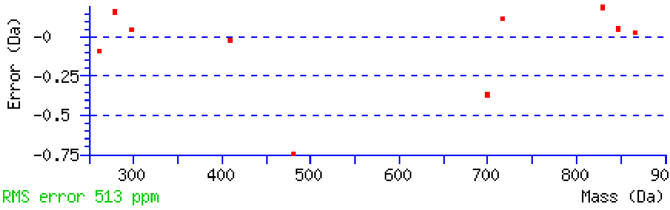
Match to Query 2396: 994.475678 from(498.245115,2+) index(1199)
Title: Elution from: 19.740 to 19.740 scan no 1751 cid35.00 polarity:+
Data file D6h-2_1.mgf

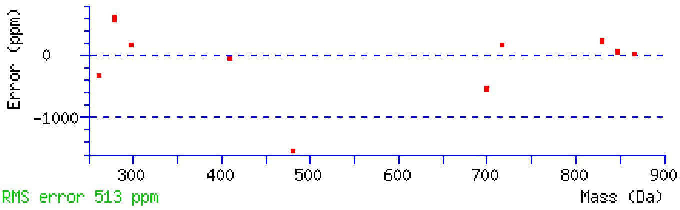
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.4750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.04
Matches : 16/82 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							9
2	***279.1618***	140.0845	261.1382	131.0727			F	**865.3933**	433.2003	847.3697	424.1885	847.3827	424.1950	8
3	337.1803	169.0938	319.1567	160.0820			G	**717.3278**	359.1675	699.3042	350.1558	699.3172	350.1623	7
4	***409.2144***	205.1108	391.1908	196.0990			A	659.3093	330.1583	641.2857	321.1465	641.2987	321.1530	6
5	***481.2486***	241.1279	463.2250	232.1161			A	587.2752	294.1412	569.2516	285.1294	569.2646	285.1359	5
6	597.2725	299.1399	579.2489	290.1281	579.2620	290.1346	D	515.2410	258.1241	497.2174	249.1124	497.2304	249.1189	4
7	***699.3172***	350.1623	681.2937	341.1505	681.3067	341.1570	T	399.2170	200.1122	381.1935	191.1004	381.2065	191.1069	3
8	***847.3827***	424.1950	829.3591	415.1832	829.3721	415.1897	F	**297.1723**	149.0898	279.1487	140.0780			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KFGAADTFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	994.4750	0.0007	KFGAADTFK

AT2G20900.1

19.7	994.4750	0.0007	KFTDAQFK
17.9	994.4750	0.0007	YLSAAGFGAK
13.6	994.4784	-0.0027	KTVAMAYGK
13.4	994.4784	-0.0027	EYAKMAKK
12.5	994.4750	0.0007	KTQADFFK
12.4	994.4777	-0.0020	EFFRQVR
11.7	994.4784	-0.0027	KAKFTDMK
11.6	994.4784	-0.0027	MKGSIFTGK
11.1	994.4784	-0.0027	FIQSKSMK

Mascot: http://www.matrixscience.com/

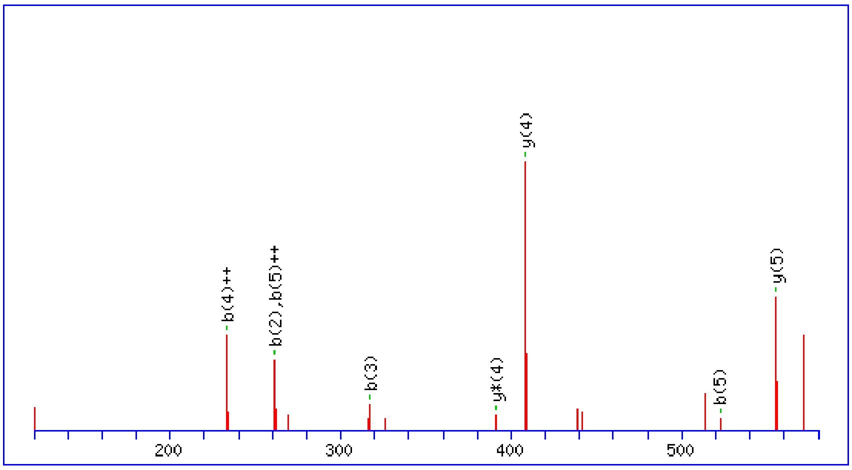
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFGFGK**
Found in **AT2G20960.1** in **TAIR_Arabidopsis**, Symbols: pEARLI4 | pEARLI4 | chr2:9014170-9016692 FORWARD

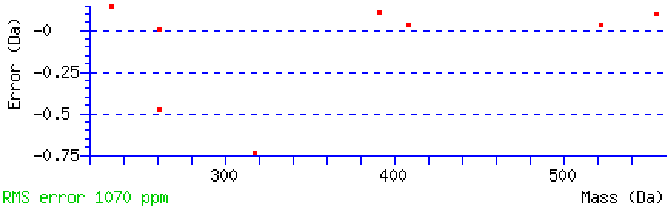
Match to Query 516: 667.369168 from(334.691860,2+) index(3797)
Title: Elution from: 37.098 to 37.098 scan no 4869 cid35.00 polarity:+
Data file D1d-2_3.mgf

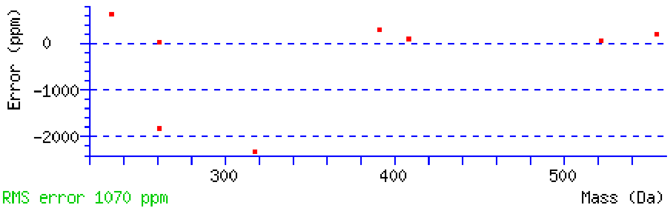
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 667.3694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.024
Matches : 8/30 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.0913	57.5493	L					6
2	***261.1598***	131.0835	F	***555.2926***	278.1499	538.2660	269.6366	5
3	***318.1812***	159.5942	G	***408.2241***	204.6157	391.1976	196.1024	4
4	465.2496	***233.1285***	F	351.2027	176.1050	334.1761	167.5917	3
5	***522.2711***	***261.6392***	G	204.1343	102.5708	187.1077	94.0575	2
6			K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of LFGFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.6	667.3694	-0.0002	LFGFGK
16.6	667.3693	-0.0002	LFFNK
10.8	667.3693	-0.0002	FLFNK
9.3	667.3693	-0.0002	IFNFK

AT2G20960.1

9.3	667.3693	-0.0002	LFNFK
5.2	667.3693	-0.0002	FNFLK
4.5	667.3694	-0.0002	FGIGFK
4.5	667.3694	-0.0002	FGLGFK
0.3	667.3693	-0.0002	FFLNK

AT2G21130.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVVFGQVVEGLDVVK**
Found in **AT2G21130.1** in **TAIR_Arabidopsis**, Symbols: | peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase | chr2:9062700-9063224 REVERSE

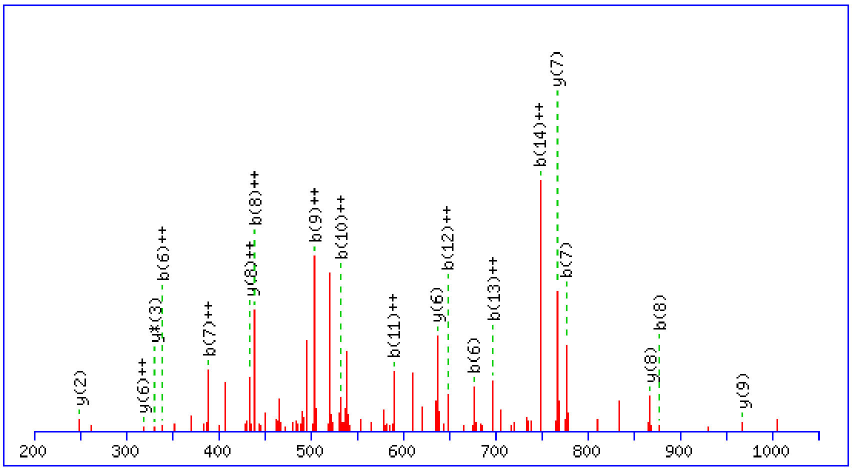
Match to Query 7561: 1642.842684 from(548.621504,3+) index(7462)
Title: Elution from: 66.739 to 66.739 scan no 9821 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

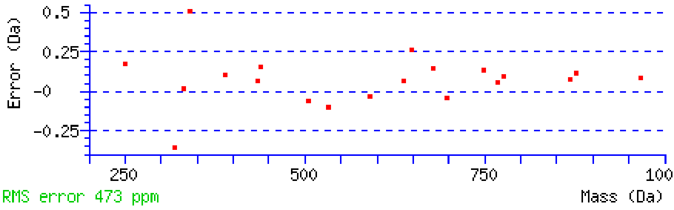
Label all possible matches ○ Label matches used for scoring ●

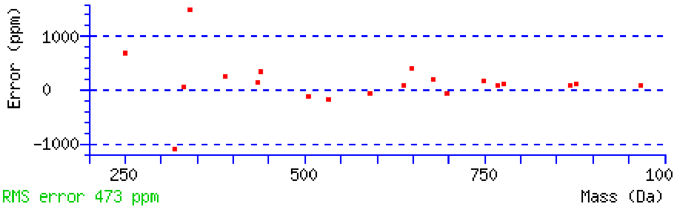
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1642.8421
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.8e-005
Matches : 20/136 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	141.0573	71.0323					**H**							**15**
2	241.1227	121.0650					**V**	1503.7994	752.4033	1485.7758	743.3915	1485.7888	743.3980	**14**
3	341.1882	171.0977					**V**	1403.7339	702.3706	1385.7103	693.3588	1385.7234	693.3653	**13**
4	489.2536	245.1305					**F**	1303.6685	652.3379	1285.6449	643.3261	1285.6579	643.3326	**12**
5	547.2721	274.1397					**G**	1155.6030	578.3051	1137.5794	569.2934	1137.5925	569.2999	**11**
6	**677.3248**	***339.1660***	659.3012	330.1542			**Q**	1097.5845	549.2959	1079.5609	540.2841	1079.5740	540.2906	**10**
7	**777.3902**	***389.1988***	759.3667	380.1870			**V**	**967.5319**	484.2696	949.5083	475.2578	949.5213	475.2643	**9**
8	**877.4557**	***439.2315***	859.4321	430.2197			**V**	**867.4664**	434.2369	849.4428	425.2251	849.4559	425.2316	**8**
9	1007.4953	***504.2513***	989.4717	495.2395	989.4847	495.2460	**E**	**767.4010**	384.2041	749.3774	375.1923	749.3904	375.1988	**7**
10	1065.5138	***533.2605***	1047.4902	524.2488	1047.5032	524.2553	**G**	**637.3613**	319.1843	619.3378	310.1725	619.3508	310.1790	**6**
11	1179.5949	***590.3011***	1161.5713	581.2893	1161.5843	581.2958	**L**	579.3428	290.1751	561.3193	281.1633	561.3323	281.1698	**5**
12	1295.6189	***648.3131***	1277.5953	639.3013	1277.6083	639.3078	**D**	465.2617	233.1345	447.2382	224.1227	447.2512	224.1292	**4**
13	1395.6843	***698.3458***	1377.6608	689.3340	1377.6738	689.3405	**V**	349.2378	175.1225	331.2142	166.1107			**3**
14	1495.7498	***748.3785***	1477.7262	739.3667	1477.7392	739.3732	**V**	**249.1723**	125.0898	231.1487	116.0780			**2**
15							**K**	149.1069	75.0571	131.0833	66.0453			**1**





AT2G21130.1

NCBI **BLAST** search of HVVFGQVVEGLDVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.7	1642.8421	0.0006	HVVFGQVVEGLDVVK
13.6	1642.8421	0.0006	EHVVWTDEKLKLK
6.8	1642.8398	0.0028	VIQKALDVIEPDQR
0.5	1642.8399	0.0028	ELESHIRLIKEEK

AT2G21170.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVIGEKDEFIGKK**
Found in **AT2G21170.1** in **TAIR_Arabidopsis**, Symbols: TIM | TIM (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr2:9078128-9080187 REVERSE

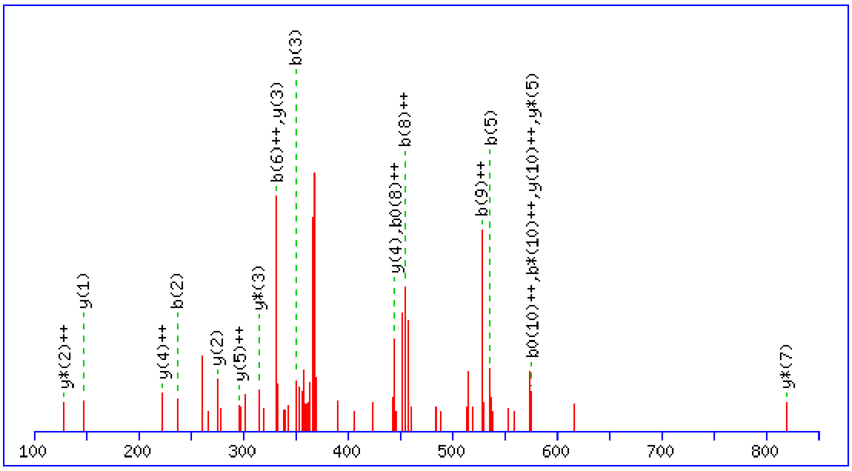
Match to Query 6029: 1498.814748 from(375.710963,4+) index(919)
Title: Elution from: 13.624 to 13.624 scan no 1263 cid35.00 polarity:+
Data file D12h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 850 Da Full range

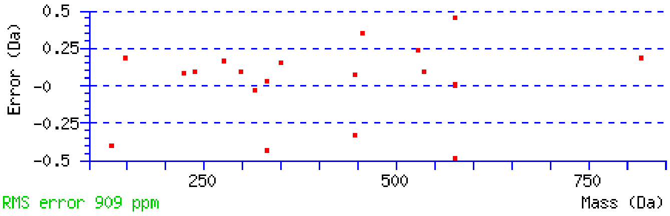
Label all possible matches ○ Label matches used for scoring ●

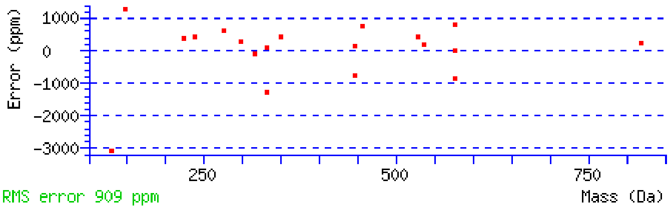
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1498.8144
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.04
Matches : 20/116 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					**H**							**13**
2	***237.1346***	119.0709					**V**	1362.7627	681.8850	1345.7362	673.3717	1344.7522	672.8797	**12**
3	***350.2187***	175.6130					**I**	1263.6943	632.3508	1246.6678	623.8375	1245.6838	623.3455	**11**
4	407.2401	204.1237					**G**	1150.6103	575.8088	1133.5837	567.2955	1132.5997	566.8035	**10**
5	***536.2827***	268.6450			518.2722	259.6397	**E**	1093.5888	547.2980	1076.5623	538.7848	1075.5782	538.2928	**9**
6	664.3777	**332.6925**	647.3511	324.1792	646.3671	323.6872	**K**	964.5462	482.7767	947.5197	474.2635	946.5356	473.7715	**8**
7	779.4046	390.2060	762.3781	381.6927	761.3941	381.2007	**D**	836.4512	418.7293	819.4247	410.2160	818.4407	409.7240	**7**
8	908.4472	**454.7272**	891.4207	446.2140	890.4367	445.7220	**E**	721.4243	361.2158	704.3978	352.7025	703.4137	352.2105	**6**
9	1055.5156	**528.2615**	1038.4891	519.7482	1037.5051	519.2562	**F**	592.3817	296.6945	575.3552	288.1812			**5**
10	1168.5997	584.8035	1151.5732	576.2902	1150.5891	575.7982	**I**	***445.3133***	223.1603	428.2867	214.6470			**4**
11	1225.6212	613.3142	1208.5946	604.8009	1207.6106	604.3089	**G**	***332.2292***	166.6183	315.2027	158.1050			**3**
12	1353.7161	677.3617	1336.6896	668.8484	1335.7056	668.3564	**K**	***275.2078***	138.1075	258.1812	129.5942			**2**
13							**K**	***147.1128***	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of HVIGEKDEFIGKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G21170.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.6	1498.8144	0.0004	HVIGEKDEFIGKK
11.7	1498.8105	0.0042	MLAIFVVFLDSTK
3.3	1498.8184	-0.0036	QVAEFFEFVKKK
0.9	1498.8143	0.0004	ILREIDWEALNK

AT2G21250.1

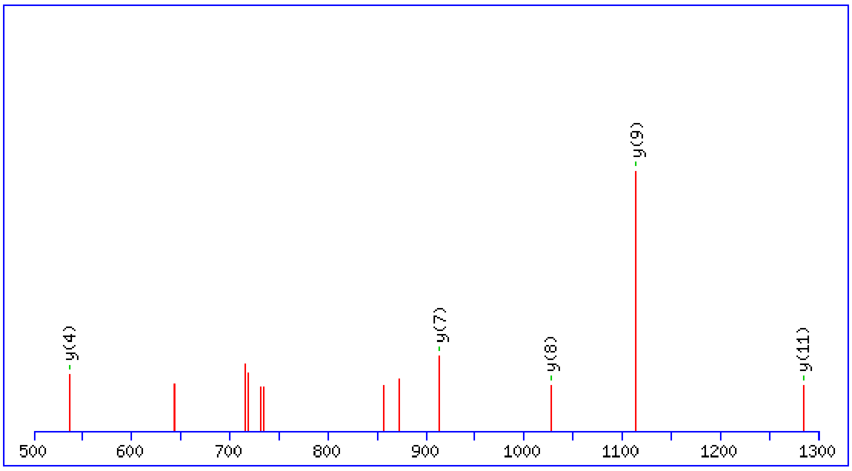
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIGISNYDVFLTR**
Found in **AT2G21250.1** in **TAIR_Arabidopsis**, Symbols: | mannose 6-phosphate reductase (NADPH-dependent), putative | chr2:9110489-9112197 REVERSE

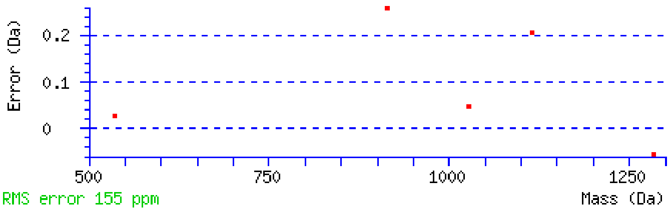
Match to Query 6368: 1483.766546 from(742.890549,2+) index(8897)
Title: Elution from: 79.745 to 79.745 scan no 11893 cid35.00 polarity:+
Data file D12h-3_1.mgf

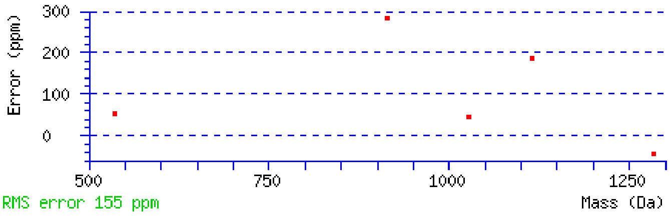
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1483.7671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00026
Matches : 5/132 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	201.1234	101.0653			183.1128	92.0600	I	1397.7423	699.3748	1380.7158	690.8615	1379.7318	690.3695	12
3	258.1448	129.5761			240.1343	120.5708	G	***1284.6583***	642.8328	1267.6317	634.3195	1266.6477	633.8275	11
4	371.2289	186.1181			353.2183	177.1128	I	1227.6368	614.3220	1210.6103	605.8088	1209.6262	605.3168	10
5	458.2609	229.6341			440.2504	220.6288	S	***1114.5527***	557.7800	1097.5262	549.2667	1096.5422	548.7747	9
6	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	N	***1027.5207***	514.2640	1010.4942	505.7507	1009.5102	505.2587	8
7	735.3672	368.1872	718.3406	359.6740	717.3566	359.1819	Y	***913.4778***	457.2425	896.4512	448.7293	895.4672	448.2373	7
8	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	D	750.4145	375.7109	733.3879	367.1976	732.4039	366.7056	6
9	949.4625	475.2349	932.4360	466.7216	931.4520	466.2296	V	635.3875	318.1974	618.3610	309.6841	617.3770	309.1921	5
10	1096.5310	548.7691	1079.5044	540.2558	1078.5204	539.7638	F	***536.3191***	268.6632	519.2926	260.1499	518.3085	259.6579	4
11	1209.6150	605.3111	1192.5885	596.7979	1191.6044	596.3059	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
12	1310.6627	655.8350	1293.6361	647.3217	1292.6521	646.8297	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SIGISNYDVFLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G21250.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.8	1483.7671	-0.0005	SIGISNYDVFLTR
2.0	1483.7704	-0.0039	CIELVEEKLKSH

Mascot: http://www.matrixscience.com/

AT2G21330.1

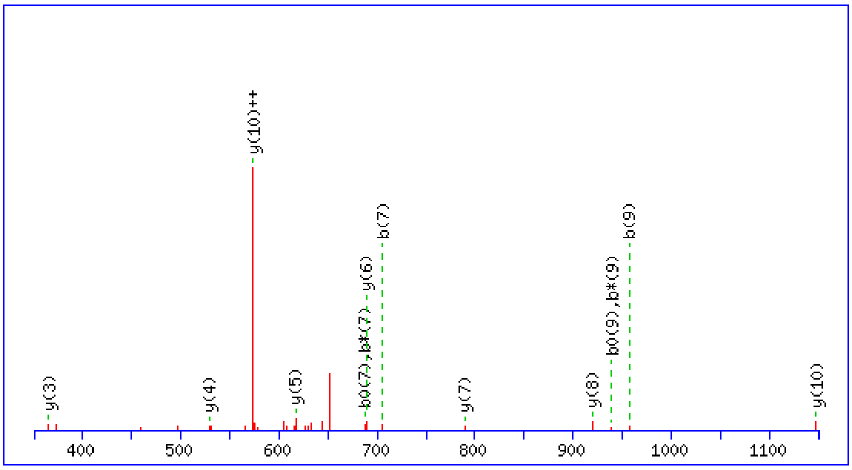
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATPEQVASYTLK**
Found in **AT2G21330.1** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr2:9135497-9137233 REVERSE

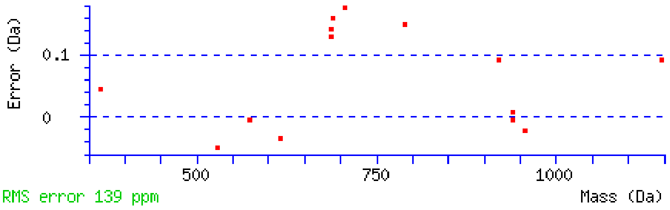
Match to Query 5240: 1320.638190 from(661.326371,2+) index(4505)
Title: Elution from: 41.637 to 41.637 scan no 5601 cid35.00 polarity:+
Data file 0-1_1.mgf

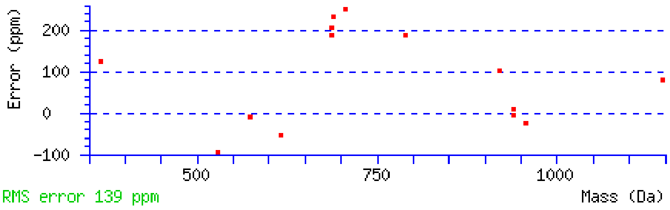
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.6354
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 2.3e-005
Matches : 14/118 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244					A							12
2	175.0861	88.0467			157.0756	79.0414	T	1249.6085	625.3079	1231.5849	616.2961	1231.5979	616.3026	11
3	273.1359	137.0716			255.1254	128.0663	P	***1147.5638***	574.2855	1129.5402	565.2737	1129.5532	565.2802	10
4	403.1756	202.0914			385.1650	193.0861	E	1049.5140	525.2606	1031.4904	516.2488	1031.5034	516.2553	9
5	533.2282	267.1177	515.2046	258.1060	515.2176	258.1125	Q	***919.4744***	460.2408	901.4508	451.2290	901.4638	451.2355	8
6	633.2937	317.1505	615.2701	308.1387	615.2831	308.1452	V	***789.4217***	395.2145	771.3981	386.2027	771.4111	386.2092	7
7	**705.3278**	353.1675	687.3042	344.1558	687.3172	344.1623	A	***689.3563***	345.1818	671.3327	336.1700	671.3457	336.1765	6
8	793.3569	397.1821	775.3333	388.1703	775.3463	388.1768	S	***617.3221***	309.1647	599.2985	300.1529	599.3115	300.1594	5
9	**957.4172**	479.2123	939.3937	470.2005	939.4067	470.2070	Y	***529.2931***	265.1502	511.2695	256.1384	511.2825	256.1449	4
10	1059.4620	530.2346	1041.4384	521.2228	1041.4514	521.2293	T	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
11	1173.5430	587.2752	1155.5195	578.2634	1155.5325	578.2699	L	263.1880	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ATPEQVASYTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G21330.1

Score	Mr(calc)	Delta	Sequence
57.2	1320.6354	0.0028	ATPEQVASYTLK
0.0	1320.6380	0.0001	QLNPDISKAYR

AT2G21510.1

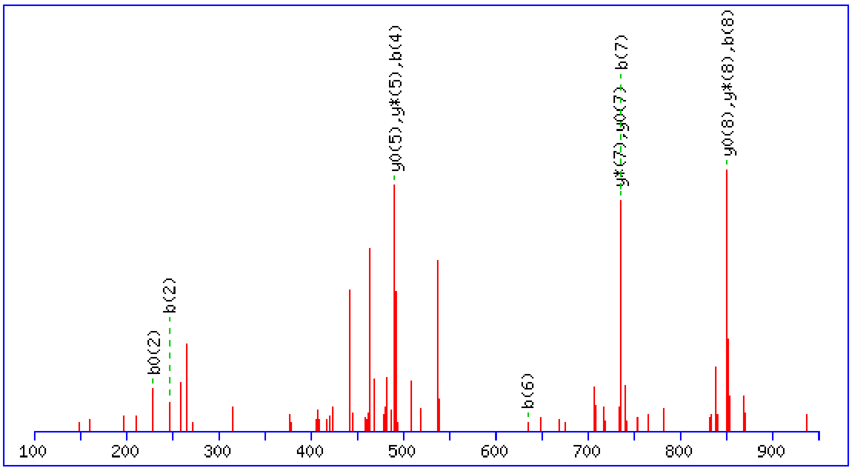
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDKLAATLK**
Found in **AT2G21510.1** in **TAIR_Arabidopsis**, Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:9217921-9219779 REVERSE

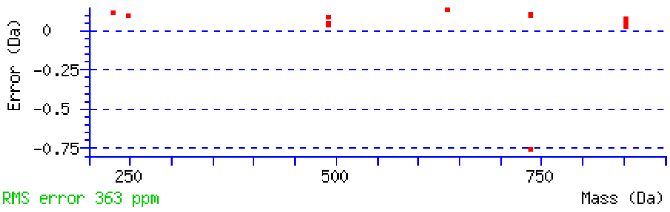
Match to Query 2441: 998.527936 from(500.271244,2+) index(1237)
Title: Elution from: 19.152 to 19.152 scan no 1764 cid35.00 polarity:+
Data file 0-1_2.mgf

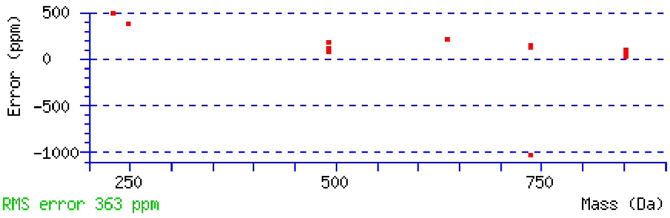
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 998.5274
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.038
Matches : 12/88 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							9
2	***247.0709***	124.0391			229.0603	115.0338	D	869.4951	435.2512	851.4715	426.2394	851.4845	426.2459	8
3	377.1599	189.0836	359.1363	180.0718	359.1494	180.0783	K	753.4711	377.2392	735.4475	368.2274	735.4606	368.2339	7
4	***491.2410***	246.1241	473.2174	237.1124	473.2304	237.1189	L	623.3821	312.1947	605.3585	303.1829	605.3715	303.1894	6
5	563.2752	282.1412	545.2516	273.1294	545.2646	273.1359	A	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	5
6	***635.3093***	318.1583	617.2857	309.1465	617.2987	309.1530	A	437.2668	219.1371	419.2433	210.1253	419.2563	210.1318	4
7	***737.3540***	369.1807	719.3304	360.1689	719.3435	360.1754	T	365.2327	183.1200	347.2091	174.1082	347.2221	174.1147	3
8	***851.4351***	426.2212	833.4115	417.2094	833.4246	417.2159	L	263.1880	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EDKLAATLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G21510.1

24.5	998.5274	0.0005	EDKLAATLK
19.3	998.5301	-0.0022	AGVVRELGGK
15.2	998.5301	-0.0022	RDLAQAAIK
12.3	998.5275	0.0005	IAASELSGLK
12.3	998.5301	-0.0022	DKDVKPRK
11.8	998.5274	0.0005	LLATISQDK
11.8	998.5301	-0.0022	LLDLRNNK
10.2	998.5297	-0.0017	AAITEFLPK
8.9	998.5283	-0.0004	MMKLQPIK
7.7	998.5275	0.0005	EIANLTSIK

AT2G21530.1

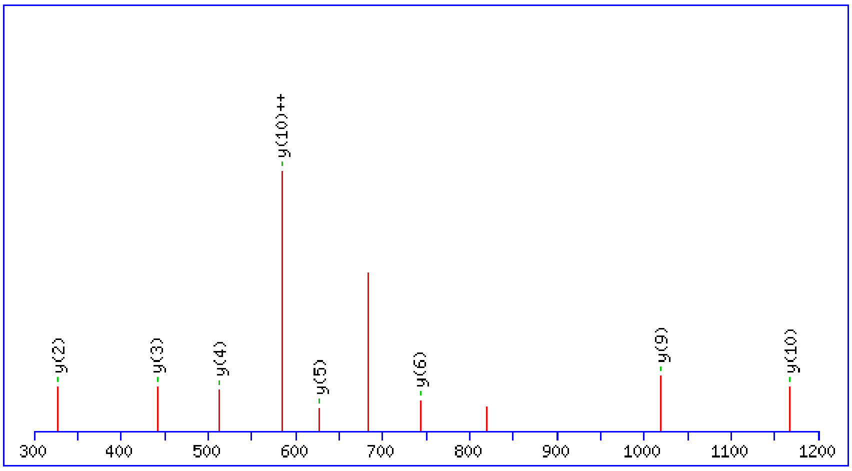
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITFGDTNLAIFR**
Found in **AT2G21530.1** in **TAIR_Arabidopsis**, Symbols: | forkhead-associated domain-containing protein / FHA domain-containing protein | chr2:9226452-9227544 FORWARD

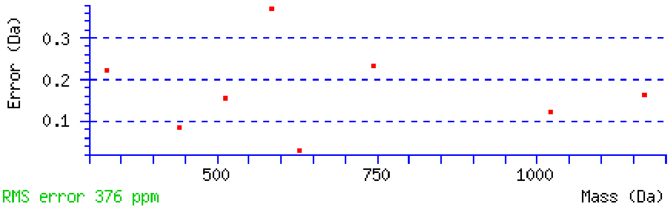
Match to Query 5349: 1382.677886 from(692.346219,2+) index(9080)
Title: Elution from: 81.080 to 81.080 scan no 12206 cid35.00 polarity:+
Data file D12h-1_2.mgf

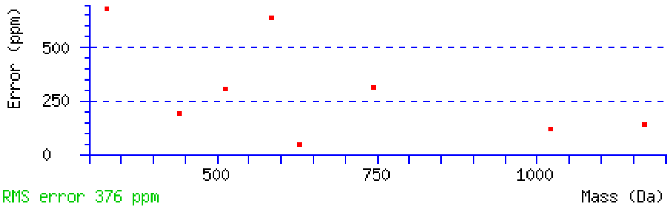
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.6770
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 3.5e-006
Matches : 8/106 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**I**							**12**
2	217.1331	109.0702			199.1225	100.0649	**T**	1269.6032	635.3053	1251.5797	626.2935	1251.5927	626.3000	**11**
3	365.1985	183.1029			347.1880	174.0976	**F**	***1167.5585***	584.2829	1149.5349	575.2711	1149.5480	575.2776	**10**
4	423.2170	212.1122			405.2065	203.1069	**G**	***1019.4931***	510.2502	1001.4695	501.2384	1001.4825	501.2449	**9**
5	539.2410	270.1241			521.2304	261.1189	**D**	961.4746	481.2409	943.4510	472.2291	943.4640	472.2356	**8**
6	641.2857	321.1465			623.2752	312.1412	**T**	845.4506	423.2289	827.4270	414.2171	827.4400	414.2237	**7**
7	757.3227	379.1650	739.2991	370.1532	739.3122	370.1597	**N**	***743.4059***	372.2066	725.3823	363.1948			**6**
8	871.4038	436.2055	853.3802	427.1938	853.3933	427.2003	**L**	***627.3689***	314.1881	609.3453	305.1763			**5**
9	943.4380	472.2226	925.4144	463.2108	925.4274	463.2173	**A**	***513.2878***	257.1475	495.2642	248.1357			**4**
10	1057.5191	529.2632	1039.4955	520.2514	1039.5085	520.2579	**I**	***441.2536***	221.1305	423.2301	212.1187			**3**
11	1205.5845	603.2959	1187.5609	594.2841	1187.5740	594.2906	**F**	***327.1725***	164.0899	309.1490	155.0781			**2**
12							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of ITFGDTNLAIFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G21530.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.5	1382.6770	0.0009	ITFGDTNLAIFR
22.3	1382.6793	-0.0014	FFAAAASGSWILK
10.2	1382.6793	-0.0014	TFIDSWIFIAR
6.0	1382.6744	0.0035	TIFLFGSEEISK
4.3	1382.6748	0.0031	LTDSKGRTVDFK
3.9	1382.6748	0.0031	LQSDRSTATLFK
2.9	1382.6748	0.0031	TPYSRTILSNSK
2.1	1382.6775	0.0004	LIIRSHEGPDAR
1.5	1382.6804	-0.0025	VFMDIGRVSSIK
0.9	1382.6771	0.0008	QPALKSPSPWEK

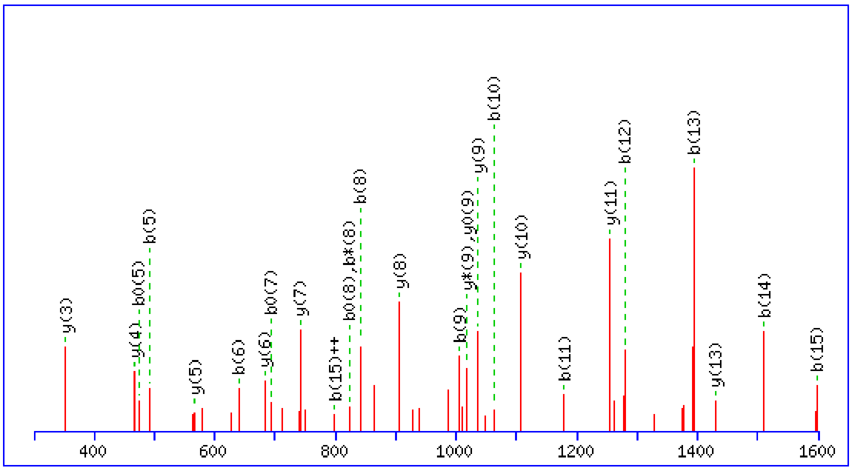
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALETAFAQYGDVIDSK**
Found in **AT2G21660.1** in **TAIR_Arabidopsis**, Symbols: GR-RBP7, GRP7, CCR2, ATGRP7 | ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding | chr2:9272557-9273396 REVERSE

Match to Query 8451: 1744.792564 from(873.403558,2+) index(8123)
Title: Elution from: 71.635 to 71.635 scan no 10667 cid35.00 polarity:+
Data file D6h-3_1.mgf

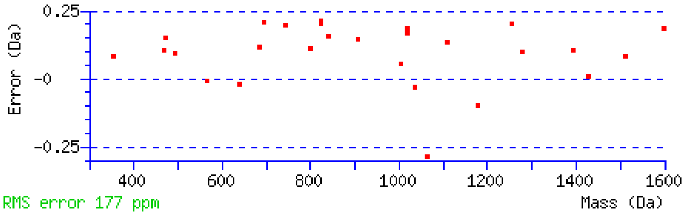
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

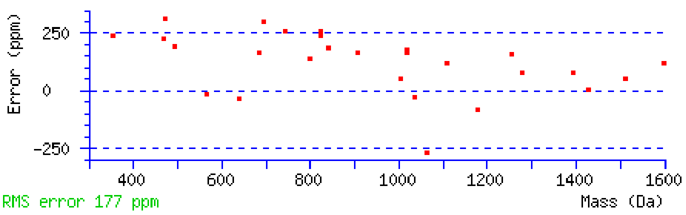


Monoisotopic mass of neutral peptide Mr(calc): 1744.7880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 1.4e-010
Matches : 27/160 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							16
2	187.1225	94.0649					L	1673.7611	837.3842	1655.7376	828.3724	1655.7506	828.3789	15
3	317.1622	159.0847			299.1516	150.0794	E	1559.6800	780.3437	1541.6565	771.3319	1541.6695	771.3384	14
4	419.2069	210.1071			401.1963	201.1018	T	***1429.6404***	715.3238	1411.6168	706.3121	1411.6298	706.3186	13
5	***491.2410***	246.1241			473.2304	237.1189	A	1327.5957	664.3015	1309.5721	655.2897	1309.5851	655.2962	12
6	***639.3065***	320.1569			621.2959	311.1516	F	***1255.5615***	628.2844	1237.5380	619.2726	1237.5510	619.2791	11
7	711.3406	356.1739			693.3300	347.1687	A	***1107.4961***	554.2517	1089.4725	545.2399	1089.4855	545.2464	10
8	***841.3933***	421.2003	823.3697	412.1885	823.3827	412.1950	Q	***1035.4620***	518.2346	1017.4384	509.2228	1017.4514	509.2293	9
9	***1005.4536***	503.2304	987.4300	494.2187	987.4431	494.2252	Y	***905.4093***	453.2083	887.3857	444.1965	887.3987	444.2030	8
10	***1063.4721***	532.2397	1045.4485	523.2279	1045.4616	523.2344	G	***741.3489***	371.1781	723.3254	362.1663	723.3384	362.1728	7
11	***1179.4961***	590.2517	1161.4725	581.2399	1161.4855	581.2464	D	***683.3304***	342.1689	665.3069	333.1571	665.3199	333.1636	6
12	***1279.5615***	640.2844	1261.5380	631.2726	1261.5510	631.2791	V	***567.3065***	284.1569	549.2829	275.1451	549.2959	275.1516	5
13	***1393.6426***	697.3250	1375.6191	688.3132	1375.6321	688.3197	I	***467.2410***	234.1241	449.2174	225.1124	449.2304	225.1189	4
14	***1509.6666***	755.3370	1491.6430	746.3252	1491.6561	746.3317	D	***353.1599***	177.0836	335.1363	168.0718	335.1493	168.0783	3
15	***1597.6957***	799.3515	1579.6721	790.3397	1579.6851	790.3462	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT2G21660.1





NCBI **BLAST** search of ALETAFAQYGDVIDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.0	1744.7880	0.0046	ALETAFAQYGDVIDSK
13.0	1744.7892	0.0034	NKSSTITTPSTVMESK
7.1	1744.7893	0.0033	VMGSSLRGMSKQEWK
4.4	1744.7941	-0.0015	MSVVENFSSEPKAKR
0.4	1744.7945	-0.0019	TQRQMRTLDISNNK

Mascot: http://www.matrixscience.com/

AT2G21870.1

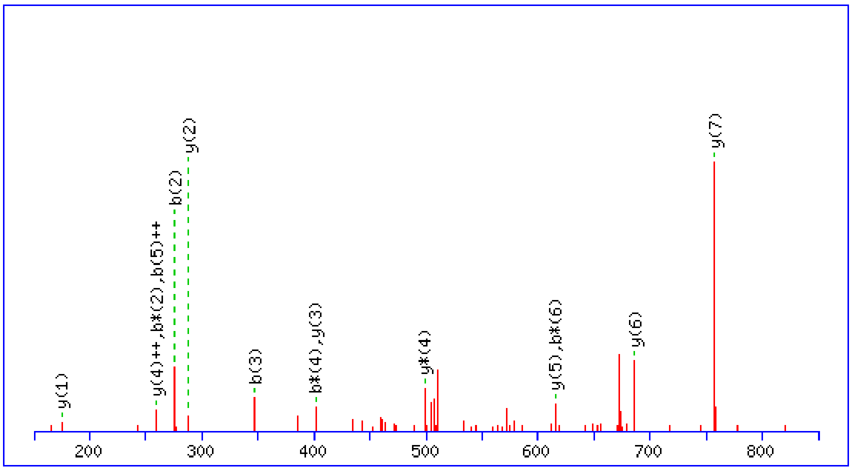
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQAAVDILR**
Found in **AT2G21870.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Probable ATP synthase 24 kDa subunit, mitochondrial precursor [Arabidopsis Thaliana] (GB:Q9SJ12;GB:Q8LBN3); similar to unnamed protein product [Vitis vinifera] (GB:CAO71749.1) | chr2:9327536-9329698 REVERSE

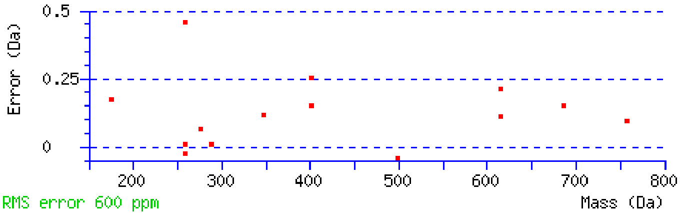
Match to Query 2597: 1031.576468 from(516.795510,2+) index(5590)
Title: Elution from: 49.296 to 49.296 scan no 7096 cid35.00 polarity:+
Data file 0-3_3.mgf

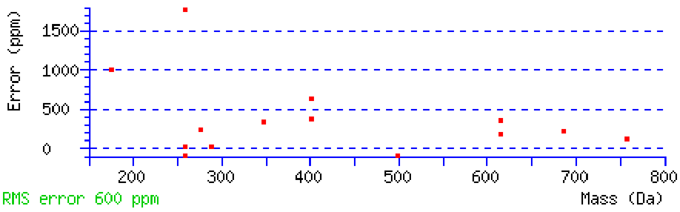
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1031.5764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0004
Matches : 14/78 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							9
2	**276.1343**	138.5708	259.1077	130.0575			Q	885.5152	443.2613	868.4887	434.7480	867.5047	434.2560	8
3	**347.1714**	174.0893	330.1448	165.5761			A	***757.4567***	379.2320	740.4301	370.7187	739.4461	370.2267	7
4	418.2085	209.6079	401.1819	201.0946			A	***686.4196***	343.7134	669.3930	335.2001	668.4090	334.7081	6
5	517.2769	259.1421	500.2504	250.6288			V	***615.3824***	308.1949	598.3559	299.6816	597.3719	299.1896	5
6	632.3039	316.6556	615.2773	308.1423	614.2933	307.6503	D	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
7	745.3879	373.1976	728.3614	364.6843	727.3774	364.1923	I	***401.2871***	201.1472	384.2605	192.6339			3
8	858.4720	429.7396	841.4454	421.2264	840.4614	420.7343	L	***288.2030***	144.6051	271.1765	136.0919			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FQAAVDILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G21870.1

38.5	1031.5764	0.0001	FQAAVDILR

Mascot: http://www.matrixscience.com/

AT2G22140.1

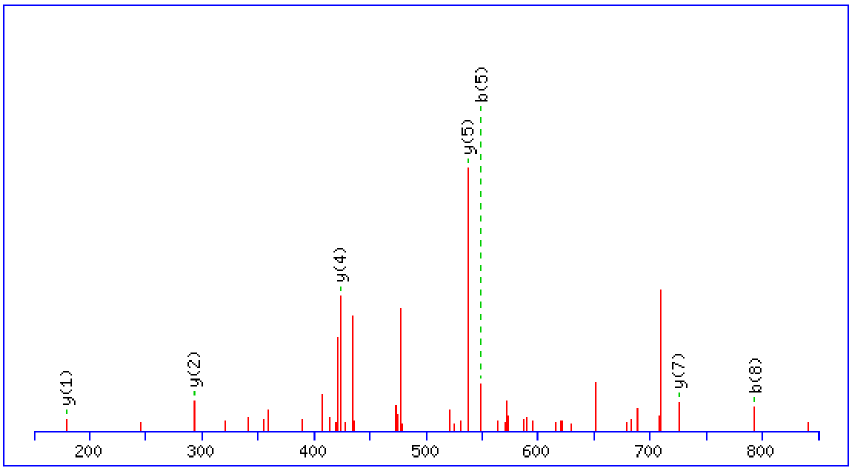
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NESVLAGLR**
Found in **AT2G22140.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G21800.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71735.1) | chr2:9421975-9425664 REVERSE

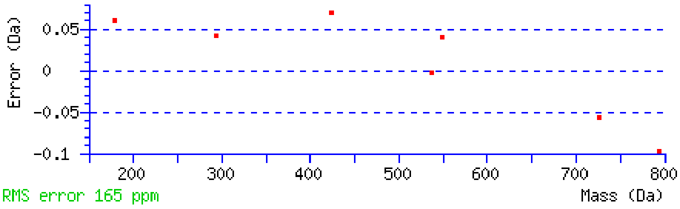
Match to Query 2087: 970.483392 from(486.248972,2+) index(5786)
Title: Elution from: 50.868 to 50.868 scan no 7359 cid35.00 polarity:+
Data file 0-3_3.mgf

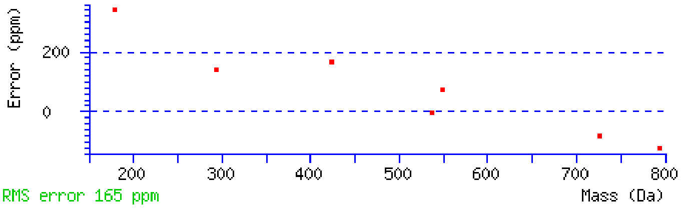
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 970.4858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0077
Matches : 7/82 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	247.0839	124.0456	229.0603	115.0338	229.0733	115.0403	E	855.4561	428.2317	837.4325	419.2199	837.4455	419.2264	8
3	335.1130	168.0601	317.0894	159.0483	317.1024	159.0548	S	***725.4165***	363.2119	707.3929	354.2001	707.4059	354.2066	7
4	435.1784	218.0928	417.1548	209.0811	417.1678	209.0876	V	637.3874	319.1973	619.3638	310.1855			6
5	**549.2595**	275.1334	531.2359	266.1216	531.2489	266.1281	L	***537.3219***	269.1646	519.2984	260.1528			5
6	621.2937	311.1505	603.2701	302.1387	603.2831	302.1452	A	***423.2408***	212.1241	405.2173	203.1123			4
7	679.3122	340.1597	661.2886	331.1479	661.3016	331.1544	G	351.2067	176.1070	333.1831	167.0952			3
8	**793.3933**	397.2003	775.3697	388.1885	775.3827	388.1950	L	***293.1882***	147.0977	275.1646	138.0859			2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NESVLAGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G22140.1

32.2	970.4858	-0.0024	NESVLAGLR
16.7	970.4858	-0.0024	LKEGNEIR
16.5	970.4858	-0.0024	ELKNGLER
10.6	970.4858	-0.0024	QLDLISNR
10.4	970.4858	-0.0024	QAVEDIKR
10.0	970.4831	0.0003	EIDSSLLGK
9.7	970.4858	-0.0024	QIIEKDGR
9.3	970.4810	0.0023	HMRVTGLK
9.0	970.4811	0.0023	HKMEKLR
9.0	970.4858	-0.0024	LTNNVELR

AT2G22170.1

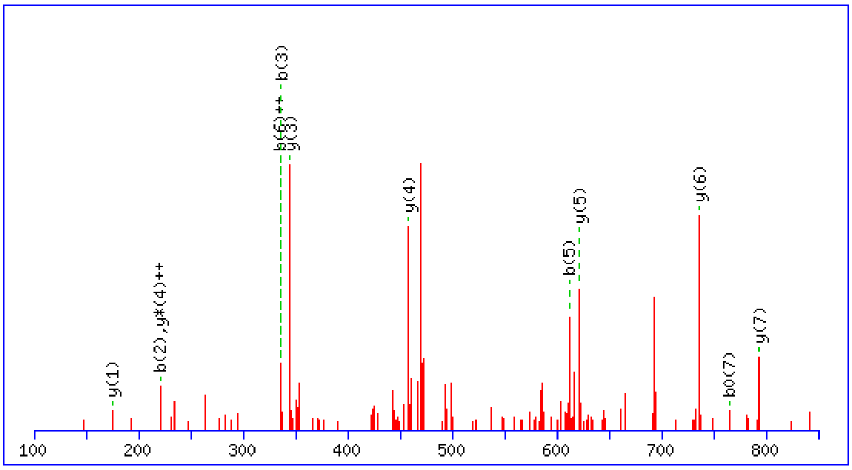
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGDYIGIR**
Found in **AT2G22170.1** in **TAIR_Arabidopsis**, Symbols: | lipid-associated family protein | chr2:9434090-9434822 REVERSE

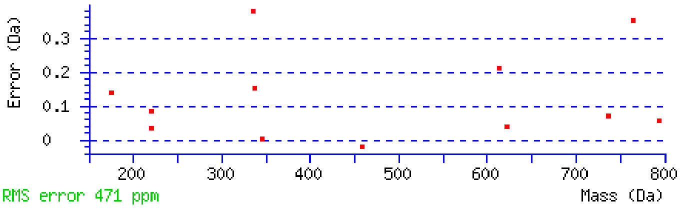
Match to Query 1777: 955.475280 from(478.744916,2+) index(3560)
Title: Elution from: 37.437 to 37.437 scan no 4579 cid35.00 polarity:+
Data file D1d-1_1.mgf

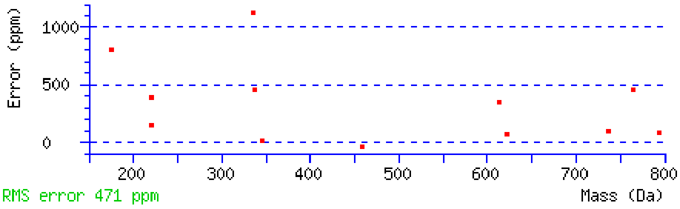
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 955.4763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00015
Matches : 12/56 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							8
2	**221.0921**	111.0497			G	***793.4203***	397.2138	776.3937	388.7005	775.4097	388.2085	7
3	**336.1190**	168.5631	318.1084	159.5579	D	***736.3988***	368.7030	719.3723	360.1898	718.3883	359.6978	6
4	499.1823	250.0948	481.1718	241.0895	Y	***621.3719***	311.1896	604.3453	302.6763			5
5	**612.2664**	306.6368	594.2558	297.6316	I	***458.3085***	229.6579	441.2820	221.1446			4
6	669.2879	335.1476	651.2773	326.1423	G	***345.2245***	173.1159	328.1979	164.6026			3
7	782.3719	391.6896	764.3614	382.6843	I	288.2030	144.6051	271.1765	136.0919			2
8					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YGDYIGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.4	955.4763	-0.0010	YGDYIGIR
4.5	955.4763	-0.0010	YVPAYSTR

AT2G22170.1

1.8	955.4763	-0.0011	YVDGISFR
1.6	955.4763	-0.0010	DYYINIR

Mascot: http://www.matrixscience.com/

AT2G22230.1

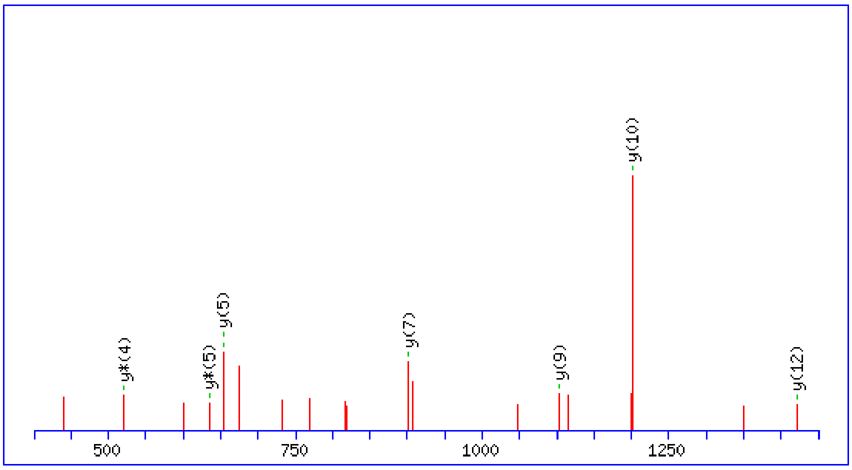
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPAFPTVMDINQIR**
Found in **AT2G22230.1** in **TAIR_Arabidopsis**, Symbols: | beta-hydroxyacyl-ACP dehydratase, putative | chr2:9457122-9458507 FORWARD

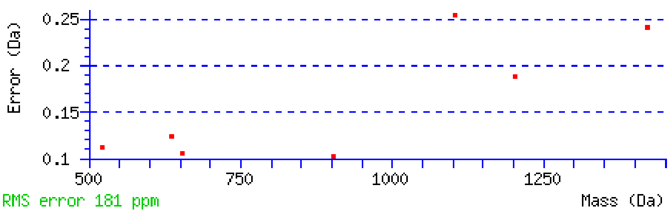
Match to Query 7826: 1666.786846 from(834.400699,2+) index(9923)
Title: Elution from: 91.016 to 91.016 scan no 13783 cid35.00 polarity:+
Data file C7-1_2.mgf

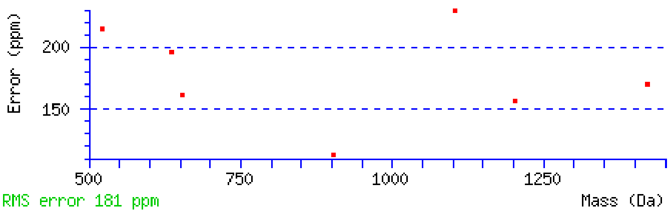
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1666.7879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0011
Matches : 7/116 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					F							14
2	247.1225	124.0649					P	1519.7298	760.3685	1501.7062	751.3567	1501.7192	751.3633	13
3	319.1567	160.0820					A	***1421.6800***	711.3436	1403.6564	702.3318	1403.6694	702.3384	12
4	467.2221	234.1147					F	1349.6458	675.3266	1331.6223	666.3148	1331.6353	666.3213	11
5	565.2719	283.1396					P	***1201.5804***	601.2938	1183.5568	592.2820	1183.5698	592.2886	10
6	667.3166	334.1620			649.3061	325.1567	T	***1103.5306***	552.2689	1085.5070	543.2571	1085.5200	543.2637	9
7	767.3821	384.1947			749.3715	375.1894	V	1001.4859	501.2466	983.4623	492.2348	983.4753	492.2413	8
8	899.4196	450.2134			881.4090	441.2082	M	***901.4204***	451.2139	883.3968	442.2021	883.4099	442.2086	7
9	1015.4436	508.2254			997.4330	499.2201	D	769.3829	385.1951	751.3593	376.1833	751.3723	376.1898	6
10	1129.5247	565.2660			1111.5141	556.2607	I	***653.3589***	327.1831	635.3353	318.1713			5
11	1245.5617	623.2845	1227.5381	614.2727	1227.5511	614.2792	N	539.2778	270.1426	521.2543	261.1308			4
12	1375.6143	688.3108	1357.5907	679.2990	1357.6038	679.3055	Q	423.2408	212.1241	405.2173	203.1123			3
13	1489.6954	745.3513	1471.6718	736.3396	1471.6849	736.3461	I	293.1882	147.0977	275.1646	138.0859			2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FPAFPTVMDINQIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G22230.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.7	1666.7879	-0.0011	FPAFPTVMDINQIR
2.3	1666.7882	-0.0014	SDLKDLREVSTAEGK
1.1	1666.7909	-0.0040	AGTTPLSVTRNSANQK

AT2G22330.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDTLASNSSDLTTK**
Found in **AT2G22330.1** in **TAIR_Arabidopsis**, Symbols: CYP79B3 | CYP79B3 (cytochrome P450, family 79, subfamily B, polypeptide 3); oxygen binding | chr2:9495681-9498063 FORWARD

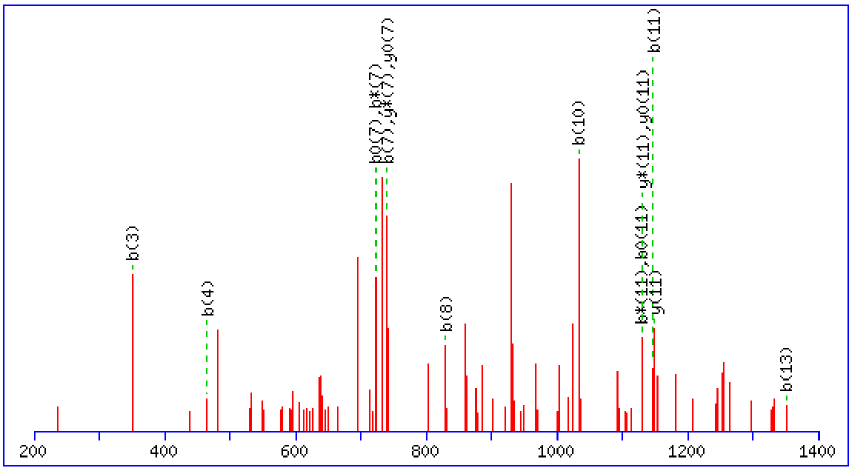
Match to Query 6178: 1498.639920 from(750.327236,2+) index(6309)
Title: Elution from: 54.588 to 54.588 scan no 8081 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

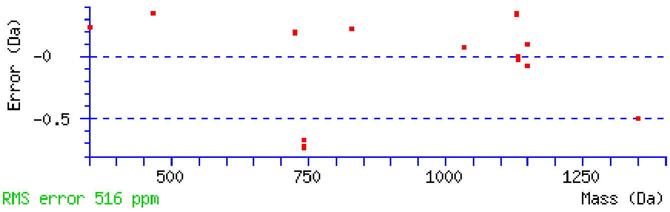
Label all possible matches ○ Label matches used for scoring ●

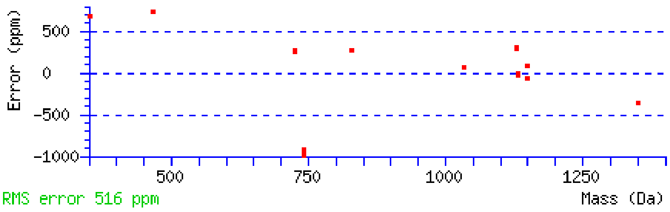
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1498.6397
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.01
Matches : 16/140 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							14
2	249.0688	125.0380			231.0582	116.0327	D	1367.6095	684.3084	1349.5859	675.2966	1349.5989	675.3031	13
3	***351.1135***	176.0604			333.1029	167.0551	T	1251.5855	626.2964	1233.5619	617.2846	1233.5750	617.2911	12
4	***465.1946***	233.1009			447.1840	224.0956	L	1149.5408	575.2740	1131.5172	566.2623	1131.5302	566.2688	11
5	537.2287	269.1180			519.2182	260.1127	A	1035.4597	518.2335	1017.4361	509.2217	1017.4491	509.2282	10
6	625.2578	313.1325			607.2472	304.1273	S	963.4256	482.2164	945.4020	473.2046	945.4150	473.2111	9
7	***741.2948***	371.1510	723.2712	362.1392	723.2842	362.1458	N	875.3965	438.2019	857.3729	429.1901	857.3859	429.1966	8
8	***829.3239***	415.1656	811.3003	406.1538	811.3133	406.1603	S	759.3595	380.1834	741.3359	371.1716	741.3489	371.1781	7
9	917.3529	459.1801	899.3293	450.1683	899.3424	450.1748	S	671.3304	336.1689	653.3069	327.1571	653.3199	327.1636	6
10	***1033.3769***	517.1921	1015.3533	508.1803	1015.3663	508.1868	D	583.3014	292.1543	565.2778	283.1425	565.2908	283.1490	5
11	***1147.4580***	574.2326	1129.4344	565.2208	1129.4474	565.2274	L	467.2774	234.1423	449.2538	225.1305	449.2668	225.1371	4
12	1249.5027	625.2550	1231.4791	616.2432	1231.4921	616.2497	T	353.1963	177.1018	335.1727	168.0900	335.1857	168.0965	3
13	***1351.5474***	676.2773	1333.5238	667.2656	1333.5369	667.2721	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MDTLASNSSDLTTK

AT2G22330.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.4	1498.6397	0.0002	MDTLASNSSDLTTK
5.8	1498.6377	0.0023	GMCNEGKVEVGRK
5.6	1498.6370	0.0029	MSNGRYNNVLHR
3.9	1498.6364	0.0036	QEELIHEEEAEK
2.9	1498.6399	-0.0000	NSVIMHPCHLEK
2.4	1498.6370	0.0030	AANQGRRCTWEK
2.3	1498.6372	0.0027	CGKMDEAEVLFGK
2.0	1498.6424	-0.0025	MATNGSASSAQLSQK
1.9	1498.6417	-0.0018	SFSCFMFVLFGK

AT2G23350.1

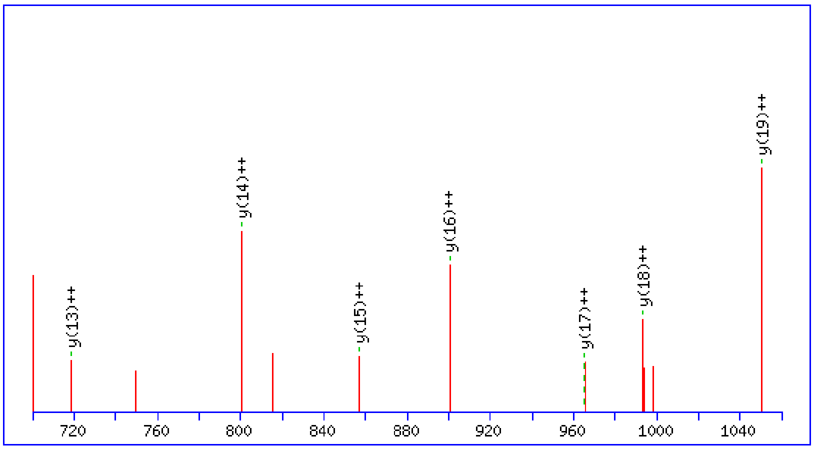
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLLGESLYPLVDQIESEHAAK**
Found in **AT2G23350.1** in **TAIR_Arabidopsis**, Symbols: PAB4 | PAB4 (POLY(A) BINDING PROTEIN 4); RNA binding / translation initiation factor | chr2:9950289-9953121 FORWARD

Match to Query 10324: 2312.194260 from(771.738696,3+) index(10116)
Title: Elution from: 94.904 to 94.904 scan no 14136 cid35.00 polarity:+
Data file D1d-2_1.mgf

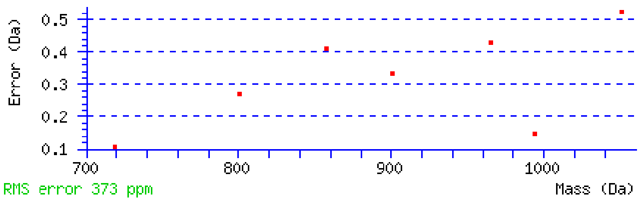
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 700 to 1060 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

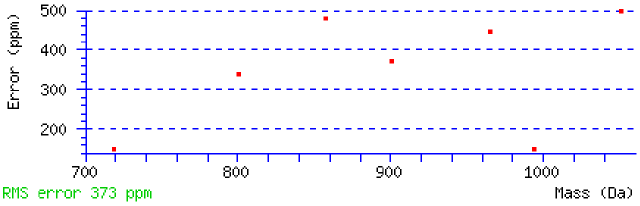


Monoisotopic mass of neutral peptide Mr(calc): 2312.1900
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 3.6e-005
Matches : 7/208 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							21
2	215.1390	108.0731			197.1285	99.0679	L	2212.1496	1106.5784	2195.1230	1098.0652	2194.1390	1097.5732	20
3	328.2231	164.6152			310.2125	155.6099	L	2099.0655	1050.0364	2082.0390	1041.5231	2081.0550	1041.0311	19
4	385.2445	193.1259			367.2340	184.1206	G	1985.9815	993.4944	1968.9549	984.9811	1967.9709	984.4891	18
5	514.2871	257.6472			496.2766	248.6419	E	1928.9600	964.9836	1911.9335	956.4704	1910.9494	955.9784	17
6	601.3192	301.1632			583.3086	292.1579	S	1799.9174	900.4623	1782.8909	891.9491	1781.9068	891.4571	16
7	714.4032	357.7053			696.3927	348.7000	L	1712.8854	856.9463	1695.8588	848.4331	1694.8748	847.9410	15
8	877.4666	439.2369			859.4560	430.2316	Y	1599.8013	800.4043	1582.7748	791.8910	1581.7907	791.3990	14
9	974.5193	487.7633			956.5088	478.7580	P	1436.7380	718.8726	1419.7114	710.3594	1418.7274	709.8673	13
10	1087.6034	544.3053			1069.5928	535.3000	L	1339.6852	670.3462	1322.6587	661.8330	1321.6747	661.3410	12
11	1186.6718	593.8395			1168.6612	584.8343	V	1226.6012	613.8042	1209.5746	605.2909	1208.5906	604.7989	11
12	1301.6987	651.3530			1283.6882	642.3477	D	1127.5327	564.2700	1110.5062	555.7567	1109.5222	555.2647	10
13	1429.7573	715.3823	1412.7308	706.8690	1411.7468	706.3770	Q	1012.5058	506.7565	995.4793	498.2433	994.4952	497.7513	9
14	1542.8414	771.9243	1525.8148	763.4111	1524.8308	762.9190	I	884.4472	442.7272	867.4207	434.2140	866.4367	433.7220	8
15	1671.8840	836.4456	1654.8574	827.9324	1653.8734	827.4403	E	771.3632	386.1852	754.3366	377.6719	753.3526	377.1799	7
16	1758.9160	879.9616	1741.8895	871.4484	1740.9054	870.9564	S	642.3206	321.6639	625.2940	313.1506	624.3100	312.6586	6
17	1887.9586	944.4829	1870.9321	935.9697	1869.9480	935.4777	E	555.2885	278.1479	538.2620	269.6346	537.2780	269.1426	5
18	2025.0175	1013.0124	2007.9910	1004.4991	2007.0069	1004.0071	H	426.2459	213.6266	409.2194	205.1133			4
19	2096.0546	1048.5310	2079.0281	1040.0177	2078.0441	1039.5257	A	289.1870	145.0972	272.1605	136.5839			3
20	2167.0917	1084.0495	2150.0652	1075.5362	2149.0812	1075.0442	A	218.1499	109.5786	201.1234	101.0653			2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT2G23350.1





NCBI **BLAST** search of TLLGESLYPLVDQIESEHAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.0	2312.1900	0.0043	TLLGESLYPLVDQIESEHAAK
8.3	2312.1913	0.0029	NVLSVVRDEQFSVLYQNFR
4.8	2312.1985	-0.0043	SPVTQDSGGFSGRTRALAQHLK
2.5	2312.1947	-0.0004	LAQRMTLNYYRGITSPSVDK

Mascot: http://www.matrixscience.com/

AT2G23450.1

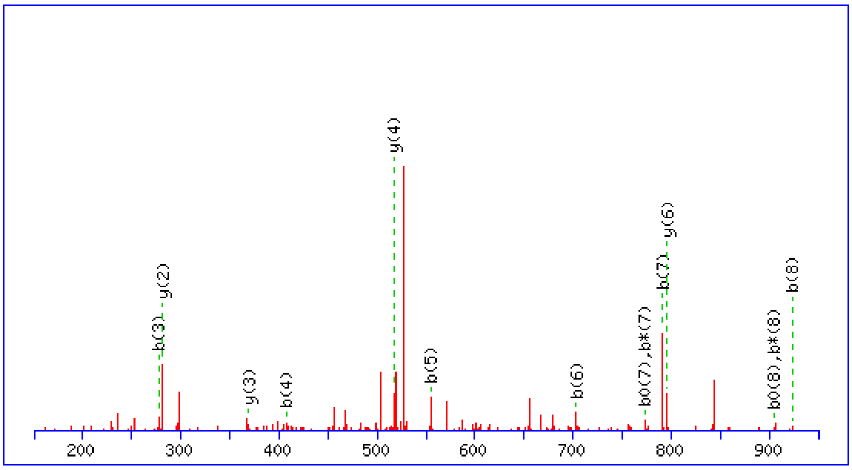
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSAKFFSMK**
Found in **AT2G23450.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr2:9996006-9998324 REVERSE

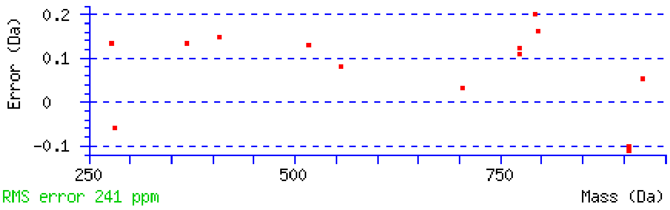
Match to Query 3037: 1070.487606 from(536.251079,2+) index(5079)
Title: Elution from: 45.767 to 45.767 scan no 6437 cid35.00 polarity:+
Data file D6h-3_2.mgf

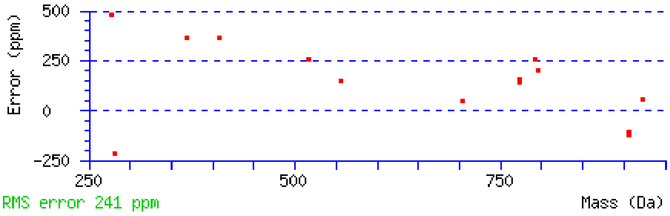
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1070.4863
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.029
Matches : 14/90 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			**N**							9
2	205.0733	103.0403	187.0498	94.0285	187.0628	94.0350	**S**	955.4566	478.2319	937.4330	469.2201	937.4460	469.2267	8
3	***277.1075***	139.0574	259.0839	130.0456	259.0969	130.0521	**A**	867.4275	434.2174	849.4040	425.2056	849.4170	425.2121	7
4	***407.1965***	204.1019	389.1729	195.0901	389.1860	195.0966	**K**	**795.3934**	398.2003	777.3698	389.1885	777.3828	389.1950	6
5	***555.2620***	278.1346	537.2384	269.1228	537.2514	269.1293	**F**	665.3044	333.1558	647.2808	324.1440	647.2938	324.1505	5
6	***703.3274***	352.1673	685.3038	343.1556	685.3169	343.1621	**F**	**517.2389**	259.1231	499.2153	250.1113	499.2283	250.1178	4
7	***791.3565***	396.1819	773.3329	387.1701	773.3459	387.1766	**S**	**369.1735**	185.0904	351.1499	176.0786	351.1629	176.0851	3
8	***923.3940***	462.2006	905.3704	453.1888	905.3834	453.1954	**M**	**281.1444**	141.0758	263.1208	132.0640			2
9							**K**	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NSAKFFSMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.8	1070.4863	0.0013	NSAKFFSMK

AT2G23450.1

11.7	1070.4897	-0.0021	IHLMAESMK
7.3	1070.4863	0.0013	MIERFGYK

AT2G23670.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAEEEAVEIVK**
Found in **AT2G23670.1** in **TAIR_Arabidopsis**, Symbols: YCF37 | YCF37 (Arabidopsis homolog of Synechocystis YCF37) | chr2:10070387-10070890 REVERSE

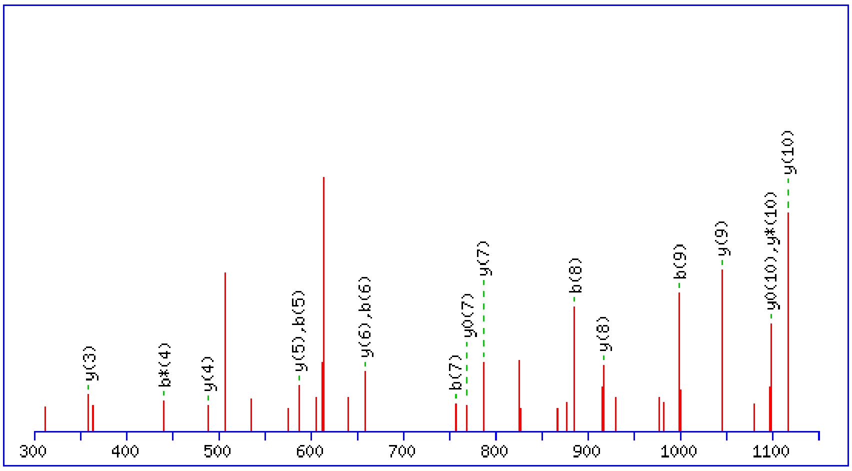
Match to Query 4696: 1243.665542 from(622.840047,2+) index(1877)
Title: Elution from: 22.549 to 22.549 scan no 2440 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1150 Da Full range

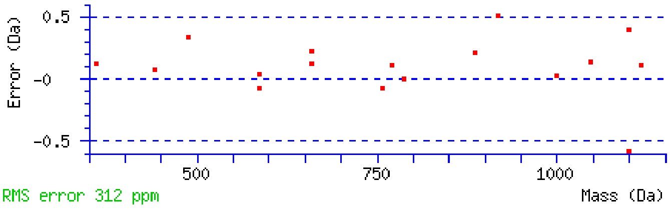
Label all possible matches ○ Label matches used for scoring ●

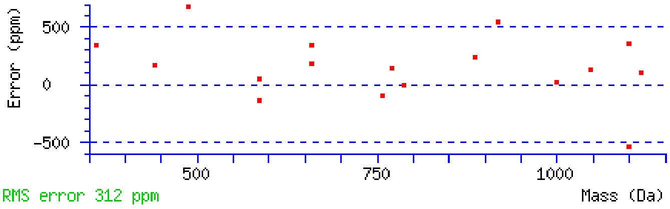
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1243.6659
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 4.2e-007
Matches : 18/110 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							11
2	200.1394	100.5733	183.1128	92.0600			A	***1116.5783***	558.7928	1099.5517	550.2795	1098.5677	549.7875	10
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	E	***1045.5412***	523.2742	1028.5146	514.7610	1027.5306	514.2689	9
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	E	***916.4986***	458.7529	899.4720	450.2397	898.4880	449.7477	8
5	***587.2671***	294.1372	570.2406	285.6239	569.2566	285.1319	E	***787.4560***	394.2316	770.4294	385.7184	769.4454	385.2264	7
6	***658.3042***	329.6558	641.2777	321.1425	640.2937	320.6505	A	***658.4134***	329.7103	641.3869	321.1971	640.4028	320.7051	6
7	***757.3727***	379.1900	740.3461	370.6767	739.3621	370.1847	V	***587.3763***	294.1918	570.3497	285.6785	569.3657	285.1865	5
8	***886.4153***	443.7113	869.3887	435.1980	868.4047	434.7060	E	***488.3079***	244.6576	471.2813	236.1443	470.2973	235.6523	4
9	***999.4993***	500.2533	982.4728	491.7400	981.4888	491.2480	I	***359.2653***	180.1363	342.2387	171.6230			3
10	***1098.5677***	549.7875	1081.5412	541.2742	1080.5572	540.7822	V	246.1812	123.5942	229.1547	115.0810			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KAEEEAVEIVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G23670.1

Score	Mr(calc)	Delta	Sequence
71.0	1243.6659	-0.0004	KAEEEAVEIVK
18.8	1243.6633	0.0022	AQRTDTGGVIAR
13.3	1243.6633	0.0023	QAIQKATNNTR
2.7	1243.6660	-0.0004	LITENADLVEK
1.6	1243.6633	0.0023	TGNRGQQEKVK
1.5	1243.6634	0.0021	KAAYLAYSVMK

AT2G24020.1

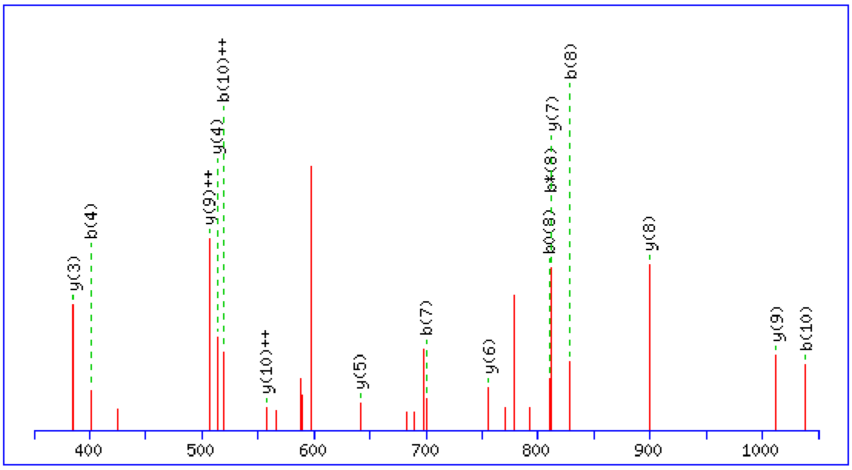
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLSGNQQPIR**
Found in **AT2G24020.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G30620.1); similar to unknown [Picea sitchensis] (GB:ABK26000.1); similar to Os02g0180200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046090.1); contains InterPro domain

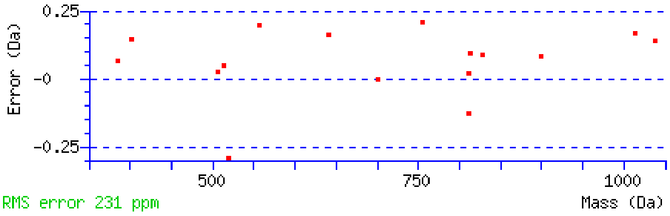
Match to Query 4106: 1211.665764 from(606.840158,2+) index(1749)
Title: Elution from: 21.948 to 21.948 scan no 2297 cid35.00 polarity:+
Data file D6h-1_3.mgf

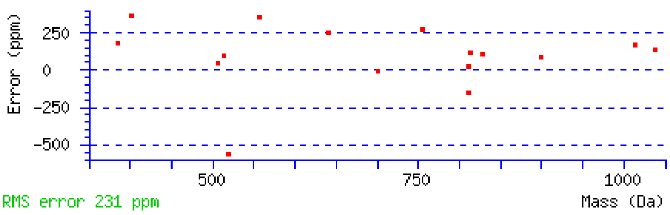
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1211.6622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 2.4e-006
Matches : 16/94 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							11
2	201.1234	101.0653			183.1128	92.0600	T	1113.6011	557.3042	1096.5745	548.7909	1095.5905	548.2989	10
3	314.2074	157.6074			296.1969	148.6021	L	***1012.5534***	506.7803	995.5269	498.2671	994.5429	497.7751	9
4	**401.2395**	201.1234			383.2289	192.1181	S	***899.4694***	450.2383	882.4428	441.7250	881.4588	441.2330	8
5	458.2609	229.6341			440.2504	220.6288	G	***812.4373***	406.7223	795.4108	398.2090			7
6	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	N	***755.4159***	378.2116	738.3893	369.6983			6
7	**700.3624**	350.6849	683.3359	342.1716	682.3519	341.6796	Q	***641.3729***	321.1901	624.3464	312.6768			5
8	**828.4210**	414.7141	811.3945	406.2009	810.4104	405.7089	Q	***513.3144***	257.1608	496.2878	248.6475			4
9	925.4738	463.2405	908.4472	454.7272	907.4632	454.2352	P	***385.2558***	193.1315	368.2292	184.6183			3
10	**1038.5578**	519.7826	1021.5313	511.2693	1020.5473	510.7773	I	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VTLSGNQQPIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G24020.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.9	1211.6622	0.0035	VTLSGNQQPIR
8.6	1211.6622	0.0036	EASLAALERPR
2.1	1211.6669	-0.0012	MHSVSRLARR
1.5	1211.6622	0.0036	SNIERPPGSKK

AT2G24200.1

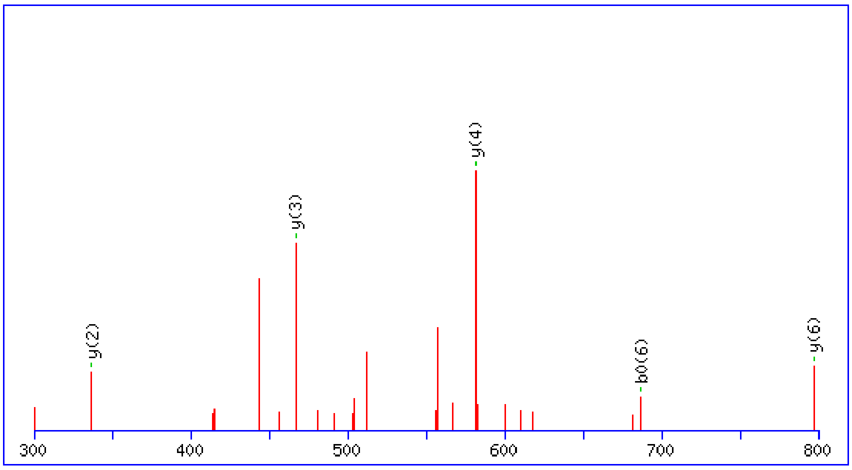
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIDVIEWK**
Found in **AT2G24200.1** in **TAIR_Arabidopsis**, Symbols: | cytosol aminopeptidase | chr2:10294097-10296530 REVERSE

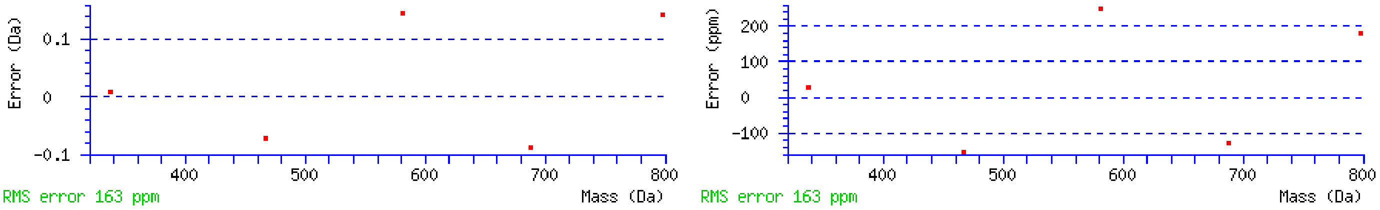
Match to Query 2905: 1040.502868 from(521.258710,2+) index(6597)
Title: Elution from: 57.508 to 57.508 scan no 8454 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1040.5038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0027
Matches : 5/66 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							8
2	245.1280	123.0676	227.1174	114.0624	I	911.4715	456.2394	893.4479	447.2276	893.4609	447.2341	7
3	361.1520	181.0796	343.1414	172.0743	D	***797.3904***	399.1988	779.3668	390.1871	779.3798	390.1936	6
4	461.2174	231.1124	443.2069	222.1071	V	681.3664	341.1869	663.3428	332.1751	663.3559	332.1816	5
5	575.2985	288.1529	557.2880	279.1476	I	***581.3010***	291.1541	563.2774	282.1423	563.2904	282.1488	4
6	705.3382	353.1727	687.3276	344.1674	E	***467.2199***	234.1136	449.1963	225.1018	449.2093	225.1083	3
7	893.4115	447.2094	875.4010	438.2041	W	***337.1803***	169.0938	319.1567	160.0820			2
8					K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of EIDVIEWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.9	1040.5038	-0.0010	EIDVIEWK
1.2	1040.5043	-0.0014	GIAPGDGTAIR

AT2G24200.1

Mascot: http://www.matrixscience.com/

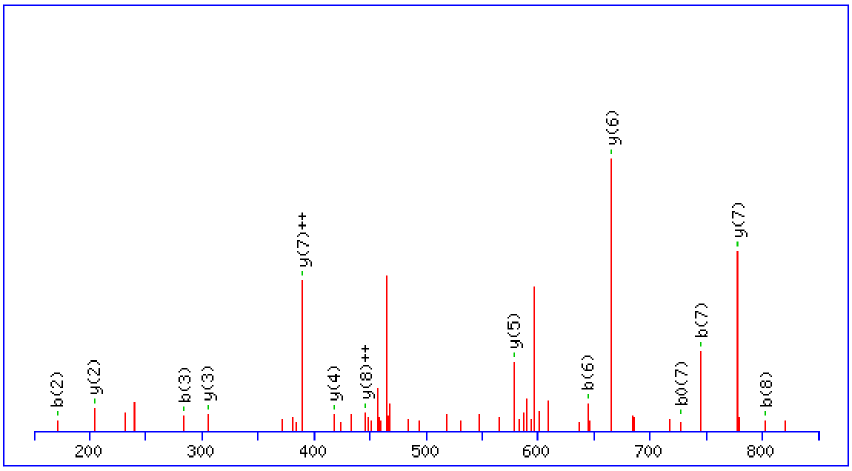
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLISCITGK**
Found in **AT2G24270.1** in **TAIR_Arabidopsis**, Symbols: ALDH11A3 | ALDH11A3 (Aldehyde dehydrogenase 11A3); 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+) | chr2:10334405-10336681 REVERSE

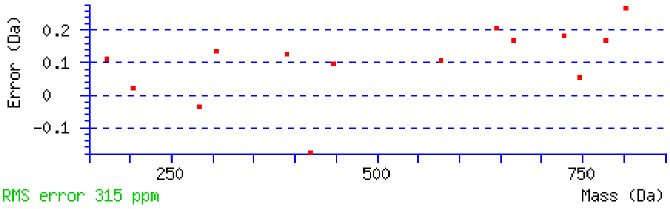
Match to Query 2132: 947.511928 from(474.763240,2+) index(5161)
Title: Elution from: 45.879 to 45.879 scan no 6445 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

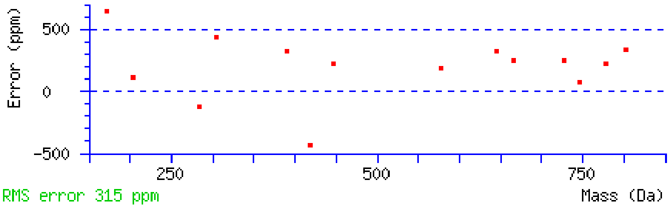


Monoisotopic mass of neutral peptide Mr(calc): 947.5110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0083
Matches : 14/70 fragment ions using 37 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180			G							9
2	***171.1128***	86.0600			L	891.4968	446.2520	874.4703	437.7388	873.4863	437.2468	8
3	***284.1969***	142.6021			I	***778.4128***	389.7100	761.3862	381.1967	760.4022	380.7047	7
4	371.2289	186.1181	353.2183	177.1128	S	***665.3287***	333.1680	648.3021	324.6547	647.3181	324.1627	6
5	531.2595	266.1334	513.2490	257.1281	C	***578.2967***	289.6520	561.2701	281.1387	560.2861	280.6467	5
6	***644.3436***	322.6754	626.3330	313.6702	I	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	4
7	***745.3913***	373.1993	727.3807	364.1940	T	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	3
8	***802.4128***	401.7100	784.4022	392.7047	G	***204.1343***	102.5708	187.1077	94.0575			2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 315 ppm



RMS error 315 ppm

NCBI **BLAST** search of GLISCITGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G24270.1

28.7	947.5110	0.0009	GLISCITGK
1.9	947.5110	0.0010	LSMALELR

Mascot: http://www.matrixscience.com/

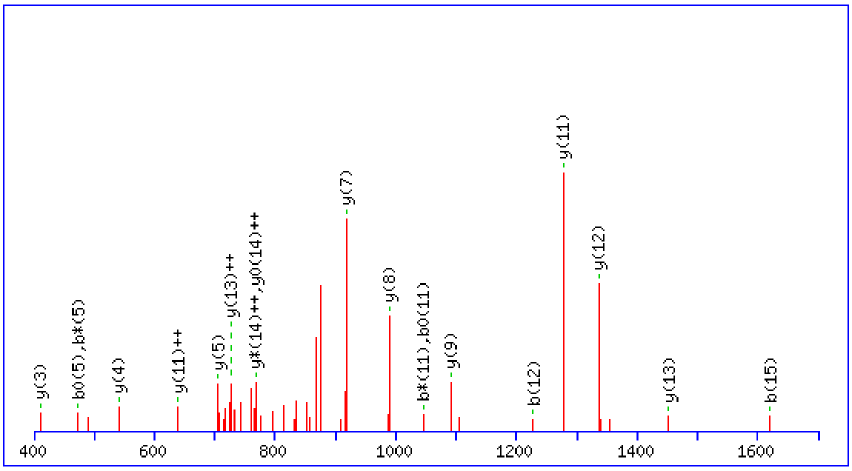
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDVNGPSTAPIYEFLK**
Found in **AT2G25080.1** in **TAIR_Arabidopsis**, Symbols: ATGPX1 | ATGPX1 (GLUTATHIONE PEROXIDASE 1); glutathione peroxidase | chr2:10675213-10676907 FORWARD

Match to Query 8137: 1766.844408 from(884.429480,2+) index(8905)
Title: Elution from: 79.665 to 79.665 scan no 12113 cid35.00 polarity:+
Data file 0-2_3.mgf

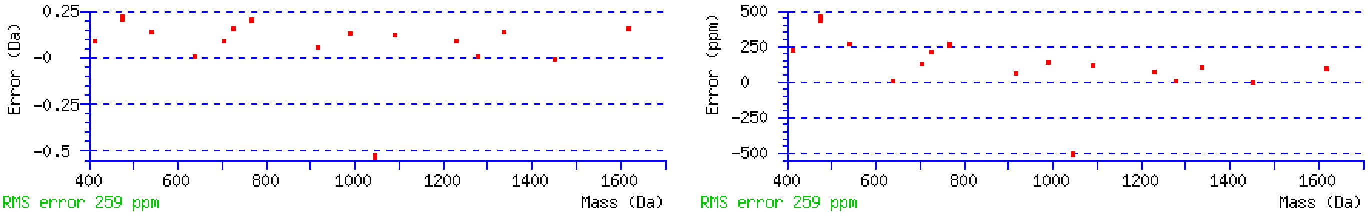
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1766.8451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 89 **Expect:** 1.3e-008
Matches : 19/166 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							16
2	217.0967	109.0520			199.0861	100.0467	D	1667.7870	834.3971	1649.7634	825.3853	1649.7764	825.3918	15
3	317.1622	159.0847			299.1516	150.0794	V	1551.7630	776.3851	1533.7394	767.3733	1533.7524	767.3798	14
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	N	***1451.6975***	726.3524	1433.6739	717.3406	1433.6870	717.3471	13
5	491.2176	246.1125	473.1941	237.1007	473.2071	237.1072	G	***1335.6605***	668.3339	1317.6370	659.3221	1317.6500	659.3286	12
6	589.2674	295.1374	571.2439	286.1256	571.2569	286.1321	P	***1277.6420***	639.3247	1259.6185	630.3129	1259.6315	630.3194	11
7	677.2965	339.1519	659.2729	330.1401	659.2859	330.1466	S	1179.5922	590.2998	1161.5687	581.2880	1161.5817	581.2945	10
8	779.3412	390.1742	761.3176	381.1625	761.3307	381.1690	T	***1091.5632***	546.2852	1073.5396	537.2734	1073.5526	537.2799	9
9	851.3754	426.1913	833.3518	417.1795	833.3648	417.1860	A	***989.5185***	495.2629	971.4949	486.2511	971.5079	486.2576	8
10	949.4252	475.2162	931.4016	466.2044	931.4146	466.2109	P	***917.4843***	459.2458	899.4607	450.2340	899.4737	450.2405	7
11	1063.5063	532.2568	1045.4827	523.2450	1045.4957	523.2515	I	819.4345	410.2209	801.4109	401.2091	801.4239	401.2156	6
12	**1227.5666**	614.2870	1209.5431	605.2752	1209.5561	605.2817	Y	***705.3534***	353.1803	687.3298	344.1686	687.3428	344.1751	5
13	1357.6063	679.3068	1339.5827	670.2950	1339.5957	670.3015	E	***541.2930***	271.1502	523.2695	262.1384	523.2825	262.1449	4
14	1505.6717	753.3395	1487.6481	744.3277	1487.6611	744.3342	F	***411.2534***	206.1303	393.2298	197.1186			3
15	**1619.7528**	810.3800	1601.7292	801.3683	1601.7422	801.3748	L	263.1880	132.0976	245.1644	123.0858			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT2G25080.1



NCBI **BLAST** search of VDVNGPSTAPIYEFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.8	1766.8451	-0.0007	VDVNGPSTAPIYEFLK
3.2	1766.8489	-0.0045	MVEELKLENQQKTR
0.5	1766.8429	0.0015	EVTVVSDLPASFSLER
0.4	1766.8463	-0.0018	DSLVAKTLMQEQLEK

Mascot: http://www.matrixscience.com/

AT2G25160.1

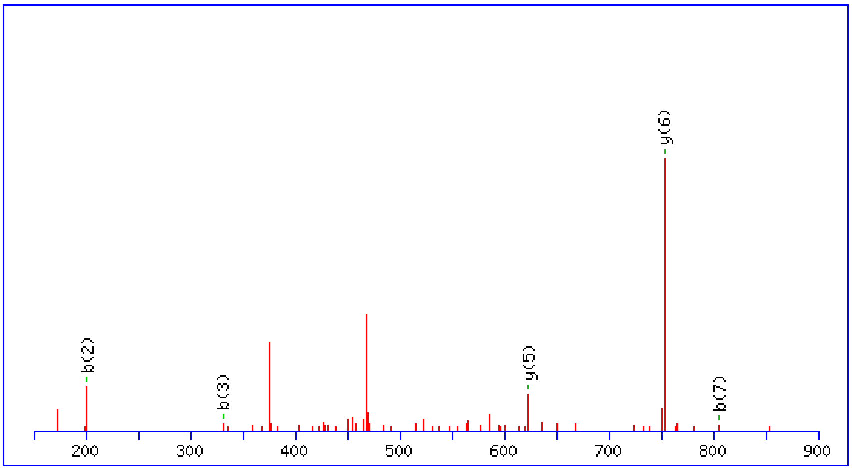
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEELDIK**
Found in **AT2G25160.1** in **TAIR_Arabidopsis**, Symbols: CYP82F1 | CYP82F1 (cytochrome P450, family 82, subfamily F, polypeptide 1); oxygen binding | chr2:10716315-10718290 REVERSE

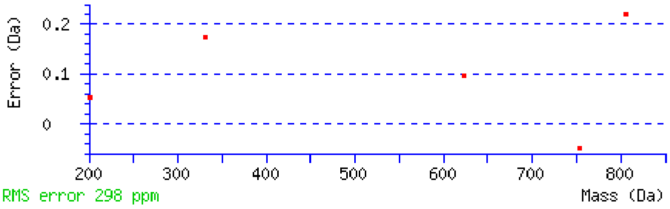
Match to Query 1929: 952.495488 from(477.255020,2+) index(2752)
Title: Elution from: 27.859 to 27.859 scan no 3441 cid35.00 polarity:+
Data file 0-3_3.mgf

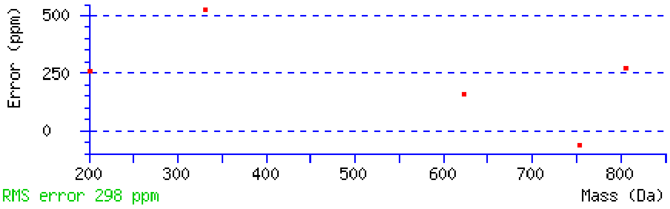
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 952.4959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.0054
Matches : 5/62 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							8
2	***201.1382***	101.0727			V	853.4378	427.2225	835.4142	418.2107	835.4272	418.2172	7
3	***331.1778***	166.0925	313.1672	157.0873	E	**753.3723**	377.1898	735.3487	368.1780	735.3617	368.1845	6
4	461.2174	231.1124	443.2069	222.1071	E	**623.3327**	312.1700	605.3091	303.1582	605.3221	303.1647	5
5	575.2985	288.1529	557.2880	279.1476	L	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
6	691.3225	346.1649	673.3119	337.1596	D	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
7	***805.4036***	403.2054	787.3930	394.2002	I	263.1880	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VVEELDIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	952.4959	-0.0004	VVEELDIK

AT2G25160.1

Mascot: http://www.matrixscience.com/

AT2G25560.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLANDFAGAR**
Found in **AT2G25560.1** in **TAIR_Arabidopsis**, Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:10888868-10890838 FORWARD

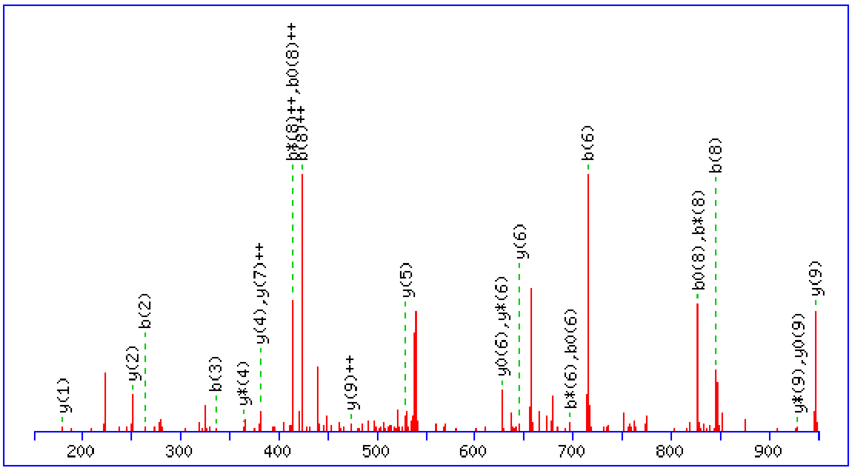
Match to Query 3270: 1094.493678 from(548.254115,2+) index(2209)
Title: Elution from: 24.924 to 24.924 scan no 2810 cid35.00 polarity:+
Data file D6h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

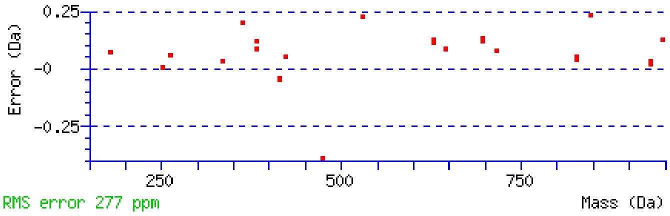
Label all possible matches ○ Label matches used for scoring ●

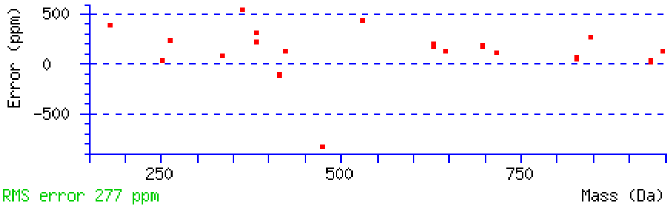
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1094.4937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.048
Matches : 24/84 fragment ions using 76 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					F							10
2	***263.1538***	132.0805					L	***947.4356***	474.2214	929.4120	465.2096	929.4250	465.2161	9
3	***335.1880***	168.0976					A	833.3545	417.1809	815.3309	408.1691	815.3439	408.1756	8
4	451.2250	226.1161	433.2014	217.1043			N	761.3203	381.1638	743.2967	372.1520	743.3097	372.1585	7
5	567.2489	284.1281	549.2254	275.1163	549.2384	275.1228	D	***645.2833***	323.1453	627.2597	314.1335	627.2728	314.1400	6
6	***715.3144***	358.1608	697.2908	349.1490	697.3038	349.1556	F	***529.2593***	265.1333	511.2358	256.1215			5
7	787.3485	394.1779	769.3250	385.1661	769.3380	385.1726	A	***381.1939***	191.1006	363.1703	182.0888			4
8	***845.3670***	423.1872	827.3435	414.1754	827.3565	414.1819	G	309.1597	155.0835	291.1362	146.0717			3
9	917.4012	459.2042	899.3776	450.1924	899.3906	450.1990	A	***251.1412***	126.0743	233.1177	117.0625			2
10							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FLANDFAGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G25560.1

Score	Mr(calc)	Delta	Sequence
20.8	1094.4937	-0.0000	FLANDFAGAR
15.0	1094.4944	-0.0008	YGIMEINTK
12.1	1094.4944	-0.0008	MEKFVASEK
10.2	1094.4915	0.0022	TENFTGGARK
6.5	1094.4944	-0.0008	GLSSFESVMK
6.5	1094.4915	0.0022	GNGEEYRKK
3.7	1094.4910	0.0026	FSEFEAQVK
3.6	1094.4944	-0.0007	STGGEMFLVK
3.3	1094.4910	0.0026	FETPKDGYK
2.0	1094.4915	0.0022	NLSYDNKAR

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTYLLVDDPKR**
Found in **AT2G25600.1** in **TAIR_Arabidopsis**, Symbols: AKT6, SPIK | SPIK (SHAKER POLLEN INWARD K+ CHANNEL); cyclic nucleotide binding / inward rectifier potassium channel/ potassium channel | chr2:10901681-10905447 FORWARD

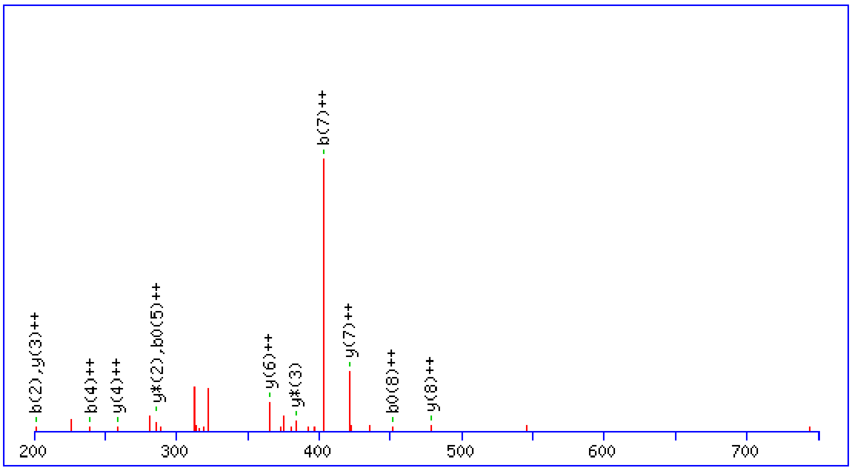
Match to Query 4811: 1317.730200 from(330.439826,4+) index(2675)
Title: Elution from: 27.661 to 27.661 scan no 3333 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 750 Da Full range

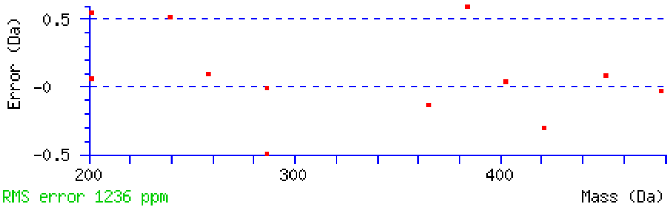
Label all possible matches ○ Label matches used for scoring ●

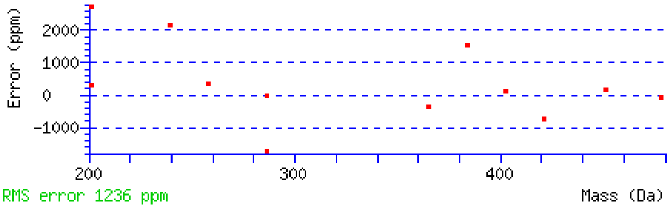
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1317.7292
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.047
Matches : 12/94 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							11
2	201.1234	101.0653			183.1128	92.0600	T	1219.6681	610.3377	1202.6416	601.8244	1201.6575	601.3324	10
3	364.1867	182.5970			346.1761	173.5917	Y	1118.6204	559.8139	1101.5939	551.3006	1100.6099	550.8086	9
4	477.2708	**239.1390**			459.2602	230.1337	L	955.5571	478.2822	938.5306	469.7689	937.5465	469.2769	8
5	590.3548	295.6811			572.3443	286.6758	L	842.4730	421.7402	825.4465	413.2269	824.4625	412.7349	7
6	689.4232	345.2153			671.4127	336.2100	V	729.3890	365.1981	712.3624	356.6849	711.3784	356.1928	6
7	804.4502	**402.7287**			786.4396	393.7234	D	630.3206	315.6639	613.2940	307.1506	612.3100	306.6586	5
8	919.4771	460.2422			901.4666	451.2369	D	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	4
9	1016.5299	508.7686			998.5193	499.7633	P	400.2667	200.6370	383.2401	192.1237			3
10	1144.6249	572.8161	1127.5983	564.3028	1126.6143	563.8108	K	303.2139	152.1106	286.1874	143.5973			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VTYLLVDDPKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G25600.1

Score	Mr(calc)	Delta	Sequence
19.6	1317.7292	0.0010	VTYLLVDDPKR
10.9	1317.7306	-0.0004	IGGHLPGVHYIR
5.1	1317.7326	-0.0024	RMLDIELTTVK
3.7	1317.7292	0.0010	KTTAWSLVEVGK
0.9	1317.7339	-0.0037	QIQQMVRFIR
0.6	1317.7292	0.0010	LIGIDSLGFDLR

AT2G25660.1

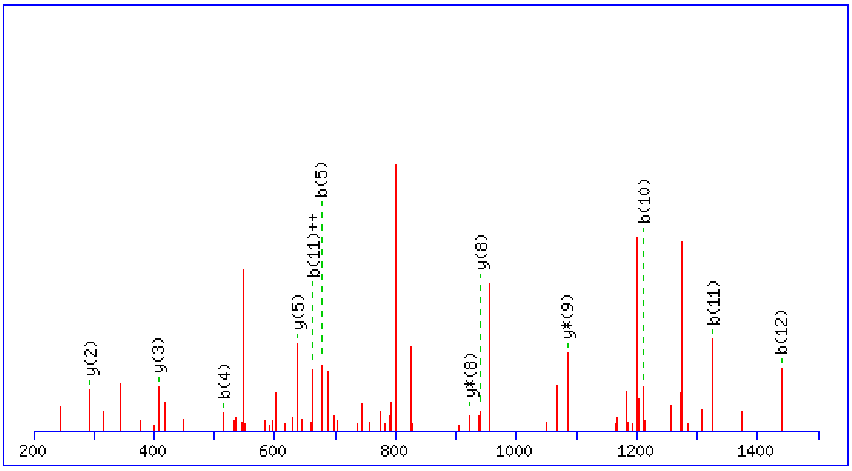
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSQFCGKNVQLLR**
Found in **AT2G25660.1** in **TAIR_Arabidopsis**, Symbols: EMB2410 | EMB2410 (EMBRYO DEFECTIVE 2410) | chr2:10923534-10934468 REVERSE

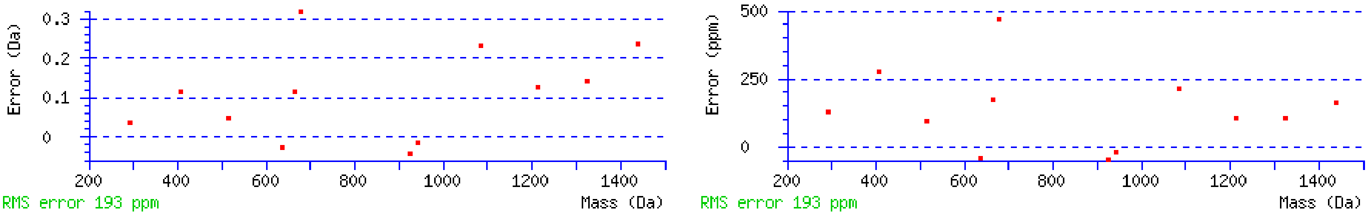
Match to Query 7636: 1616.766482 from(809.390517,2+) index(9103)
Title: Elution from: 80.995 to 80.995 scan no 12143 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1616.7619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.04
Matches : 12/116 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	149.0727	75.0400					F							13
2	237.1018	119.0545			219.0912	110.0492	S	1469.7038	735.3555	1451.6802	726.3437	1451.6932	726.3503	12
3	367.1544	184.0809	349.1309	175.0691	349.1439	175.0756	Q	1381.6747	691.3410	1363.6511	682.3292			11
4	***515.2199***	258.1136	497.1963	249.1018	497.2093	249.1083	F	1251.6221	626.3147	1233.5985	617.3029			10
5	***677.2446***	339.1259	659.2210	330.1141	659.2340	330.1207	C	1103.5566	552.2820	1085.5330	543.2702			9
6	735.2631	368.1352	717.2395	359.1234	717.2525	359.1299	G	***941.5319***	471.2696	923.5083	462.2578			8
7	865.3521	433.1797	847.3286	424.1679	847.3416	424.1744	K	883.5134	442.2603	865.4898	433.2486			7
8	981.3891	491.1982	963.3655	482.1864	963.3786	482.1929	N	753.4244	377.2158	735.4008	368.2040			6
9	1081.4546	541.2309	1063.4310	532.2191	1063.4440	532.2256	V	***637.3874***	319.1973	619.3638	310.1855			5
10	***1211.5072***	606.2573	1193.4836	597.2455	1193.4967	597.2520	Q	537.3219	269.1646	519.2984	260.1528			4
11	***1325.5883***	663.2978	1307.5647	654.2860	1307.5778	654.2925	L	***407.2693***	204.1383	389.2457	195.1265			3
12	***1439.6694***	720.3384	1421.6458	711.3266	1421.6589	711.3331	L	***293.1882***	147.0977	275.1646	138.0859			2
13							R	179.1071	90.0572	161.0835	81.0454			1



NCBI **BLAST** search of FSQFCGKNVQLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G25660.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1616.7619	0.0045	FSQFCGKNVQLLR
6.7	1616.7672	-0.0007	ANVSGKPKHSLDANR
3.8	1616.7701	-0.0036	LDLAGRDLTDHLMK
3.6	1616.7689	-0.0024	TFADPFEIYRALR
3.1	1616.7645	0.0020	QNFTSKKASSETIR
1.2	1616.7711	-0.0047	GPVSGFGLGFVPFYR
0.8	1616.7674	-0.0009	VLEMVAEELGIEPR
0.1	1616.7644	0.0020	KALEDVATIAGEHSR

AT2G25850.1

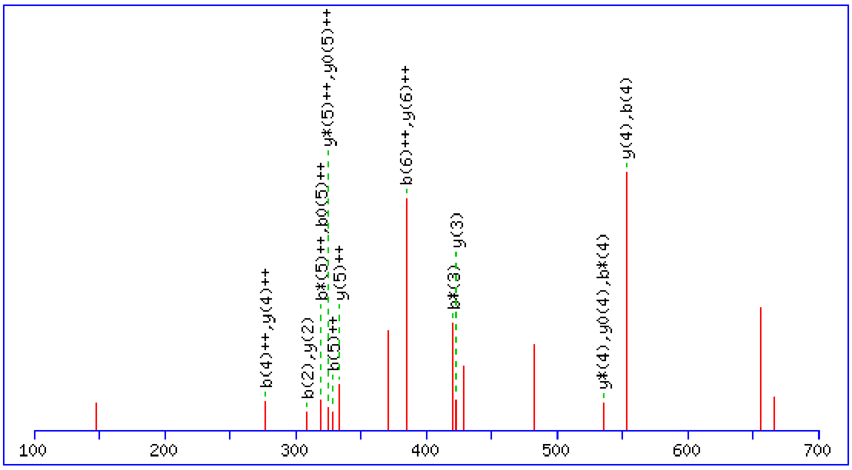
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FRQLTLKIER**
Found in **AT2G25850.1** in **TAIR_Arabidopsis**, Symbols: | nucleotidyltransferase family protein | chr2:11033126-11037518 REVERSE

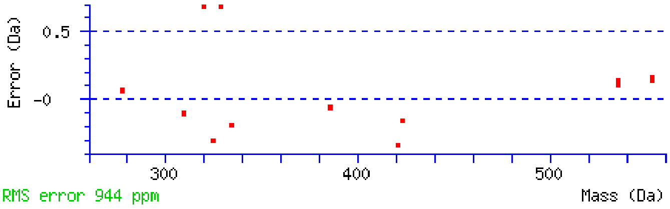
Match to Query 4814: 1320.720627 from(441.247485,3+) index(7762)
Title: Elution from: 68.864 to 68.864 scan no 10229 cid35.00 polarity:+
Data file D12h-3_2.mgf

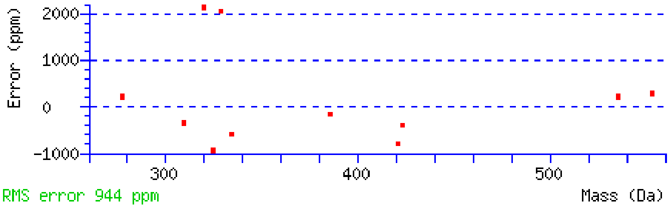
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.7238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.021
Matches : 19/96 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							10
2	**309.1620**	155.0846	291.1384	146.0728			R	1173.6657	587.3365	1155.6421	578.3247	1155.6551	578.3312	9
3	439.2146	220.1109	421.1910	211.0992			Q	1013.5764	507.2918	995.5528	498.2801	995.5658	498.2866	8
4	***553.2957***	***277.1515***	535.2721	268.1397			L	883.5238	442.2655	865.5002	433.2537	865.5132	433.2602	7
5	655.3404	***328.1739***	637.3169	319.1621	637.3299	319.1686	T	769.4427	385.2250	751.4191	376.2132	751.4321	376.2197	6
6	769.4215	***385.2144***	751.3980	376.2026	751.4110	376.2091	L	667.3980	334.2026	649.3744	325.1908	649.3874	325.1973	5
7	899.5106	450.2589	881.4870	441.2471	881.5000	441.2536	K	***553.3169***	277.1621	535.2933	268.1503	535.3063	268.1568	4
8	1013.5917	507.2995	995.5681	498.2877	995.5811	498.2942	I	***423.2278***	212.1175	405.2042	203.1058	405.2173	203.1123	3
9	1143.6313	572.3193	1125.6077	563.3075	1125.6207	563.3140	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FRQLTLKIER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G25850.1

21.4	1320.7238	-0.0032	FRQLTLKIER
1.7	1320.7211	-0.0005	IGLKGYELGKTK

Mascot: http://www.matrixscience.com/

AT2G26040.1

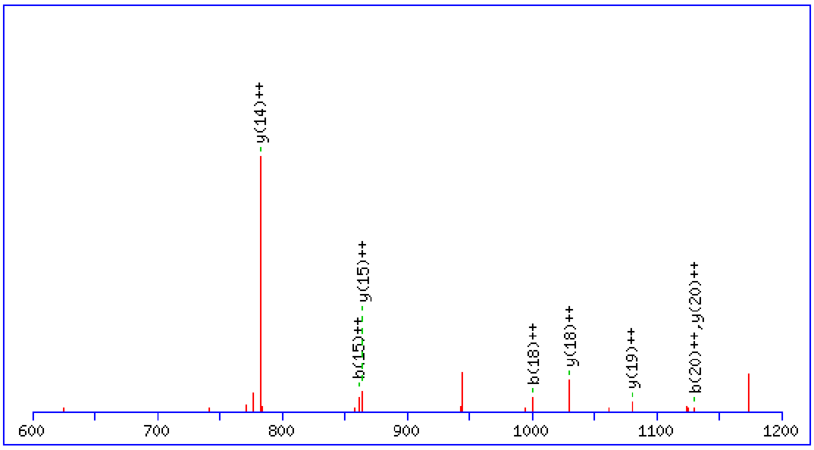
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYTVVLESYTVDIPEGNTEEDTK**
Found in **AT2G26040.1** in **TAIR_Arabidopsis**, Symbols: | Bet v I allergen family protein | chr2:11101910-11102482 REVERSE

Match to Query 10662: 2625.156618 from(876.059482,3+) index(10405)
Title: Elution from: 97.898 to 97.898 scan no 14769 cid35.00 polarity:+
Data file C7-1_2.mgf

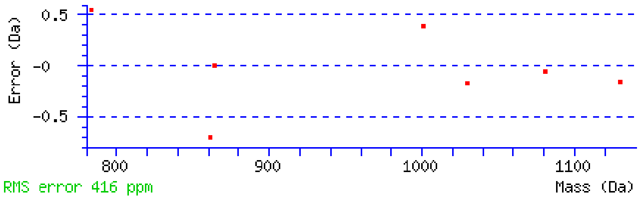
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

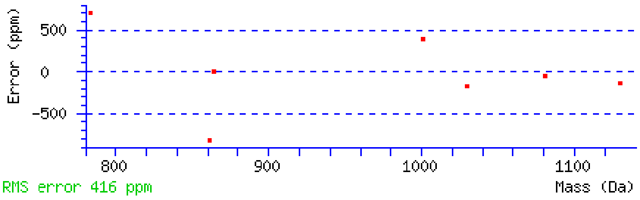


Monoisotopic mass of neutral peptide Mr(calc): 2625.1640
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.049
Matches : 8/226 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							23
2	265.1331	133.0702					Y	2526.1058	1263.5566	2508.0822	1254.5448	2508.0953	1254.5513	22
3	367.1778	184.0925			349.1672	175.0873	T	2362.0455	1181.5264	2344.0219	1172.5146	2344.0349	1172.5211	21
4	467.2433	234.1253			449.2327	225.1200	V	2260.0007	1130.5040	2241.9772	1121.4922	2241.9902	1121.4987	20
5	567.3087	284.1580			549.2981	275.1527	V	2159.9353	1080.4713	2141.9117	1071.4595	2141.9247	1071.4660	19
6	681.3898	341.1985			663.3792	332.1933	L	2059.8698	1030.4386	2041.8463	1021.4268	2041.8593	1021.4333	18
7	811.4294	406.2184			793.4189	397.2131	E	1945.7888	973.3980	1927.7652	964.3862	1927.7782	964.3927	17
8	899.4585	450.2329			881.4479	441.2276	S	1815.7491	908.3782	1797.7255	899.3664	1797.7386	899.3729	16
9	1063.5189	532.2631			1045.5083	523.2578	Y	1727.7201	864.3637	1709.6965	855.3519	1709.7095	855.3584	15
10	1165.5636	583.2854			1147.5530	574.2801	T	1563.6597	782.3335	1545.6361	773.3217	1545.6491	773.3282	14
11	1265.6290	633.3181			1247.6185	624.3129	V	1461.6150	731.3111	1443.5914	722.2993	1443.6044	722.3058	13
12	1381.6530	691.3301			1363.6424	682.3249	D	1361.5495	681.2784	1343.5259	672.2666	1343.5390	672.2731	12
13	1495.7341	748.3707			1477.7235	739.3654	I	1245.5256	623.2664	1227.5020	614.2546	1227.5150	614.2611	11
14	1593.7839	797.3956			1575.7733	788.3903	P	1131.4445	566.2259	1113.4209	557.2141	1113.4339	557.2206	10
15	1723.8235	***862.4154***			1705.8130	853.4101	E	1033.3947	517.2010	1015.3711	508.1892	1015.3841	508.1957	9
16	1781.8420	891.4246			1763.8315	882.4194	G	903.3550	452.1812	885.3314	443.1694	885.3445	443.1759	8
17	1897.8790	949.4431	1879.8554	940.4314	1879.8685	940.4379	N	845.3365	423.1719	827.3129	414.1601	827.3260	414.1666	7
18	1999.9237	***1000.4655***	1981.9001	991.4537	1981.9132	991.4602	T	729.2995	365.1534	711.2759	356.1416	711.2890	356.1481	6
19	2129.9634	1065.4853	2111.9398	1056.4735	2111.9528	1056.4800	E	627.2548	314.1310	609.2312	305.1193	609.2443	305.1258	5
20	2260.0030	***1130.5051***	2241.9794	1121.4933	2241.9924	1121.4998	E	497.2152	249.1112	479.1916	240.0994	479.2046	240.1060	4
21	2376.0270	1188.5171	2358.0034	1179.5053	2358.0164	1179.5118	D	367.1756	184.0914	349.1520	175.0796	349.1650	175.0861	3
22	2478.0717	1239.5395	2460.0481	1230.5277	2460.0611	1230.5342	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
23							K	149.1069	75.0571	131.0833	66.0453			1

AT2G26040.1





NCBI **BLAST** search of VYTVVLESYTVDIPEGNTEEDTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.2	2625.1640	-0.0073	VYTVVLESYTVDIPEGNTEEDTK
19.3	2625.1612	-0.0046	ITASSRNWEHNVFSSFSSVDVPK
8.9	2625.1597	-0.0031	SGEMQEGNKDFVGELSVTLVNAQK
8.4	2625.1622	-0.0056	SESSIGDSGIEKSSDSSVVDRVIDK
5.7	2625.1541	0.0026	GDEIVPPANQLAADNLENDGSTVQK
5.3	2625.1630	-0.0064	EASMGGEVKTLSEKVDSLAQEMTR
5.0	2625.1547	0.0019	KSGFVAALMCFSCWVGSSFLAVR
5.0	2625.1502	0.0064	LSRVAMVENGECVICLEEWRK
4.5	2625.1565	0.0001	SNLLTEYPWSPRWEVGRMAER
4.5	2625.1557	0.0009	SMEMEIQSLLEKLLDINDSMSR

Mascot: http://www.matrixscience.com/

AT2G26080.1

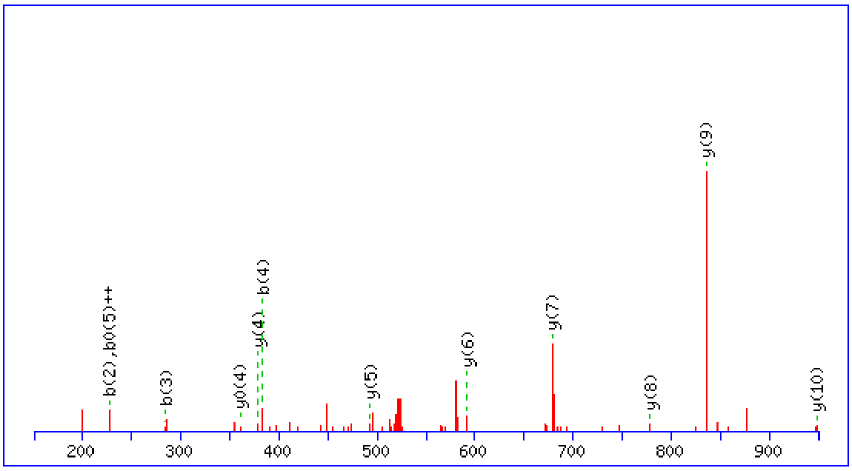
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGVSVDSSGK**
Found in **AT2G26080.1** in **TAIR_Arabidopsis**, Symbols: ATGLDP2 | ATGLDP2 (ARABIDOPSIS THALIANA GLYCINE DECARBOXYLASE P-PROTEIN 2); glycine dehydrogenase (decarboxylating) | chr2:11116408-11120864 REVERSE

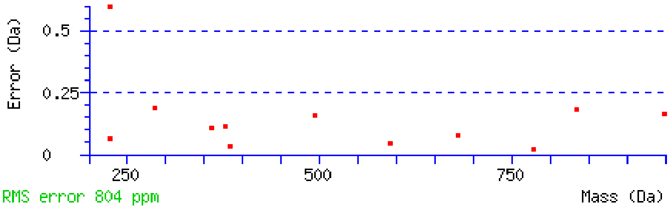
Match to Query 2692: 1060.576168 from(531.295360,2+) index(2439)
Title: Elution from: 28.428 to 28.428 scan no 3160 cid35.00 polarity:+
Data file D1d-2_1.mgf

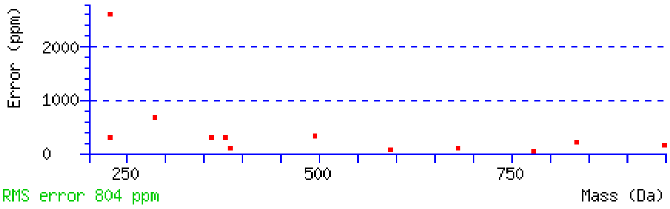
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1060.5764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0049
Matches : 12/88 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			I							11
2	**227.1754**	114.0913			I	***948.4997***	474.7535	931.4731	466.2402	930.4891	465.7482	10
3	**284.1969**	142.6021			G	***835.4156***	418.2114	818.3890	409.6982	817.4050	409.2061	9
4	**383.2653**	192.1363			V	***778.3941***	389.7007	761.3676	381.1874	760.3836	380.6954	8
5	470.2973	235.6523	452.2867	226.6470	S	***679.3257***	340.1665	662.2992	331.6532	661.3151	331.1612	7
6	569.3657	285.1865	551.3552	276.1812	V	***592.2937***	296.6505	575.2671	288.1372	574.2831	287.6452	6
7	684.3927	342.7000	666.3821	333.6947	D	***493.2253***	247.1163	476.1987	238.6030	475.2147	238.1110	5
8	771.4247	386.2160	753.4141	377.2107	S	***378.1983***	189.6028	361.1718	181.0895	360.1878	180.5975	4
9	858.4567	429.7320	840.4462	420.7267	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
10	915.4782	458.2427	897.4676	449.2374	G	204.1343	102.5708	187.1077	94.0575			2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IIGVSVDSSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G26080.1

Score	Mr(calc)	Delta	Sequence
29.2	1060.5764	-0.0003	IIGVSVDSSGK
2.3	1060.5773	-0.0011	SPVAKGMMIK

Mascot: http://www.matrixscience.com/

AT2G26420.1

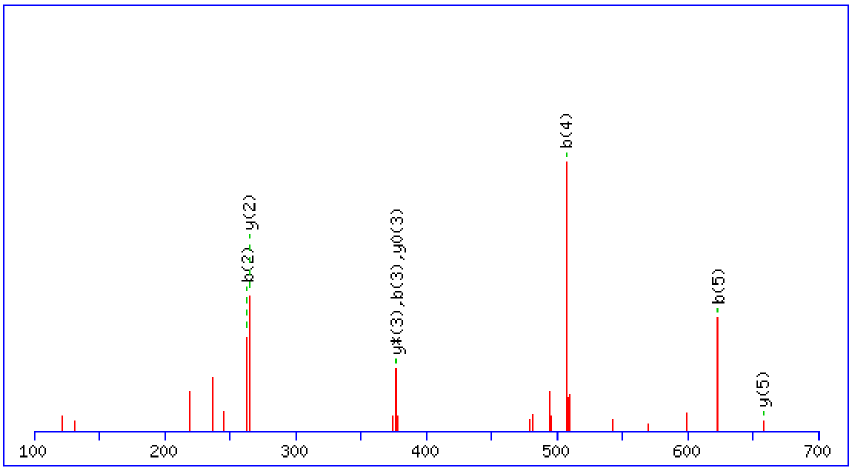
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFIEDK**
Found in **AT2G26420.1** in **TAIR_Arabidopsis**, Symbols: PIP5K3 | PIP5K3; 1-phosphatidylinositol-4-phosphate 5-kinase | chr2:11246512-11249317 REVERSE

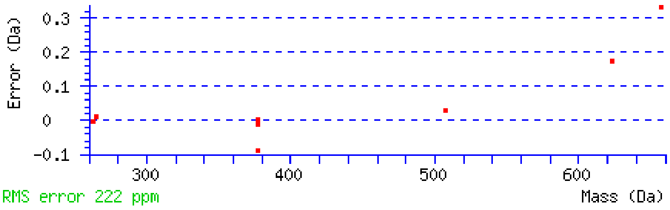
Match to Query 717: 770.391054 from(386.202803,2+) index(4735)
Title: Elution from: 44.281 to 44.281 scan no 6049 cid35.00 polarity:+
Data file D12h-2_3.mgf

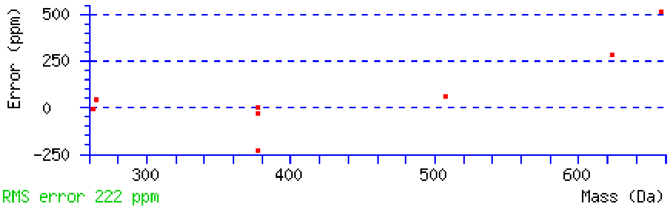
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.3908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.03
Matches : 8/42 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							6
2	***263.1538***	132.0805			F	**657.3170**	329.1622	639.2934	320.1504	639.3065	320.1569	5
3	***377.2349***	189.1211			I	509.2516	255.1294	491.2280	246.1176	491.2410	246.1241	4
4	***507.2746***	254.1409	489.2640	245.1356	E	395.1705	198.0889	377.1469	189.0771	377.1599	189.0836	3
5	***623.2985***	312.1529	605.2880	303.1476	D	**265.1309**	133.0691	247.1073	124.0573	247.1203	124.0638	2
6					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IFIEDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.9	770.3908	0.0002	IFIEDK
18.5	770.3913	-0.0002	IRTEGGK
18.5	770.3913	-0.0002	TLRENK

AT2G26420.1

17.3	770.3908	0.0002	LEFLDK
16.9	770.3908	0.0002	FDIELK
16.9	770.3908	0.0002	FDLELK
16.2	770.3913	-0.0002	LERTNK
16.1	770.3908	0.0002	IFEDLK
13.8	770.3908	0.0002	LEFDLK
13.5	770.3913	-0.0002	ELRTGGK

AT2G27020.1

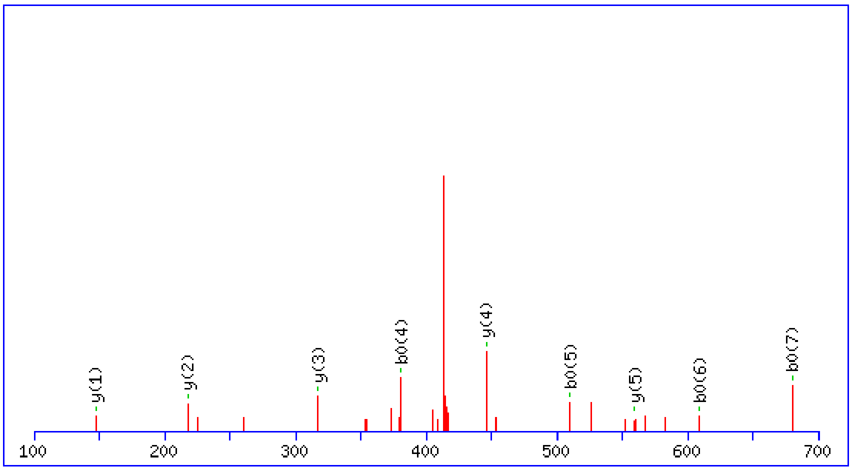
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGVIEVAK**
Found in **AT2G27020.1** in **TAIR_Arabidopsis**, Symbols: PAG1 | PAG1 (20S proteasome alpha subunit G1); peptidase | chr2:11535593-11537936 REVERSE

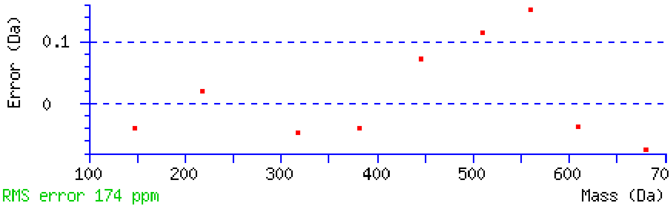
Match to Query 1368: 843.470156 from(422.742354,2+) index(1538)
Title: Elution from: 19.310 to 19.310 scan no 2016 cid35.00 polarity:+
Data file D1d-3_2.mgf

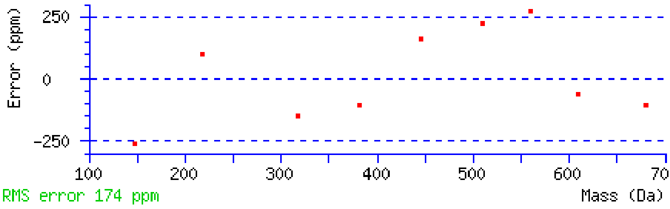
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 843.4702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.033
Matches : 9/64 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	**E**							**8**
2	187.0713	94.0393	169.0608	85.0340	**G**	715.4349	358.2211	698.4083	349.7078	697.4243	349.2158	**7**
3	286.1397	143.5735	268.1292	134.5682	**V**	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	**6**
4	399.2238	200.1155	381.2132	191.1103	**I**	***559.3450***	280.1761	542.3184	271.6629	541.3344	271.1709	**5**
5	528.2664	264.6368	510.2558	255.6316	**E**	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	**4**
6	627.3348	314.1710	609.3243	305.1658	**V**	***317.2183***	159.1128	300.1918	150.5995			**3**
7	698.3719	349.6896	680.3614	340.6843	**A**	***218.1499***	109.5786	201.1234	101.0653			**2**
8					**K**	***147.1128***	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EGVIEVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	843.4702	-0.0000	EGVIEVAK

AT2G27020.1

13.1	843.4702	-0.0000	DVAGELLK
11.9	843.4702	-0.0000	GIEVVEAK
9.9	843.4702	-0.0000	ELAVLGDK
8.8	843.4702	-0.0000	GLLDGLEK
8.3	843.4702	-0.0000	EAVLLGDK
7.3	843.4702	-0.0000	EDQVLIK
7.3	843.4702	-0.0000	EDVQLLK
7.3	843.4702	0.0000	ENVEILK
7.3	843.4702	0.0000	NEIDILK

AT2G27140.1

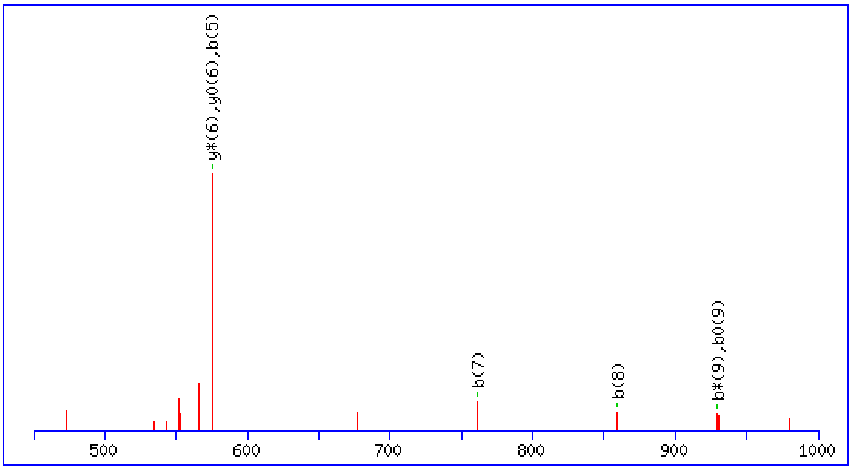
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENPNLPSPSAK**
Found in **AT2G27140.1** in **TAIR_Arabidopsis**, Symbols: | heat shock family protein | chr2:11605574-11606342 REVERSE

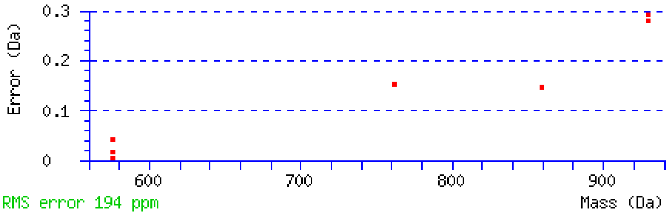
Match to Query 3745: 1166.532692 from(584.273622,2+) index(1217)
Title: Elution from: 17.257 to 17.257 scan no 1664 cid35.00 polarity:+
Data file 0-3_3.mgf

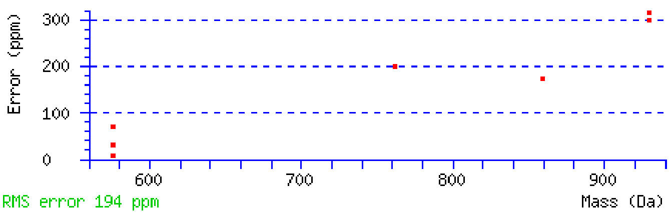
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1166.5360
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.035
Matches : 7/114 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	**E**							**11**
2	247.0839	124.0456	229.0603	115.0338	229.0733	115.0403	**N**	1037.5036	519.2555	1019.4801	510.2437	1019.4931	510.2502	**10**
3	345.1337	173.0705	327.1101	164.0587	327.1231	164.0652	**P**	921.4666	461.2370	903.4431	452.2252	903.4561	452.2317	**9**
4	461.1707	231.0890	443.1471	222.0772	443.1601	222.0837	**N**	823.4168	412.2121	805.3933	403.2003	805.4063	403.2068	**8**
5	***575.2518***	288.1295	557.2282	279.1177	557.2412	279.1243	**L**	707.3798	354.1936	689.3563	345.1818	689.3693	345.1883	**7**
6	673.3016	337.1544	655.2780	328.1426	655.2910	328.1492	**P**	593.2987	297.1530	575.2752	288.1412	575.2882	288.1477	**6**
7	***761.3307***	381.1690	743.3071	372.1572	743.3201	372.1637	**S**	495.2489	248.1281	477.2254	239.1163	477.2384	239.1228	**5**
8	***859.3805***	430.1939	841.3569	421.1821	841.3699	421.1886	**P**	407.2199	204.1136	389.1963	195.1018	389.2093	195.1083	**4**
9	947.4095	474.2084	929.3859	465.1966	929.3990	465.2031	**S**	309.1701	155.0887	291.1465	146.0769	291.1595	146.0834	**3**
10	1019.4437	510.2255	1001.4201	501.2137	1001.4331	501.2202	**A**	221.1410	111.0741	203.1174	102.0624			**2**
11							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of ENPNLPSPSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G27140.1

Score	Mr(calc)	Delta	Sequence
23.2	1166.5360	-0.0033	ENPNLPSPSAK
6.7	1166.5360	-0.0033	DVQAPIEPER
6.1	1166.5328	-0.0001	RFPAWGFGGR
4.8	1166.5346	-0.0019	VAVMQGMTRK
4.6	1166.5317	0.0010	KNVGGRMSAGR

AT2G27170.1

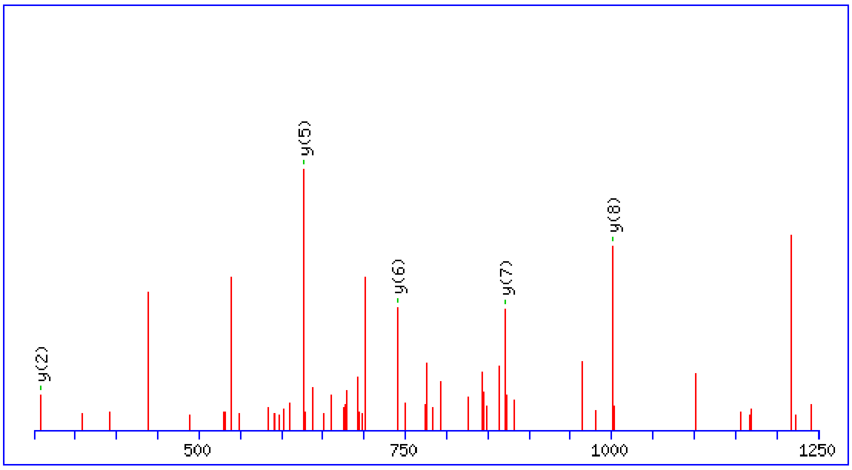
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDALEQLNTVER**
Found in **AT2G27170.1** in **TAIR_Arabidopsis**, Symbols: SMC3, TTN7 | TTN7 (TITAN7); ATP binding | chr2:11616397-11624142 REVERSE

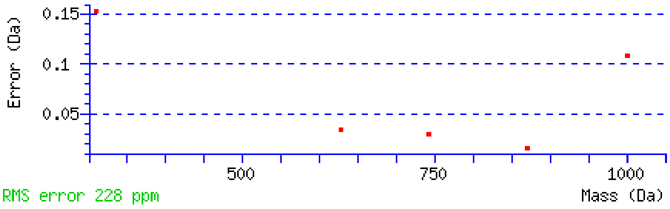
Match to Query 5651: 1418.639074 from(710.326813,2+) index(4947)
Title: Elution from: 46.088 to 46.088 scan no 6243 cid35.00 polarity:+
Data file D6h-2_1.mgf

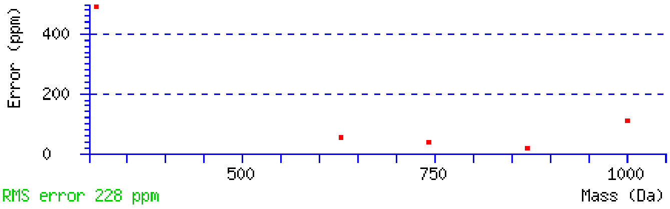
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1418.6362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.016
Matches : 5/128 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							12
2	233.0683	117.0378	215.0447	108.0260	215.0577	108.0325	D	1303.6065	652.3069	1285.5829	643.2951	1285.5959	643.3016	11
3	305.1024	153.0548	287.0788	144.0430	287.0918	144.0496	A	1187.5825	594.2949	1169.5589	585.2831	1169.5719	585.2896	10
4	419.1835	210.0954	401.1599	201.0836	401.1729	201.0901	L	1115.5484	558.2778	1097.5248	549.2660	1097.5378	549.2725	9
5	549.2231	275.1152	531.1995	266.1034	531.2126	266.1099	E	***1001.4673***	501.2373	983.4437	492.2255	983.4567	492.2320	8
6	679.2758	340.1415	661.2522	331.1297	661.2652	331.1362	Q	***871.4276***	436.2175	853.4040	427.2057	853.4171	427.2122	7
7	793.3569	397.1821	775.3333	388.1703	775.3463	388.1768	L	***741.3750***	371.1911	723.3514	362.1793	723.3644	362.1858	6
8	909.3939	455.2006	891.3703	446.1888	891.3833	446.1953	N	***627.2939***	314.1506	609.2703	305.1388	609.2833	305.1453	5
9	1011.4386	506.2229	993.4150	497.2111	993.4280	497.2176	T	511.2569	256.1321	493.2333	247.1203	493.2463	247.1268	4
10	1111.5040	556.2557	1093.4804	547.2439	1093.4935	547.2504	V	409.2122	205.1097	391.1886	196.0979	391.2016	196.1044	3
11	1241.5437	621.2755	1223.5201	612.2637	1223.5331	612.2702	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NDALEQLNTVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G27170.1

Score	Mr(calc)	Delta	Sequence
26.0	1418.6362	0.0029	NDALEQLNTVER
17.5	1418.6418	-0.0027	LSPLEMDSLNQR
0.0	1418.6362	0.0029	AEVLNEENTNLR

AT2G27250.1

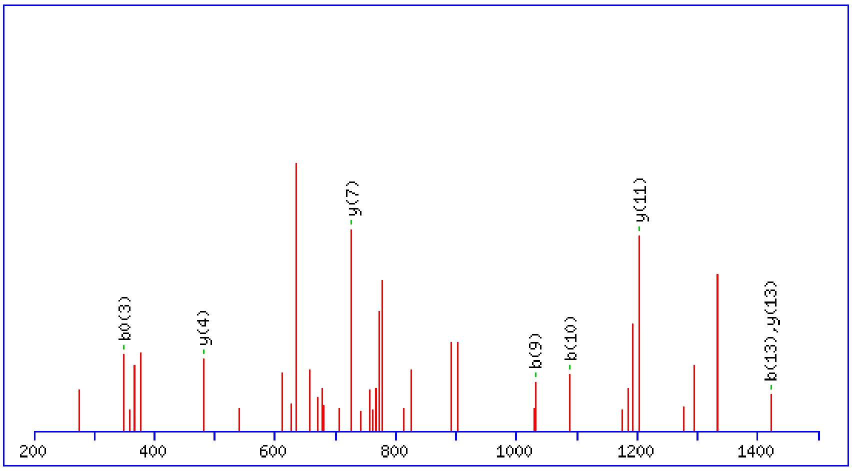
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MESEWVGANGEAEK**
Found in **AT2G27250.1** in **TAIR_Arabidopsis**, Symbols: CLV3 | CLV3 (CLAVATA3); kinase activator/ receptor binding | chr2:11672264-11672548 REVERSE

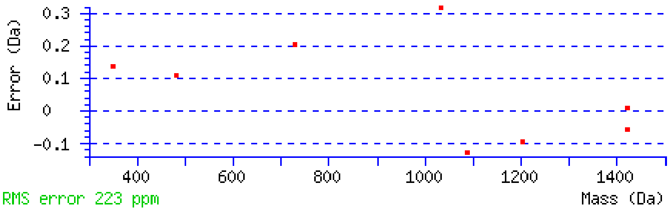
Match to Query 6897: 1568.599878 from(785.307215,2+) index(1600)
Title: Elution from: 21.016 to 21.016 scan no 2141 cid35.00 polarity:+
Data file 0-2_2.mgf

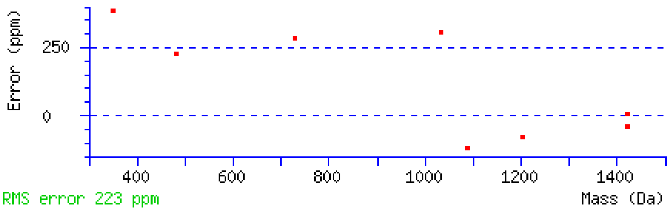
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1568.6007
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.0076
Matches : 8/196 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235					M							14
2	279.0793	140.0433			261.0688	131.0380	E	***1421.5756***	711.2914	1403.5520	702.2796	1403.5650	702.2861	13
3	367.1084	184.0578			349.0978	175.0526	S	1291.5359	646.2716	1273.5124	637.2598	1273.5254	637.2663	12
4	497.1480	249.0777			479.1375	240.0724	E	***1203.5069***	602.2571	1185.4833	593.2453	1185.4963	593.2518	11
5	685.2214	343.1143			667.2108	334.1091	W	1073.4673	537.2373	1055.4437	528.2255	1055.4567	528.2320	10
6	785.2869	393.1471			767.2763	384.1418	V	885.3939	443.2006	867.3703	434.1888	867.3833	434.1953	9
7	843.3054	422.1563			825.2948	413.1510	G	785.3284	393.1678	767.3048	384.1561	767.3179	384.1626	8
8	915.3395	458.1734			897.3289	449.1681	A	***727.3099***	364.1586	709.2863	355.1468	709.2994	355.1533	7
9	***1031.3765***	516.1919	1013.3529	507.1801	1013.3659	507.1866	N	655.2758	328.1415	637.2522	319.1297	637.2652	319.1362	6
10	***1089.3950***	545.2011	1071.3714	536.1893	1071.3844	536.1959	G	539.2388	270.1230	521.2152	261.1112	521.2282	261.1177	5
11	1219.4346	610.2210	1201.4110	601.2092	1201.4241	601.2157	E	***481.2203***	241.1138	463.1967	232.1020	463.2097	232.1085	4
12	1291.4688	646.2380	1273.4452	637.2262	1273.4582	637.2327	A	351.1807	176.0940	333.1571	167.0822	333.1701	167.0887	3
13	***1421.5084***	711.2578	1403.4848	702.2461	1403.4978	702.2526	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
14							K	149.1069	75.0571	131.0833	66.0453			1





AT2G27250.1

NCBI **BLAST** search of MESEWVGANGEAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.2	1568.6007	-0.0008	MESEWVGANGEAEK
0.2	1568.5985	0.0014	DEEPSAEGMGTSVSR

AT2G27280.1

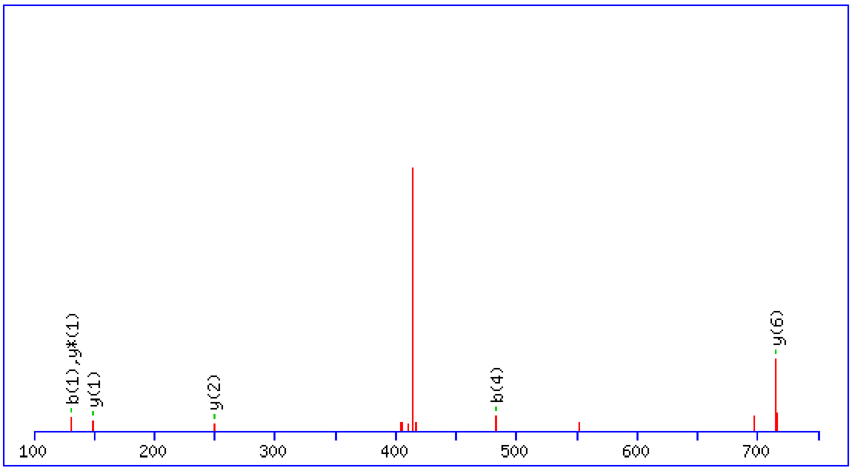
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSNFLVK**
Found in **AT2G27280.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27285.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN79937.1) | chr2:11680904-11682691 REVERSE

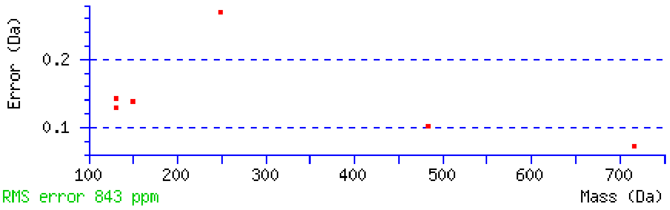
Match to Query 1319: 844.465754 from(423.240153,2+) index(489)
Title: Elution from: 10.458 to 10.458 scan no 757 cid35.00 polarity:+
Data file D12h-3_1.mgf

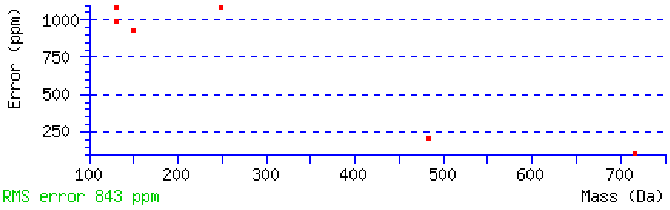
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 844.4667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0092
Matches : 6/60 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	***131.0963***	66.0518	113.0727	57.0400			**K**							**7**
2	219.1254	110.0663	201.1018	101.0545	201.1148	101.0610	**S**	***715.3849***	358.1961	697.3613	349.1843	697.3744	349.1908	**6**
3	335.1624	168.0848	317.1388	159.0730	317.1518	159.0795	**N**	627.3559	314.1816	609.3323	305.1698			**5**
4	***483.2278***	242.1175	465.2042	233.1058	465.2173	233.1123	**F**	511.3189	256.1631	493.2953	247.1513			**4**
5	597.3089	299.1581	579.2853	290.1463	579.2984	290.1528	**L**	363.2534	182.1303	345.2298	173.1186			**3**
6	697.3744	349.1908	679.3508	340.1790	679.3638	340.1855	**V**	***249.1723***	125.0898	231.1487	116.0780			**2**
7							**K**	***149.1069***	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of KSNFLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.0	844.4667	-0.0009	KSNFLVK
23.4	844.4667	-0.0009	KASAFIAK

AT2G27280.1

23.4	844.4667	-0.0009	KYNVAIK
23.4	844.4667	-0.0009	KFSLNVK
23.4	844.4667	-0.0009	KKEFGVK
23.4	844.4667	-0.0009	KNSIFVK
23.4	844.4667	-0.0009	KSIFNVK
21.7	844.4667	-0.0009	EIVPHLK
20.7	844.4667	-0.0009	KLVGGSFK
12.4	844.4667	-0.0009	YGQKLVK

AT2G27530.1

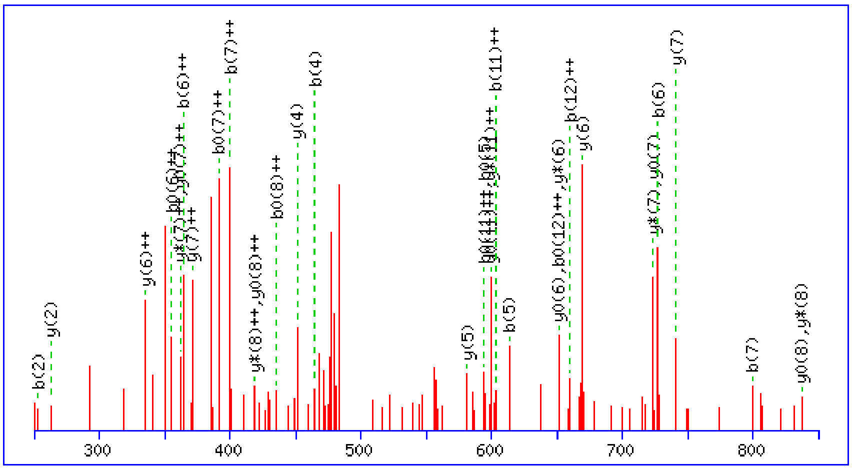
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYHAFLASESVIK**
Found in **AT2G27530.1** in **TAIR_Arabidopsis**, Symbols: PGY1 | 60S ribosomal protein L10A (RPL10aB) | chr2:11770520-11771647 REVERSE

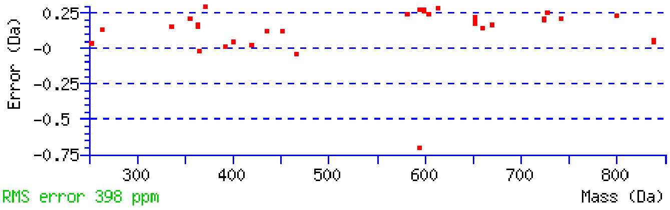
Match to Query 5734: 1466.697033 from(489.906287,3+) index(4609)
Title: Elution from: 45.327 to 45.327 scan no 5921 cid35.00 polarity:+
Data file D1d-1_1.mgf

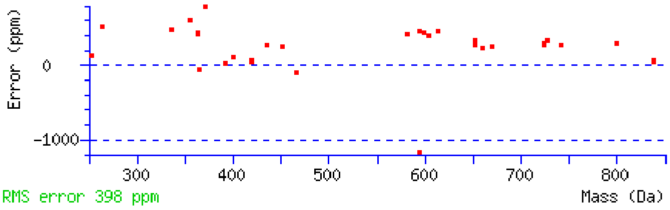
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1466.6982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.035
Matches : 34/114 fragment ions using 55 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218	71.0258	36.0165	S							13
2	***253.0967***	127.0520	235.0861	118.0467	Y	1379.6764	690.3418	1361.6528	681.3300	1361.6658	681.3366	12
3	393.1467	197.0770	375.1362	188.0717	H	1215.6160	608.3117	1197.5925	599.2999	1197.6055	599.3064	11
4	***465.1809***	233.0941	447.1703	224.0888	A	1075.5660	538.2866	1057.5424	529.2749	1057.5555	529.2814	10
5	***613.2463***	307.1268	595.2358	298.1215	F	1003.5319	502.2696	985.5083	493.2578	985.5213	493.2643	9
6	***727.3274***	**364.1673**	709.3169	355.1621	L	855.4664	428.2368	837.4428	419.2251	837.4559	419.2316	8
7	***799.3616***	**400.1844**	781.3510	391.1791	A	***741.3853***	371.1963	723.3617	362.1845	723.3748	362.1910	7
8	887.3906	444.1990	869.3801	435.1937	S	***669.3512***	335.1792	651.3276	326.1674	651.3406	326.1739	6
9	1017.4303	509.2188	999.4197	500.2135	E	***581.3221***	291.1647	563.2985	282.1529	563.3115	282.1594	5
10	1105.4593	553.2333	1087.4488	544.2280	S	***451.2825***	226.1449	433.2589	217.1331	433.2719	217.1396	4
11	1205.5248	**603.2660**	1187.5142	594.2607	V	363.2534	182.1303	345.2298	173.1186			3
12	1319.6059	**660.3066**	1301.5953	651.3013	I	***263.1880***	132.0976	245.1644	123.0858			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SYHAFLASESVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G27530.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.6	1466.6982	-0.0012	SYHAFLASESVIK
6.0	1466.6959	0.0011	QSAVIGSFEEQKK

Mascot: http://www.matrixscience.com/

AT2G27660.1

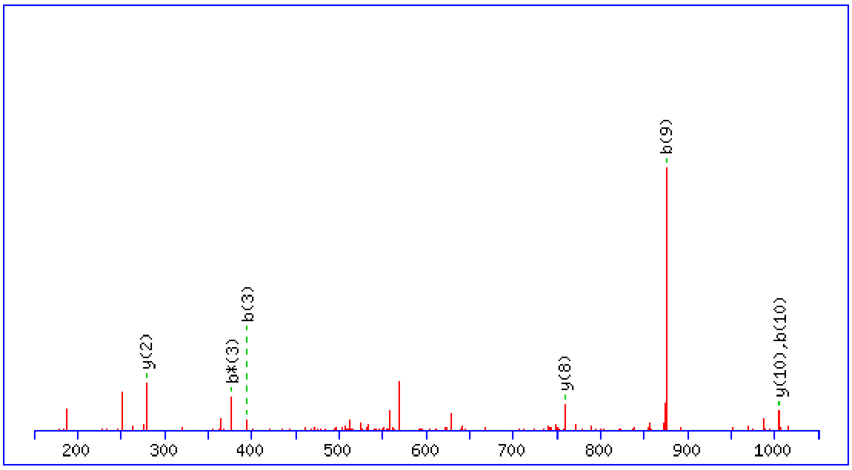
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MNQGSGGGRKK**
Found in **AT2G27660.1** in **TAIR_Arabidopsis**, Symbols: | DC1 domain-containing protein | chr2:11805771-11807927 REVERSE

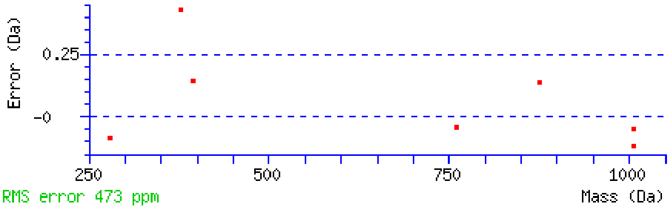
Match to Query 3754: 1152.500658 from(577.257605,2+) index(4344)
Title: Elution from: 40.011 to 40.011 scan no 5460 cid35.00 polarity:+
Data file C7-3_3.mgf

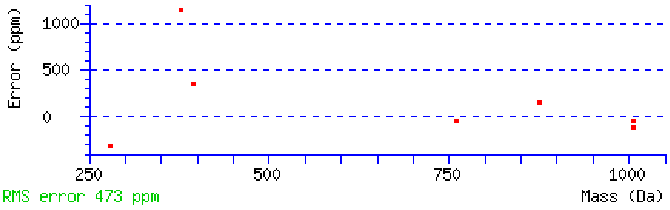
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1152.5030
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.046
Matches : 7/148 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							11
2	265.0767	133.0420	247.0531	124.0302			N	***1005.4779***	503.2426	987.4543	494.2308	987.4673	494.2373	10
3	***395.1294***	198.0683	377.1058	189.0565			Q	889.4409	445.2241	871.4173	436.2123	871.4303	436.2188	9
4	453.1479	227.0776	435.1243	218.0658			G	***759.3882***	380.1977	741.3646	371.1860	741.3777	371.1925	8
5	541.1769	271.0921	523.1533	262.0803	523.1664	262.0868	S	701.3697	351.1885	683.3461	342.1767	683.3592	342.1832	7
6	599.1954	300.1013	581.1718	291.0896	581.1849	291.0961	G	613.3407	307.1740	595.3171	298.1622			6
7	657.2139	329.1106	639.1903	320.0988	639.2034	320.1053	G	555.3222	278.1647	537.2986	269.1529			5
8	715.2324	358.1198	697.2088	349.1081	697.2218	349.1146	G	497.3037	249.1555	479.2801	240.1437			4
9	***875.3217***	438.1645	857.2981	429.1527	857.3111	429.1592	R	439.2852	220.1462	421.2616	211.1344			3
10	***1005.4107***	503.2090	987.3871	494.1972	987.4001	494.2037	K	***279.1959***	140.1016	261.1723	131.0898			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MNQGSGGGRKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G27660.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1152.5030	-0.0023	MNQGSGGGRKK
13.3	1152.4996	0.0010	FQEDRRER
12.8	1152.5026	-0.0019	QMDLLFSNR
7.8	1152.5033	-0.0026	MESLSSITMK
7.2	1152.4986	0.0021	MMTINMKEK
6.8	1152.5026	-0.0019	EAETRMFQK
6.0	1152.5026	-0.0019	FQKCVDQSK
6.0	1152.5004	0.0003	MATTANGNSKK
5.4	1152.5003	0.0003	RSSSDVQMTK
4.5	1152.5026	-0.0019	FEMKGGEVAR

AT2G27680.1

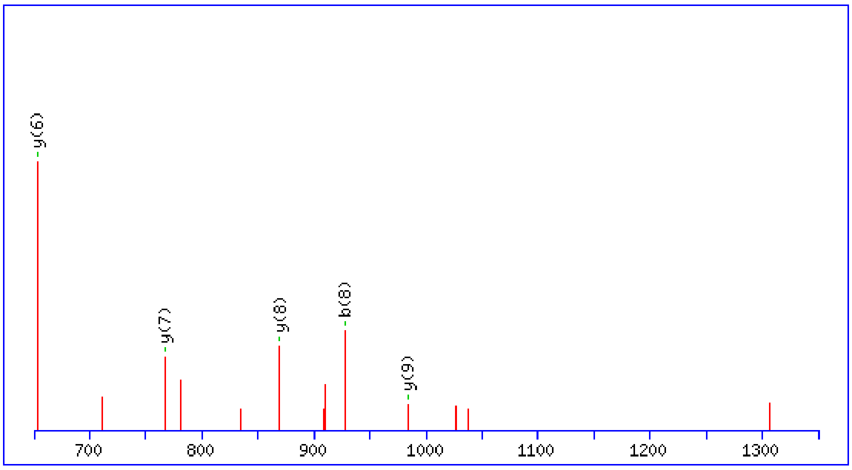
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLDTNLTIPFAGPR**
Found in **AT2G27680.1** in **TAIR_Arabidopsis**, Symbols: | aldo/keto reductase family protein | chr2:11811058-11813042 REVERSE

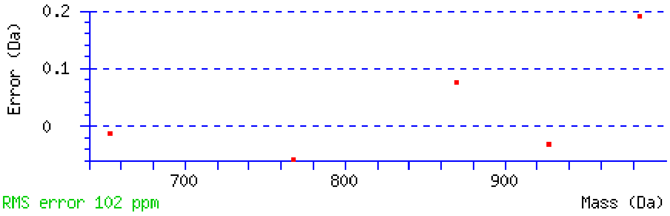
Match to Query 6719: 1578.774280 from(790.394416,2+) index(8999)
Title: Elution from: 82.242 to 82.242 scan no 12383 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

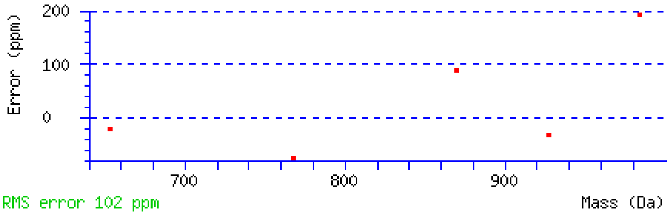


Monoisotopic mass of neutral peptide Mr(calc): 1578.7766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.026
Matches : 5/130 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							14
2	263.1538	132.0805					L	1431.7185	716.3629	1413.6949	707.3511	1413.7079	707.3576	13
3	379.1778	190.0925			361.1672	181.0873	D	1317.6374	659.3223	1299.6138	650.3105	1299.6268	650.3170	12
4	481.2225	241.1149			463.2120	232.1096	T	1201.6134	601.3103	1183.5898	592.2985	1183.6028	592.3051	11
5	597.2595	299.1334	579.2359	290.1216	579.2489	290.1281	N	1099.5687	550.2880	1081.5451	541.2762	1081.5581	541.2827	10
6	711.3406	356.1739	693.3170	347.1622	693.3300	347.1687	L	***983.5317***	492.2695	965.5081	483.2577	965.5211	483.2642	9
7	813.3853	407.1963	795.3617	398.1845	795.3748	398.1910	T	***869.4506***	435.2289	851.4270	426.2171	851.4400	426.2237	8
8	927.4664	464.2368	909.4428	455.2251	909.4559	455.2316	I	***767.4059***	384.2066	749.3823	375.1948			7
9	1025.5162	513.2617	1007.4926	504.2500	1007.5057	504.2565	P	***653.3248***	327.1660	635.3012	318.1542			6
10	1173.5817	587.2945	1155.5581	578.2827	1155.5711	578.2892	F	555.2750	278.1411	537.2514	269.1293			5
11	1245.6158	623.3115	1227.5922	614.2998	1227.6053	614.3063	A	407.2095	204.1084	389.1860	195.0966			4
12	1303.6343	652.3208	1285.6107	643.3090	1285.6238	643.3155	G	335.1754	168.0913	317.1518	159.0795			3
13	1401.6841	701.3457	1383.6605	692.3339	1383.6736	692.3404	P	277.1569	139.0821	259.1333	130.0703			2
14							R	179.1071	90.0572	161.0835	81.0454			1



RMS error 102 ppm



RMS error 102 ppm

NCBI **BLAST** search of FLDTNLTIPFAGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G27680.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.6	1578.7766	-0.0024	FLDTNLTIPFAGPR
7.2	1578.7701	0.0042	AVSRRATLHEMIR
2.9	1578.7778	-0.0035	ERKLPMSLLTDNK
2.6	1578.7778	-0.0035	LSSVPKLEDARAMK

AT2G27710.1

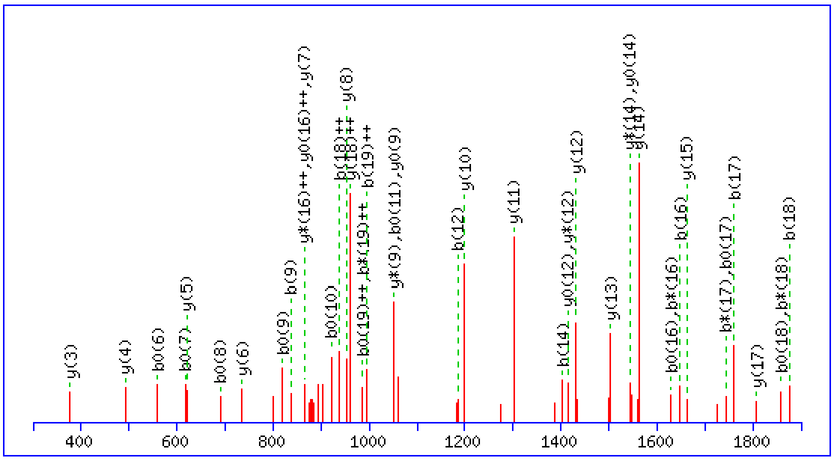
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TILGSVGAETEDSQIELLLK**
Found in **AT2G27710.1** in **TAIR_Arabidopsis**, Symbols: | 60S acidic ribosomal protein P2 (RPP2B) | chr2:11824006-11824747 FORWARD

Match to Query 9769: 2137.064428 from(1069.539490,2+) index(10039)
Title: Elution from: 92.631 to 92.631 scan no 14026 cid35.00 polarity:+
Data file C7-1_2.mgf

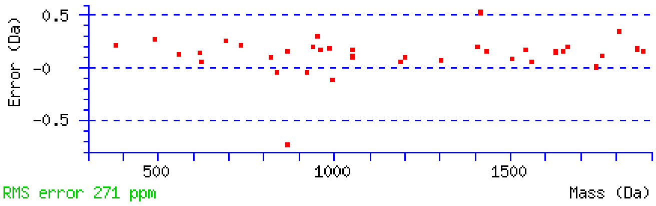
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

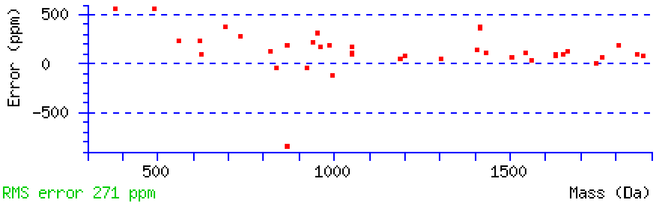


`Monoisotopic mass of neutral peptide Mr(calc):` 2137.0658
`Fixed modifications:` Carbamidomethyl (C) (apply to specified residues or termini only)
`Ions Score:` 103 `Expect:` 2.5e-010
`Matches :` 44/194 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							20
2	217.1331	109.0702			199.1225	100.0649	I	2036.0284	1018.5178	2018.0048	1009.5061	2018.0178	1009.5126	19
3	331.2142	166.1107			313.2036	157.1054	L	1921.9473	961.4773	1903.9237	952.4655	1903.9367	952.4720	18
4	389.2327	195.1200			371.2221	186.1147	G	***1807.8662***	904.4367	1789.8426	895.4250	1789.8556	895.4315	17
5	477.2617	239.1345			459.2512	230.1292	S	1749.8477	875.4275	1731.8241	866.4157	1731.8372	866.4222	16
6	577.3272	289.1672			559.3166	280.1620	V	***1661.8187***	831.4130	1643.7951	822.4012	1643.8081	822.4077	15
7	635.3457	318.1765			617.3351	309.1712	G	***1561.7532***	781.3802	1543.7296	772.3684	1543.7426	772.3750	14
8	707.3798	354.1936			689.3693	345.1883	A	***1503.7347***	752.3710	1485.7111	743.3592	1485.7241	743.3657	13
9	**837.4195**	419.2134			819.4089	410.2081	E	***1431.7006***	716.3539	1413.6770	707.3421	1413.6900	707.3486	12
10	939.4642	470.2357			921.4536	461.2304	T	***1301.6609***	651.3341	1283.6373	642.3223	1283.6504	642.3288	11
11	1069.5038	535.2555			1051.4933	526.2503	E	***1199.6162***	600.3117	1181.5926	591.3000	1181.6056	591.3065	10
12	**1185.5278**	593.2675			1167.5172	584.2623	D	1069.5766	535.2919	1051.5530	526.2801	1051.5660	526.2866	9
13	1273.5569	637.2821			1255.5463	628.2768	S	***953.5526***	477.2799	935.5290	468.2682	935.5420	468.2747	8
14	**1403.6095**	702.3084	1385.5859	693.2966	1385.5989	693.3031	Q	***865.5235***	433.2654	847.5000	424.2536	847.5130	424.2601	7
15	1517.6906	759.3489	1499.6670	750.3371	1499.6800	750.3437	I	***735.4709***	368.2391	717.4473	359.2273	717.4603	359.2338	6
16	**1647.7302**	824.3688	1629.7066	815.3570	1629.7197	815.3635	E	***621.3898***	311.1985	603.3662	302.1867	603.3792	302.1933	5
17	**1761.8113**	881.4093	1743.7877	872.3975	1743.8008	872.4040	L	***491.3502***	246.1787	473.3266	237.1669			4
18	**1875.8924**	938.4499	1857.8688	929.4381	1857.8819	929.4446	L	***377.2691***	189.1382	359.2455	180.1264			3
19	1989.9735	995.4904	1971.9499	986.4786	1971.9630	986.4851	L	263.1880	132.0976	245.1644	123.0858			2
20							K	149.1069	75.0571	131.0833	66.0453			1

AT2G27710.1





NCBI **BLAST** search of TILGSVGAETEDSQIELLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
103.4	2137.0658	-0.0014	TILGSVGAETEDSQIELLLK
6.9	2137.0604	0.0040	TIEVGAEQGALLWGALLSAGR
5.8	2137.0707	-0.0063	GISDIITIPGLVNVDFADVR
4.4	2137.0638	0.0006	DVKLLITLLNQNCESPVR
1.3	2137.0660	-0.0016	MLHFKPGGVNSIIQVTDLK
0.3	2137.0685	-0.0041	VLVATSIREAAAGAEDDALLK

Mascot: http://www.matrixscience.com/

AT2G27720.1

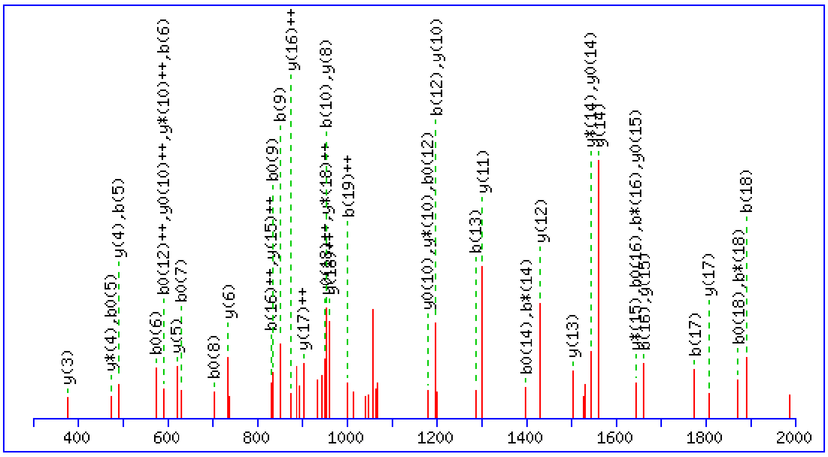
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILGSVGAETEDSQIELLLK**
Found in **AT2G27720.1** in **TAIR_Arabidopsis**, Symbols: | 60S acidic ribosomal protein P2 (RPP2A) | chr2:11825773-11826447 FORWARD

Match to Query 9717: 2151.042542 from(1076.528547,2+) index(10569)
Title: Elution from: 102.109 to 102.109 scan no 15174 cid35.00 polarity:+
Data file D12h-1_2.mgf

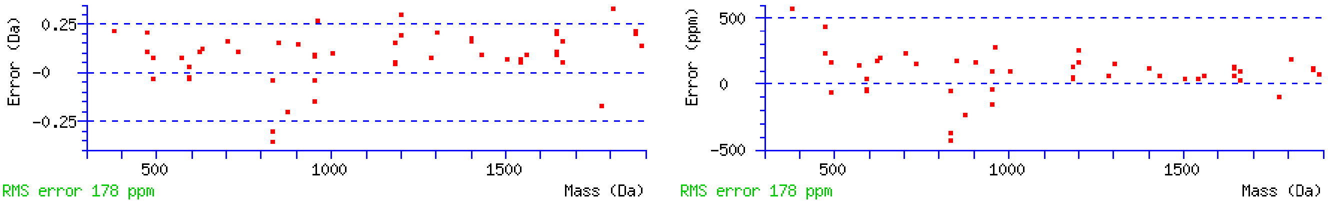
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2151.0451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 97 **Expect:** 1.4e-009
Matches : 51/194 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	**D**							**20**
2	231.1124	116.0598			213.1018	107.0545	**I**	2036.0284	1018.5178	2018.0048	1009.5061	2018.0178	1009.5126	**19**
3	345.1935	173.1004			327.1829	164.0951	**L**	1921.9473	961.4773	1903.9237	952.4655	1903.9367	952.4720	**18**
4	403.2120	202.1096			385.2014	193.1043	**G**	***1807.8662***	904.4367	1789.8426	895.4250	1789.8556	895.4315	**17**
5	***491.2410***	246.1241			473.2304	237.1189	**S**	1749.8477	875.4275	1731.8241	866.4157	1731.8372	866.4222	**16**
6	***591.3065***	296.1569			573.2959	287.1516	**V**	***1661.8187***	831.4130	1643.7951	822.4012	1643.8081	822.4077	**15**
7	649.3250	325.1661			631.3144	316.1608	**G**	***1561.7532***	781.3802	1543.7296	772.3684	1543.7426	772.3750	**14**
8	721.3591	361.1832			703.3485	352.1779	**A**	***1503.7347***	752.3710	1485.7111	743.3592	1485.7241	743.3657	**13**
9	***851.3987***	426.2030			833.3882	417.1977	**E**	***1431.7006***	716.3539	1413.6770	707.3421	1413.6900	707.3486	**12**
10	***953.4435***	477.2254			935.4329	468.2201	**T**	***1301.6609***	651.3341	1283.6373	642.3223	1283.6504	642.3288	**11**
11	1083.4831	542.2452			1065.4725	533.2399	**E**	***1199.6162***	600.3117	1181.5926	591.3000	1181.6056	591.3065	**10**
12	***1199.5071***	600.2572			1181.4965	591.2519	**D**	1069.5766	535.2919	1051.5530	526.2801	1051.5660	526.2866	**9**
13	***1287.5361***	644.2717			1269.5256	635.2664	**S**	***953.5526***	477.2799	935.5290	468.2681	935.5420	468.2747	**8**
14	1417.5888	709.2980	1399.5652	700.2862	1399.5782	700.2927	**Q**	865.5235	433.2654	847.5000	424.2536	847.5130	424.2601	**7**
15	1531.6699	766.3386	1513.6463	757.3268	1513.6593	757.3333	**I**	***735.4709***	368.2391	717.4473	359.2273	717.4603	359.2338	**6**
16	***1661.7095***	831.3584	1643.6859	822.3466	1643.6989	822.3531	**E**	***621.3898***	311.1985	603.3662	302.1867	603.3792	302.1933	**5**
17	***1775.7906***	888.3989	1757.7670	879.3871	1757.7800	879.3937	**L**	***491.3502***	246.1787	473.3266	237.1669			**4**
18	***1889.8717***	945.4395	1871.8481	936.4277	1871.8611	936.4342	**L**	***377.2691***	189.1382	359.2455	180.1264			**3**
19	2003.9528	1002.4800	1985.9292	993.4682	1985.9422	993.4748	**L**	263.1880	132.0976	245.1644	123.0858			**2**
20							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT2G27720.1



NCBI **BLAST** search of DILGSVGAETEDSQIELLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
97.0	2151.0451	-0.0025	DILGSVGAETEDSQIELLLK
5.3	2151.0392	0.0033	LIDDIDLFISKEDFYKR
0.7	2151.0460	-0.0034	AELDIDGTVICALPMISALK
0.1	2151.0383	0.0042	QMIISQRTLEVICRYSK
0.1	2151.0430	-0.0005	IKAMLEEKIDELSQGLHR

Mascot: http://www.matrixscience.com/

AT2G27840.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPNGAFEIAKGGKK**
Found in **AT2G27840.1** in **TAIR_Arabidopsis**, Symbols: HDA13, HDT04 | HDT4 (histone deacetylase 13) | chr2:11869162-11870784 FORWARD

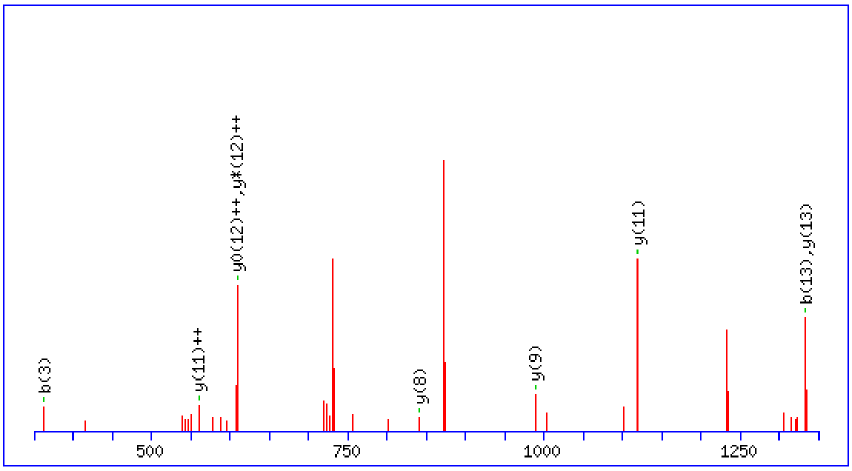
Match to Query 6250: 1480.709884 from(741.362218,2+) index(2507)
Title: Elution from: 26.513 to 26.513 scan no 3142 cid35.00 polarity:+
Data file C7-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1350 Da Full range

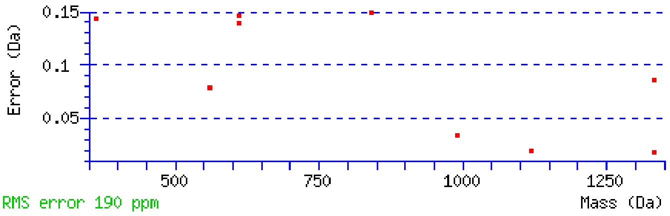
Label all possible matches ○ Label matches used for scoring ●

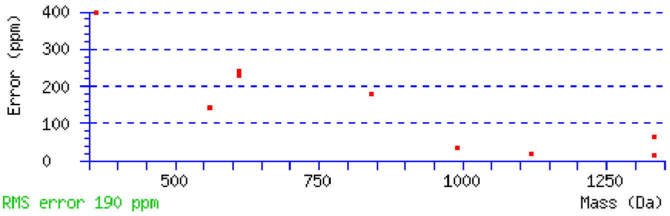
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1480.7069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.045
Matches : 9/188 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							14
2	247.0895	124.0484					P	***1333.6817***	667.3445	1315.6581	658.3327	1315.6711	658.3392	13
3	**363.1265**	182.0669	345.1029	173.0551			N	1235.6319	618.3196	1217.6083	609.3078	1217.6213	609.3143	12
4	421.1450	211.0761	403.1214	202.0643			G	***1119.5949***	560.3011	1101.5713	551.2893	1101.5843	551.2958	11
5	493.1792	247.0932	475.1556	238.0814			A	1061.5764	531.2918	1043.5528	522.2801	1043.5658	522.2866	10
6	641.2446	321.1259	623.2210	312.1141			F	***989.5423***	495.2748	971.5187	486.2630	971.5317	486.2695	9
7	771.2842	386.1458	753.2606	377.1340	753.2737	377.1405	E	***841.4768***	421.2420	823.4532	412.2303	823.4662	412.2368	8
8	885.3653	443.1863	867.3417	434.1745	867.3548	434.1810	I	711.4372	356.2222	693.4136	347.2104			7
9	957.3995	479.2034	939.3759	470.1916	939.3889	470.1981	A	597.3561	299.1817	579.3325	290.1699			6
10	1087.4885	544.2479	1069.4649	535.2361	1069.4779	535.2426	K	525.3219	263.1646	507.2984	254.1528			5
11	1145.5070	573.2571	1127.4834	564.2454	1127.4964	564.2519	G	395.2329	198.1201	377.2093	189.1083			4
12	1203.5255	602.2664	1185.5019	593.2546	1185.5149	593.2611	G	337.2144	169.1108	319.1908	160.0990			3
13	**1333.6145**	667.3109	1315.5910	658.2991	1315.6040	658.3056	K	279.1959	140.1016	261.1723	131.0898			2
14							K	149.1069	75.0571	131.0833	66.0453			1





AT2G27840.1

NCBI **BLAST** search of MPNGAFEIAKGGKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	1480.7069	0.0030	MPNGAFEIAKGGKK
9.5	1480.7116	-0.0017	TGAESAQYLGLLNK
7.9	1480.7091	0.0008	FTYNILIHGVCK
6.9	1480.7129	-0.0030	IVMNMDGRRKPK
4.5	1480.7068	0.0030	LTYPKVMGVDNAR
2.3	1480.7138	-0.0039	DTKHFFSETLLK
2.1	1480.7094	0.0005	VSSSASAQKSGDVIK
1.8	1480.7076	0.0023	LDMTEKQMTLLK
1.2	1480.7064	0.0034	YPYVCLSEIPVK
1.1	1480.7102	-0.0004	RLMISSIEMQQK

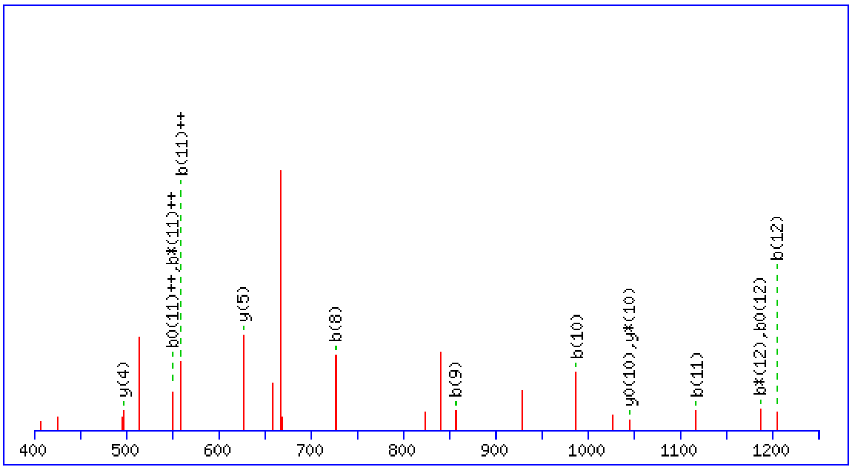
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVSVASSSKEESK**
Found in **AT2G27880.1** in **TAIR_Arabidopsis**, Symbols: | argonaute protein, putative / AGO, putative | chr2:11878565-11883789 FORWARD

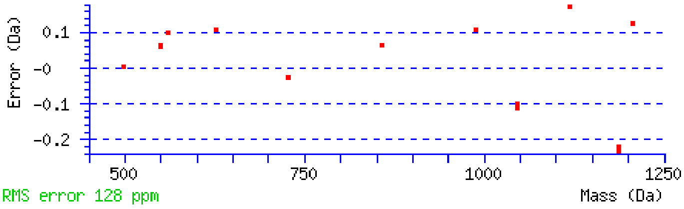
Match to Query 5156: 1352.619490 from(677.317021,2+) index(1665)
Title: Elution from: 22.928 to 22.928 scan no 2274 cid35.00 polarity:+
Data file D6h-2_1.mgf

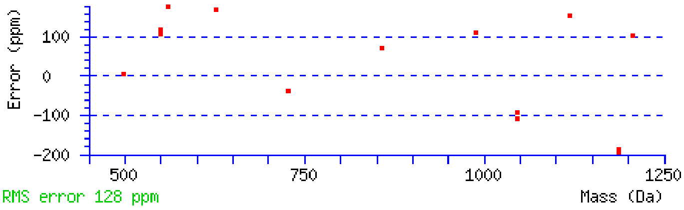
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1352.6230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.013
Matches : 14/126 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							13
2	203.1174	102.0624			185.1069	93.0571	V	1251.5855	626.2964	1233.5619	617.2846	1233.5750	617.2911	12
3	291.1465	146.0769			273.1359	137.0716	S	1151.5201	576.2637	1133.4965	567.2519	1133.5095	567.2584	11
4	391.2120	196.1096			373.2014	187.1043	V	1063.4910	532.2491	1045.4674	523.2374	1045.4804	523.2439	10
5	463.2461	232.1267			445.2355	223.1214	A	963.4256	482.2164	945.4020	473.2046	945.4150	473.2111	9
6	551.2752	276.1412			533.2646	267.1359	S	891.3914	446.1993	873.3678	437.1876	873.3808	437.1941	8
7	639.3042	320.1558			621.2937	311.1505	S	803.3624	402.1848	785.3388	393.1730	785.3518	393.1795	7
8	***727.3333***	364.1703			709.3227	355.1650	S	715.3333	358.1703	697.3097	349.1585	697.3227	349.1650	6
9	***857.4223***	429.2148	839.3987	420.2030	839.4118	420.2095	K	**627.3042**	314.1558	609.2806	305.1440	609.2937	305.1505	5
10	***987.4619***	494.2346	969.4384	485.2228	969.4514	485.2293	E	**497.2152**	249.1112	479.1916	240.0994	479.2046	240.1060	4
11	***1117.5016***	559.2544	1099.4780	550.2426	1099.4910	550.2491	E	367.1756	184.0914	349.1520	175.0796	349.1650	175.0861	3
12	***1205.5306***	603.2690	1187.5071	594.2572	1187.5201	594.2637	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TVSVASSSKEESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G27880.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.6	1352.6230	-0.0035	TVSVASSSKEESK
28.5	1352.6161	0.0034	CMQALVRVQGR
19.9	1352.6182	0.0013	TMPETKSGSGSKK
16.7	1352.6205	-0.0010	ESFQKLEVACK
14.9	1352.6182	0.0013	KMQVSGASDLASK
13.9	1352.6205	-0.0010	VENMFKDIQSK
13.7	1352.6209	-0.0014	KSEQMVNAQKR
12.3	1352.6198	-0.0003	YAQLWNEQRK
11.1	1352.6182	0.0013	MSSGQKEKVEAK
9.3	1352.6175	0.0020	QKVSRNSDWSK

Mascot: http://www.matrixscience.com/

AT2G28000.1

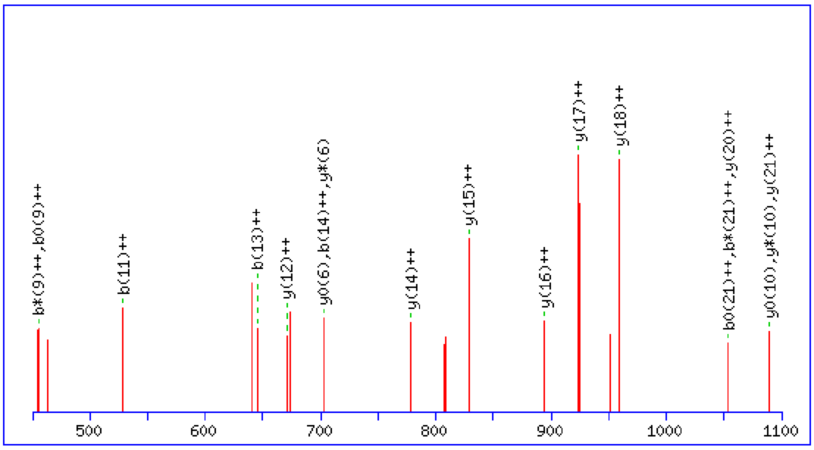
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CALQNAASVAGMVLTTQAIVVDKPKPK**
Found in **AT2G28000.1** in **TAIR_Arabidopsis**, Symbols: CH-CPN60A, SLP, CPN60A | CPN60A (chloroplast / 60 kDa chaperonin alpha subunit); ATP binding / protein binding / unfolded protein binding | chr2:11933680-11936261 FORWARD

Match to Query 10706: 2843.423908 from(711.863253,4+) index(9328)
Title: Elution from: 83.629 to 83.629 scan no 12656 cid35.00 polarity:+
Data file C7-3_2.mgf

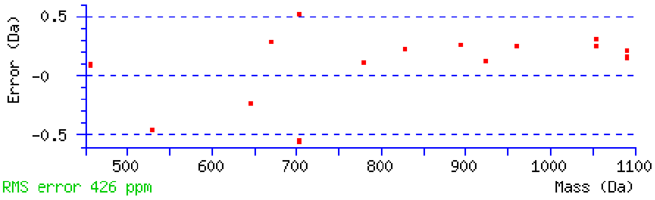
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

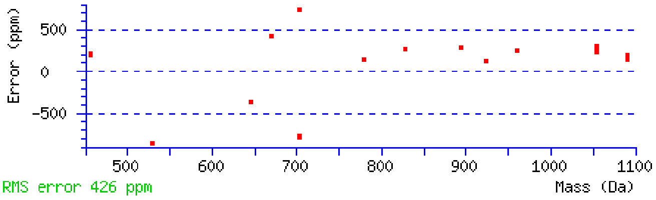


Monoisotopic mass of neutral peptide Mr(calc): 2843.4186
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2e-005
Matches : 19/282 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	163.0320	82.0196					C							27
2	235.0661	118.0367					A	2682.4012	1341.7042	2664.3776	1332.6924	2664.3906	1332.6989	26
3	349.1472	175.0773					L	2610.3670	1305.6871	2592.3434	1296.6753	2592.3564	1296.6819	25
4	479.1999	240.1036	461.1763	231.0918			Q	2496.2859	1248.6466	2478.2623	1239.6348	2478.2753	1239.6413	24
5	595.2369	298.1221	577.2133	289.1103			N	2366.2333	1183.6203	2348.2097	1174.6085	2348.2227	1174.6150	23
6	667.2710	334.1392	649.2475	325.1274			A	2250.1963	1125.6018	2232.1727	1116.5900	2232.1857	1116.5965	22
7	739.3052	370.1562	721.2816	361.1444			A	2178.1621	1089.5847	2160.1385	1080.5729	2160.1515	1080.5794	21
8	827.3342	414.1708	809.3107	405.1590	809.3237	405.1655	S	2106.1280	1053.5676	2088.1044	1044.5558	2088.1174	1044.5623	20
9	927.3997	464.2035	909.3761	455.1917	909.3891	455.1982	V	2018.0989	1009.5531	2000.0753	1000.5413	2000.0883	1000.5478	19
10	999.4338	500.2206	981.4103	491.2088	981.4233	491.2153	A	1918.0335	959.5204	1900.0099	950.5086	1900.0229	950.5151	18
11	1057.4523	**529.2298**	1039.4288	520.2180	1039.4418	520.2245	G	1845.9993	923.5033	1827.9757	914.4915	1827.9887	914.4980	17
12	1189.4899	595.2486	1171.4663	586.2368	1171.4793	586.2433	M	1787.9808	894.4940	1769.9572	885.4822	1769.9702	885.4888	16
13	1289.5553	**645.2813**	1271.5317	636.2695	1271.5447	636.2760	V	1655.9433	828.4753	1637.9197	819.4635	1637.9327	819.4700	15
14	1403.6364	**702.3218**	1385.6128	693.3101	1385.6258	693.3166	L	1555.8778	778.4426	1537.8543	769.4308	1537.8673	769.4373	14
15	1505.6811	753.3442	1487.6575	744.3324	1487.6706	744.3389	T	1441.7967	721.4020	1423.7732	712.3902	1423.7862	712.3967	13
16	1607.7258	804.3666	1589.7023	795.3548	1589.7153	795.3613	T	1339.7520	670.3796	1321.7284	661.3679	1321.7415	661.3744	12
17	1737.7785	869.3929	1719.7549	860.3811	1719.7679	860.3876	Q	1237.7073	619.3573	1219.6837	610.3455	1219.6967	610.3520	11
18	1809.8126	905.4100	1791.7890	896.3982	1791.8021	896.4047	A	1107.6547	554.3310	1089.6311	545.3192	1089.6441	545.3257	10
19	1923.8937	962.4505	1905.8701	953.4387	1905.8832	953.4452	I	1035.6205	518.3139	1017.5969	509.3021	1017.6099	509.3086	9
20	2023.9592	1012.4832	2005.9356	1003.4714	2005.9486	1003.4779	V	921.5394	461.2733	903.5158	452.2616	903.5288	452.2681	8
21	2124.0246	1062.5160	2106.0010	1053.5042	2106.0141	1053.5107	V	821.4740	411.2406	803.4504	402.2288	803.4634	402.2353	7
22	2240.0486	1120.5279	2222.0250	1111.5162	2222.0380	1111.5227	D	721.4085	361.2079	703.3849	352.1961	703.3980	352.2026	6
23	2370.1376	1185.5725	2352.1141	1176.5607	2352.1271	1176.5672	K	605.3845	303.1959	587.3610	294.1841			5
24	2468.1874	1234.5974	2450.1639	1225.5856	2450.1769	1225.5921	P	475.2955	238.1514	457.2719	229.1396			4

25	2598.2765	1299.6419	2580.2529	1290.6301	2580.2659	1290.6366	**K**	377.2457	189.1265	359.2221	180.1147			**3**
26	2696.3263	1348.6668	2678.3027	1339.6550	2678.3157	1339.6615	**P**	247.1567	124.0820	229.1331	115.0702			**2**
27							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of CALQNAASVAGMVLTTQAIVVDKPKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.5	2843.4186	0.0053	CALQNAASVAGMVLTTQAIVVDKPKPK
5.6	2843.4226	0.0013	SGRKGQLSVATEVFEVAPSLHVVELR
1.8	2843.4201	0.0038	LSQFSEAPRLAHQQAVMKILHYIK
0.3	2843.4233	0.0006	ARLLCTAEANPQELLEKIITISEAK

Mascot: http://www.matrixscience.com/

AT2G28720.1

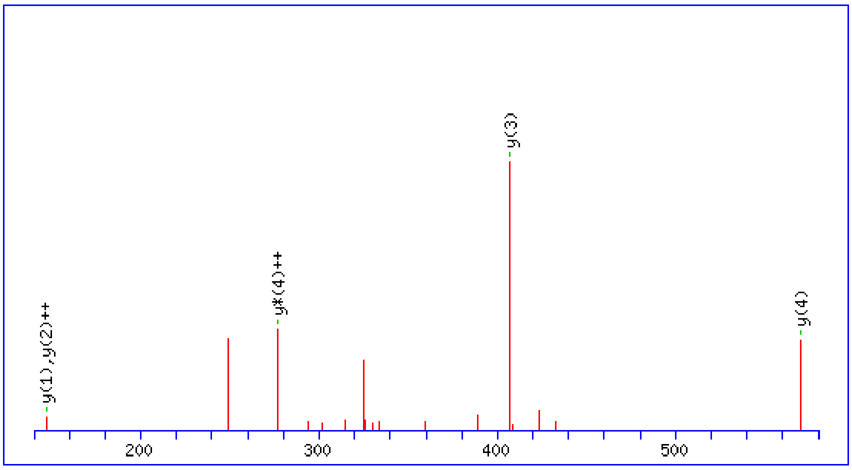
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYIFK**
Found in **AT2G28720.1** in **TAIR_Arabidopsis**

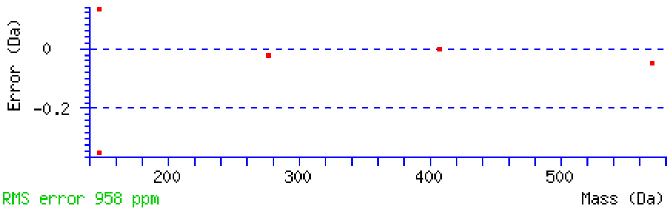
Match to Query 564: 682.404858 from(342.209705,2+) index(3928)
Title: Elution from: 36.577 to 36.577 scan no 4889 cid35.00 polarity:+
Data file D12h-1_3.mgf

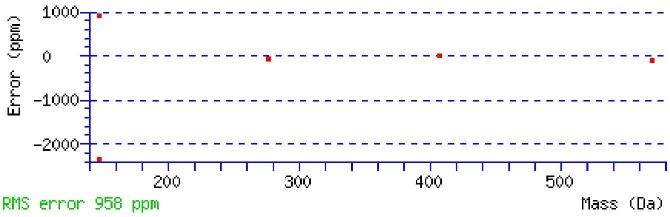
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 682.4054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0014
Matches : 7/24 fragment ions using 4 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	114.0913	57.5493	**I**					**5**
2	277.1547	139.0810	**Y**	***570.3286***	285.6679	553.3021	277.1547	**4**
3	390.2387	195.6230	**I**	***407.2653***	204.1363	390.2387	195.6230	**3**
4	537.3071	269.1572	**F**	294.1812	147.5942	277.1547	139.0810	**2**
5			**K**	***147.1128***	74.0600	130.0863	65.5468	**1**





NCBI **BLAST** search of IYIFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.3	682.4054	-0.0005	IYIFK
29.3	682.4054	-0.0005	IYLFK
18.9	682.4054	-0.0005	IFLYK
13.5	682.4054	-0.0005	YLLFK
10.7	682.4054	-0.0005	LIFYK

AT2G28720.1

10.7	682.4054	-0.0005	YLFLK
5.2	682.4054	-0.0005	IFPPLP

Mascot: http://www.matrixscience.com/

AT2G28820.1

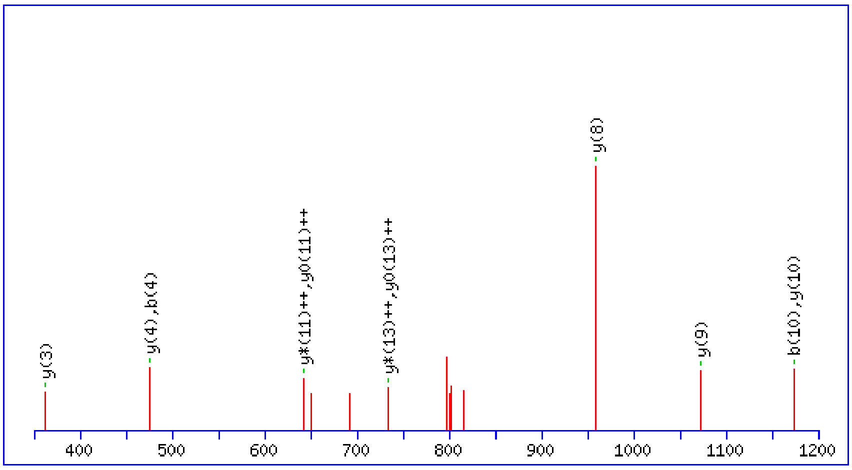
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YALQTLEPAWITSR**
Found in **AT2G28820.1** in **TAIR_Arabidopsis**, Symbols: | structural constituent of ribosome | chr2:12374078-12375141 REVERSE

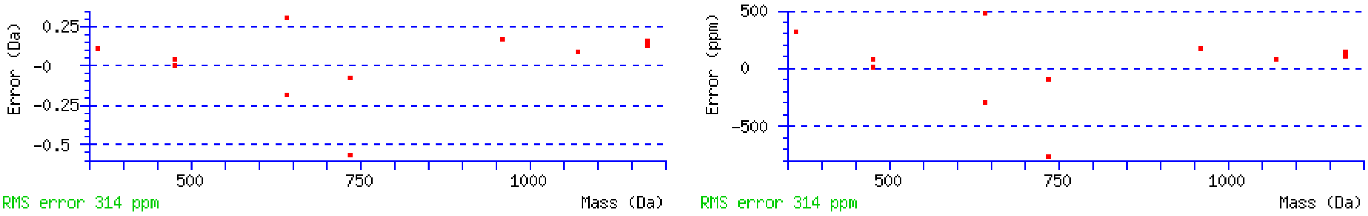
Match to Query 7999: 1647.860772 from(824.937662,2+) index(9278)
Title: Elution from: 81.782 to 81.782 scan no 12286 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1647.8620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00041
Matches : 11/140 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							14
2	235.1077	118.0575					A	1485.8060	743.4066	1468.7795	734.8934	1467.7954	734.4014	13
3	348.1918	174.5995					L	1414.7689	707.8881	1397.7423	699.3748	1396.7583	698.8828	12
4	**476.2504**	238.6288	459.2238	230.1155			Q	1301.6848	651.3461	1284.6583	642.8328	1283.6743	642.3408	11
5	577.2980	289.1527	560.2715	280.6394	559.2875	280.1474	T	***1173.6263***	587.3168	1156.5997	578.8035	1155.6157	578.3115	10
6	690.3821	345.6947	673.3556	337.1814	672.3715	336.6894	L	***1072.5786***	536.7929	1055.5520	528.2796	1054.5680	527.7876	9
7	819.4247	410.2160	802.3981	401.7027	801.4141	401.2107	E	***959.4945***	480.2509	942.4680	471.7376	941.4839	471.2456	8
8	916.4775	458.7424	899.4509	450.2291	898.4669	449.7371	P	830.4519	415.7296	813.4254	407.2163	812.4413	406.7243	7
9	987.5146	494.2609	970.4880	485.7477	969.5040	485.2556	A	733.3992	367.2032	716.3726	358.6899	715.3886	358.1979	6
10	**1173.5939**	587.3006	1156.5673	578.7873	1155.5833	578.2953	W	662.3620	331.6847	645.3355	323.1714	644.3515	322.6794	5
11	1286.6780	643.8426	1269.6514	635.3293	1268.6674	634.8373	I	***476.2827***	238.6450	459.2562	230.1317	458.2722	229.6397	4
12	1387.7256	694.3665	1370.6991	685.8532	1369.7151	685.3612	T	***363.1987***	182.1030	346.1721	173.5897	345.1881	173.0977	3
13	1474.7577	737.8825	1457.7311	729.3692	1456.7471	728.8772	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of YALQTLEPAWITSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G28820.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.3	1647.8620	-0.0013	YALQTLEPAWITSR

AT2G28880.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSFISLPCR**
Found in **AT2G28880.1** in **TAIR_Arabidopsis**, Symbols: EMB1997 | EMB1997 (EMBRYO DEFECTIVE 1997); anthranilate synthase/ catalytic/ oxo-acid-lyase | chr2:12406014-12410185 REVERSE

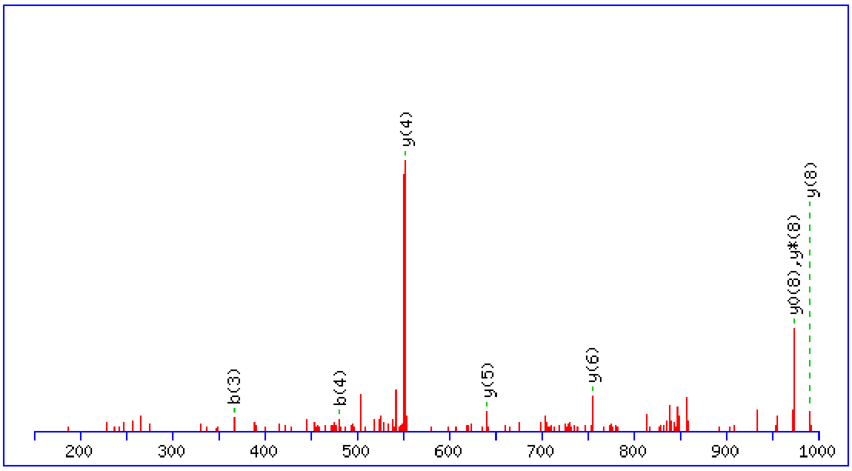
Match to Query 3526: 1120.550356 from(561.282454,2+) index(3023)
Title: Elution from: 30.318 to 30.318 scan no 3761 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

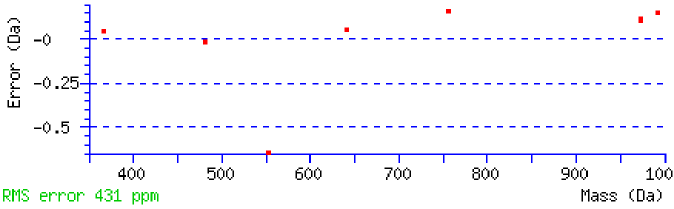
Label all possible matches ○ Label matches used for scoring ●

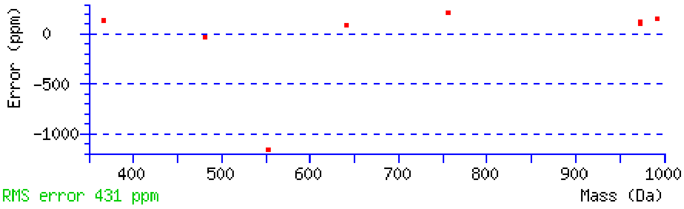
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1120.5491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.009
Matches : 8/86 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							9
2	219.1254	110.0663	201.1018	101.0545	201.1148	101.0610	S	***991.4674***	496.2373	973.4438	487.2255	973.4568	487.2320	8
3	**367.1908**	184.0990	349.1672	175.0873	349.1803	175.0938	F	903.4383	452.2228	885.4147	443.2110	885.4278	443.2175	7
4	**481.2719**	241.1396	463.2483	232.1278	463.2614	232.1343	I	***755.3729***	378.1901	737.3493	369.1783	737.3623	369.1848	6
5	569.3010	285.1541	551.2774	276.1423	551.2904	276.1488	S	***641.2918***	321.1495	623.2682	312.1377	623.2812	312.1442	5
6	683.3821	342.1947	665.3585	333.1829	665.3715	333.1894	L	***553.2627***	277.1350	535.2391	268.1232			4
7	781.4319	391.2196	763.4083	382.2078	763.4213	382.2143	P	439.1816	220.0944	421.1580	211.0827			3
8	943.4566	472.2319	925.4330	463.2201	925.4460	463.2267	C	341.1318	171.0695	323.1082	162.0578			2
9							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KSFISLPCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G28880.1

27.0	1120.5491	0.0012	KSFISLPCR
8.6	1120.5517	-0.0013	QKIDSSSKSK
8.6	1120.5516	-0.0013	KAATTGTSKDK
8.5	1120.5514	-0.0010	KAVGFMAAWK
3.6	1120.5518	-0.0014	TGKMGLRWR
3.4	1120.5514	-0.0010	FVMVNGWKK
1.1	1120.5491	0.0012	DFVQMLARK
1.0	1120.5491	0.0012	KSLICSFPR
0.8	1120.5496	0.0008	LVQRRMER
0.6	1120.5491	0.0012	FILTCNIAR

AT2G28900.1

Mascot Search Results

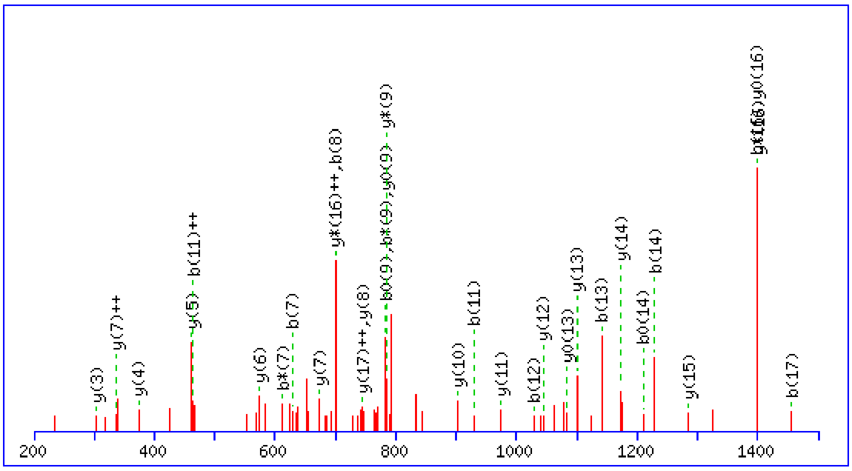
Peptide View

MS/MS Fragmentation of **NAMLAGAATGAVLSAVGK**
Found in **AT2G28900.1** in **TAIR_Arabidopsis**, Symbols: ATOEP16-L, ATOEP16-1, OEP16 | OEP16 (OUTER ENVELOPE PROTEIN 16); P-P-bond-hydrolysis-driven protein transmembrane transporter | chr2:12421500-12422536 REVERSE

Match to Query 6937: 1600.860974 from(801.437763,2+) index(7905)
Title: Elution from: 70.431 to 70.431 scan no 10419 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

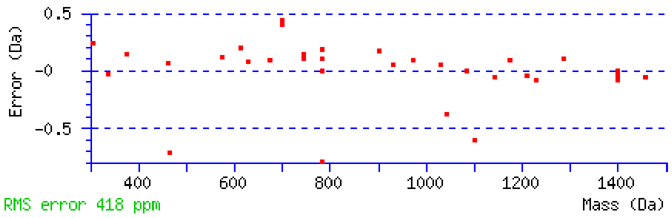
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

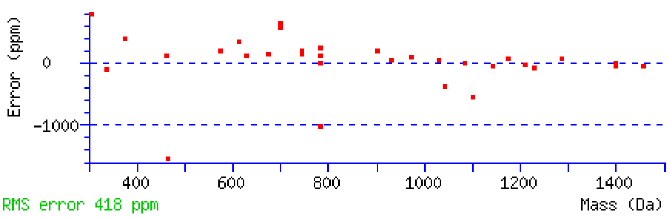


Monoisotopic mass of neutral peptide Mr(calc): 1600.8607
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.4e-007
Matches : 33/180 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							18
2	186.0873	93.5473	169.0608	85.0340			A	1487.8250	744.4162	1470.7985	735.9029	1469.8145	735.4109	17
3	317.1278	159.0675	300.1013	150.5543			M	1416.7879	708.8976	1399.7614	700.3843	1398.7773	699.8923	16
4	430.2119	215.6096	413.1853	207.0963			L	***1285.7474***	643.3774	1268.7209	634.8641	1267.7369	634.3721	15
5	501.2490	251.1281	484.2224	242.6149			A	***1172.6634***	586.8353	1155.6368	578.3220	1154.6528	577.8300	14
6	558.2704	279.6389	541.2439	271.1256			G	***1101.6263***	551.3168	1084.5997	542.8035	1083.6157	542.3115	13
7	**629.3076**	315.1574	612.2810	306.6441			A	***1044.6048***	522.8060	1027.5782	514.2928	1026.5942	513.8007	12
8	**700.3447**	350.6760	683.3181	342.1627			A	***973.5677***	487.2875	956.5411	478.7742	955.5571	478.2822	11
9	801.3924	401.1998	784.3658	392.6865	783.3818	392.1945	T	***902.5306***	451.7689	885.5040	443.2556	884.5200	442.7636	10
10	858.4138	429.7105	841.3873	421.1973	840.4033	420.7053	G	801.4829	401.2451	784.4563	392.7318	783.4723	392.2398	9
11	**929.4509**	465.2291	912.4244	456.7158	911.4404	456.2238	A	***744.4614***	372.7343	727.4349	364.2211	726.4509	363.7291	8
12	**1028.5193**	514.7633	1011.4928	506.2500	1010.5088	505.7580	V	***673.4243***	337.2158	656.3978	328.7025	655.4137	328.2105	7
13	**1141.6034**	571.3053	1124.5769	562.7921	1123.5928	562.3001	L	***574.3559***	287.6816	557.3293	279.1683	556.3453	278.6763	6
14	**1228.6354**	614.8214	1211.6089	606.3081	1210.6249	605.8161	S	***461.2718***	231.1396	444.2453	222.6263	443.2613	222.1343	5
15	1299.6725	650.3399	1282.6460	641.8266	1281.6620	641.3346	A	***374.2398***	187.6235	357.2132	179.1103			4
16	**1398.7410**	699.8741	1381.7144	691.3608	1380.7304	690.8688	V	***303.2027***	152.1050	286.1761	143.5917			3
17	**1455.7624**	728.3849	1438.7359	719.8716	1437.7519	719.3796	G	204.1343	102.5708	187.1077	94.0575			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT2G28900.1





NCBI **BLAST** search of NAMLAGAATGAVLSAVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.0	1600.8607	0.0003	NAMLAGAATGAVLSAVGK
0.1	1600.8607	0.0003	LGKEILECTPKGTR
0.0	1600.8573	0.0037	RDWVEKLITNAEK

Mascot: http://www.matrixscience.com/

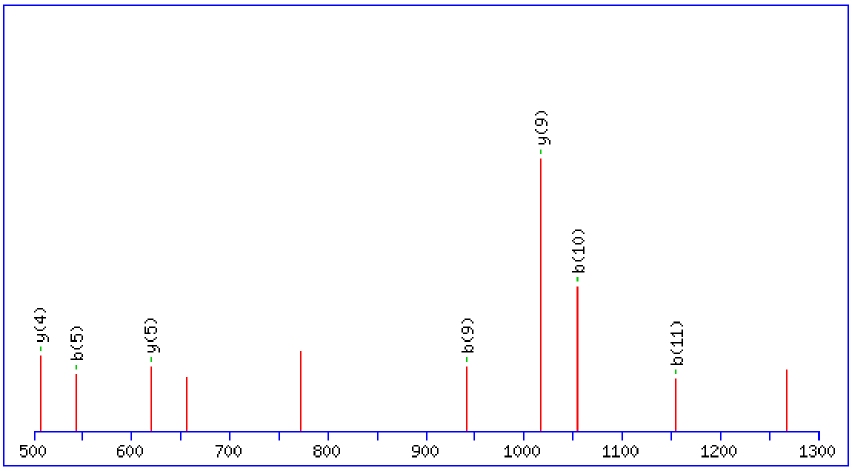
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GWEGIGLEVITEEK**
Found in **AT2G29450.1** in **TAIR_Arabidopsis**, Symbols: ATGSTU1, AT103-1A, ATGSTU5 | ATGSTU5 (Arabidopsis thaliana Glutathione S-transferase (class tau) 5); glutathione transferase | chr2:12631851-12632643 REVERSE

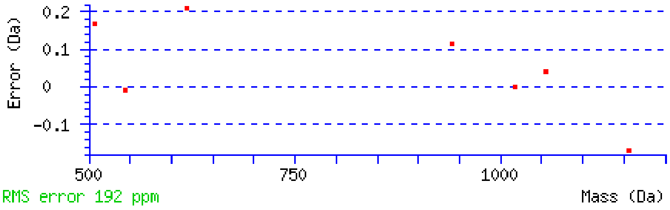
Match to Query 6685: 1558.789896 from(780.402224,2+) index(9008)
Title: Elution from: 81.359 to 81.359 scan no 12240 cid35.00 polarity:+
Data file D12h-3_2.mgf

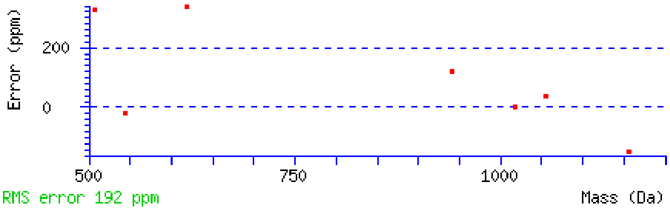
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1558.7879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0034
Matches : 7/124 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180			**G**							**14**
2	244.1081	122.5577			**W**	1502.7737	751.8905	1485.7472	743.3772	1484.7631	742.8852	**13**
3	373.1506	187.0790	355.1401	178.0737	**E**	1316.6944	658.8508	1299.6678	650.3376	1298.6838	649.8456	**12**
4	430.1721	215.5897	412.1615	206.5844	**G**	1187.6518	594.3295	1170.6252	585.8163	1169.6412	585.3243	**11**
5	***543.2562***	272.1317	525.2456	263.1264	**I**	1130.6303	565.8188	1113.6038	557.3055	1112.6198	556.8135	**10**
6	600.2776	300.6425	582.2671	291.6372	**G**	**1017.5463**	509.2768	1000.5197	500.7635	999.5357	500.2715	**9**
7	713.3617	357.1845	695.3511	348.1792	**L**	960.5248	480.7660	943.4983	472.2528	942.5142	471.7608	**8**
8	842.4043	421.7058	824.3937	412.7005	**E**	847.4407	424.2240	830.4142	415.7107	829.4302	415.2187	**7**
9	***941.4727***	471.2400	923.4621	462.2347	**V**	718.3981	359.7027	701.3716	351.1894	700.3876	350.6974	**6**
10	***1054.5568***	527.7820	1036.5462	518.7767	**I**	**619.3297**	310.1685	602.3032	301.6552	601.3192	301.1632	**5**
11	***1155.6045***	578.3059	1137.5939	569.3006	**T**	**506.2457**	253.6265	489.2191	245.1132	488.2351	244.6212	**4**
12	1284.6470	642.8272	1266.6365	633.8219	**E**	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	**3**
13	1413.6896	707.3485	1395.6791	698.3432	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
14					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GWEGIGLEVITEEK

AT2G29450.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.1	1558.7879	0.0020	GWEGIGLEVITEEK

AT2G29630.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDGIAENLNWEVFR**
Found in **AT2G29630.1** in **TAIR_Arabidopsis**, Symbols: | thiamine biosynthesis family protein / thiC family protein | chr2:12674472-12676646 FORWARD

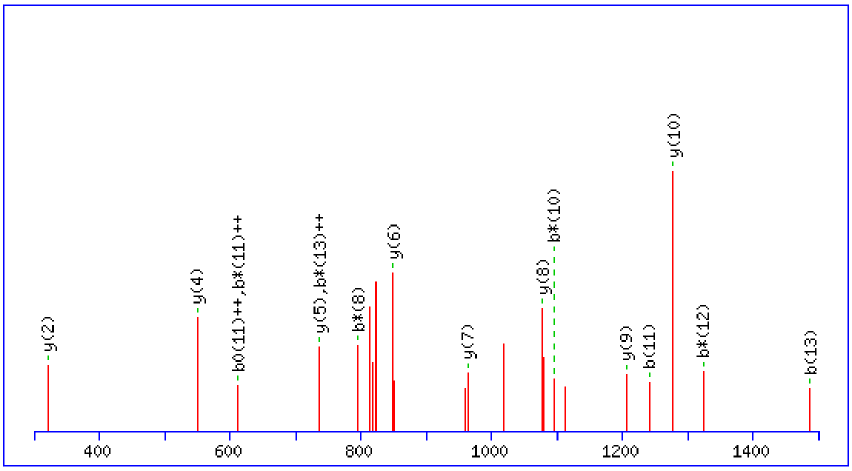
Match to Query 7977: 1660.817554 from(831.416053,2+) index(9678)
Title: Elution from: 88.088 to 88.088 scan no 13207 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

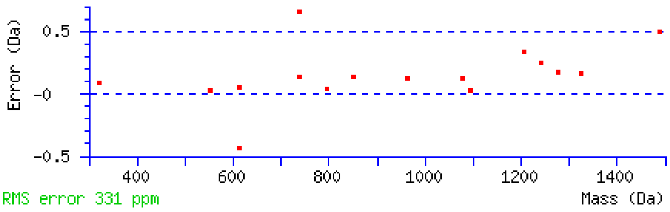
Label all possible matches ○ Label matches used for scoring ●

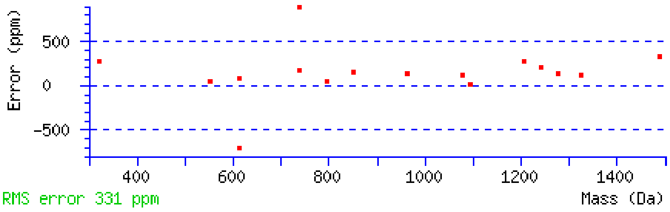
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1660.8209
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 8.9e-007
Matches : 16/136 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							14
2	215.1026	108.0550			197.0921	99.0497	D	1562.7598	781.8835	1545.7332	773.3703	1544.7492	772.8782	13
3	272.1241	136.5657			254.1135	127.5604	G	1447.7328	724.3701	1430.7063	715.8568	1429.7223	715.3648	12
4	385.2082	193.1077			367.1976	184.1024	I	1390.7114	695.8593	1373.6848	687.3461	1372.7008	686.8540	11
5	456.2453	228.6263			438.2347	219.6210	A	***1277.6273***	639.3173	1260.6008	630.8040	1259.6167	630.3120	10
6	585.2879	293.1476			567.2773	284.1423	E	***1206.5902***	603.7987	1189.5636	595.2855	1188.5796	594.7935	9
7	699.3308	350.1690	682.3042	341.6558	681.3202	341.1638	N	***1077.5476***	539.2774	1060.5211	530.7642	1059.5370	530.2722	8
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	L	***963.5047***	482.2560	946.4781	473.7427	945.4941	473.2507	7
9	926.4578	463.7325	909.4312	455.2193	908.4472	454.7272	N	***850.4206***	425.7139	833.3941	417.2007	832.4100	416.7087	6
10	1112.5371	556.7722	1095.5106	548.2589	1094.5265	547.7669	W	***736.3777***	368.6925	719.3511	360.1792	718.3671	359.6872	5
11	**1241.5797**	621.2935	1224.5531	612.7802	1223.5691	612.2882	E	***550.2984***	275.6528	533.2718	267.1396	532.2878	266.6475	4
12	1340.6481	670.8277	1323.6216	662.3144	1322.6375	661.8224	V	421.2558	211.1315	404.2292	202.6183			3
13	**1487.7165**	744.3619	1470.6900	735.8486	1469.7060	735.3566	F	***322.1874***	161.5973	305.1608	153.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VDGIAENLNWEVFR

AT2G29630.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.5	1660.8209	-0.0034	VDGIAENLNWEVFR

Mascot: http://www.matrixscience.com/

AT2G29760.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LHEVMEKLK**
Found in **AT2G29760.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:12719961-12722177 FORWARD

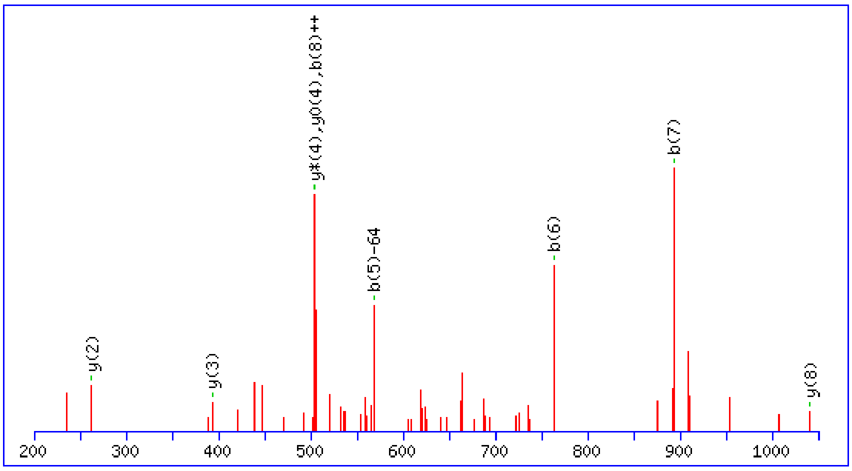
Match to Query 3914: 1154.581160 from(578.297856,2+) index(7360)
Title: Elution from: 65.825 to 65.825 scan no 9580 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

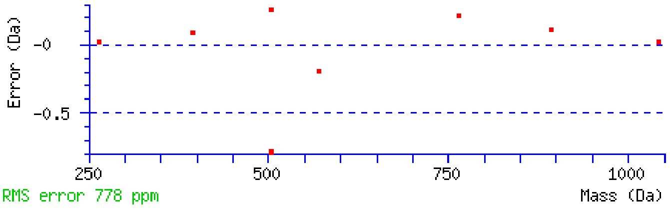
Label all possible matches ○ Label matches used for scoring ●

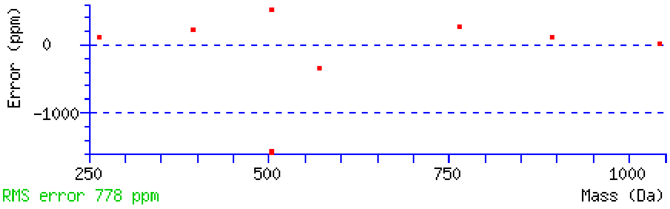
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.5780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 18 **Expect:** 0.041
Matches : 9/118 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							9
2	255.1384	128.0728					H	***1041.5042***	521.2557	1023.4806	512.2439	1023.4936	512.2504	8
3	385.1780	193.0926			367.1675	184.0874	E	901.4541	451.2307	883.4306	442.2189	883.4436	442.2254	7
4	485.2435	243.1254			467.2329	234.1201	V	771.4145	386.2109	753.3909	377.1991	753.4040	377.2056	6
5	633.2759	317.1416			615.2653	308.1363	M	671.3491	336.1782	653.3255	327.1664	653.3385	327.1729	5
6	**763.3155**	382.1614			745.3050	373.1561	E	523.3166	262.1620	505.2930	253.1502	505.3061	253.1567	4
7	**893.4046**	447.2059	875.3810	438.1941	875.3940	438.2006	K	***393.2770***	197.1421	375.2534	188.1303			3
8	1007.4857	504.2465	989.4621	495.2347	989.4751	495.2412	L	***263.1880***	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LHEVMEKLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G29760.1

Score	Mr(calc)	Delta	Sequence
18.4	1154.5780	0.0032	LHEVMEKLK
12.0	1154.5827	-0.0016	TPTNIEEVLK
6.9	1154.5827	-0.0016	LDDALNLIEK
3.5	1154.5827	-0.0016	IPDTVASEAIK
3.2	1154.5827	-0.0015	QVADIEIVEK
3.2	1154.5827	-0.0015	VPTVDGTVDLK
2.8	1154.5827	-0.0016	LAELEEALQK
1.9	1154.5836	-0.0024	MKILKGMYK
1.8	1154.5802	0.0009	AIWMLDPGIK
1.1	1154.5827	-0.0016	AVEAELAELAK

AT2G29990.1

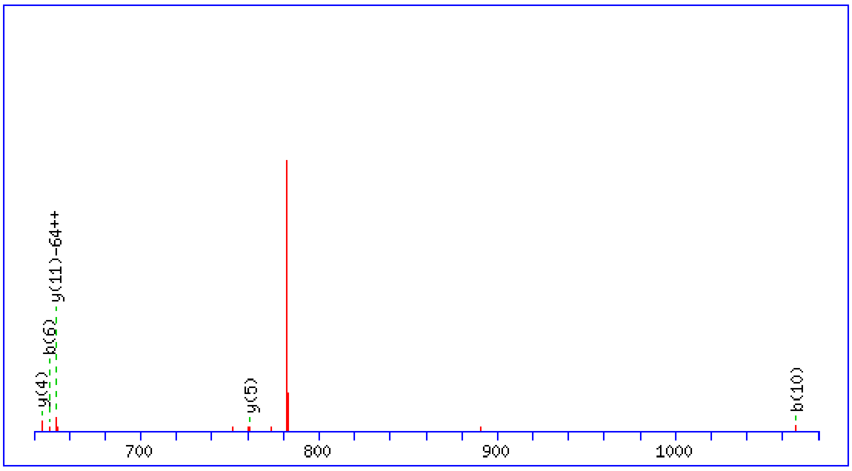
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPTGRIGIDEWMR**
Found in **AT2G29990.1** in **TAIR_Arabidopsis**, Symbols: NDA2 | NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); NADH dehydrogenase | chr2:12800639-12802990 REVERSE

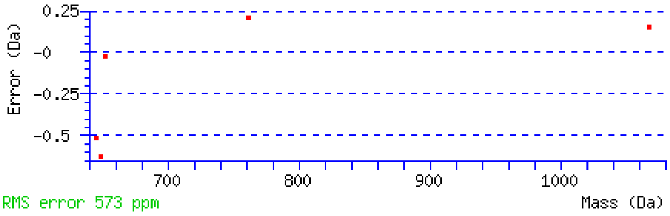
Match to Query 7011: 1580.678782 from(791.346667,2+) index(7207)
Title: Elution from: 64.060 to 64.060 scan no 9432 cid35.00 polarity:+
Data file 0-2_2.mgf

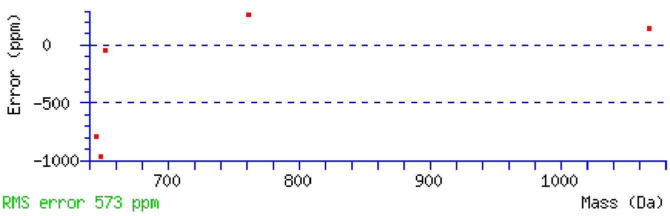
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 640 to 1080 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1580.6761
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.041
Matches : 5/198 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							13
2	215.0811	108.0442			197.0705	99.0389	P	1465.6595	733.3334	1447.6359	724.3216	1447.6489	724.3281	12
3	317.1258	159.0665			299.1152	150.0612	T	1367.6097	684.3085	1349.5861	675.2967	1349.5991	675.3032	11
4	375.1443	188.0758			357.1337	179.0705	G	1265.5650	633.2861	1247.5414	624.2743	1247.5544	624.2808	10
5	535.2335	268.1204	517.2099	259.1086	517.2230	259.1151	R	1207.5465	604.2769	1189.5229	595.2651	1189.5359	595.2716	9
6	***649.3146***	325.1609	631.2910	316.1492	631.3040	316.1557	I	1047.4572	524.2322	1029.4336	515.2205	1029.4466	515.2270	8
7	707.3331	354.1702	689.3095	345.1584	689.3225	345.1649	G	933.3761	467.1917	915.3525	458.1799	915.3655	458.1864	7
8	821.4142	411.2107	803.3906	402.1990	803.4036	402.2055	I	875.3576	438.1824	857.3340	429.1707	857.3470	429.1772	6
9	937.4382	469.2227	919.4146	460.2109	919.4276	460.2175	D	***761.2765***	381.1419	743.2529	372.1301	743.2660	372.1366	5
10	***1067.4778***	534.2425	1049.4542	525.2308	1049.4673	525.2373	E	***645.2525***	323.1299	627.2290	314.1181	627.2420	314.1246	4
11	1255.5512	628.2792	1237.5276	619.2674	1237.5406	619.2740	W	515.2129	258.1101	497.1893	249.0983			3
12	1403.5836	702.2955	1385.5601	693.2837	1385.5731	693.2902	M	327.1395	164.0734	309.1159	155.0616			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DPTGRIGIDEWMR

AT2G29990.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.8	1580.6761	0.0026	DPTGRIGIDEWMR
5.4	1580.6757	0.0030	AMYQEYFESLLR
5.1	1580.6795	-0.0008	MKKELQMEHDTR
5.0	1580.6832	-0.0044	LGELFSPSNEWER
4.9	1580.6788	-0.0001	NQEITPHMRNYR

AT2G30110.1

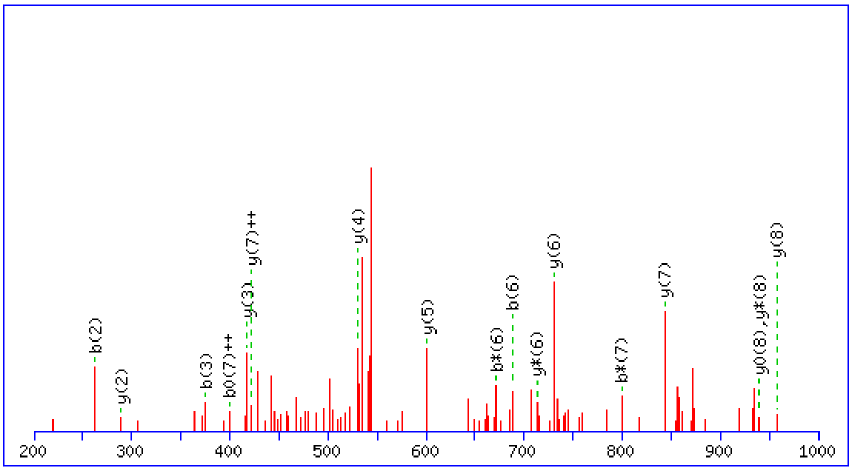
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNIEALQNR**
Found in **AT2G30110.1** in **TAIR_Arabidopsis**, Symbols: MOS5, ATUBA1 | ATUBA1 (ARABIDOPSIS THALIANA UBIQUITIN-ACTIVATING ENZYME 1); ubiquitin activating enzyme | chr2:12859709-12864446 REVERSE

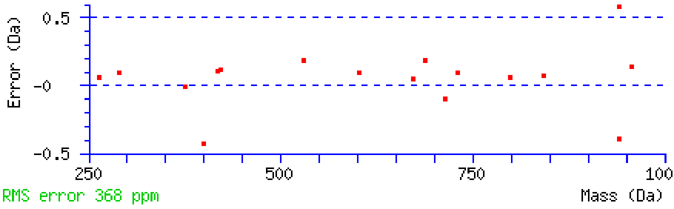
Match to Query 3170: 1103.571998 from(552.793275,2+) index(4886)
Title: Elution from: 43.493 to 43.493 scan no 6155 cid35.00 polarity:+
Data file D6h-3_3.mgf

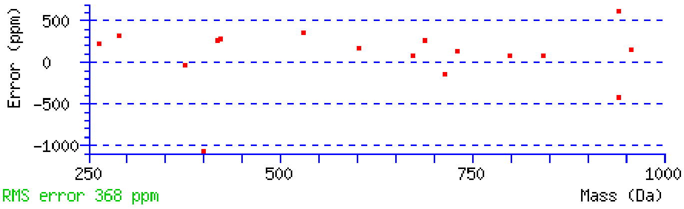
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1103.5723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00042
Matches : 17/78 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							9
2	**262.1186**	131.5629	245.0921	123.0497			N	***957.5112***	479.2592	940.4847	470.7460	939.5007	470.2540	8
3	**375.2027**	188.1050	358.1761	179.5917			I	***843.4683***	422.2378	826.4417	413.7245	825.4577	413.2325	7
4	504.2453	252.6263	487.2187	244.1130	486.2347	243.6210	E	***730.3842***	365.6958	713.3577	357.1825	712.3737	356.6905	6
5	575.2824	288.1448	558.2558	279.6316	557.2718	279.1395	A	***601.3416***	301.1745	584.3151	292.6612			5
6	**688.3665**	344.6869	671.3399	336.1736	670.3559	335.6816	L	***530.3045***	265.6559	513.2780	257.1426			4
7	816.4250	408.7162	799.3985	400.2029	798.4145	399.7109	Q	***417.2205***	209.1139	400.1939	200.6006			3
8	930.4680	465.7376	913.4414	457.2243	912.4574	456.7323	N	***289.1619***	145.0846	272.1353	136.5713			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FNIEALQNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G30110.1

38.6	1103.5723	-0.0003	FNIEALQNR
4.0	1103.5710	0.0010	GLSLEEIESK
2.9	1103.5723	-0.0003	FNQLNEALR
2.9	1103.5723	-0.0003	GSIALQSWSR

AT2G30490.1

Mascot Search Results

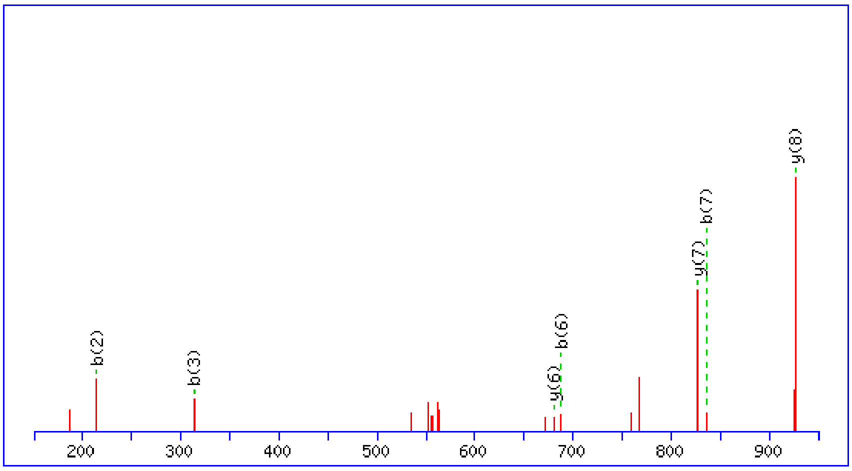
Peptide View

MS/MS Fragmentation of **NVVFDIFTGK**
Found in **AT2G30490.1** in **TAIR_Arabidopsis**, Symbols: ATC4H, C4H, CYP73A5 | ATC4H/C4H/CYP73A5 (CINNAMATE 4-HYDROXYLASE, CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase | chr2:13000938-13002760 REVERSE

Match to Query 3534: 1138.601054 from(570.307803,2+) index(8747)
Title: Elution from: 78.445 to 78.445 scan no 11878 cid35.00 polarity:+
Data file 0-3_3.mgf

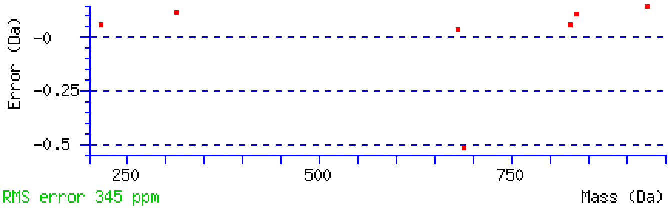
Click mouse within plot area to zoom in by factor of two about that point

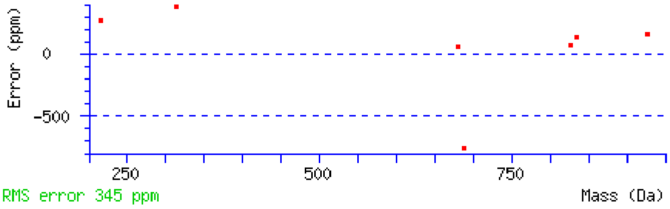
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1138.6023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0069
Matches : 7/96 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							10
2	***214.1186***	107.5629	197.0921	99.0497			V	1025.5666	513.2869	1008.5401	504.7737	1007.5560	504.2817	9
3	***313.1870***	157.0972	296.1605	148.5839			V	***926.4982***	463.7527	909.4716	455.2395	908.4876	454.7475	8
4	460.2554	230.6314	443.2289	222.1181			F	***827.4298***	414.2185	810.4032	405.7053	809.4192	405.2132	7
5	575.2824	288.1448	558.2558	279.6316	557.2718	279.1395	D	***680.3614***	340.6843	663.3348	332.1710	662.3508	331.6790	6
6	***688.3665***	344.6869	671.3399	336.1736	670.3559	335.6816	I	565.3344	283.1709	548.3079	274.6576	547.3239	274.1656	5
7	***835.4349***	418.2211	818.4083	409.7078	817.4243	409.2158	F	452.2504	226.6288	435.2238	218.1155	434.2398	217.6235	4
8	936.4825	468.7449	919.4560	460.2316	918.4720	459.7396	T	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
9	993.5040	497.2556	976.4775	488.7424	975.4934	488.2504	G	204.1343	102.5708	187.1077	94.0575			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NVVFDIFTGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G30490.1

Score	Mr(calc)	Delta	Sequence
27.1	1138.6023	-0.0012	NVVFDIFTGK

Mascot: http://www.matrixscience.com/

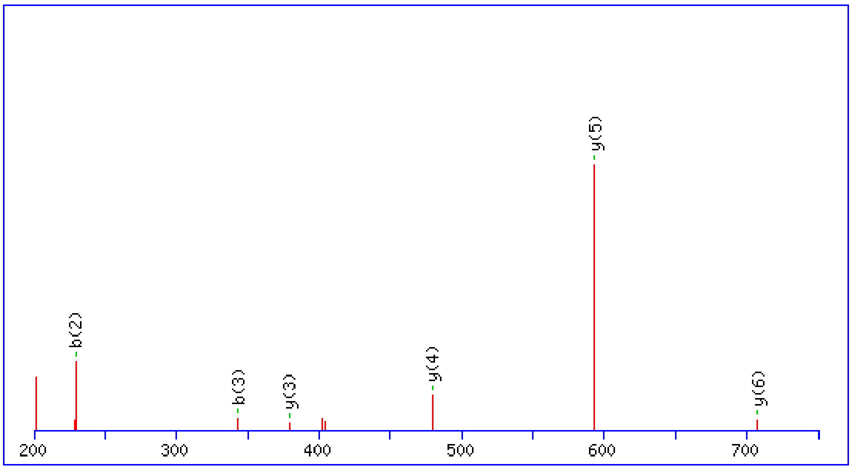
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLVNLK**
Found in **AT2G30620.1** in **TAIR_Arabidopsis**, Symbols: | histone H1.2 | chr2:13052437-13053344 FORWARD

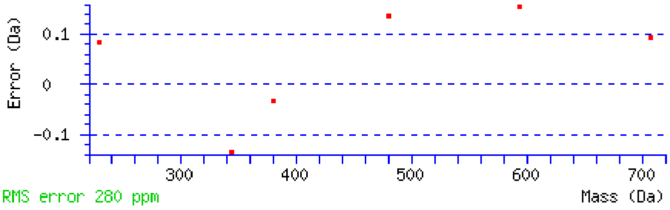
Match to Query 1118: 820.526352 from(411.270452,2+) index(6088)
Title: Elution from: 54.592 to 54.592 scan no 7730 cid35.00 polarity:+
Data file 0-3_1.mgf

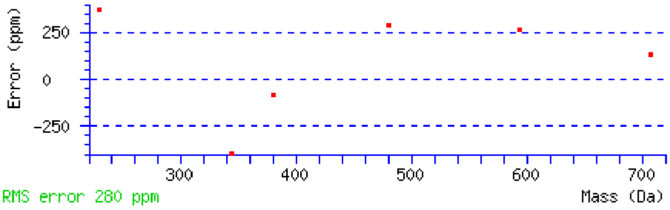
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 820.5264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00017
Matches : 6/40 fragment ions using 9 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	115.0884	58.0478			L					7
2	**229.1695**	115.0884			L	***707.4526***	354.2299	689.4290	345.2182	6
3	**343.2506**	172.1289			L	***593.3715***	297.1894	575.3479	288.1776	5
4	443.3160	222.1616			V	***479.2904***	240.1488	461.2668	231.1371	4
5	559.3530	280.1801	541.3294	271.1684	N	***379.2250***	190.1161	361.2014	181.1043	3
6	673.4341	337.2207	655.4105	328.2089	L	263.1880	132.0976	245.1644	123.0858	2
7					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LLLVNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.7	820.5264	-0.0001	LLLVNLK
18.8	820.5264	-0.0001	LIVLNLK
9.5	820.5264	-0.0001	LIVQVLK

AT2G30620.1

9.5	820.5264	-0.0001	LLAIIAAK

Mascot: http://www.matrixscience.com/

AT2G30790.1

Mascot Search Results

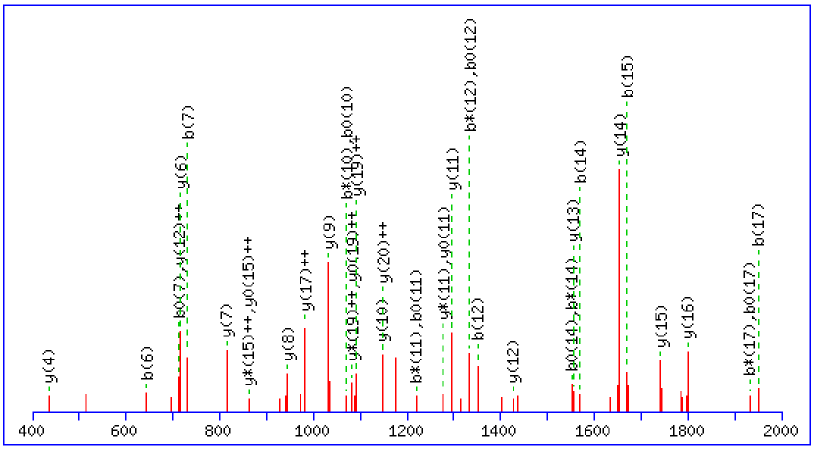
Peptide View

MS/MS Fragmentation of **SITDYGSPEQFLSQVNYLLGK**
Found in **AT2G30790.1** in **TAIR_Arabidopsis**, Symbols: PSBP-2 | PSBP-2 (photosystem II subunit P-2); calcium ion binding | chr2:13126124-13127167 REVERSE

Match to Query 9788: 2383.093064 from(1192.553808,2+) index(10571)
Title: Elution from: 120.434 to 120.434 scan no 16285 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

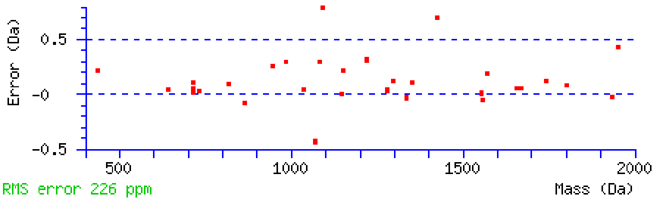
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

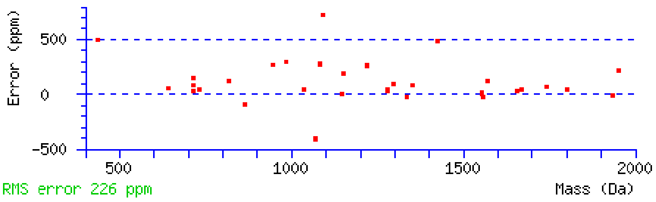


Monoisotopic mass of neutral peptide Mr(calc): 2383.1002
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 1.4e-008
Matches : 39/206 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							21
2	203.1174	102.0624			185.1069	93.0571	I	2296.0784	1148.5429	2278.0548	1139.5311	2278.0679	1139.5376	20
3	305.1622	153.0847			287.1516	144.0794	T	2181.9973	1091.5023	2163.9737	1082.4905	2163.9868	1082.4970	19
4	421.1861	211.0967			403.1756	202.0914	D	2079.9526	1040.4799	2061.9290	1031.4682	2061.9421	1031.4747	18
5	585.2465	293.1269			567.2359	284.1216	Y	1963.9286	982.4680	1945.9051	973.4562	1945.9181	973.4627	17
6	**643.2650**	322.1361			625.2544	313.1309	G	***1799.8683***	900.4378	1781.8447	891.4260	1781.8577	891.4325	16
7	**731.2941**	366.1507			713.2835	357.1454	S	***1741.8498***	871.4285	1723.8262	862.4167	1723.8392	862.4232	15
8	829.3439	415.1756			811.3333	406.1703	P	***1653.8207***	827.4140	1635.7971	818.4022	1635.8101	818.4087	14
9	959.3835	480.1954			941.3729	471.1901	E	***1555.7709***	778.3891	1537.7473	769.3773	1537.7603	769.3838	13
10	1089.4361	545.2217	1071.4125	536.2099	1071.4256	536.2164	Q	***1425.7313***	713.3693	1407.7077	704.3575	1407.7207	704.3640	12
11	1237.5016	619.2544	1219.4780	610.2426	1219.4910	610.2491	F	***1295.6786***	648.3430	1277.6551	639.3312	1277.6681	639.3377	11
12	**1351.5827**	676.2950	1333.5591	667.2832	1333.5721	667.2897	L	***1147.6132***	574.3102	1129.5896	565.2984	1129.6026	565.3050	10
13	1439.6117	720.3095	1421.5882	711.2977	1421.6012	711.3042	S	***1033.5321***	517.2697	1015.5085	508.2579	1015.5215	508.2644	9
14	**1569.6644**	785.3358	1551.6408	776.3240	1551.6538	776.3305	Q	***945.5030***	473.2552	927.4794	464.2434			8
15	**1669.7298**	835.3686	1651.7063	826.3568	1651.7193	826.3633	V	***815.4504***	408.2288	797.4268	399.2170			7
16	1785.7668	893.3871	1767.7432	884.3753	1767.7563	884.3818	N	***715.3849***	358.1961	697.3613	349.1843			6
17	**1949.8272**	975.4172	1931.8036	966.4054	1931.8166	966.4120	Y	599.3479	300.1776	581.3244	291.1658			5
18	2063.9083	1032.4578	2045.8847	1023.4460	2045.8977	1023.4525	L	***435.2876***	218.1474	417.2640	209.1356			4
19	2177.9894	1089.4983	2159.9658	1080.4865	2159.9788	1080.4931	L	321.2065	161.1069	303.1829	152.0951			3
20	2236.0079	1118.5076	2217.9843	1109.4958	2217.9973	1109.5023	G	207.1254	104.0663	189.1018	95.0545			2
21							K	149.1069	75.0571	131.0833	66.0453			1

AT2G30790.1





NCBI **BLAST** search of SITDYGSPEQFLSQVNYLLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.5	2383.1002	-0.0071	SITDYGSPEQFLSQVNYLLGK
84.3	2383.0872	0.0059	SITDYGSPEEFLSQVNYLLGK

Mascot: http://www.matrixscience.com/

AT2G30860.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **RALVTLIEK**
Found in **AT2G30860.1** in **TAIR_Arabidopsis**, Symbols: GLUTTR, ATGSTF7, ATGSTF9 | ATGSTF9 (Arabidopsis thaliana Glutathione S-transferase (class phi) 9); glutathione transferase | chr2:13146209-13147134 FORWARD

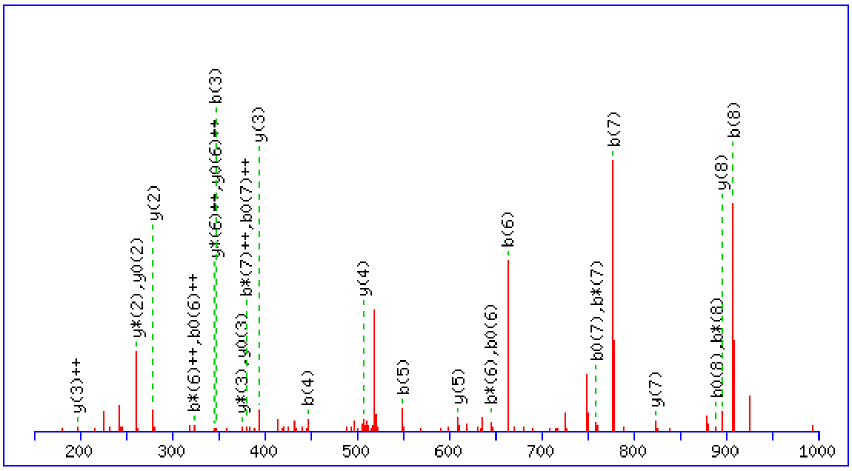
Match to Query 2875: 1054.616142 from(528.315347,2+) index(3293)
Title: Elution from: 33.565 to 33.565 scan no 4120 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

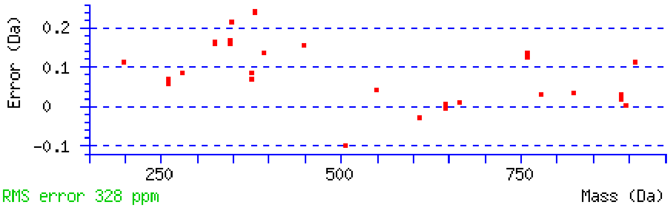
Label all possible matches ○ Label matches used for scoring ●

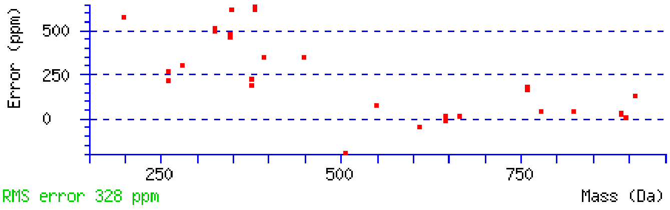
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1054.6161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0046
Matches : 29/86 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							9
2	233.1307	117.0690	215.1071	108.0572			A	***895.5341***	448.2707	877.5105	439.2589	877.5235	439.2654	8
3	***347.2118***	174.1095	329.1882	165.0977			L	***823.5000***	412.2536	805.4764	403.2418	805.4894	403.2483	7
4	***447.2772***	224.1422	429.2536	215.1305			V	709.4189	355.2131	691.3953	346.2013	691.4083	346.2078	6
5	***549.3219***	275.1646	531.2984	266.1528	531.3114	266.1593	T	***609.3534***	305.1803	591.3298	296.1686	591.3428	296.1751	5
6	***663.4030***	332.2052	645.3795	323.1934	645.3925	323.1999	L	***507.3087***	254.1580	489.2851	245.1462	489.2981	245.1527	4
7	***777.4841***	389.2457	759.4606	380.2339	759.4736	380.2404	I	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
8	***907.5238***	454.2655	889.5002	445.2537	889.5132	445.2602	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RALVTLIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G30860.1

30.1	1054.6161	0.0001	RALVTLIEK
13.6	1054.6183	-0.0022	ELVKWLKK
13.6	1054.6161	0.0001	ISLVNKIQK
13.6	1054.6161	0.0001	ITNPKTLKK
1.5	1054.6161	0.0001	KQGLGILVSK
1.3	1054.6161	0.0001	ILKLGNKEK
1.3	1054.6161	0.0001	LNIKLSVAGK
1.3	1054.6161	0.0001	NIVKIAKEK
1.3	1054.6161	0.0001	TLLLRIGEK
1.3	1054.6161	0.0001	TVKVLLNQK

AT2G30870.1

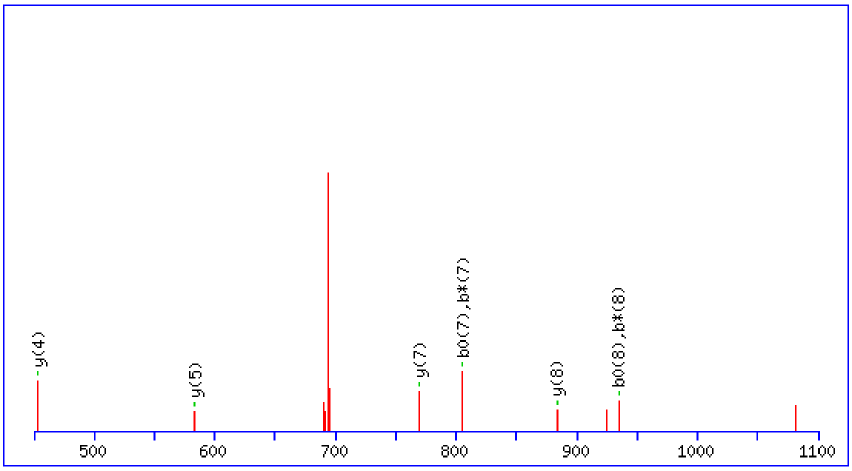
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPEYLAIQPFGK**
Found in **AT2G30870.1** in **TAIR_Arabidopsis**, Symbols: ERD13, ATGSTF4, ATGSTF10 | ATGSTF10 (EARLY DEHYDRATION-INDUCED 13); glutathione transferase | chr2:13148567-13149469 FORWARD

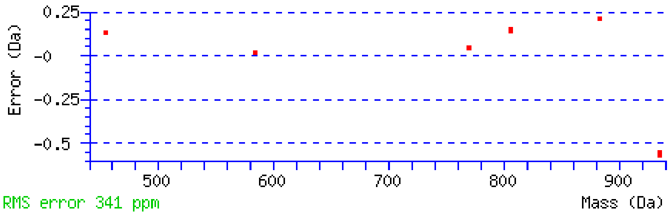
Match to Query 5236: 1404.688412 from(703.351482,2+) index(6836)
Title: Elution from: 60.000 to 60.000 scan no 8925 cid35.00 polarity:+
Data file 0-2_3.mgf

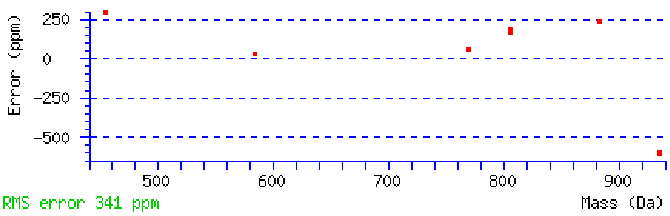
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1404.6848
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.017
Matches : 8/110 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							12
2	229.1097	115.0585	211.0861	106.0467			P	1275.6394	638.3233	1257.6158	629.3115	1257.6288	629.3181	11
3	359.1493	180.0783	341.1258	171.0665	341.1388	171.0730	E	1177.5896	589.2984	1159.5660	580.2866	1159.5790	580.2932	10
4	523.2097	262.1085	505.1861	253.0967	505.1991	253.1032	Y	1047.5500	524.2786	1029.5264	515.2668			9
5	637.2908	319.1490	619.2672	310.1373	619.2802	310.1438	L	***883.4896***	442.2484	865.4660	433.2367			8
6	709.3250	355.1661	691.3014	346.1543	691.3144	346.1608	A	***769.4085***	385.2079	751.3849	376.1961			7
7	823.4061	412.2067	805.3825	403.1949	805.3955	403.2014	I	697.3744	349.1908	679.3508	340.1790			6
8	953.4587	477.2330	935.4351	468.2212	935.4481	468.2277	Q	***583.2933***	292.1503	565.2697	283.1385			5
9	1051.5085	526.2579	1033.4849	517.2461	1033.4979	517.2526	P	***453.2406***	227.1239	435.2170	218.1122			4
10	1199.5740	600.2906	1181.5504	591.2788	1181.5634	591.2853	F	355.1908	178.0990	337.1672	169.0873			3
11	1257.5925	629.2999	1239.5689	620.2881	1239.5819	620.2946	G	207.1254	104.0663	189.1018	95.0545			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QPEYLAIQPFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G30870.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.2	1404.6848	0.0036	QPEYLAIQPFGK
5.5	1404.6859	0.0025	QQLQALMETLSK
4.8	1404.6908	-0.0024	SMIRSGYLPHVK

AT2G30930.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEAAAAPDKASGVSTQAK**
Found in **AT2G30930.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G06540.1) | chr2:13169535-13170233 FORWARD

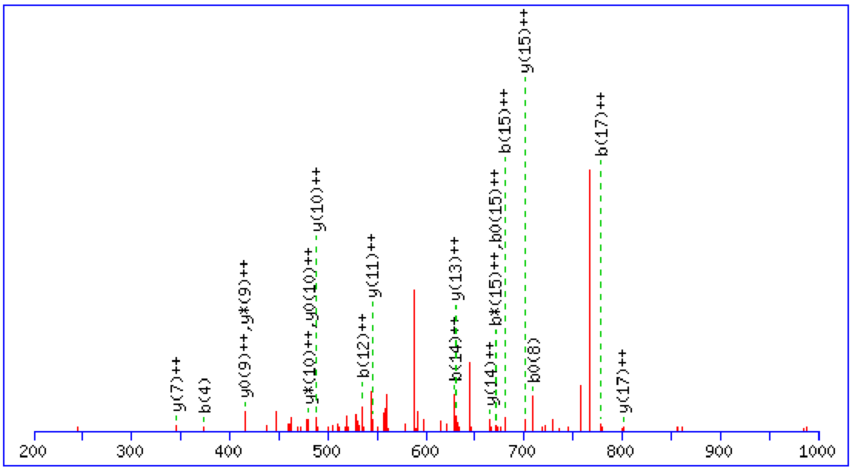
Match to Query 7626: 1701.853215 from(568.291681,3+) index(4959)
Title: Elution from: 47.757 to 47.757 scan no 6372 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, [Plot from] [200] to [1000] Da [Full range]

Label all possible matches ○ Label matches used for scoring ●

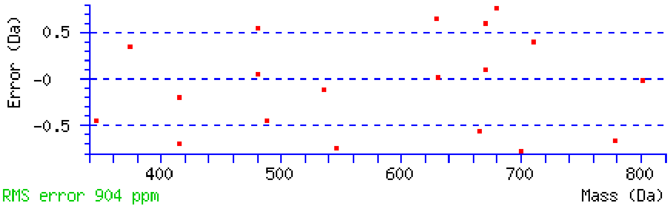
Show Y-axis ☐

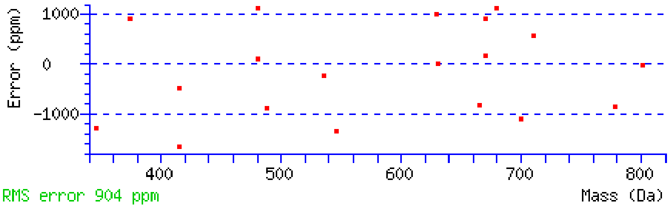


Monoisotopic mass of neutral peptide Mr(calc): 1701.8533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.046
Matches : 19/182 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**18**
2	231.0975	116.0524			213.0870	107.0471	**E**	1601.8129	801.4101	1584.7864	792.8968	1583.8024	792.4048	**17**
3	302.1347	151.5710			284.1241	142.5657	**A**	1472.7703	736.8888	1455.7438	728.3755	1454.7598	727.8835	**16**
4	373.1718	187.0895			355.1612	178.0842	**A**	1401.7332	701.3703	1384.7067	692.8570	1383.7227	692.3650	**15**
5	444.2089	222.6081			426.1983	213.6028	**A**	1330.6961	665.8517	1313.6696	657.3384	1312.6856	656.8464	**14**
6	515.2460	258.1266			497.2354	249.1214	**A**	1259.6590	630.3331	1242.6325	621.8199	1241.6484	621.3279	**13**
7	612.2988	306.6530			594.2882	297.6477	**P**	1188.6219	594.8146	1171.5953	586.3013	1170.6113	585.8093	**12**
8	727.3257	364.1665			709.3151	355.1612	**D**	1091.5691	546.2882	1074.5426	537.7749	1073.5586	537.2829	**11**
9	855.4207	428.2140	838.3941	419.7007	837.4101	419.2087	**K**	976.5422	488.7747	959.5156	480.2615	958.5316	479.7694	**10**
10	926.4578	463.7325	909.4312	455.2193	908.4472	454.7272	**A**	848.4472	424.7272	831.4207	416.2140	830.4367	415.7220	**9**
11	1013.4898	507.2485	996.4633	498.7353	995.4793	498.2433	**S**	777.4101	389.2087	760.3836	380.6954	759.3995	380.2034	**8**
12	1070.5113	***535.7593***	1053.4847	527.2460	1052.5007	526.7540	**G**	690.3781	345.6927	673.3515	337.1794	672.3675	336.6874	**7**
13	1169.5797	585.2935	1152.5531	576.7802	1151.5691	576.2882	**V**	633.3566	317.1819	616.3301	308.6687	615.3461	308.1767	**6**
14	1256.6117	***628.8095***	1239.5852	620.2962	1238.6012	619.8042	**S**	534.2882	267.6477	517.2617	259.1345	516.2776	258.6425	**5**
15	1357.6594	***679.3333***	1340.6329	670.8201	1339.6488	670.3281	**T**	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	**4**
16	1485.7180	743.3626	1468.6914	734.8494	1467.7074	734.3573	**Q**	346.2085	173.6079	329.1819	165.0946			**3**
17	1556.7551	***778.8812***	1539.7285	770.3679	1538.7445	769.8759	**A**	218.1499	109.5786	201.1234	101.0653			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT2G30930.1





NCBI **BLAST** search of TEAAAAPDKASGVSTQAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.6	1701.8533	-0.0001	TEAAAAPDKASGVSTQAK
7.2	1701.8547	-0.0014	SVDIINPNGNRGQYR
2.8	1701.8508	0.0024	KSDDLWKHCVSISK
1.2	1701.8573	-0.0041	TSLEYYVGKQSNSVK
0.9	1701.8508	0.0024	GLIRDWDAMEDLLR
0.4	1701.8508	0.0024	AIGESTECGIPVWRK
0.2	1701.8573	-0.0041	HELLYSEDEVIISR

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVSVDVPDVK**
Found in **AT2G30950.1** in **TAIR_Arabidopsis**, Symbols: FTSH2, VAR2 | VAR2 (VARIEGATED 2); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding | chr2:13181769-13184141 FORWARD

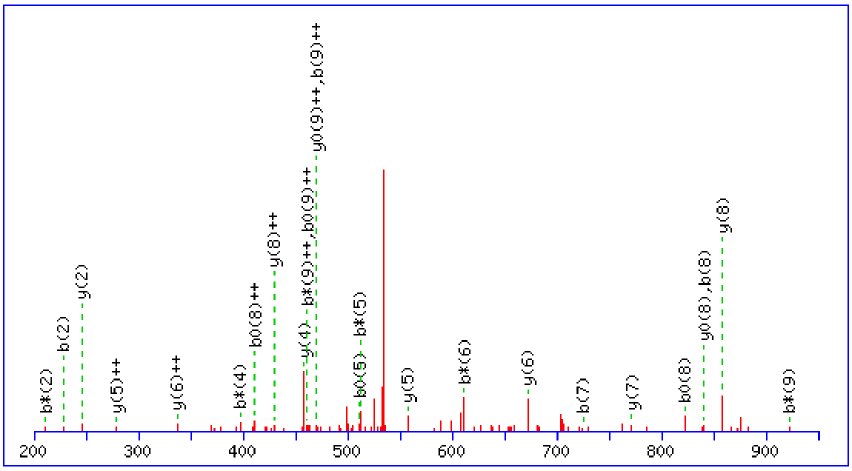
Match to Query 3171: 1084.573878 from(543.294215,2+) index(3572)
Title: Elution from: 34.318 to 34.318 scan no 4455 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

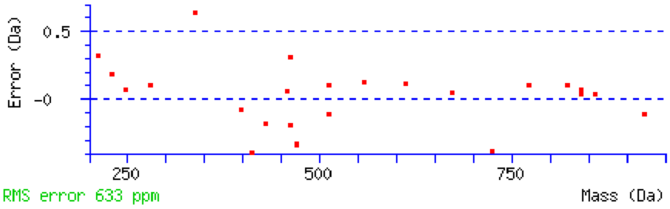
Label all possible matches ○ Label matches used for scoring ●

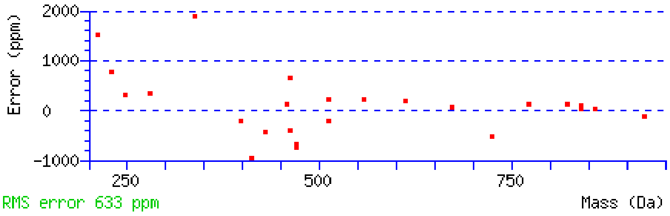
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1084.5765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0013
Matches : 25/100 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							10
2	**228.1343**	114.5708	211.1077	106.0575			V	957.5251	479.2662	940.4986	470.7529	939.5146	470.2609	9
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	S	***858.4567***	429.7320	841.4302	421.2187	840.4462	420.7267	8
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	V	***771.4247***	386.2160	754.3981	377.7027	753.4141	377.2107	7
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	D	***672.3563***	336.6818	655.3297	328.1685	654.3457	327.6765	6
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	V	***557.3293***	279.1683	540.3028	270.6550	539.3188	270.1630	5
7	**725.3828**	363.1951	708.3563	354.6818	707.3723	354.1898	P	***458.2609***	229.6341	441.2344	221.1208	440.2504	220.6288	4
8	**840.4098**	420.7085	823.3832	412.1953	822.3992	411.7032	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
9	939.4782	470.2427	922.4516	461.7295	921.4676	461.2374	V	***246.1812***	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of QVSVDVPDVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G30950.1

Score	Mr(calc)	Delta	Sequence
32.1	1084.5765	-0.0026	QVSVDVPDVK
6.3	1084.5737	0.0002	ADNLAAQRAR
0.8	1084.5737	0.0001	RASGGINSAPR

AT2G30970.1

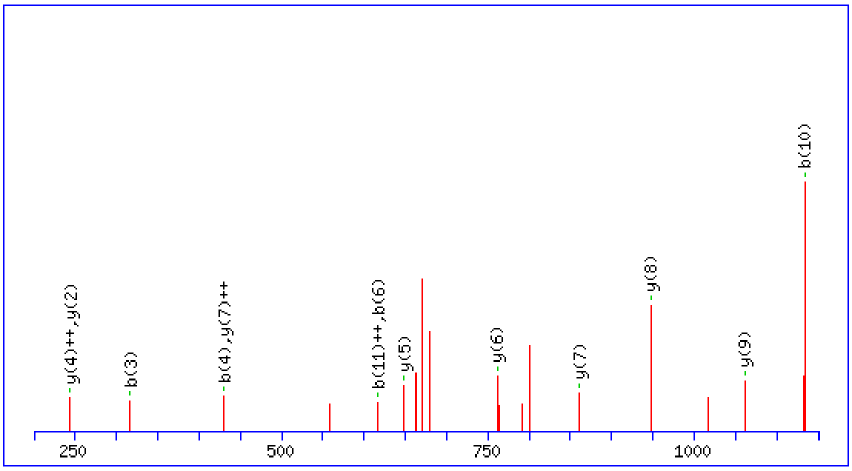
Mascot Search Results

Peptide View

MS/MS Fragmentation of VGCLSVLCEDPK
Found in AT2G30970.1 in TAIR_Arabidopsis, Symbols: ASP1 | ASP1 (ASPARTATE AMINOTRANSFERASE 1) | chr2:13186089-13188763 FORWARD

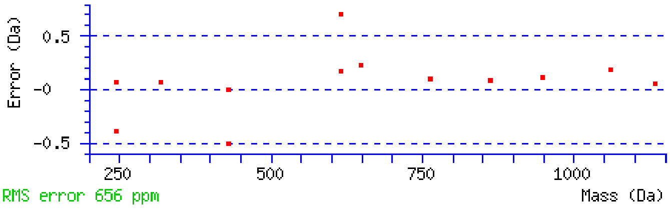
Match to Query 5530: 1375.644626 from(688.829589,2+) index(5032)
Title: Elution from: 45.655 to 45.655 scan no 6314 cid35.00 polarity:+
Data file 0-2_1.mgf

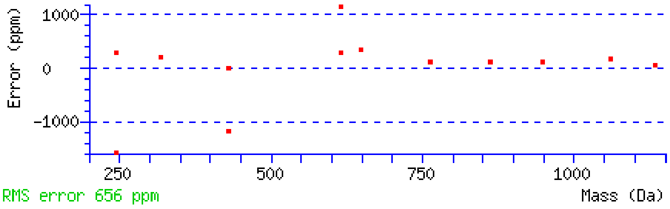
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1375.6476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00036
Matches : 13/98 fragment ions using 21 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415			V							12
2	157.0972	79.0522			G	1277.5864	639.2969	1260.5599	630.7836	1259.5759	630.2916	11
3	**317.1278**	159.0675			C	1220.5650	610.7861	1203.5384	602.2728	1202.5544	601.7808	10
4	**430.2119**	215.6096			L	***1060.5343***	530.7708	1043.5078	522.2575	1042.5238	521.7655	9
5	517.2439	259.1256	499.2333	250.1203	S	***947.4503***	474.2288	930.4237	465.7155	929.4397	465.2235	8
6	**616.3123**	308.6598	598.3017	299.6545	V	***860.4182***	430.7128	843.3917	422.1995	842.4077	421.7075	7
7	729.3964	365.2018	711.3858	356.1965	L	***761.3498***	381.1785	744.3233	372.6653	743.3393	372.1733	6
8	889.4270	445.2171	871.4165	436.2119	C	***648.2658***	324.6365	631.2392	316.1232	630.2552	315.6312	5
9	1018.4696	509.7384	1000.4591	500.7332	E	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	4
10	**1133.4966**	567.2519	1115.4860	558.2466	D	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
11	1230.5493	615.7783	1212.5388	606.7730	P	***244.1656***	122.5864	227.1390	114.0731			2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VGCLSVLCEDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G30970.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.2	1375.6476	-0.0030	VGCLSVLCEDPK
11.0	1375.6476	-0.0029	DENQMPLLCLK
2.7	1375.6442	0.0004	GGPECDSLPFIGK

AT2G31240.1

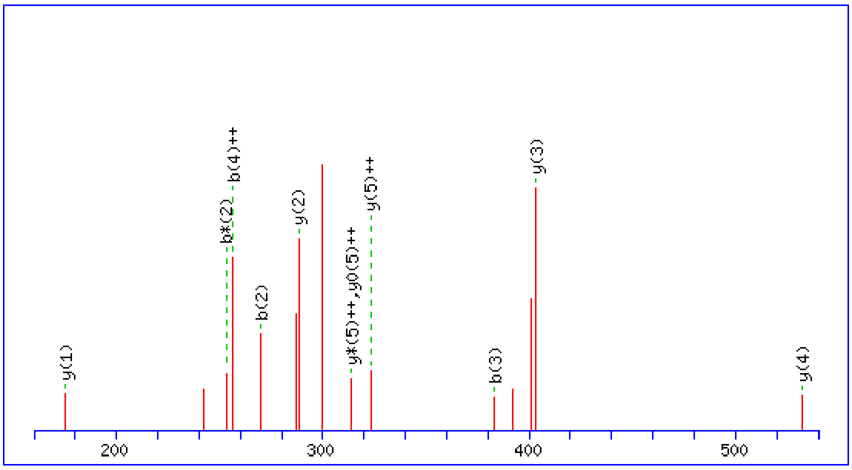
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RLLEDLR**
Found in **AT2G31240.1** in **TAIR_Arabidopsis**, Symbols: | tetratricopeptide repeat (TPR)-containing protein | chr2:13324647-13326595 REVERSE

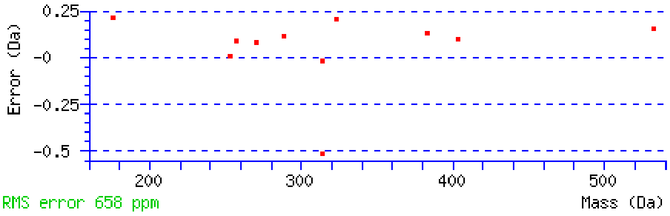
Match to Query 1692: 913.534014 from(305.518614,3+) index(3261)
Title: Elution from: 32.163 to 32.163 scan no 4054 cid35.00 polarity:+
Data file D6h-1_3.mgf

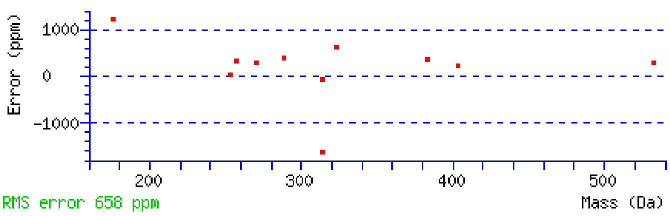
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 540 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 913.5345
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.024
Matches : 12/62 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							7
2	**270.1925**	135.5999	253.1659	127.0866			L	758.4407	379.7240	741.4141	371.2107	740.4301	370.7187	6
3	**383.2765**	192.1419	366.2500	183.6286			L	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
4	512.3191	**256.6632**	495.2926	248.1499	494.3085	247.6579	E	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
5	627.3461	**314.1767**	610.3195	305.6634	609.3355	305.1714	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
6	740.4301	370.7187	723.4036	362.2054	722.4196	361.7134	L	***288.2030***	144.6051	271.1765	136.0919			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of RLLEDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	913.5345	-0.0005	RLLEDLR
13.6	913.5345	-0.0005	LRLVEER
11.7	913.5345	-0.0005	NNIVVSLR

AT2G31240.1

8.8	913.5345	-0.0005	IDREILR
8.6	913.5345	-0.0005	LREEVIR
7.3	913.5345	-0.0005	RVEELLR
7.1	913.5345	-0.0005	LIDREIR
6.5	913.5345	-0.0005	NQLASLLR
4.4	913.5345	-0.0005	GTQLLNLR
4.1	913.5345	-0.0005	KKTSSHVK

AT2G31390.1

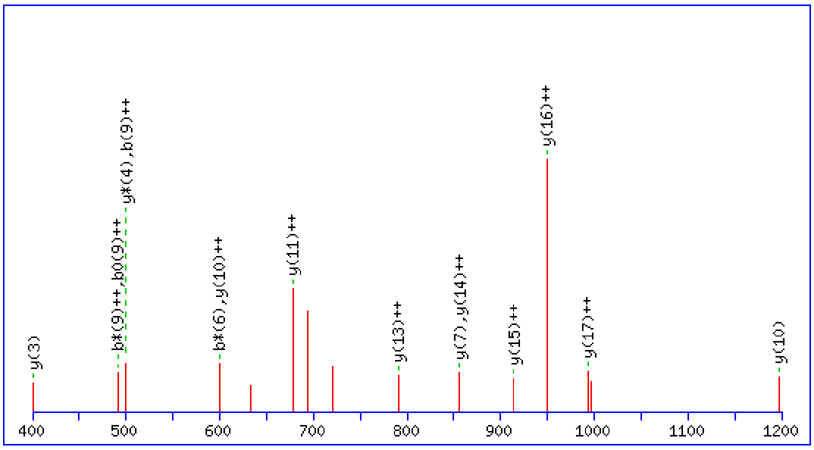
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPSADMLLRPDELNLDLIR**
Found in **AT2G31390.1** in **TAIR_Arabidopsis**, Symbols: | pfkB-type carbohydrate kinase family protein | chr2:13390712-13393193 REVERSE

Match to Query 9547: 2194.139754 from(732.387194,3+) index(9749)
Title: Elution from: 90.491 to 90.491 scan no 13626 cid35.00 polarity:+
Data file D12h-3_2.mgf

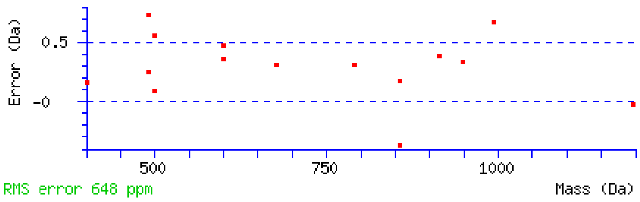
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

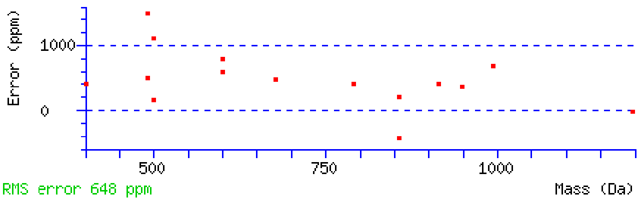


Monoisotopic mass of neutral peptide Mr(calc): 2194.1416
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 5e-005
Matches : 15/206 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							19
2	212.1030	106.5551	195.0764	98.0418			P	2081.1060	1041.0566	2064.0794	1032.5433	2063.0954	1032.0513	18
3	299.1350	150.0711	282.1084	141.5579	281.1244	141.0659	S	1984.0532	992.5302	1967.0266	984.0170	1966.0426	983.5249	17
4	370.1721	185.5897	353.1456	177.0764	352.1615	176.5844	A	1897.0212	949.0142	1879.9946	940.5009	1879.0106	940.0089	16
5	485.1991	243.1032	468.1725	234.5899	467.1885	234.0979	D	1825.9840	913.4957	1808.9575	904.9824	1807.9735	904.4904	15
6	616.2395	308.6234	599.2130	300.1101	598.2290	299.6181	M	1710.9571	855.9822	1693.9306	847.4689	1692.9465	846.9769	14
7	729.3236	365.1654	712.2971	356.6522	711.3130	356.1602	L	1579.9166	790.4619	1562.8901	781.9487	1561.9061	781.4567	13
8	842.4077	421.7075	825.3811	413.1942	824.3971	412.7022	L	1466.8326	733.9199	1449.8060	725.4066	1448.8220	724.9146	12
9	998.5088	499.7580	981.4822	491.2448	980.4982	490.7527	R	1353.7485	677.3779	1336.7219	668.8646	1335.7379	668.3726	11
10	1095.5615	548.2844	1078.5350	539.7711	1077.5510	539.2791	P	**1197.6474**	599.3273	1180.6208	590.8141	1179.6368	590.3220	10
11	1210.5885	605.7979	1193.5619	597.2846	1192.5779	596.7926	D	1100.5946	550.8009	1083.5681	542.2877	1082.5840	541.7957	9
12	1339.6311	670.3192	1322.6045	661.8059	1321.6205	661.3139	E	985.5677	493.2875	968.5411	484.7742	967.5571	484.2822	8
13	1452.7151	726.8612	1435.6886	718.3479	1434.7046	717.8559	L	**856.5251**	428.7662	839.4985	420.2529	838.5145	419.7609	7
14	1566.7581	783.8827	1549.7315	775.3694	1548.7475	774.8774	N	743.4410	372.2241	726.4145	363.7109	725.4304	363.2189	6
15	1679.8421	840.4247	1662.8156	831.9114	1661.8316	831.4194	L	629.3981	315.2027	612.3715	306.6894	611.3875	306.1974	5
16	1794.8691	897.9382	1777.8425	889.4249	1776.8585	888.9329	D	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
17	1907.9531	954.4802	1890.9266	945.9669	1889.9426	945.4749	L	**401.2871**	201.1472	384.2605	192.6339			3
18	2021.0372	1011.0222	2004.0107	1002.5090	2003.0266	1002.0170	I	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT2G31390.1





NCBI **BLAST** search of NPSADMLLRPDELNLDLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.0	2194.1416	-0.0018	NPSADMLLRPDELNLDLIR
5.4	2194.1344	0.0054	ALDLMGDSLEFLAKWALSAK
0.2	2194.1344	0.0054	FMIEEDHTVATFIKLIGSK
0.2	2194.1456	-0.0058	RGMEWELSVANALIVLYSK

Mascot: http://www.matrixscience.com/

AT2G31570.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIYDFTVK**
Found in **AT2G31570.1** in **TAIR_Arabidopsis**, Symbols: ATGPX2 | ATGPX2 (GLUTATHIONE PEROXIDASE 2); glutathione peroxidase | chr2:13445288-13446852 REVERSE

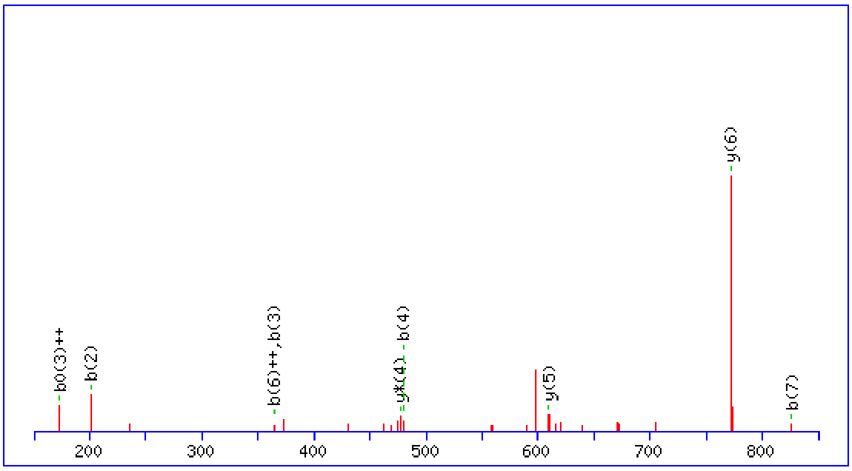
Match to Query 2093: 971.496476 from(486.755514,2+) index(5489)
Title: Elution from: 48.470 to 48.470 scan no 6956 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

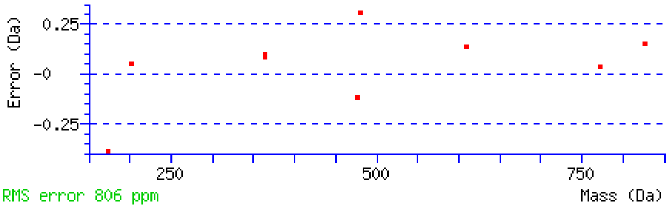
Label all possible matches ○ Label matches used for scoring ●

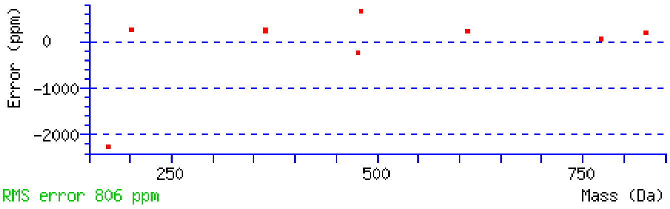
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 971.4964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.024
Matches : 9/66 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							8
2	***201.1234***	101.0653	183.1128	92.0600	I	885.4716	443.2395	868.4451	434.7262	867.4611	434.2342	7
3	***364.1867***	182.5970	346.1761	173.5917	Y	**772.3876**	386.6974	755.3610	378.1842	754.3770	377.6921	6
4	***479.2136***	240.1105	461.2031	231.1052	D	**609.3243**	305.1658	592.2977	296.6525	591.3137	296.1605	5
5	626.2821	313.6447	608.2715	304.6394	F	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
6	727.3297	364.1685	709.3192	355.1632	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
7	***826.3981***	413.7027	808.3876	404.6974	V	246.1812	123.5942	229.1547	115.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SIYDFTVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.4	971.4964	0.0001	SIYDFTVK

AT2G31570.1

18.4	971.4964	0.0001	SLYDFTVK
4.0	971.4937	0.0028	WNGGRSPAK

AT2G31610.1

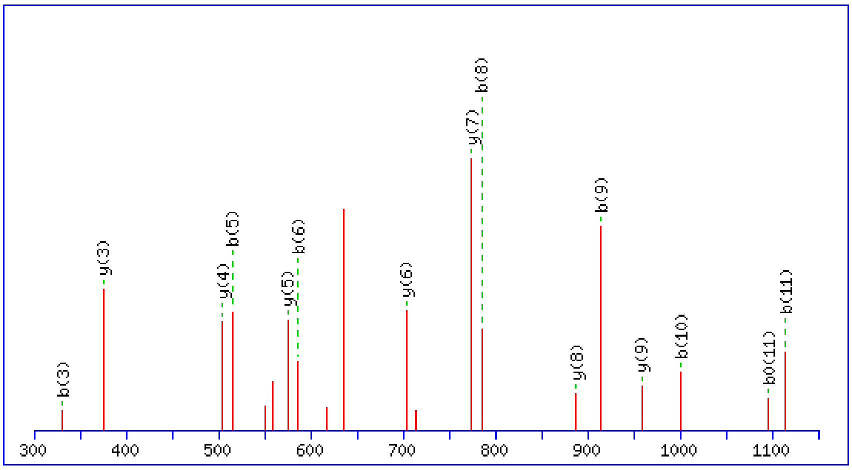
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLCAIAQAESLR**
Found in **AT2G31610.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S3 (RPS3A) | chr2:13457461-13458746 FORWARD

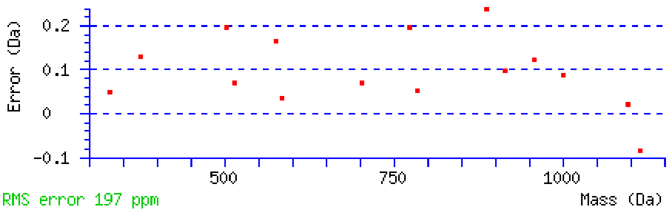
Match to Query 4905: 1287.658876 from(644.836714,2+) index(5641)
Title: Elution from: 50.286 to 50.286 scan no 7097 cid35.00 polarity:+
Data file 0-2_1.mgf

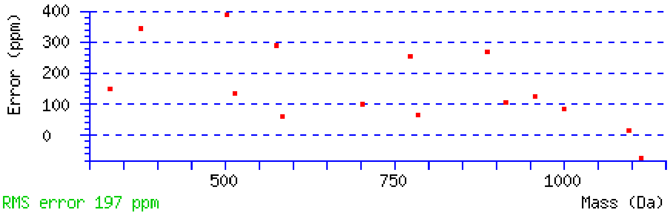
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1287.6605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 4e-009
Matches : 15/100 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							12
2	171.1128	86.0600					L	1231.6463	616.3268	1214.6198	607.8135	1213.6358	607.3215	11
3	***331.1435***	166.0754					C	1118.5623	559.7848	1101.5357	551.2715	1100.5517	550.7795	10
4	402.1806	201.5939					A	***958.5316***	479.7694	941.5051	471.2562	940.5211	470.7642	9
5	***515.2646***	258.1360					I	***887.4945***	444.2509	870.4680	435.7376	869.4839	435.2456	8
6	***586.3017***	293.6545					A	***774.4104***	387.7089	757.3839	379.1956	756.3999	378.7036	7
7	714.3603	357.6838	697.3338	349.1705			Q	***703.3733***	352.1903	686.3468	343.6770	685.3628	343.1850	6
8	***785.3974***	393.2024	768.3709	384.6891			A	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
9	***914.4400***	457.7237	897.4135	449.2104	896.4295	448.7184	E	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
10	***1001.4721***	501.2397	984.4455	492.7264	983.4615	492.2344	S	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
11	***1114.5561***	557.7817	1097.5296	549.2684	1096.5456	548.7764	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GLCAIAQAESLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G31610.1

Score	Mr(calc)	Delta	Sequence
90.6	1287.6605	-0.0016	GLCAIAQAESLR
11.0	1287.6605	-0.0016	ASGSMSPGVQVLR
5.6	1287.6605	-0.0016	AGDMQGVRVVEK
3.0	1287.6606	-0.0017	VVVGMLGDGNGVR
3.0	1287.6571	0.0018	KEFNLANPNNK
2.5	1287.6571	0.0018	ESLKGYIDAHR
2.0	1287.6605	-0.0016	AGMINEANSLLR
2.0	1287.6618	-0.0030	YHGRIMRSPR
1.7	1287.6605	-0.0016	IPKNGDMSALSR
1.3	1287.6571	0.0017	QTEQVKNQWK

AT2G32060.1

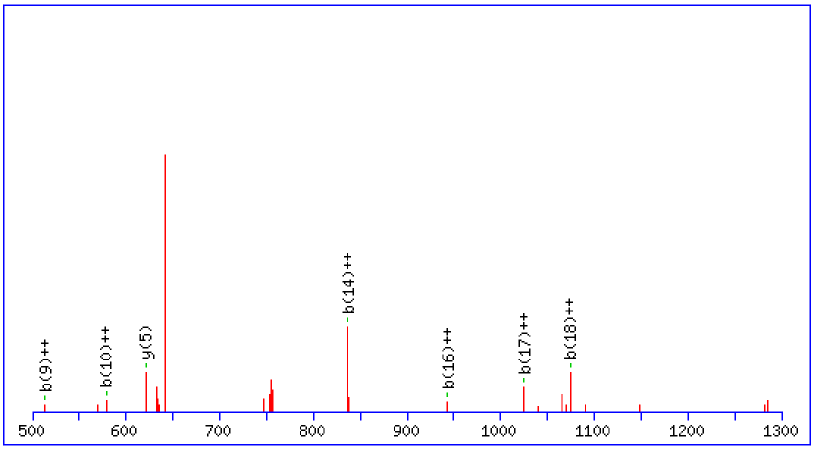
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNAQLCVLAEDCNQPDYVK**
Found in **AT2G32060.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S12 (RPS12C) | chr2:13646305-13647181 REVERSE

Match to Query 9931: 2292.063996 from(765.028608,3+) index(4464)
Title: Elution from: 41.452 to 41.452 scan no 5655 cid35.00 polarity:+
Data file 0-2_2.mgf

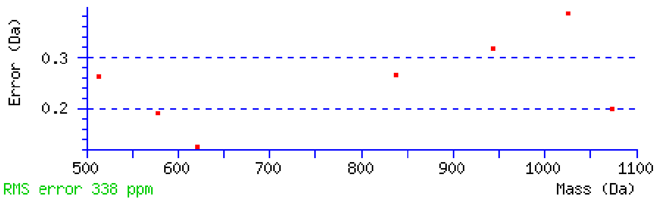
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

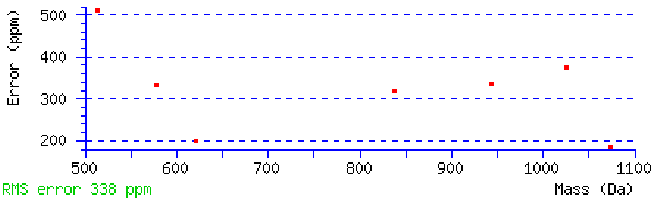


Monoisotopic mass of neutral peptide Mr(calc): 2292.0627
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.0079
Matches : 7/192 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			**R**							**19**
2	271.1513	136.0793	254.1248	127.5660			**N**	2136.9689	1068.9881	2119.9423	1060.4748	2118.9583	1059.9828	**18**
3	342.1884	171.5979	325.1619	163.0846			**A**	2022.9259	1011.9666	2005.8994	1003.4533	2004.9154	1002.9613	**17**
4	470.2470	235.6271	453.2205	227.1139			**Q**	1951.8888	976.4481	1934.8623	967.9348	1933.8783	967.4428	**16**
5	583.3311	292.1692	566.3045	283.6559			**L**	1823.8302	912.4188	1806.8037	903.9055	1805.8197	903.4135	**15**
6	743.3617	372.1845	726.3352	363.6712			**C**	1710.7462	855.8767	1693.7196	847.3635	1692.7356	846.8714	**14**
7	842.4301	421.7187	825.4036	413.2054			**V**	1550.7155	775.8614	1533.6890	767.3481	1532.7050	766.8561	**13**
8	955.5142	478.2607	938.4876	469.7475			**L**	1451.6471	726.3272	1434.6206	717.8139	1433.6366	717.3219	**12**
9	1026.5513	***513.7793***	1009.5248	505.2660			**A**	1338.5631	669.7852	1321.5365	661.2719	1320.5525	660.7799	**11**
10	1155.5939	***578.3006***	1138.5674	569.7873	1137.5833	569.2953	**E**	1267.5259	634.2666	1250.4994	625.7533	1249.5154	625.2613	**10**
11	1270.6208	635.8141	1253.5943	627.3008	1252.6103	626.8088	**D**	1138.4834	569.7453	1121.4568	561.2320	1120.4728	560.7400	**9**
12	1430.6515	715.8294	1413.6249	707.3161	1412.6409	706.8241	**C**	1023.4564	512.2318	1006.4299	503.7186	1005.4458	503.2266	**8**
13	1544.6944	772.8508	1527.6679	764.3376	1526.6839	763.8456	**N**	863.4258	432.2165	846.3992	423.7032	845.4152	423.2112	**7**
14	1672.7530	***836.8801***	1655.7265	828.3669	1654.7424	827.8749	**Q**	749.3828	375.1951	732.3563	366.6818	731.3723	366.1898	**6**
15	1769.8058	885.4065	1752.7792	876.8932	1751.7952	876.4012	**P**	621.3243	311.1658	604.2977	302.6525	603.3137	302.1605	**5**
16	1884.8327	***942.9200***	1867.8062	934.4067	1866.8221	933.9147	**D**	524.2715	262.6394	507.2449	254.1261	506.2609	253.6341	**4**
17	2047.8960	***1024.4517***	2030.8695	1015.9384	2029.8855	1015.4464	**Y**	409.2445	205.1259	392.2180	196.6126			**3**
18	2146.9645	***1073.9859***	2129.9379	1065.4726	2128.9539	1064.9806	**V**	246.1812	123.5942	229.1547	115.0810			**2**
19							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT2G32060.1





NCBI **BLAST** search of RNAQLCVLAEDCNQPDYVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.9	2292.0627	0.0013	RNAQLCVLAEDCNQPDYVK
7.6	2292.0620	0.0020	MDDWEAEDFQPLPSKVELK
5.9	2292.0667	-0.0027	RSYDVCMQLYEKELWTR
5.2	2292.0580	0.0060	VAEVDESGTQPFVDSLSQCPK
2.8	2292.0692	-0.0052	KEAAAKDPSNAAMQLEFDDNK
1.9	2292.0588	0.0052	KKFVADDSQCSICLMEYAK

Mascot: http://www.matrixscience.com/

AT2G32220.1

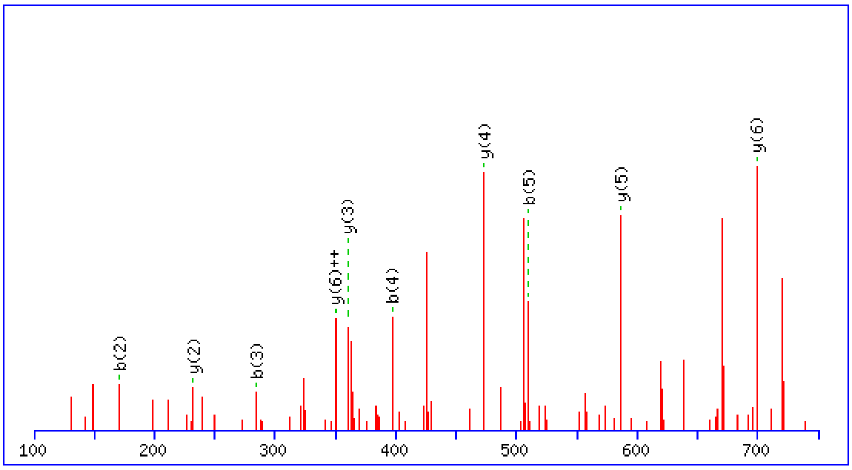
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVILLQGR**
Found in **AT2G32220.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L27 (RPL27A) | chr2:13686022-13686429 FORWARD

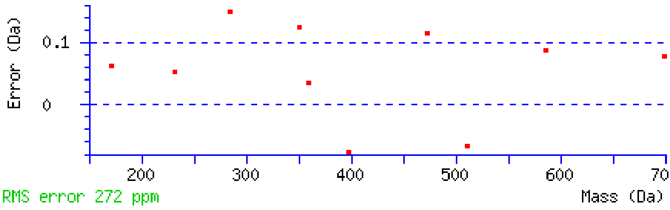
Match to Query 1405: 868.549248 from(435.281900,2+) index(3620)
Title: Elution from: 34.922 to 34.922 scan no 4529 cid35.00 polarity:+
Data file D6h-3_1.mgf

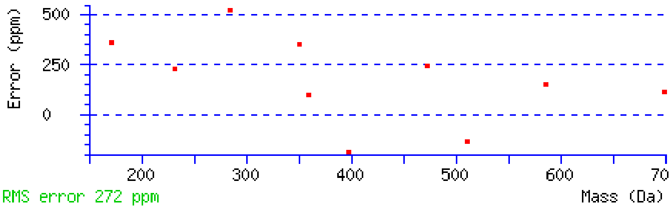
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 868.5494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.011
Matches : 10/46 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.0444	36.5258			A					8
2	**171.1128**	86.0600			V	798.5196	399.7634	781.4931	391.2502	7
3	**284.1969**	142.6021			I	***699.4512***	350.2292	682.4246	341.7160	6
4	**397.2809**	199.1441			L	***586.3671***	293.6872	569.3406	285.1739	5
5	**510.3650**	255.6861			L	***473.2831***	237.1452	456.2565	228.6319	4
6	638.4236	319.7154	621.3970	311.2022	Q	***360.1990***	180.6031	343.1724	172.0899	3
7	695.4450	348.2262	678.4185	339.7129	G	***232.1404***	116.5738	215.1139	108.0606	2
8					R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of AVILLQGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.5	868.5494	-0.0002	AVILLQGR

AT2G32220.1

Mascot: http://www.matrixscience.com/

AT2G32390.1

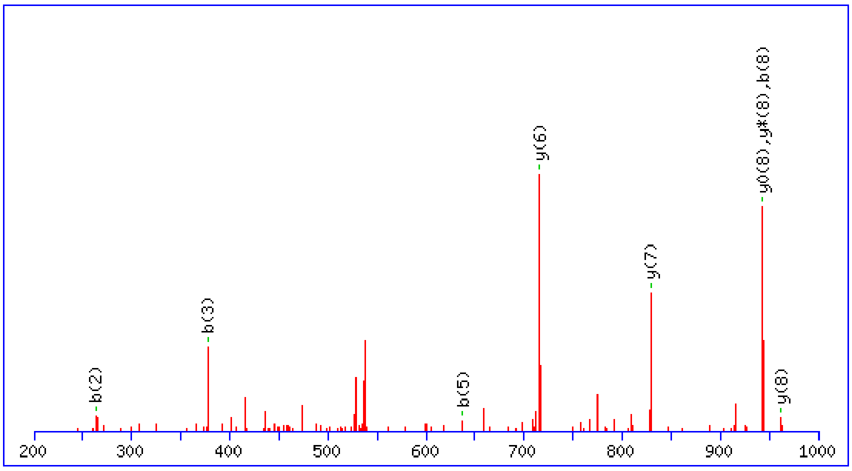
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EMLKEKSSK**
Found in **AT2G32390.1** in **TAIR_Arabidopsis**, Symbols: GLR3.5, GLR6, ATGLR3.5 | ATGLR3.5 (GLUTAMATE RECEPTOR 6) | chr2:13755545-13758834 REVERSE

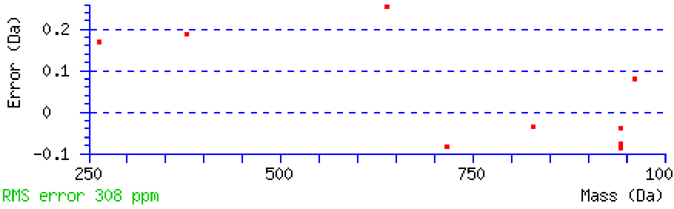
Match to Query 3221: 1090.535756 from(546.275154,2+) index(1933)
Title: Elution from: 22.101 to 22.101 scan no 2478 cid35.00 polarity:+
Data file D12h-3_3.mgf

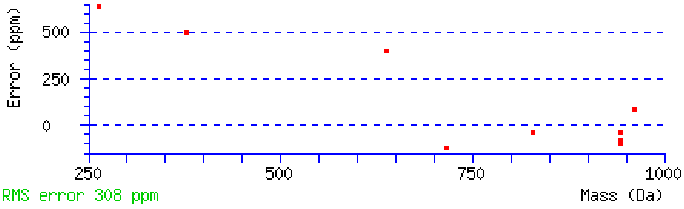
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1090.5337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0011
Matches : 9/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							9
2	***263.0844***	132.0458			245.0739	123.0406	M	***961.5013***	481.2543	943.4777	472.2425	943.4907	472.2490	8
3	***377.1655***	189.0864			359.1550	180.0811	L	***829.4638***	415.2355	811.4402	406.2237	811.4532	406.2303	7
4	507.2546	254.1309	489.2310	245.1191	489.2440	245.1256	K	***715.3827***	358.1950	697.3591	349.1832	697.3721	349.1897	6
5	***637.2942***	319.1507	619.2706	310.1389	619.2836	310.1454	E	585.2937	293.1505	567.2701	284.1387	567.2831	284.1452	5
6	767.3832	384.1952	749.3596	375.1835	749.3727	375.1900	K	455.2540	228.1307	437.2304	219.1189	437.2435	219.1254	4
7	855.4123	428.2098	837.3887	419.1980	837.4017	419.2045	S	325.1650	163.0861	307.1414	154.0743	307.1544	154.0809	3
8	***943.4413***	472.2243	925.4178	463.2125	925.4308	463.2190	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EMLKEKSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G32390.1

40.6	1090.5337	0.0021	EMLKEKSSK
27.8	1090.5359	-0.0001	EYMQGVLIK
21.5	1090.5359	-0.0001	FLLAQMETK
19.4	1090.5359	-0.0001	LYEAACLLK
19.4	1090.5386	-0.0028	YRCPQLLK
15.4	1090.5386	-0.0028	TRGMLGWLK
11.6	1090.5325	0.0032	EDAFFVKPK
10.3	1090.5337	0.0021	AMSLLSNSLK
10.2	1090.5363	-0.0006	QMVGEKRTK
3.2	1090.5325	0.0032	SPPYYNVIK

AT2G32940.1

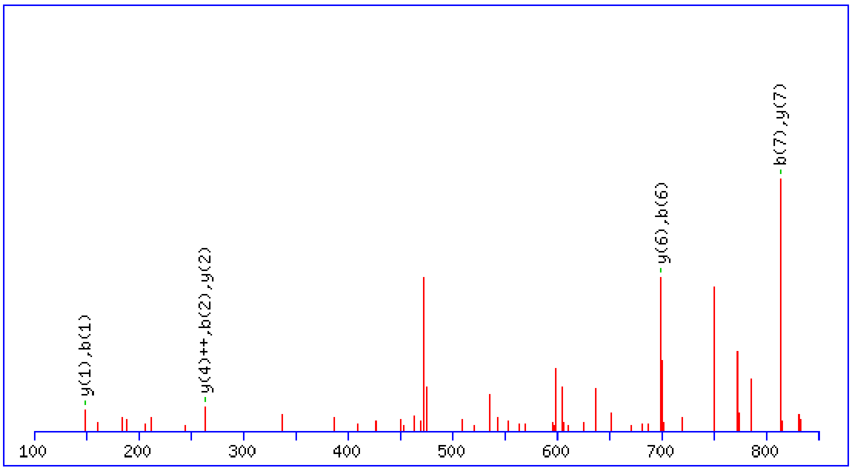
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MIATMKLK**
Found in **AT2G32940.1** in **TAIR_Arabidopsis**, Symbols: AGO6 | AGO6 (ARGONAUTE 6); nucleic acid binding | chr2:13979295-13983933 REVERSE

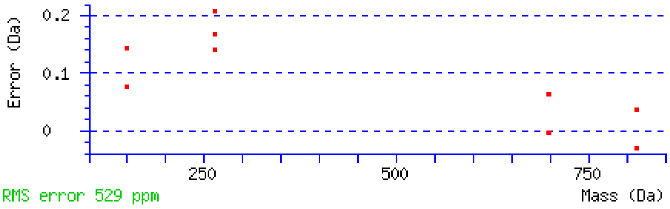
Match to Query 1811: 960.497186 from(481.255869,2+) index(2894)
Title: Elution from: 30.037 to 30.037 scan no 3663 cid35.00 polarity:+
Data file D1d-2_3.mgf

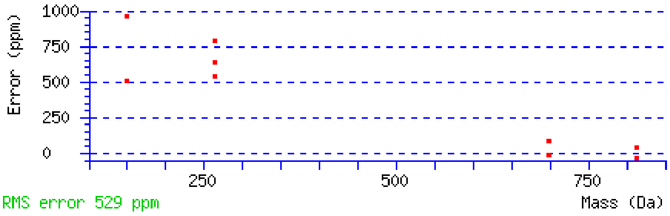
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 960.4996
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.0045
Matches : 9/86 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***149.0397***	75.0235					M							8
2	***263.1208***	132.0640					I	***813.4745***	407.2409	795.4509	398.2291	795.4639	398.2356	7
3	335.1550	168.0811					A	***699.3934***	350.2003	681.3698	341.1885	681.3828	341.1950	6
4	437.1997	219.1035			419.1891	210.0982	T	627.3592	314.1833	609.3357	305.1715	609.3487	305.1780	5
5	569.2372	285.1222			551.2266	276.1170	M	525.3145	263.1609	507.2909	254.1491			4
6	***699.3262***	350.1668	681.3026	341.1550	681.3157	341.1615	K	393.2770	197.1421	375.2534	188.1303			3
7	***813.4073***	407.2073	795.3837	398.1955	795.3968	398.2020	L	***263.1880***	132.0976	245.1644	123.0858			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MIATMKLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis

AT2G32940.1

31.0	960.4996	-0.0025	MIATMKLK	Oxidation M1 99.01%
21.8	960.4963	0.0009	MKVFIGEK	
20.5	960.4985	-0.0013	FLIWVMK	
20.5	960.4963	0.0009	FMKIGDLK	
11.0	960.4963	0.0009	IGKMDFLK	
11.0	960.4963	0.0009	LGMFTAAIK	
11.0	960.4963	0.0009	MDGLFKLK	
11.0	960.4967	0.0005	MIARALTR	
11.0	960.4996	-0.0025	MIATMKLK	Oxidation M5 0.99%
11.0	960.4996	-0.0025	MMKSTLIK	

Mascot: http://www.matrixscience.com/

AT2G32970.1

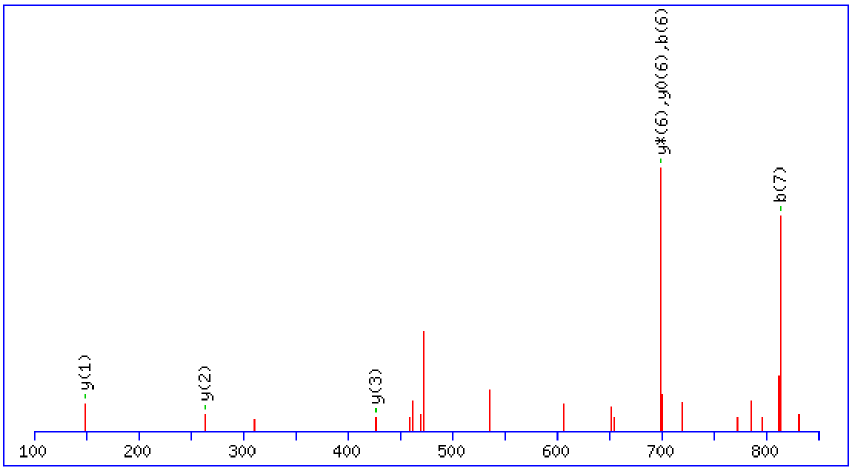
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQSSLYLK**
Found in **AT2G32970.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO24057.1) | chr2:13998821-14001159 REVERSE

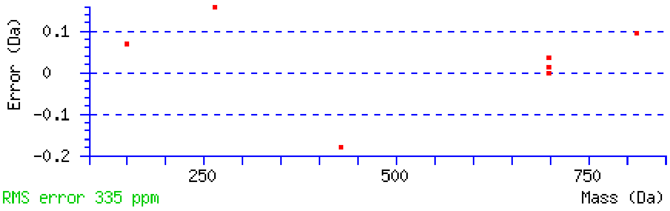
Match to Query 2051: 960.512462 from(481.263507,2+) index(3124)
Title: Elution from: 30.635 to 30.635 scan no 3867 cid35.00 polarity:+
Data file D12h-1_3.mgf

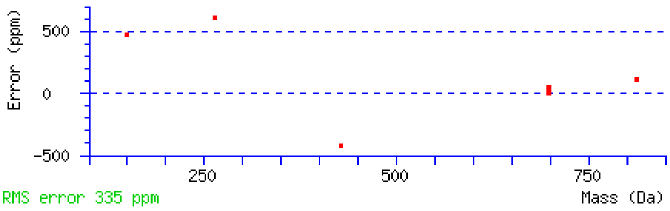
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 960.5140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.021
Matches : 7/70 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							8
2	245.1410	123.0741	227.1174	114.0624			Q	847.4402	424.2237	829.4166	415.2120	829.4296	415.2185	7
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	S	717.3876	359.1974	699.3640	350.1856	699.3770	350.1921	6
4	421.1991	211.1032	403.1756	202.0914	403.1886	202.0979	S	629.3585	315.1829	611.3349	306.1711	611.3479	306.1776	5
5	535.2802	268.1438	517.2567	259.1320	517.2697	259.1385	L	541.3294	271.1684	523.3059	262.1566			4
6	**699.3406**	350.1739	681.3170	341.1622	681.3300	341.1687	Y	***427.2483***	214.1278	409.2248	205.1160			3
7	**813.4217**	407.2145	795.3981	398.2027	795.4111	398.2092	L	***263.1880***	132.0976	245.1644	123.0858			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LQSSLYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	960.5140	-0.0016	LQSSLYLK

22.3	960.5140	-0.0016	FLKLDTSK
22.3	960.5140	-0.0016	IFSSKELK
12.8	960.5097	0.0027	CLRRTLK
12.8	960.5140	-0.0016	KSLESFLK
12.8	960.5140	-0.0016	LASSYVALK
12.8	960.5140	-0.0016	LFKESVTK
12.8	960.5140	-0.0016	SEKFSLIK
12.8	960.5140	-0.0016	SEKISFIK
12.8	960.5145	-0.0020	STRTNKLK

AT2G33040.1

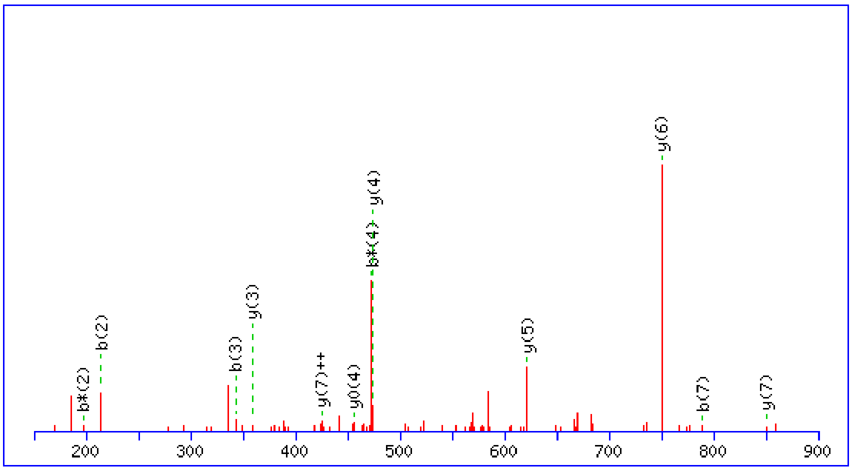
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVEFDALR**
Found in **AT2G33040.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase gamma chain, mitochondrial (ATPC) | chr2:14026055-14028124 REVERSE

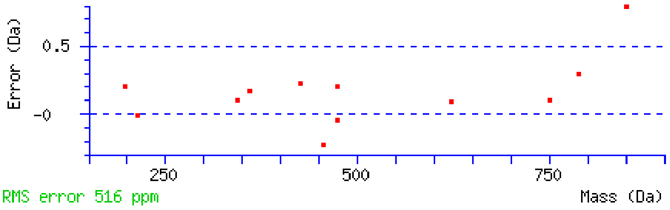
Match to Query 2132: 962.480562 from(482.247557,2+) index(4356)
Title: Elution from: 41.745 to 41.745 scan no 5504 cid35.00 polarity:+
Data file D6h-2_1.mgf

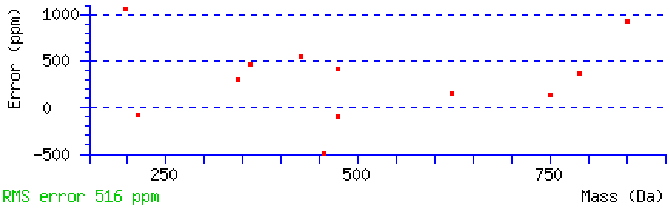
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 962.4821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.018
Matches : 12/74 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	**214.1186**	107.5629	197.0921	99.0497			V	***849.4465***	425.2269	832.4199	416.7136	831.4359	416.2216	7
3	**343.1612**	172.0842	326.1347	163.5710	325.1506	163.0790	E	***750.3781***	375.6927	733.3515	367.1794	732.3675	366.6874	6
4	490.2296	245.6185	473.2031	237.1052	472.2191	236.6132	F	***621.3355***	311.1714	604.3089	302.6581	603.3249	302.1661	5
5	605.2566	303.1319	588.2300	294.6186	587.2460	294.1266	D	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
6	676.2937	338.6505	659.2671	330.1372	658.2831	329.6452	A	***359.2401***	180.1237	342.2136	171.6104			3
7	**789.3777**	395.1925	772.3512	386.6792	771.3672	386.1872	L	288.2030	144.6051	271.1765	136.0919			2
8							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of NVEFDALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	962.4821	-0.0016	NVEFDALR

AT2G33040.1

Mascot: http://www.matrixscience.com/

AT2G33150.1

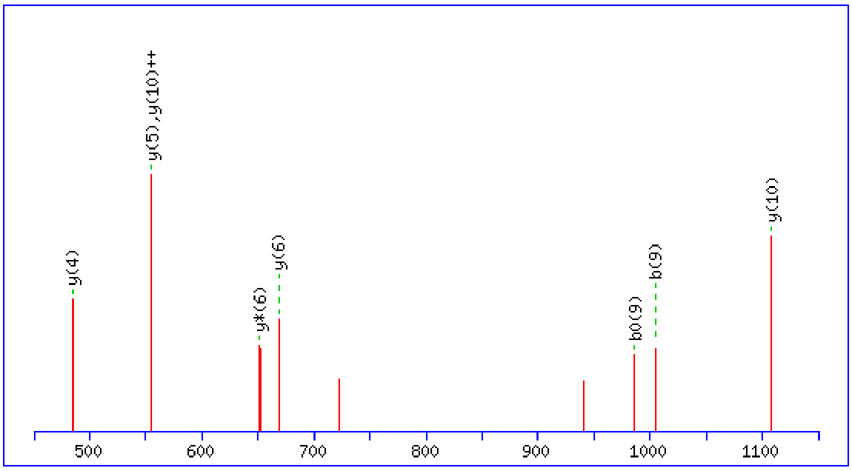
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTYPDDLLAPVLR**
Found in **AT2G33150.1** in **TAIR_Arabidopsis**, Symbols: PED1, KAT2 | KAT2/PED1 (PEROXISOME DEFECTIVE 1); acetyl-CoA C-acyltransferase | chr2:14054891-14058060 REVERSE

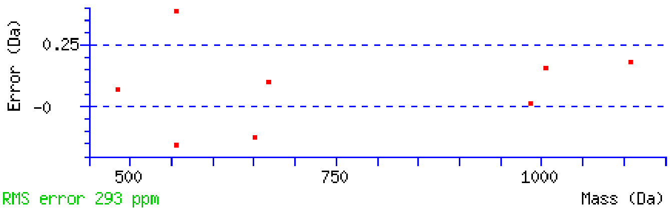
Match to Query 6273: 1486.764182 from(744.389367,2+) index(9710)
Title: Elution from: 88.375 to 88.375 scan no 13355 cid35.00 polarity:+
Data file D6h-3_1.mgf

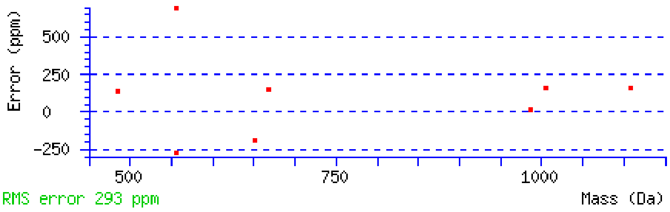
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1486.7668
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.024
Matches : 8/106 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	**D**							**13**
2	217.0819	109.0446	199.0713	100.0393	**T**	1372.7471	686.8772	1355.7205	678.3639	1354.7365	677.8719	**12**
3	380.1452	190.5763	362.1347	181.5710	**Y**	1271.6994	636.3533	1254.6729	627.8401	1253.6888	627.3481	**11**
4	477.1980	239.1026	459.1874	230.0974	**P**	***1108.6361***	554.8217	1091.6095	546.3084	1090.6255	545.8164	**10**
5	592.2249	296.6161	574.2144	287.6108	**D**	1011.5833	506.2953	994.5568	497.7820	993.5728	497.2900	**9**
6	707.2519	354.1296	689.2413	345.1243	**D**	896.5564	448.7818	879.5298	440.2686	878.5458	439.7765	**8**
7	820.3359	410.6716	802.3254	401.6663	**L**	781.5294	391.2684	764.5029	382.7551			**7**
8	933.4200	467.2136	915.4094	458.2084	**L**	***668.4454***	334.7263	651.4188	326.2130			**6**
9	1004.4571	502.7322	986.4466	493.7269	**A**	***555.3613***	278.1843	538.3348	269.6710			**5**
10	1101.5099	551.2586	1083.4993	542.2533	**P**	***484.3242***	242.6657	467.2976	234.1525			**4**
11	1200.5783	600.7928	1182.5677	591.7875	**V**	387.2714	194.1394	370.2449	185.6261			**3**
12	1313.6624	657.3348	1295.6518	648.3295	**L**	288.2030	144.6051	271.1765	136.0919			**2**
13					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DTYPDDLLAPVLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G33150.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.5	1486.7668	-0.0026	DTYPDDLLAPVLR

Mascot: http://www.matrixscience.com/

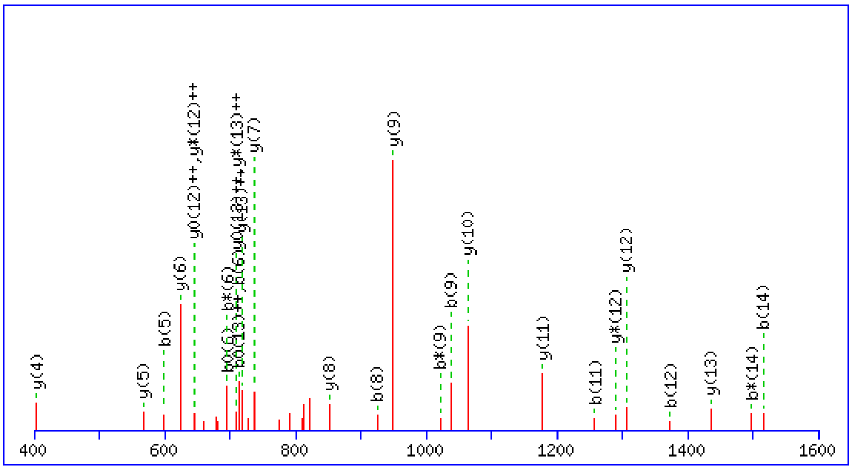
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEQDNPDLGYDAAK**
Found in **AT2G33210.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr2:14082170-14085645 REVERSE

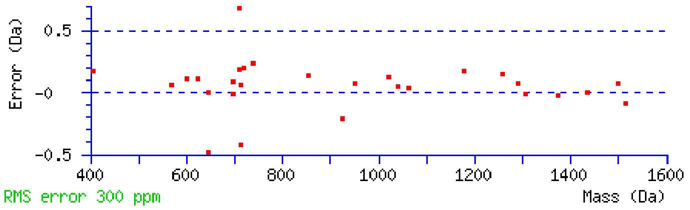
Match to Query 7619: 1660.790002 from(831.402277,2+) index(4375)
Title: Elution from: 40.367 to 40.367 scan no 5527 cid35.00 polarity:+
Data file D6h-3_2.mgf

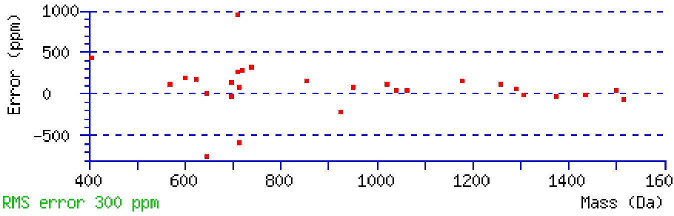
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1660.7944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 5e-011
Matches : 28/152 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							15
2	227.1754	114.0913					L	1548.7176	774.8625	1531.6911	766.3492	1530.7071	765.8572	14
3	356.2180	178.6126			338.2074	169.6074	E	***1435.6336***	718.3204	1418.6070	709.8072	1417.6230	709.3151	13
4	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	Q	***1306.5910***	653.7991	1289.5644	645.2859	1288.5804	644.7938	12
5	***599.3035***	300.1554	582.2770	291.6421	581.2930	291.1501	D	***1178.5324***	589.7698	1161.5059	581.2566	1160.5218	580.7646	11
6	***713.3464***	357.1769	696.3199	348.6636	695.3359	348.1716	N	***1063.5055***	532.2564	1046.4789	523.7431	1045.4949	523.2511	10
7	810.3992	405.7032	793.3727	397.1900	792.3886	396.6980	P	***949.4625***	475.2349	932.4360	466.7216	931.4520	466.2296	9
8	***925.4262***	463.2167	908.3996	454.7034	907.4156	454.2114	D	***852.4098***	426.7085	835.3832	418.1953	834.3992	417.7032	8
9	***1038.5102***	519.7587	1021.4837	511.2455	1020.4997	510.7535	L	***737.3828***	369.1951	720.3563	360.6818	719.3723	360.1898	7
10	1095.5317	548.2695	1078.5051	539.7562	1077.5211	539.2642	G	***624.2988***	312.6530	607.2722	304.1397	606.2882	303.6477	6
11	***1258.5950***	629.8011	1241.5685	621.2879	1240.5844	620.7959	Y	***567.2773***	284.1423	550.2508	275.6290	549.2667	275.1370	5
12	***1373.6220***	687.3146	1356.5954	678.8013	1355.6114	678.3093	D	***404.2140***	202.6106	387.1874	194.0974	386.2034	193.6053	4
13	1444.6591	722.8332	1427.6325	714.3199	1426.6485	713.8279	A	289.1870	145.0972	272.1605	136.5839			3
14	***1515.6962***	758.3517	1498.6696	749.8385	1497.6856	749.3464	A	218.1499	109.5786	201.1234	101.0653			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LLEQDNPDLGYDAAK

AT2G33210.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.2	1660.7944	-0.0044	LLEQDNPDLGYDAAK
4.0	1660.7903	-0.0003	ELNQNLNSSEEEKK

AT2G33410.1

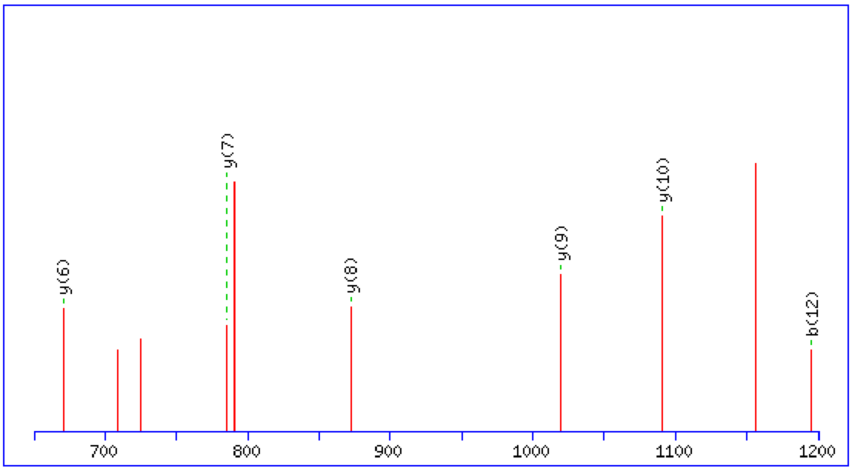
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGFVAFSDPAVIDR**
Found in **AT2G33410.1** in **TAIR_Arabidopsis**, Symbols: | heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative | chr2:14163161-14164511 FORWARD

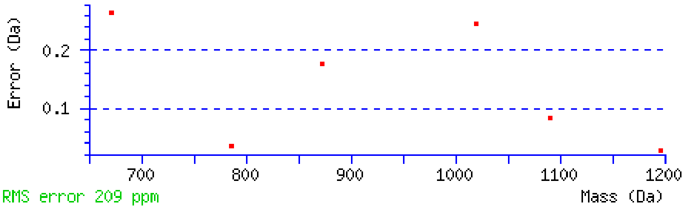
Match to Query 7187: 1596.793192 from(799.403872,2+) index(9463)
Title: Elution from: 86.563 to 86.563 scan no 13005 cid35.00 polarity:+
Data file D6h-1_2.mgf

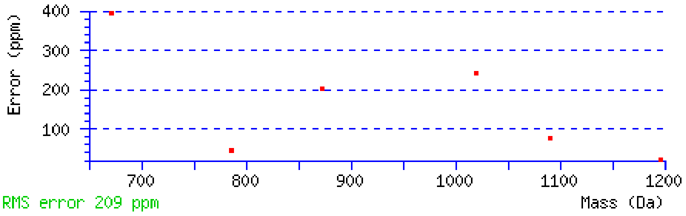
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1596.7937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0015
Matches : 6/124 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							15
2	205.0972	103.0522			F	1540.7795	770.8934	1523.7529	762.3801	1522.7689	761.8881	14
3	262.1186	131.5629			G	1393.7110	697.3592	1376.6845	688.8459	1375.7005	688.3539	13
4	409.1870	205.0972			F	1336.6896	668.8484	1319.6630	660.3352	1318.6790	659.8431	12
5	508.2554	254.6314			V	1189.6212	595.3142	1172.5946	586.8009	1171.6106	586.3089	11
6	579.2926	290.1499			A	***1090.5527***	545.7800	1073.5262	537.2667	1072.5422	536.7747	10
7	726.3610	363.6841			F	***1019.5156***	510.2615	1002.4891	501.7482	1001.5051	501.2562	9
8	813.3930	407.2001	795.3824	398.1949	S	***872.4472***	436.7272	855.4207	428.2140	854.4367	427.7220	8
9	928.4199	464.7136	910.4094	455.7083	D	***785.4152***	393.2112	768.3886	384.6980	767.4046	384.2060	7
10	1025.4727	513.2400	1007.4621	504.2347	P	***670.3883***	335.6978	653.3617	327.1845	652.3777	326.6925	6
11	1096.5098	548.7585	1078.4993	539.7533	A	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
12	1195.5782	598.2928	1177.5677	589.2875	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
13	1308.6623	654.8348	1290.6517	645.8295	I	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
14	1423.6892	712.3483	1405.6787	703.3430	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
15					R	175.1190	88.0631	158.0924	79.5498			1





AT2G33410.1

NCBI **BLAST** search of GFGFVAFSDPAVIDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.3	1596.7937	-0.0005	GFGFVAFSDPAVIDR

AT2G33540.1

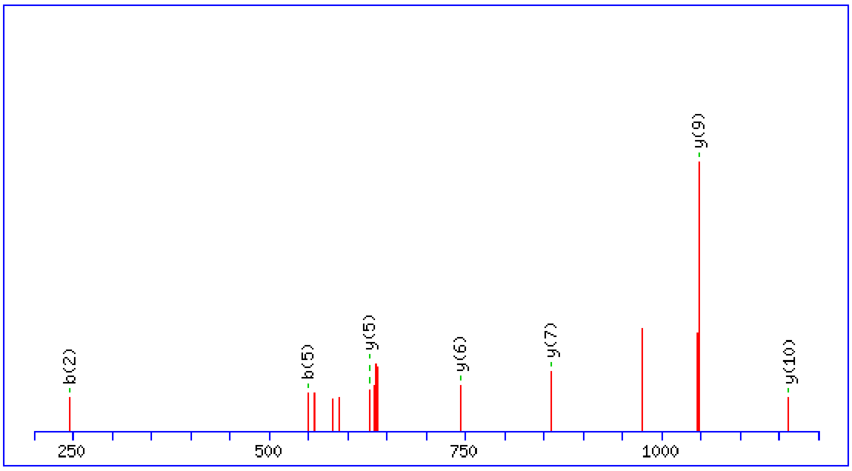
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELVSDNDDFPK**
Found in **AT2G33540.1** in **TAIR_Arabidopsis**, Symbols: CPL3 | CPL3 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 3); CTD phosphatase | chr2:14211157-14215873 REVERSE

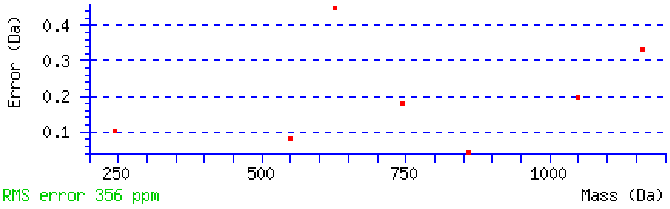
Match to Query 4798: 1290.537690 from(646.276121,2+) index(4110)
Title: Elution from: 38.073 to 38.073 scan no 5121 cid35.00 polarity:+
Data file C7-2_2.mgf

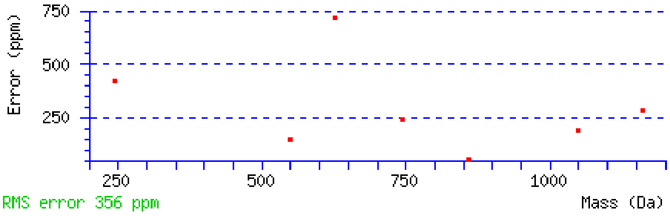
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1290.5390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00028
Matches : 7/104 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							11
2	**245.1280**	123.0676			227.1174	114.0624	L	***1161.5067***	581.2570	1143.4831	572.2452	1143.4961	572.2517	10
3	345.1935	173.1004			327.1829	164.0951	V	***1047.4256***	524.2164	1029.4020	515.2046	1029.4150	515.2111	9
4	433.2225	217.1149			415.2120	208.1096	S	947.3601	474.1837	929.3365	465.1719	929.3496	465.1784	8
5	**549.2465**	275.1269			531.2359	266.1216	D	***859.3311***	430.1692	841.3075	421.1574	841.3205	421.1639	7
6	665.2835	333.1454	647.2599	324.1336	647.2729	324.1401	N	***743.3071***	372.1572	725.2835	363.1454	725.2965	363.1519	6
7	781.3075	391.1574	763.2839	382.1456	763.2969	382.1521	D	***627.2701***	314.1387	609.2465	305.1269	609.2595	305.1334	5
8	897.3314	449.1694	879.3079	440.1576	879.3209	440.1641	D	511.2461	256.1267	493.2225	247.1149	493.2355	247.1214	4
9	1045.3969	523.2021	1027.3733	514.1903	1027.3863	514.1968	F	395.2221	198.1147	377.1985	189.1029			3
10	1143.4467	572.2270	1125.4231	563.2152	1125.4361	563.2217	P	247.1567	124.0820	229.1331	115.0702			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ELVSDNDDFPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G33540.1

Score	Mr(calc)	Delta	Sequence
41.1	1290.5390	-0.0013	ELVSDNDDFPK
9.1	1290.5403	-0.0026	EMQHLATICR
5.0	1290.5367	0.0009	QLQVDDSTEDK
1.5	1290.5395	-0.0018	SEPNSAQSTPTR
0.3	1290.5365	0.0012	EWIMEQWEK

AT2G33680.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **CGSLEDGNLVFR**
Found in **AT2G33680.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:14256684-14258867 FORWARD

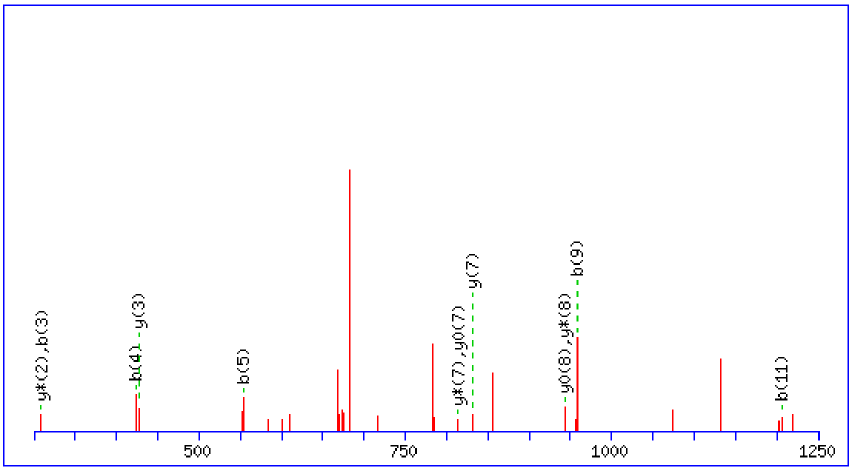
Match to Query 5380: 1382.581610 from(692.298081,2+) index(3389)
Title: Elution from: 32.139 to 32.139 scan no 4186 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1250 Da Full range

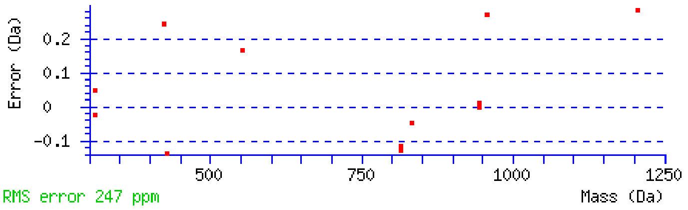
Label all possible matches ○ Label matches used for scoring ●

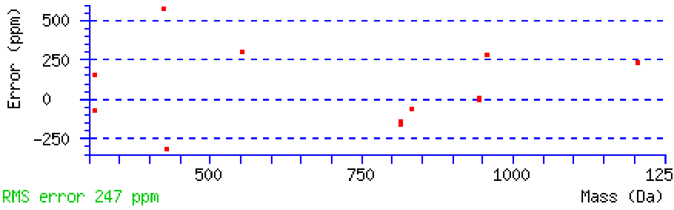
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.5843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.014
Matches : 12/102 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	163.0320	82.0196					C							12
2	221.0505	111.0289					G	1221.5669	611.2871	1203.5433	602.2753	1203.5563	602.2818	11
3	***309.0796***	155.0434			291.0690	146.0381	S	1163.5484	582.2778	1145.5248	573.2660	1145.5378	573.2725	10
4	***423.1607***	212.0840			405.1501	203.0787	L	1075.5193	538.2633	1057.4957	529.2515	1057.5087	529.2580	9
5	***553.2003***	277.1038			535.1897	268.0985	E	961.4382	481.2227	943.4146	472.2109	943.4276	472.2175	8
6	669.2243	335.1158			651.2137	326.1105	D	**831.3986**	416.2029	813.3750	407.1911	813.3880	407.1976	7
7	727.2428	364.1250			709.2322	355.1197	G	715.3746	358.1909	697.3510	349.1791			6
8	843.2798	422.1435	825.2562	413.1317	825.2692	413.1382	N	657.3561	329.1817	639.3325	320.1699			5
9	***957.3609***	479.1841	939.3373	470.1723	939.3503	470.1788	L	541.3191	271.1632	523.2955	262.1514			4
10	1057.4263	529.2168	1039.4027	520.2050	1039.4157	520.2115	V	**427.2380**	214.1226	409.2144	205.1108			3
11	***1205.4918***	603.2495	1187.4682	594.2377	1187.4812	594.2442	F	327.1725	164.0899	309.1490	155.0781			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of CGSLEDGNLVFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G33680.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.4	1382.5843	-0.0027	CGSLEDGNLVFR
6.6	1382.5829	-0.0013	VMMNAMNAPSKR
6.4	1382.5820	-0.0004	MEEERVDSSKR
5.9	1382.5818	-0.0001	RGGRGGSGGGGSGPSR
5.8	1382.5818	-0.0002	YPRAHYVGCLM
5.0	1382.5794	0.0022	TLMTSSEGEEIR
4.4	1382.5787	0.0029	GGSVWSSPSTSSAR
4.2	1382.5829	-0.0013	VMMNAMNAPSKR
4.2	1382.5829	-0.0013	VMMNAMNAPSKR
2.4	1382.5843	-0.0027	ASRTIDWDGMAK

AT2G33800.1

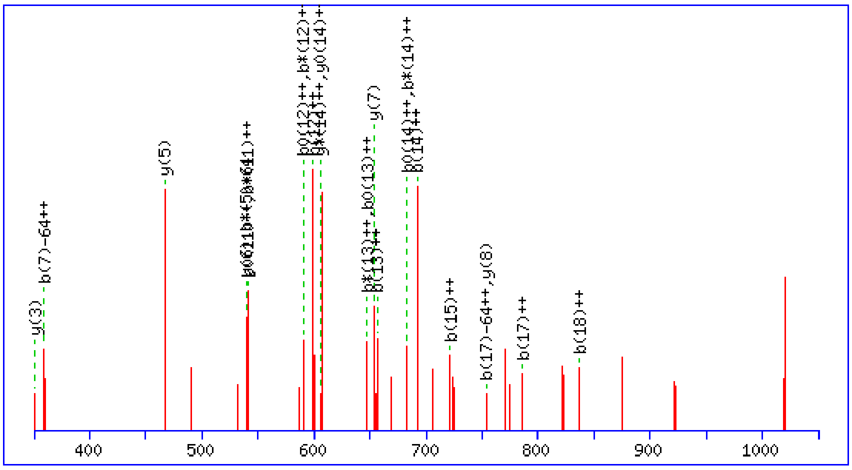
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMLRPASPGTGVIAGGAVR**
Found in **AT2G33800.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein S5 family protein | chr2:14308001-14309428 REVERSE

Match to Query 8412: 1848.926853 from(617.316227,3+) index(3413)
Title: Elution from: 34.172 to 34.172 scan no 4327 cid35.00 polarity:+
Data file D12h-2_3.mgf

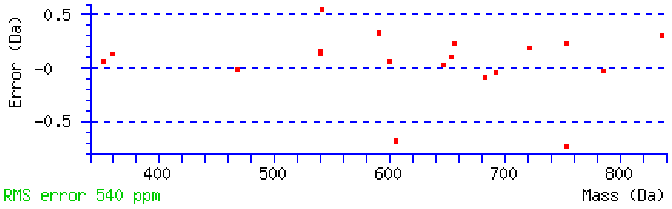
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

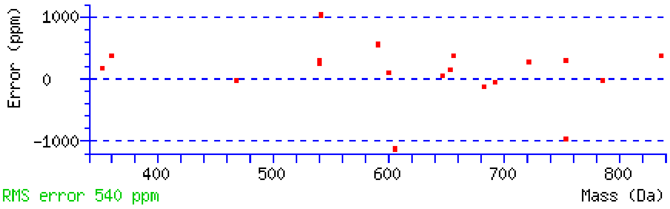


Monoisotopic mass of neutral peptide Mr(calc): 1848.9298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.041
Matches : 24/274 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							19
2	249.1052	125.0562					M	1749.8717	875.4395	1731.8481	866.4277	1731.8611	866.4342	18
3	363.1863	182.0968					L	1601.8393	801.4233	1583.8157	792.4115	1583.8287	792.4180	17
4	523.2755	262.1414	505.2519	253.1296			R	1487.7582	744.3827	1469.7346	735.3709	1469.7476	735.3774	16
5	621.3253	311.1663	603.3017	302.1545			P	1327.6689	664.3381	1309.6453	655.3263	1309.6583	655.3328	15
6	693.3595	347.1834	675.3359	338.1716			A	1229.6191	615.3132	1211.5955	606.3014	1211.6085	606.3079	14
7	781.3885	391.1979	763.3649	382.1861	763.3780	382.1926	S	1157.5850	579.2961	1139.5614	570.2843	1139.5744	570.2908	13
8	879.4383	440.2228	861.4147	431.2110	861.4278	431.2175	P	1069.5559	535.2816	1051.5323	526.2698	1051.5453	526.2763	12
9	937.4568	469.2320	919.4332	460.2203	919.4463	460.2268	G	971.5061	486.2567	953.4825	477.2449	953.4955	477.2514	11
10	1039.5015	520.2544	1021.4779	511.2426	1021.4910	511.2491	T	913.4876	457.2474	895.4640	448.2356	895.4770	448.2422	10
11	1097.5200	549.2637	1079.4964	540.2519	1079.5095	540.2584	G	811.4429	406.2251	793.4193	397.2133			9
12	1197.5855	***599.2964***	1179.5619	590.2846	1179.5749	590.2911	V	***753.4244***	377.2158	735.4008	368.2040			8
13	1311.6666	***656.3369***	1293.6430	647.3251	1293.6560	647.3316	I	***653.3589***	327.1831	635.3354	318.1713			7
14	1383.7007	***692.3540***	1365.6771	683.3422	1365.6902	683.3487	A	***539.2778***	270.1426	521.2543	261.1308			6
15	1441.7192	***721.3633***	1423.6956	712.3515	1423.7087	712.3580	G	***467.2437***	234.1255	449.2201	225.1137			5
16	1499.7377	750.3725	1481.7141	741.3607	1481.7272	741.3672	G	409.2252	205.1162	391.2016	196.1044			4
17	1571.7719	***786.3896***	1553.7483	777.3778	1553.7613	777.3843	A	***351.2067***	176.1070	333.1831	167.0952			3
18	1671.8373	***836.4223***	1653.8137	827.4105	1653.8268	827.4170	V	279.1725	140.0899	261.1490	131.0781			2
19							R	179.1071	90.0572	161.0835	81.0454			1

AT2G33800.1





NCBI **BLAST** search of VMLRPASPGTGVIAGGAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.7	1848.9298	-0.0030	VMLRPASPGTGVIAGGAVR
3.8	1848.9299	-0.0030	ALNSSCKKPPKPGNKAK
3.7	1848.9225	0.0044	LMALRSHVPIVTNMTK
0.3	1848.9240	0.0029	WKLEPRLVCLHFAR

AT2G34230.1

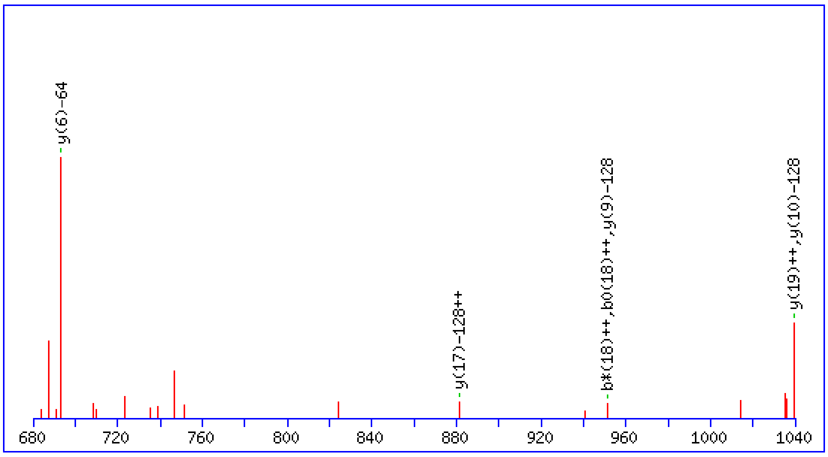
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSNAVVTVSETSTMANQMVLK**
Found in **AT2G34230.1** in **TAIR_Arabidopsis**, Symbols: | similar to MEE20 (maternal effect embryo arrest 20) [Arabidopsis thaliana] (TAIR:AT2G34220.1); contains InterPro domain Protein of unknown function DUF627 (InterPro:IPR006866); contains InterPro domain Protein of unknown function DUF629

Match to Query 10438: 2280.994398 from(761.338742,3+) index(6101)
Title: Elution from: 53.961 to 53.961 scan no 7717 cid35.00 polarity:+
Data file 0-2_1.mgf

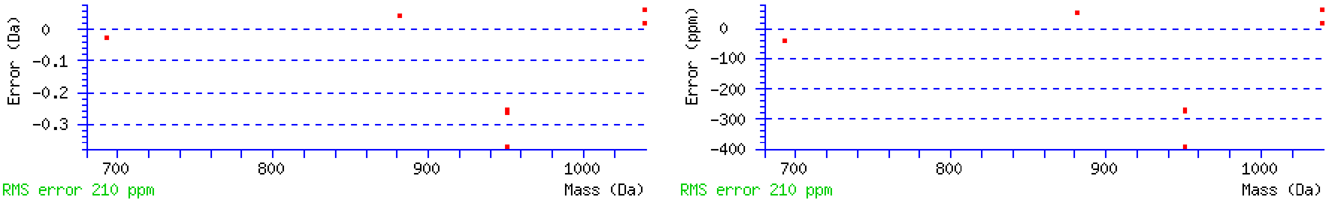
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 680 to 1040 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2281.0003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M14 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
M18 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.033
Matches : 7/356 fragment ions using 4 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							21
2	205.0733	103.0403	187.0498	94.0285	187.0628	94.0350	S	2037.9740	1019.4906	2019.9504	1010.4788	2019.9634	1010.4853	20
3	321.1103	161.0588	303.0867	152.0470	303.0998	152.0535	N	1949.9449	975.4761	1931.9213	966.4643	1931.9343	966.4708	19
4	393.1445	197.0759	375.1209	188.0641	375.1339	188.0706	A	1833.9079	917.4576	1815.8843	908.4458	1815.8973	908.4523	18
5	493.2099	247.1086	475.1863	238.0968	475.1994	238.1033	V	1761.8738	881.4405	1743.8502	872.4287	1743.8632	872.4352	17
6	593.2754	297.1413	575.2518	288.1295	575.2648	288.1360	V	1661.8083	831.4078	1643.7847	822.3960	1643.7977	822.4025	16
7	695.3201	348.1637	677.2965	339.1519	677.3095	339.1584	T	1561.7429	781.3751	1543.7193	772.3633	1543.7323	772.3698	15
8	795.3855	398.1964	777.3620	389.1846	777.3750	389.1911	V	1459.6981	730.3527	1441.6746	721.3409	1441.6876	721.3474	14
9	883.4146	442.2109	865.3910	433.1991	865.4040	433.2057	S	1359.6327	680.3200	1341.6091	671.3082	1341.6221	671.3147	13
10	1013.4542	507.2308	995.4306	498.2190	995.4437	498.2255	E	1271.6036	636.3055	1253.5800	627.2937	1253.5931	627.3002	12
11	1115.4989	558.2531	1097.4754	549.2413	1097.4884	549.2478	T	1141.5640	571.2856	1123.5404	562.2738	1123.5534	562.2804	11
12	1203.5280	602.2676	1185.5044	593.2559	1185.5174	593.2624	S	***1039.5193***	520.2633	1021.4957	511.2515	1021.5087	511.2580	10
13	1305.5727	653.2900	1287.5491	644.2782	1287.5622	644.2847	T	***951.4902***	476.2488	933.4666	467.2370	933.4797	467.2435	9
14	1389.6069	695.3071	1371.5833	686.2953	1371.5963	686.3018	M	849.4455	425.2264	831.4219	416.2146			8
15	1461.6410	731.3241	1443.6174	722.3124	1443.6305	722.3189	A	765.4114	383.2093	747.3878	374.1975			7
16	1577.6780	789.3426	1559.6544	780.3309	1559.6675	780.3374	N	***693.3772***	347.1922	675.3536	338.1805			6
17	1707.7307	854.3690	1689.7071	845.3572	1689.7201	845.3637	Q	577.3402	289.1737	559.3166	280.1620			5
18	1791.7648	896.3860	1773.7412	887.3743	1773.7543	887.3808	M	447.2876	224.1474	429.2640	215.1356			4
19	1891.8303	946.4188	1873.8067	937.4070	1873.8197	937.4135	V	363.2534	182.1303	345.2298	173.1186			3
20	2005.9114	1003.4593	1987.8878	994.4475	1987.9008	994.4540	L	263.1880	132.0976	245.1644	123.0858			2
21							K	149.1069	75.0571	131.0833	66.0453			1

AT2G34230.1



NCBI **BLAST** search of NSNAVVTVSETSTMANQMVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.5	2281.0003	-0.0059	NSNAVVTVSETSTMANQMVLK
3.5	2280.9914	0.0030	FHGATVSASAQGSPSCIQYKR
2.4	2280.9998	-0.0054	EAVDSFIEKAIMTIDTEMGK
1.5	2280.9928	0.0016	GYFVWSFMDLYELLNGYK
1.1	2280.9978	-0.0034	MYHDKIMGERSVDISSLMK

Mascot: http://www.matrixscience.com/

AT2G34310.1

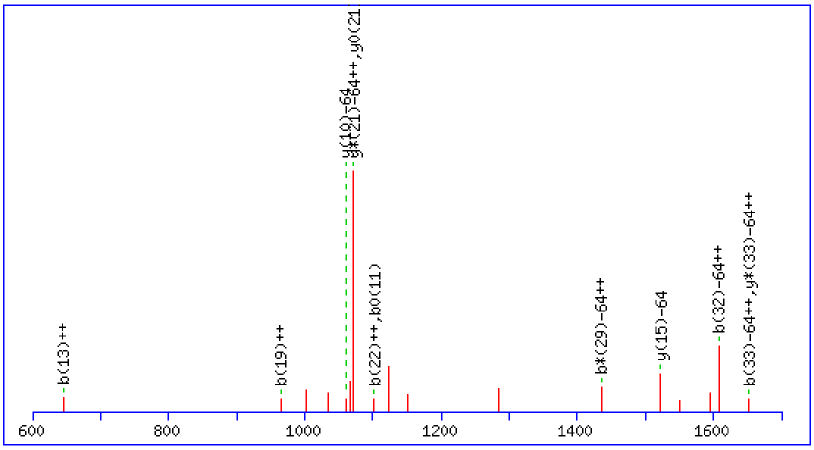
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EADSTSSLEISPALDSVKPMGSSVSKVVMSDKSK**
Found in **AT2G34310.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29530.1) | chr2:14485643-14486891 REVERSE

Match to Query 10841: 3511.724379 from(1171.582069,3+) index(10419)
Title: Elution from: 100.091 to 100.091 scan no 14697 cid35.00 polarity:+
Data file D6h-2_2.mgf

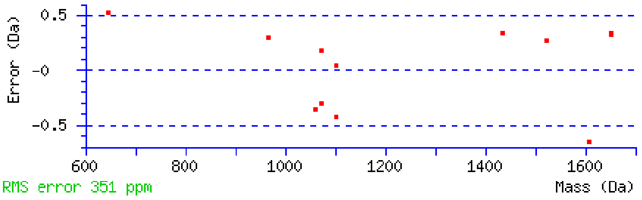
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

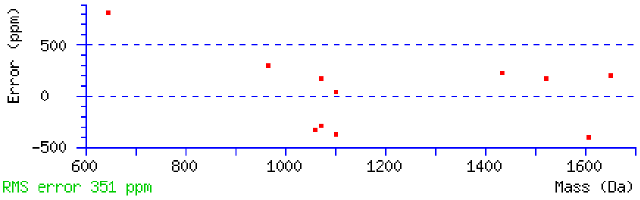


Monoisotopic mass of neutral peptide Mr(calc): 3511.7273
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M29 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.044
Matches : 12/558 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							34
2	201.0870	101.0471			183.0764	92.0418	A	3319.6937	1660.3505	3302.6672	1651.8372	3301.6832	1651.3452	33
3	316.1139	158.5606			298.1034	149.5553	D	3248.6566	1624.8320	3231.6301	1616.3187	3230.6461	1615.8267	32
4	403.1460	202.0766			385.1354	193.0713	S	3133.6297	1567.3185	3116.6031	1558.8052	3115.6191	1558.3132	31
5	504.1936	252.6005			486.1831	243.5952	T	3046.5977	1523.8025	3029.5711	1515.2892	3028.5871	1514.7972	30
6	591.2257	296.1165			573.2151	287.1112	S	2945.5500	1473.2786	2928.5234	1464.7654	2927.5394	1464.2733	29
7	678.2577	339.6325			660.2471	330.6272	S	2858.5179	1429.7626	2841.4914	1421.2493	2840.5074	1420.7573	28
8	791.3418	396.1745			773.3312	387.1692	L	2771.4859	1386.2466	2754.4594	1377.7333	2753.4754	1377.2413	27
9	920.3843	460.6958			902.3738	451.6905	E	2658.4019	1329.7046	2641.3753	1321.1913	2640.3913	1320.6993	26
10	1033.4684	517.2378			1015.4578	508.2326	I	2529.3593	1265.1833	2512.3327	1256.6700	2511.3487	1256.1780	25
11	1120.5004	560.7539			1102.4899	551.7486	S	2416.2752	1208.6412	2399.2487	1200.1280	2398.2646	1199.6360	24
12	1217.5532	609.2802			1199.5426	600.2750	P	2329.2432	1165.1252	2312.2166	1156.6119	2311.2326	1156.1199	23
13	1288.5903	***644.7988***			1270.5798	635.7935	A	2232.1904	1116.5988	2215.1639	1108.0856	2214.1798	1107.5936	22
14	1401.6744	701.3408			1383.6638	692.3355	L	2161.1533	1081.0803	2144.1267	1072.5670	2143.1427	1072.0750	21
15	1516.7013	758.8543			1498.6908	749.8490	D	2048.0692	1024.5383	2031.0427	1016.0250	2030.0587	1015.5330	20
16	1603.7334	802.3703			1585.7228	793.3650	S	1933.0423	967.0248	1916.0157	958.5115	1915.0317	958.0195	19
17	1702.8018	851.9045			1684.7912	842.8992	V	1846.0103	923.5088	1828.9837	914.9955	1827.9997	914.5035	18
18	1830.8967	915.9520	1813.8702	907.4387	1812.8862	906.9467	K	1746.9418	873.9746	1729.9153	865.4613	1728.9313	864.9693	17
19	1927.9495	***964.4784***	1910.9229	955.9651	1909.9389	955.4731	P	1618.8469	809.9271	1601.8203	801.4138	1600.8363	800.9218	16
20	2058.9900	1029.9986	2041.9634	1021.4854	2040.9794	1020.9933	M	**1521.7941**	761.4007	1504.7676	752.8874	1503.7836	752.3954	15
21	2116.0114	1058.5094	2098.9849	1049.9961	2098.0009	1049.5041	G	1390.7536	695.8805	1373.7271	687.3672	1372.7431	686.8752	14
22	2203.0435	***1102.0254***	2186.0169	1093.5121	2185.0329	1093.0201	S	1333.7322	667.3697	1316.7056	658.8564	1315.7216	658.3644	13
23	2290.0755	1145.5414	2273.0489	1137.0281	2272.0649	1136.5361	S	1246.7001	623.8537	1229.6736	615.3404	1228.6896	614.8484	12

24	2389.1439	1195.0756	2372.1174	1186.5623	2371.1333	1186.0703	**V**	1159.6681	580.3377	1142.6416	571.8244	1141.6575	571.3324	**11**
25	2476.1759	1238.5916	2459.1494	1230.0783	2458.1654	1229.5863	**S**	**1060.5997**	530.8035	1043.5732	522.2902	1042.5891	521.7982	**10**
26	2604.2709	1302.6391	2587.2444	1294.1258	2586.2603	1293.6338	**K**	973.5677	487.2875	956.5411	478.7742	955.5571	478.2822	**9**
27	2703.3393	1352.1733	2686.3128	1343.6600	2685.3288	1343.1680	**V**	845.4727	423.2400	828.4462	414.7267	827.4621	414.2347	**8**
28	2802.4077	1401.7075	2785.3812	1393.1942	2784.3972	1392.7022	**V**	746.4043	373.7058	729.3777	365.1925	728.3937	364.7005	**7**
29	2885.4448	1443.2261	2868.4183	1434.7128	2867.4343	1434.2208	**M**	647.3359	324.1716	630.3093	315.6583	629.3253	315.1663	**6**
30	2972.4769	1486.7421	2955.4503	1478.2288	2954.4663	1477.7368	**S**	564.2988	282.6530	547.2722	274.1397	546.2882	273.6477	**5**
31	3087.5038	1544.2555	3070.4773	1535.7423	3069.4933	1535.2503	**D**	477.2667	239.1370	460.2402	230.6237	459.2562	230.1317	**4**
32	3215.5988	***1608.3030***	3198.5722	1599.7898	3197.5882	1599.2977	**K**	362.2398	181.6235	345.2132	173.1103	344.2292	172.6183	**3**
33	3302.6308	***1651.8190***	3285.6043	1643.3058	3284.6202	1642.8138	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
34							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EADSTSSLEISPALDSVKPMGSSVSKVVMSDKSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
19.1	3511.7273	-0.0029	EADSTSSLEISPALDSVKPMGSSVSKVVMSDKSK	Oxidation M29 89.27%
9.9	3511.7273	-0.0029	EADSTSSLEISPALDSVKPMGSSVSKVVMSDKSK	Oxidation M20 10.73%
3.0	3511.7161	0.0083	YSTIIYVHIVYLGEKQHDDPEFVTESHHR	
1.5	3511.7149	0.0095	MSIIELKPGGKDTSVTNENKMQYIHAMADYK	
1.0	3511.7228	0.0016	VCNHPYLIPGTEPESGSLEFLHDMRIKASAK	
0.9	3511.7334	-0.0090	EQLVQLMFETFNVSGFYASEQAVLSLYAVGR	

Mascot: http://www.matrixscience.com/

AT2G34400.1

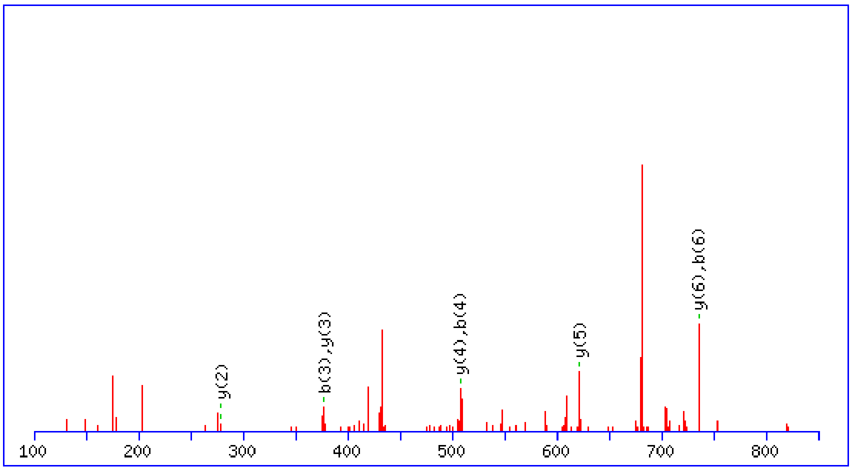
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLIKPEK**
Found in **AT2G34400.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:14523317-14525265 FORWARD

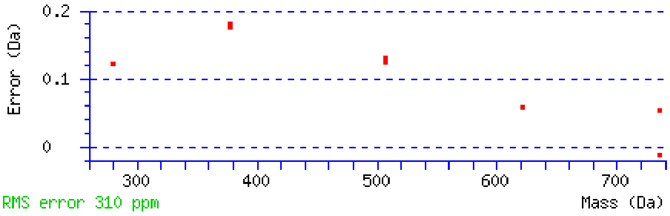
Match to Query 1476: 882.473940 from(442.244246,2+) index(1833)
Title: Elution from: 22.344 to 22.344 scan no 2388 cid35.00 polarity:+
Data file D12h-3_2.mgf

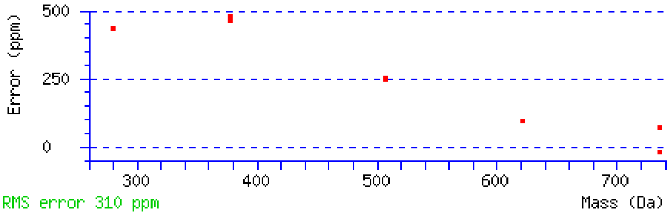
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 882.4727
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.0092
Matches : 8/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							7
2	263.1208	132.0640					L	*735.4475*	368.2274	717.4239	359.2156	717.4370	359.2221	6
3	**377.2019**	189.1046					I	*621.3664*	311.1869	603.3428	302.1751	603.3559	302.1816	5
4	**507.2909**	254.1491	489.2674	245.1373			K	*507.2853*	254.1463	489.2617	245.1345	489.2748	245.1410	4
5	605.3407	303.1740	587.3172	294.1622			P	*377.1963*	189.1018	359.1727	180.0900	359.1857	180.0965	3
6	**735.3804**	368.1938	717.3568	359.1820	717.3698	359.1885	E	*279.1465*	140.0769	261.1229	131.0651	261.1359	131.0716	2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MLIKPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.4	882.4727	0.0012	MLIKPEK

AT2G34400.1

9.4	882.4727	0.0013	ICLDILK
6.1	882.4727	0.0013	LMAEGILK
3.9	882.4720	0.0020	FHKALQK
2.1	882.4720	0.0020	KFAHLQK
1.5	882.4727	0.0013	CIEIIVK
1.1	882.4720	0.0019	KPPNLFR

AT2G34420.1

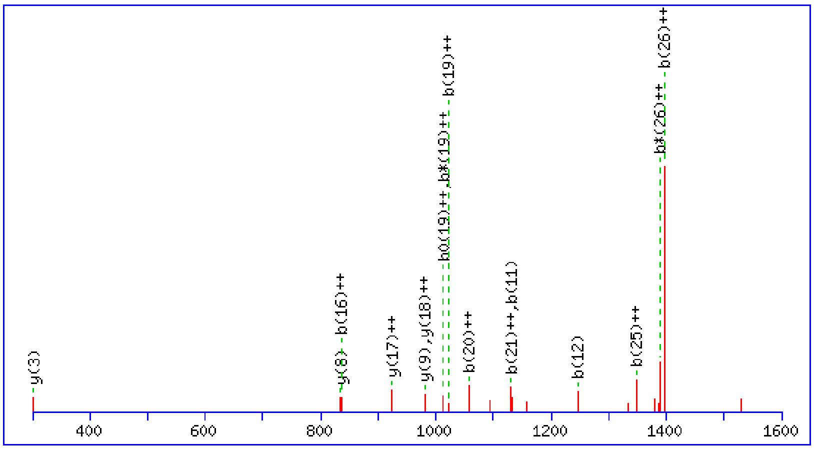
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPLENLADHLADPVNNNAWAFATNFVPGK**
Found in **AT2G34420.1** in **TAIR_Arabidopsis**, Symbols: LHCB1.5, LHB1B2 | LHB1B2 (Photosystem II light harvesting complex gene 1.5); chlorophyll binding | chr2:14529795-14530592 REVERSE

Match to Query 11215: 3091.517241 from(1031.513023,3+) index(11188)
Title: Elution from: 112.196 to 112.196 scan no 16172 cid35.00 polarity:+
Data file 0-2_1.mgf

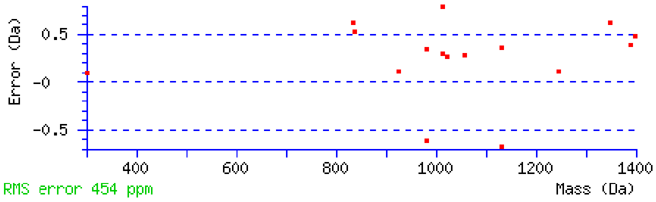
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

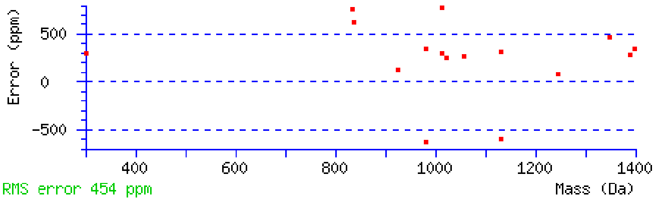


Monoisotopic mass of neutral peptide Mr(calc): 3091.5152
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00032
Matches : 16/310 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							29
2	155.0815	78.0444					P	3035.5010	1518.2541	3018.4744	1509.7409	3017.4904	1509.2489	28
3	268.1656	134.5864					L	2938.4482	1469.7278	2921.4217	1461.2145	2920.4377	1460.7225	27
4	397.2082	199.1077			379.1976	190.1024	E	2825.3642	1413.1857	2808.3376	1404.6724	2807.3536	1404.1804	26
5	511.2511	256.1292	494.2245	247.6159	493.2405	247.1239	N	2696.3216	1348.6644	2679.2950	1340.1512	2678.3110	1339.6591	25
6	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	L	2582.2786	1291.6430	2565.2521	1283.1297	2564.2681	1282.6377	24
7	695.3723	348.1898	678.3457	339.6765	677.3617	339.1845	A	2469.1946	1235.1009	2452.1680	1226.5877	2451.1840	1226.0956	23
8	810.3992	405.7032	793.3727	397.1900	792.3886	396.6980	D	2398.1575	1199.5824	2381.1309	1191.0691	2380.1469	1190.5771	22
9	947.4581	474.2327	930.4316	465.7194	929.4476	465.2274	H	2283.1305	1142.0689	2266.1040	1133.5556	2265.1200	1133.0636	21
10	1060.5422	530.7747	1043.5156	522.2615	1042.5316	521.7694	L	2146.0716	1073.5394	2129.0451	1065.0262	2128.0610	1064.5342	20
11	**1131.5793**	566.2933	1114.5528	557.7800	1113.5687	557.2880	A	2032.9876	1016.9974	2015.9610	1008.4841	2014.9770	1007.9921	19
12	**1246.6062**	623.8068	1229.5797	615.2935	1228.5957	614.8015	D	1961.9504	981.4789	1944.9239	972.9656	1943.9399	972.4736	18
13	1343.6590	672.3331	1326.6325	663.8199	1325.6484	663.3279	P	1846.9235	923.9654	1829.8969	915.4521	1828.9129	914.9601	17
14	1442.7274	721.8673	1425.7009	713.3541	1424.7169	712.8621	V	1749.8707	875.4390	1732.8442	866.9257	1731.8602	866.4337	16
15	1556.7703	778.8888	1539.7438	770.3755	1538.7598	769.8835	N	1650.8023	825.9048	1633.7758	817.3915	1632.7918	816.8995	15
16	1670.8133	***835.9103***	1653.7867	827.3970	1652.8027	826.9050	N	1536.7594	768.8833	1519.7328	760.3701	1518.7488	759.8780	14
17	1784.8562	892.9317	1767.8297	884.4185	1766.8456	883.9265	N	1422.7165	711.8619	1405.6899	703.3486	1404.7059	702.8566	13
18	1855.8933	928.4503	1838.8668	919.9370	1837.8828	919.4450	A	1308.6735	654.8404	1291.6470	646.3271	1290.6630	645.8351	12
19	2041.9726	***1021.4900***	2024.9461	1012.9767	2023.9621	1012.4847	W	1237.6364	619.3218	1220.6099	610.8086	1219.6259	610.3166	11
20	2113.0097	***1057.0085***	2095.9832	1048.4952	2094.9992	1048.0032	A	1051.5571	526.2822	1034.5306	517.7689	1033.5465	517.2769	10
21	2260.0782	***1130.5427***	2243.0516	1122.0294	2242.0676	1121.5374	F	**980.5200**	490.7636	963.4934	482.2504	962.5094	481.7584	9
22	2331.1153	1166.0613	2314.0887	1157.5480	2313.1047	1157.0560	A	**833.4516**	417.2294	816.4250	408.7162	815.4410	408.2241	8
23	2432.1629	1216.5851	2415.1364	1208.0718	2414.1524	1207.5798	T	762.4145	381.7109	745.3879	373.1976	744.4039	372.7056	7
24	2546.2059	1273.6066	2529.1793	1265.0933	2528.1953	1264.6013	N	661.3668	331.1870	644.3402	322.6738			6

25	2693.2743	***1347.1408***	2676.2477	1338.6275	2675.2637	1338.1355	**F**	547.3239	274.1656	530.2973	265.6523			**5**
26	2792.3427	***1396.6750***	2775.3162	1388.1617	2774.3321	1387.6697	**V**	400.2554	200.6314	383.2289	192.1181			**4**
27	2889.3955	1445.2014	2872.3689	1436.6881	2871.3849	1436.1961	**P**	**301.1870**	151.0972	284.1605	142.5839			**3**
28	2946.4169	1473.7121	2929.3904	1465.1988	2928.4064	1464.7068	**G**	204.1343	102.5708	187.1077	94.0575			**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GPLENLADHLADPVNNNAWAFATNFVPGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.5	3091.5152	0.0021	GPIENLADHLADPVNNNAWAFATNFVPGK
39.5	3091.5152	0.0021	GPLENLADHLADPVNNNAWAFATNFVPGK

Mascot: http://www.matrixscience.com/

AT2G34430.1

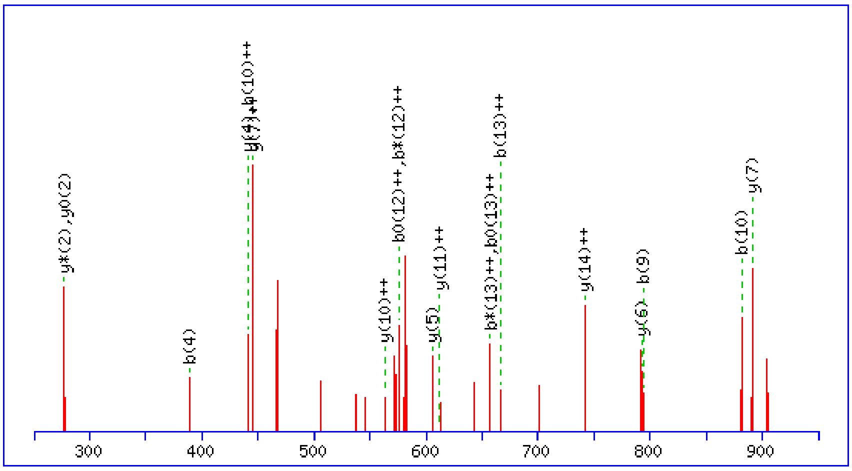
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASKPTGPSGSPWYGSDR**
Found in **AT2G34430.1** in **TAIR_Arabidopsis**, Symbols: LHCB1.4, LHB1B1 | LHB1B1 (Photosystem II light harvesting complex gene 1.4); chlorophyll binding | chr2:14531897-14532697 FORWARD

Match to Query 8852: 1770.744810 from(591.255546,3+) index(2367)
Title: Elution from: 26.380 to 26.380 scan no 3022 cid35.00 polarity:+
Data file D12h-1_1.mgf

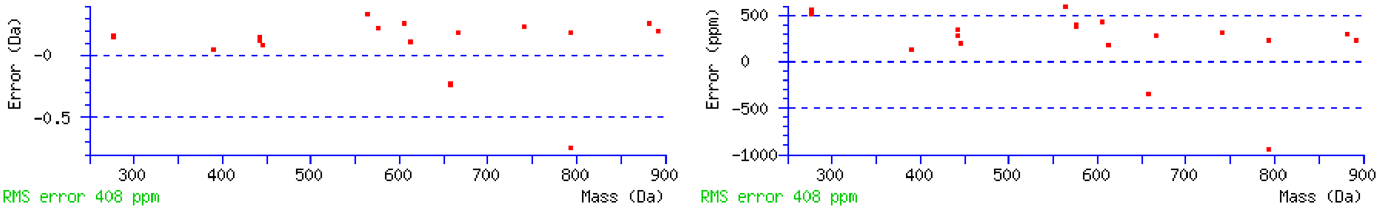
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1770.7466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.039
Matches : 19/184 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							17
2	161.0705	81.0389			143.0599	72.0336	S	1699.7197	850.3635	1681.6961	841.3517	1681.7091	841.3582	16
3	291.1595	146.0834	273.1359	137.0716	273.1490	137.0781	K	1611.6906	806.3490	1593.6671	797.3372	1593.6801	797.3437	15
4	***389.2093***	195.1083	371.1857	186.0965	371.1988	186.1030	P	1481.6016	741.3044	1463.5780	732.2927	1463.5910	732.2992	14
5	491.2540	246.1307	473.2304	237.1189	473.2435	237.1254	T	1383.5518	692.2795	1365.5282	683.2678	1365.5412	683.2743	13
6	549.2725	275.1399	531.2489	266.1281	531.2620	266.1346	G	1281.5071	641.2572	1263.4835	632.2454	1263.4965	632.2519	12
7	647.3223	324.1648	629.2987	315.1530	629.3118	315.1595	P	1223.4886	612.2479	1205.4650	603.2361	1205.4780	603.2427	11
8	735.3514	368.1793	717.3278	359.1675	717.3408	359.1741	S	1125.4388	563.2230	1107.4152	554.2112	1107.4282	554.2178	10
9	***793.3699***	397.1886	775.3463	388.1768	775.3593	388.1833	G	1037.4097	519.2085	1019.3862	510.1967	1019.3992	510.2032	9
10	***881.3990***	441.2031	863.3754	432.1913	863.3884	432.1978	S	979.3912	490.1993	961.3677	481.1875	961.3807	481.1940	8
11	979.4488	490.2280	961.4252	481.2162	961.4382	481.2227	P	***891.3622***	446.1847	873.3386	437.1729	873.3516	437.1794	7
12	1167.5221	584.2647	1149.4986	575.2529	1149.5116	575.2594	W	***793.3124***	397.1598	775.2888	388.1480	775.3018	388.1545	6
13	1331.5825	666.2949	1313.5589	657.2831	1313.5719	657.2896	Y	***605.2390***	303.1231	587.2154	294.1113	587.2284	294.1179	5
14	1389.6010	695.3041	1371.5774	686.2923	1371.5904	686.2989	G	***441.1786***	221.0930	423.1550	212.0812	423.1681	212.0877	4
15	1477.6301	739.3187	1459.6065	730.3069	1459.6195	730.3134	S	383.1601	192.0837	365.1365	183.0719	365.1496	183.0784	3
16	1593.6540	797.3307	1575.6305	788.3189	1575.6435	788.3254	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
17							R	179.1071	90.0572	161.0835	81.0454			1

AT2G34430.1



NCBI **BLAST** search of ASKPTGPSGSPWYGSDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.4	1770.7466	-0.0018	ASKPTGPSGSPWYGSDR
0.7	1770.7473	-0.0025	VVYMDEPSTGLDPASR
0.6	1770.7427	0.0021	RHMIKWVCECWK

Mascot: http://www.matrixscience.com/

AT2G34460.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFVAGATGQTGK**
Found in **AT2G34460.1** in **TAIR_Arabidopsis**, Symbols: | flavin reductase-related | chr2:14536714-14537811 FORWARD

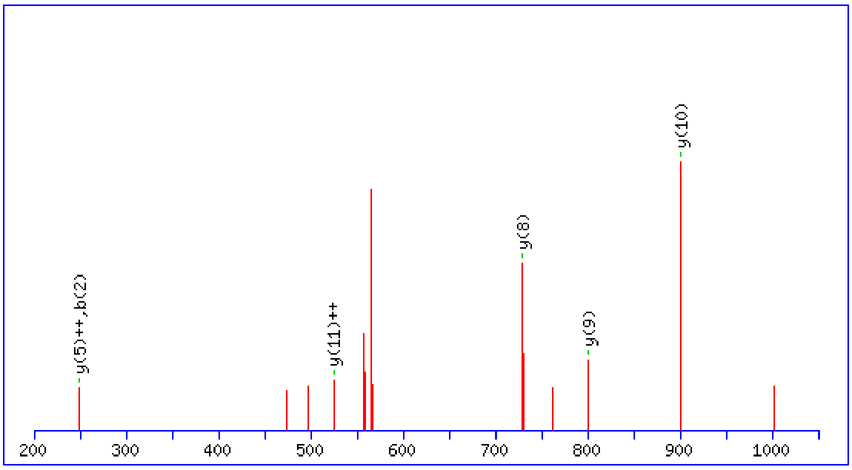
Match to Query 3858: 1148.560072 from(575.287312,2+) index(1152)
Title: Elution from: 17.513 to 17.513 scan no 1616 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

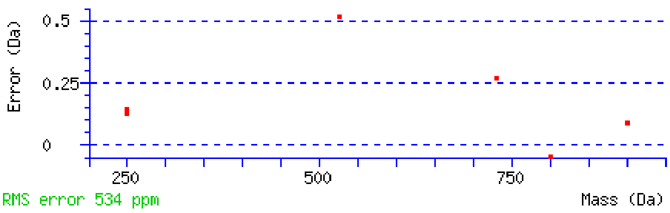
Label all possible matches ○ Label matches used for scoring ●

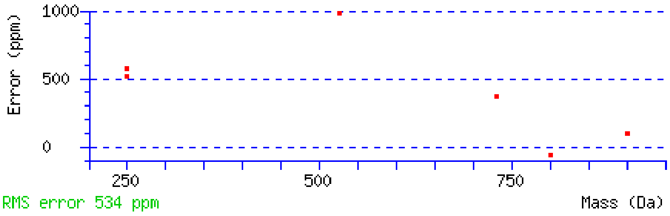
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1148.5618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.019
Matches : 6/100 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							12
2	249.1382	125.0727					F	1049.5036	525.2555	1031.4801	516.2437	1031.4931	516.2502	11
3	349.2036	175.1054					V	***901.4382***	451.2227	883.4146	442.2109	883.4276	442.2175	10
4	421.2378	211.1225					A	***801.3727***	401.1900	783.3492	392.1782	783.3622	392.1847	9
5	479.2563	240.1318					G	***729.3386***	365.1729	711.3150	356.1611	711.3280	356.1677	8
6	551.2904	276.1488					A	671.3201	336.1637	653.2965	327.1519	653.3095	327.1584	7
7	653.3351	327.1712			635.3246	318.1659	T	599.2859	300.1466	581.2624	291.1348	581.2754	291.1413	6
8	711.3536	356.1805			693.3431	347.1752	G	497.2412	249.1243	479.2176	240.1125	479.2307	240.1190	5
9	841.4063	421.2068	823.3827	412.1950	823.3957	412.2015	Q	439.2227	220.1150	421.1991	211.1032	421.2122	211.1097	4
10	943.4510	472.2291	925.4274	463.2173	925.4404	463.2239	T	309.1701	155.0887	291.1465	146.0769	291.1595	146.0834	3
11	1001.4695	501.2384	983.4459	492.2266	983.4589	492.2331	G	207.1254	104.0663	189.1018	95.0545			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VFVAGATGQTGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G34460.1

Score	Mr(calc)	Delta	Sequence
27.4	1148.5618	-0.0017	VFVAGATGQTGK
6.2	1148.5578	0.0023	DMMKEKLVK
3.7	1148.5618	-0.0017	QNEKYQVVK
3.0	1148.5575	0.0026	RQEMARLAR
1.9	1148.5604	-0.0004	MVNICTIKR
0.9	1148.5618	-0.0017	VRFIEENTK
0.1	1148.5571	0.0030	RVTGCLFPGK
0.1	1148.5593	0.0008	HQFLGFMKK

AT2G34480.1

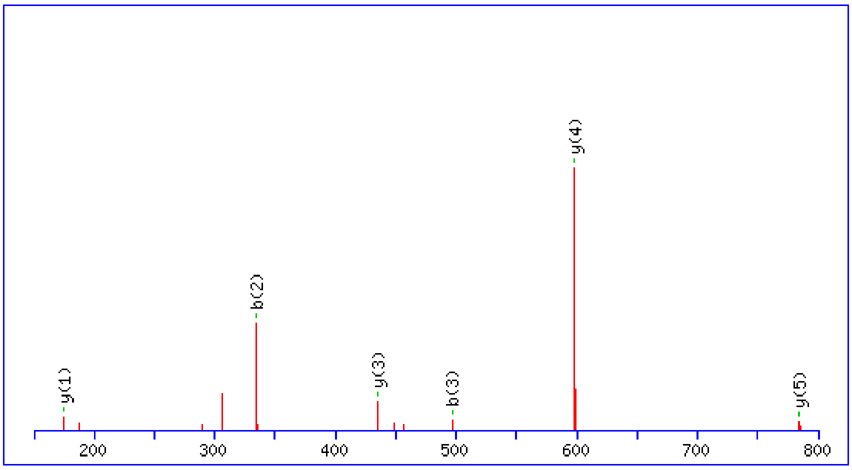
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FWYFLR**
Found in **AT2G34480.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L18A (RPL18aB) | chr2:14539995-14541240 REVERSE

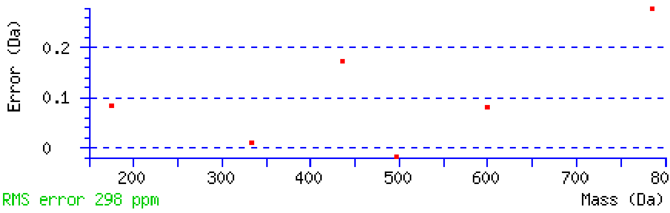
Match to Query 1994: 930.473784 from(466.244168,2+) index(8964)
Title: Elution from: 79.720 to 79.720 scan no 11915 cid35.00 polarity:+
Data file C7-3_1.mgf

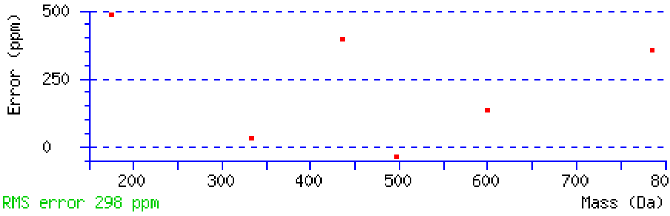
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 930.4752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 9.1e-005
Matches : 6/30 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	148.0757	74.5415	F					6
2	**334.1550**	167.5811	W	***784.4141***	392.7107	767.3875	384.1974	5
3	**497.2183**	249.1128	Y	***598.3348***	299.6710	581.3082	291.1577	4
4	644.2867	322.6470	F	***435.2714***	218.1394	418.2449	209.6261	3
5	757.3708	379.1890	L	288.2030	144.6051	271.1765	136.0919	2
6			R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of FWYFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.4	930.4752	-0.0014	FWYFLR

Mascot: http://www.matrixscience.com/

AT2G34750.1

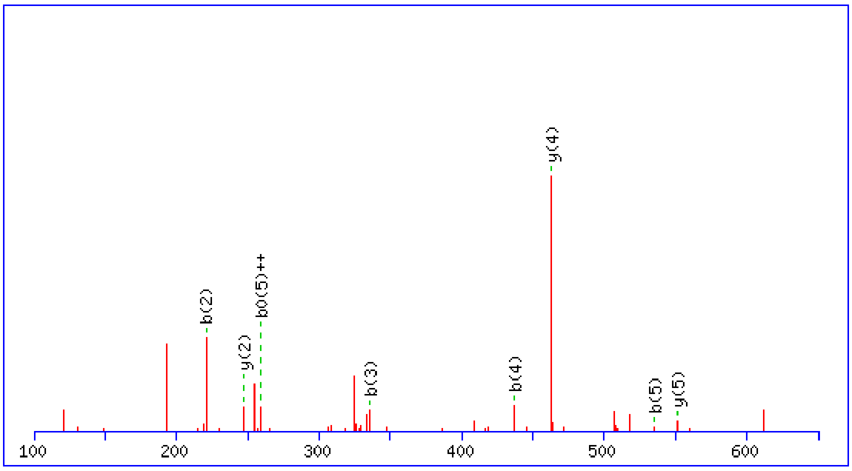
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSITPK**
Found in **AT2G34750.1** in **TAIR_Arabidopsis**, Symbols: | RNA polymerase I specific transcription initiation factor RRN3 family protein | chr2:14667528-14670871 REVERSE

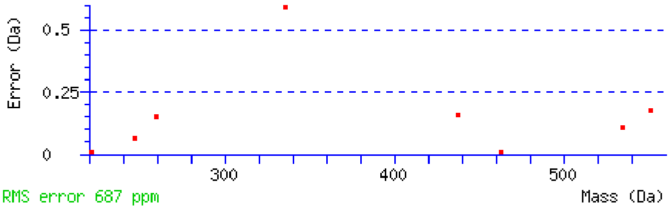
Match to Query 569: 682.343760 from(342.179156,2+) index(1801)
Title: Elution from: 21.460 to 21.460 scan no 2330 cid35.00 polarity:+
Data file 0-3_3.mgf

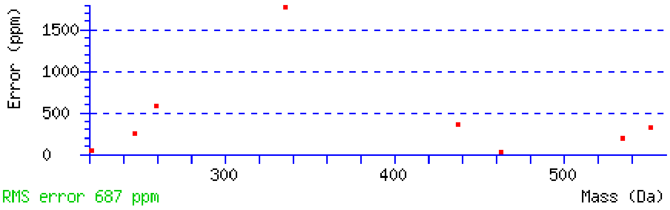
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 682.3418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.004
Matches : 8/44 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	133.0448	67.0260			M							6
2	***221.0739***	111.0406	203.0633	102.0353	S	***551.3115***	276.1594	533.2880	267.1476	533.3010	267.1541	5
3	***335.1550***	168.0811	317.1444	159.0758	I	***463.2825***	232.1449	445.2589	223.1331	445.2719	223.1396	4
4	***437.1997***	219.1035	419.1891	210.0982	T	349.2014	175.1043	331.1778	166.0925	331.1908	166.0990	3
5	***535.2495***	268.1284	517.2389	259.1231	P	***247.1567***	124.0820	229.1331	115.0702			2
6					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MSITPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.8	682.3418	0.0020	MSITPK
20.6	682.3418	0.0020	MIDVAK
16.3	682.3418	0.0020	MSLPTK

AT2G34750.1

16.3	682.3418	0.0020	MVDLAK
9.5	682.3418	0.0020	VMDLAK
9.4	682.3418	0.0020	MSTPLK
9.4	682.3418	0.0020	MVEVAK
7.4	682.3418	0.0020	MAPTIK
2.2	682.3418	0.0020	MIEVGK
2.2	682.3418	0.0020	MLDLGK

AT2G35050.1

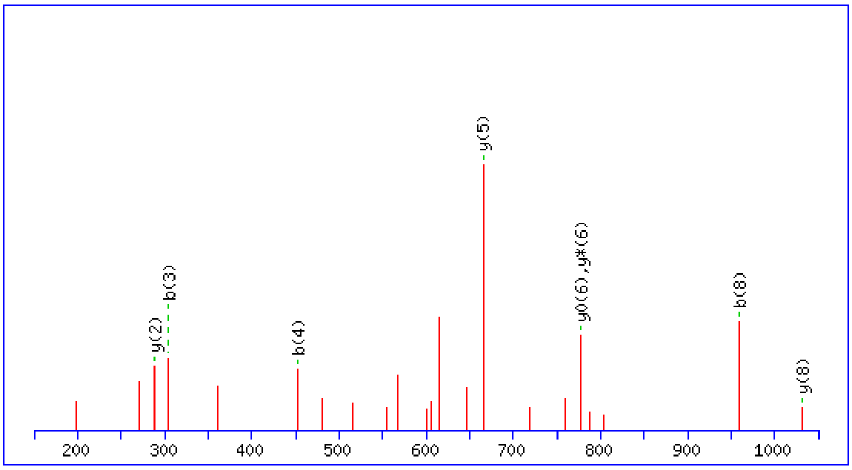
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TISFQELMHK**
Found in **AT2G35050.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr2:14776787-14781875 FORWARD

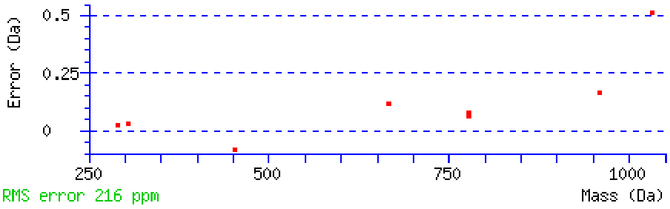
Match to Query 4592: 1246.583540 from(624.299046,2+) index(2242)
Title: Elution from: 25.520 to 25.520 scan no 2863 cid35.00 polarity:+
Data file 0-2_1.mgf

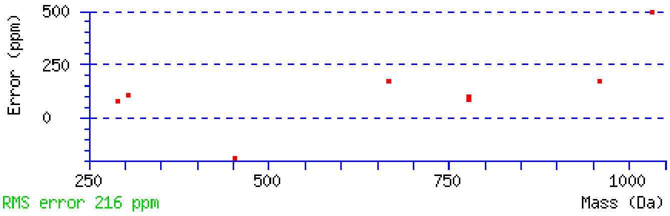
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.5808
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.017
Matches : 8/92 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							10
2	217.1331	109.0702			199.1225	100.0649	I	1145.5434	573.2753	1127.5198	564.2635	1127.5328	564.2701	9
3	***305.1622***	153.0847			287.1516	144.0794	S	***1031.4623***	516.2348	1013.4387	507.2230	1013.4517	507.2295	8
4	***453.2276***	227.1174			435.2170	218.1122	F	943.4332	472.2203	925.4097	463.2085	925.4227	463.2150	7
5	583.2802	292.1438	565.2567	283.1320	565.2697	283.1385	Q	795.3678	398.1875	777.3442	389.1757	777.3572	389.1822	6
6	713.3199	357.1636	695.2963	348.1518	695.3093	348.1583	E	***665.3151***	333.1612	647.2916	324.1494	647.3046	324.1559	5
7	827.4010	414.2041	809.3774	405.1923	809.3904	405.1988	L	535.2755	268.1414	517.2519	259.1296			4
8	***959.4385***	480.2229	941.4149	471.2111	941.4279	471.2176	M	421.1944	211.1008	403.1708	202.0891			3
9	1099.4885	550.2479	1081.4649	541.2361	1081.4779	541.2426	H	***289.1569***	145.0821	271.1333	136.0703			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TISFQELMHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G35050.1

27.2	1246.5808	0.0027	TISFQELMHK
16.9	1246.5860	-0.0024	DVADEGSLLRR
2.2	1246.5860	-0.0024	DSVLANGKDVGR
1.1	1246.5813	0.0023	MNGEKPLRER
0.8	1246.5801	0.0034	DWFKHRDVK
0.3	1246.5835	0.0000	MPKHYRPTGK

AT2G35340.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGKVGCTQPR**
Found in **AT2G35340.1** in **TAIR_Arabidopsis**, Symbols: MEE29 | MEE29 (maternal effect embryo arrest 29); ATP-dependent RNA helicase | chr2:14879807-14886694 FORWARD

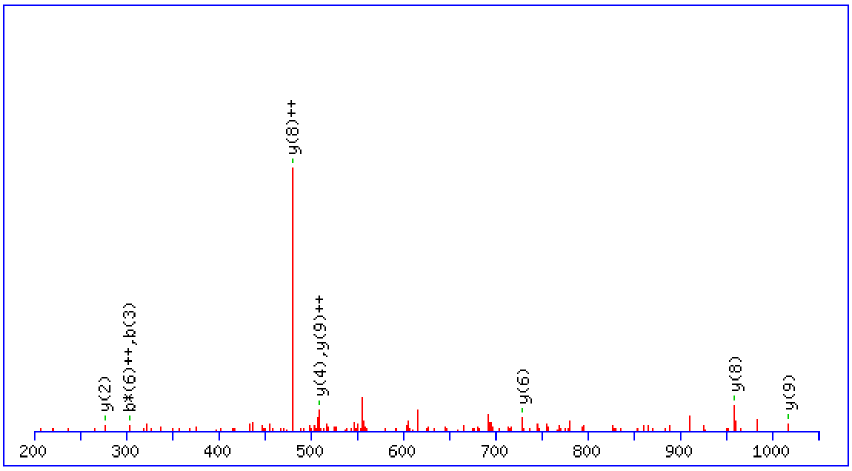
Match to Query 3619: 1130.547302 from(566.280927,2+) index(5523)
Title: Elution from: 49.654 to 49.654 scan no 7042 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

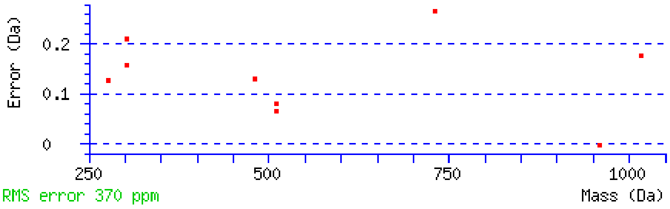
Label all possible matches ○ Label matches used for scoring ●

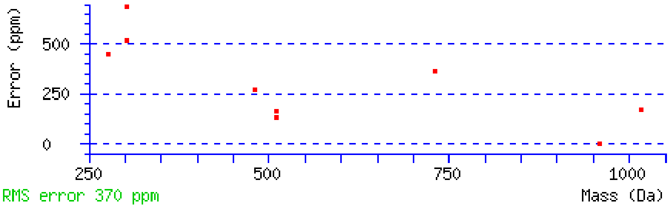
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1130.5442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.031
Matches : 9/86 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							10
2	173.1069	87.0571					G	*1017.4704*	509.2389	999.4469	500.2271	999.4599	500.2336	9
3	303.1959	152.1016	285.1723	143.0898			K	*959.4520*	480.2296	941.4284	471.2178	941.4414	471.2243	8
4	403.2614	202.1343	385.2378	193.1225			V	829.3629	415.1851	811.3393	406.1733	811.3524	406.1798	7
5	461.2799	231.1436	443.2563	222.1318			G	*729.2975*	365.1524	711.2739	356.1406	711.2869	356.1471	6
6	623.3046	312.1559	605.2810	303.1441			C	671.2790	336.1431	653.2554	327.1313	653.2684	327.1378	5
7	725.3493	363.1783	707.3257	354.1665	707.3387	354.1730	T	*509.2543*	255.1308	491.2307	246.1190	491.2437	246.1255	4
8	855.4019	428.2046	837.3783	419.1928	837.3914	419.1993	Q	407.2095	204.1084	389.1860	195.0966			3
9	953.4517	477.2295	935.4281	468.2177	935.4412	468.2242	P	*277.1569*	139.0821	259.1333	130.0703			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LGKVGCTQPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G35340.1

Score	Mr(calc)	Delta	Sequence
24.5	1130.5442	0.0031	LGKVGCTQPR
9.7	1130.5490	-0.0017	DKGNKLEQGK
9.4	1130.5472	0.0001	VAMLMDLQAK
8.2	1130.5463	0.0010	LSTDQIDLSK
7.0	1130.5490	-0.0017	IEEEKRQGK
4.8	1130.5490	-0.0017	QKLREEEGK
3.9	1130.5490	-0.0017	KDPREGSISK
3.8	1130.5490	-0.0017	IEEKRNAEK
3.4	1130.5486	-0.0013	LGDYLIEQGL
3.4	1130.5486	-0.0013	LGDYLLEQGL

AT2G35370.1

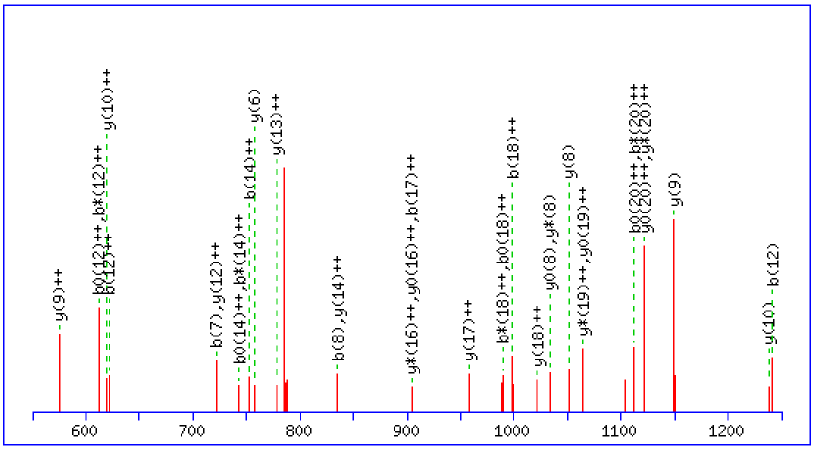
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLTESPGLINSSPYEDGWMIK**
Found in **AT2G35370.1** in **TAIR_Arabidopsis**, Symbols: GDCH | GDCH (Glycine decarboxylase complex H) | chr2:14898318-14899129 FORWARD

Match to Query 9940: 2389.093902 from(797.371910,3+) index(7472)
Title: Elution from: 66.904 to 66.904 scan no 9830 cid35.00 polarity:+
Data file D12h-2_3.mgf

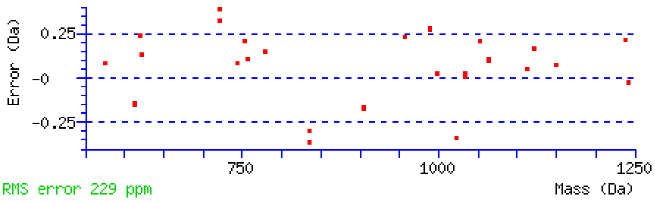
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

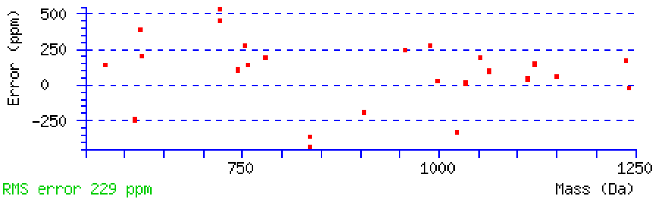


Monoisotopic mass of neutral peptide Mr(calc): 2389.0930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 5.3e-006
Matches : 36/226 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			**K**							**21**
2	245.1774	123.0923	227.1538	114.0805			**L**	2260.0113	1130.5093	2241.9877	1121.4975	2242.0007	1121.5040	**20**
3	347.2221	174.1147	329.1985	165.1029	329.2116	165.1094	**T**	2145.9302	1073.4687	2127.9066	1064.4569	2127.9196	1064.4634	**19**
4	477.2617	239.1345	459.2382	230.1227	459.2512	230.1292	**E**	2043.8855	1022.4464	2025.8619	1013.4346	2025.8749	1013.4411	**18**
5	565.2908	283.1490	547.2672	274.1373	547.2802	274.1438	**S**	1913.8458	957.4266	1895.8222	948.4148	1895.8353	948.4213	**17**
6	663.3406	332.1739	645.3170	323.1622	645.3300	323.1687	**P**	1825.8168	913.4120	1807.7932	904.4002	1807.8062	904.4067	**16**
7	**721.3591**	361.1832	703.3355	352.1714	703.3485	352.1779	**G**	1727.7670	864.3871	1709.7434	855.3753	1709.7564	855.3818	**15**
8	**835.4402**	418.2237	817.4166	409.2120	817.4296	409.2185	**L**	1669.7485	835.3779	1651.7249	826.3661	1651.7379	826.3726	**14**
9	949.5213	475.2643	931.4977	466.2525	931.5107	466.2590	**I**	1555.6674	778.3373	1537.6438	769.3255	1537.6568	769.3320	**13**
10	1065.5583	533.2828	1047.5347	524.2710	1047.5477	524.2775	**N**	1441.5863	721.2968	1423.5627	712.2850	1423.5757	712.2915	**12**
11	1153.5874	577.2973	1135.5638	568.2855	1135.5768	568.2920	**S**	1325.5493	663.2783	1307.5257	654.2665	1307.5387	654.2730	**11**
12	**1241.6164**	***621.3119***	1223.5928	612.3001	1223.6059	612.3066	**S**	**1237.5202**	619.2637	1219.4966	610.2519	1219.5096	610.2585	**10**
13	1339.6662	670.3368	1321.6426	661.3250	1321.6557	661.3315	**P**	**1149.4911**	575.2492	1131.4676	566.2374	1131.4806	566.2439	**9**
14	1503.7266	***752.3669***	1485.7030	743.3551	1485.7160	743.3617	**Y**	**1051.4413**	526.2243	1033.4178	517.2125	1033.4308	517.2190	**8**
15	1633.7662	817.3867	1615.7426	808.3750	1615.7557	808.3815	**E**	887.3810	444.1941	869.3574	435.1823	869.3704	435.1888	**7**
16	1749.7902	875.3987	1731.7666	866.3869	1731.7796	866.3935	**D**	**757.3414**	379.1743	739.3178	370.1625	739.3308	370.1690	**6**
17	1807.8087	***904.4080***	1789.7851	895.3962	1789.7981	895.4027	**G**	641.3174	321.1623	623.2938	312.1505			**5**
18	1995.8821	***998.4447***	1977.8585	989.4329	1977.8715	989.4394	**W**	583.2989	292.1531	565.2753	283.1413			**4**
19	2127.9196	***1064.4634***	2109.8960	1055.4516	2109.9090	1055.4582	**M**	395.2255	198.1164	377.2019	189.1046			**3**
20	2242.0007	***1121.5040***	2223.9771	1112.4922	2223.9901	1112.4987	**I**	263.1880	132.0976	245.1644	123.0858			**2**
21							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT2G35370.1





NCBI **BLAST** search of KLTESPGLINSSPYEDGWMIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.4	2389.0930	0.0009	KLTESPGLINSSPYEDGWMIK
1.6	2389.0991	-0.0052	SKIQLLNQTNMVDYAMDIHK
1.2	2389.0935	0.0004	IQGKTALIAHFQNSSLMNEDK
0.8	2389.0940	-0.0001	TVMVHQPGFRACLLRNQGNR
0.1	2389.0977	-0.0038	FLARSFAIPGNHLGQQSHGYR

Mascot: http://www.matrixscience.com/

AT2G35410.1

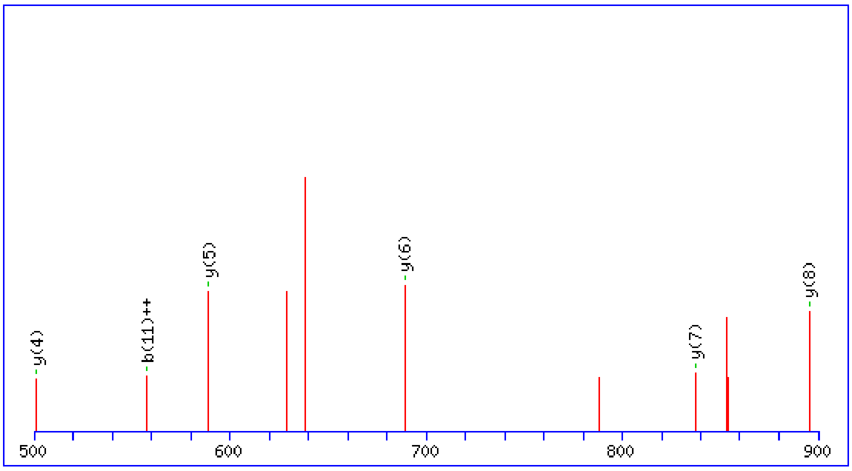
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSGYGFVSFATR**
Found in **AT2G35410.1** in **TAIR_Arabidopsis**, Symbols: | 33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative | chr2:14905420-14906669 FORWARD

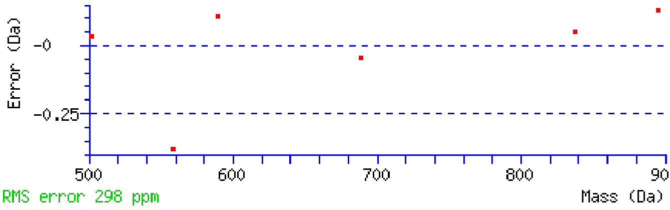
Match to Query 4773: 1292.561966 from(647.288259,2+) index(6399)
Title: Elution from: 55.792 to 55.792 scan no 8172 cid35.00 polarity:+
Data file C7-3_2.mgf

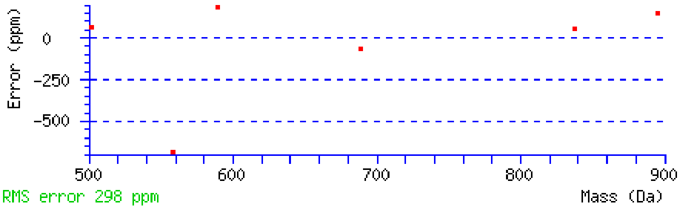
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1292.5596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0024
Matches : 6/108 fragment ions using 10 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218	71.0258	36.0165	S							12
2	177.0654	89.0363	159.0548	80.0311	S	1205.5378	603.2725	1187.5142	594.2607	1187.5272	594.2672	11
3	235.0839	118.0456	217.0733	109.0403	G	1117.5087	559.2580	1099.4851	550.2462	1099.4982	550.2527	10
4	399.1443	200.0758	381.1337	191.0705	Y	1059.4902	530.2488	1041.4666	521.2370	1041.4797	521.2435	9
5	457.1628	229.0850	439.1522	220.0797	G	***895.4299***	448.2186	877.4063	439.2068	877.4193	439.2133	8
6	605.2282	303.1177	587.2176	294.1125	F	***837.4114***	419.2093	819.3878	410.1975	819.4008	410.2040	7
7	705.2937	353.1505	687.2831	344.1452	V	***689.3459***	345.1766	671.3223	336.1648	671.3353	336.1713	6
8	793.3227	397.1650	775.3122	388.1597	S	***589.2805***	295.1439	571.2569	286.1321	571.2699	286.1386	5
9	941.3882	471.1977	923.3776	462.1924	F	***501.2514***	251.1293	483.2278	242.1175	483.2408	242.1241	4
10	1013.4223	507.2148	995.4118	498.2095	A	353.1860	177.0966	335.1624	168.0848	335.1754	168.0913	3
11	1115.4670	558.2372	1097.4565	549.2319	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
12					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SSGYGFVSFATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G35410.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.9	1292.5596	0.0024	SSGYGFVSFATR
10.4	1292.5596	0.0024	HVYVPTDYER
3.8	1292.5656	-0.0036	LPNQQVNFCR
3.0	1292.5607	0.0013	ETNNVVGEMIR
2.1	1292.5607	0.0013	DMRLEEESLR
2.1	1292.5607	0.0013	NMEVLGSQDLR
0.7	1292.5602	0.0018	HFCHKHHLR
0.7	1292.5656	-0.0037	MNAFANVHSLR
0.7	1292.5654	-0.0035	TSSEEESQILR

AT2G35490.1

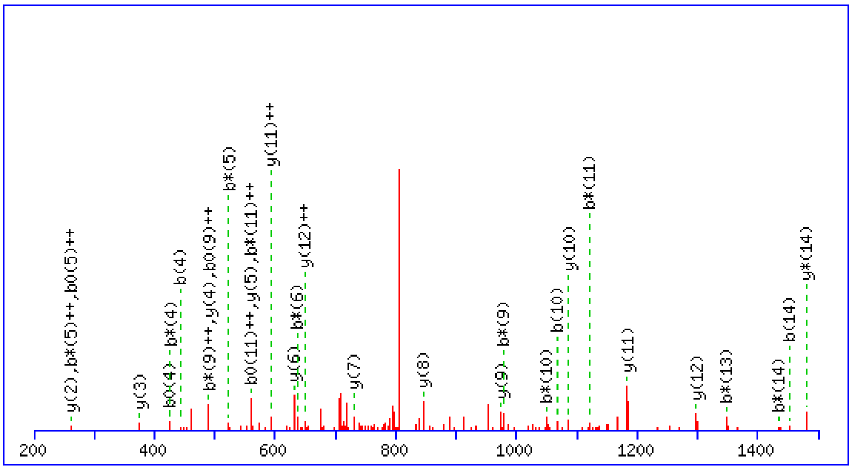
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSLNPLQDVAANISR**
Found in **AT2G35490.1** in **TAIR_Arabidopsis**, Symbols: | plastid-lipid associated protein PAP, putative | chr2:14919388-14920876 REVERSE

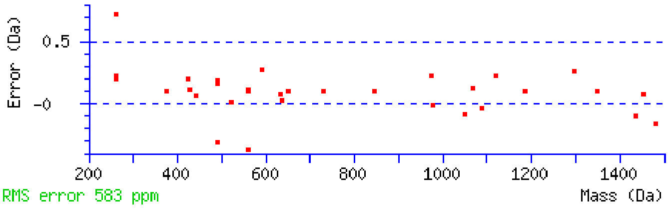
Match to Query 7356: 1624.851722 from(813.433137,2+) index(8209)
Title: Elution from: 74.490 to 74.490 scan no 10879 cid35.00 polarity:+
Data file D1d-2_1.mgf

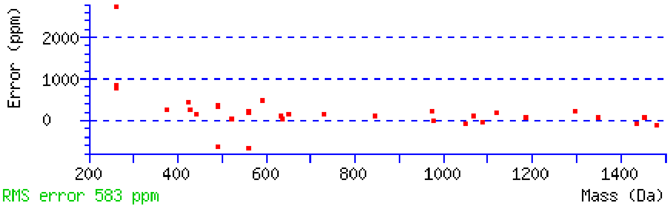
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1624.8533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.2e-006
Matches : 32/164 fragment ions using 57 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	S	1497.8020	749.4046	1480.7754	740.8914	1479.7914	740.3993	14
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	L	1410.7700	705.8886	1393.7434	697.3753	1392.7594	696.8833	13
4	**443.2249**	222.1161	426.1983	213.6028	425.2143	213.1108	N	***1297.6859***	649.3466	1280.6593	640.8333	1279.6753	640.3413	12
5	540.2776	270.6425	523.2511	262.1292	522.2671	261.6372	P	***1183.6430***	592.3251	1166.6164	583.8118	1165.6324	583.3198	11
6	653.3617	327.1845	636.3352	318.6712	635.3511	318.1792	L	***1086.5902***	543.7987	1069.5636	535.2855	1068.5796	534.7935	10
7	781.4203	391.2138	764.3937	382.7005	763.4097	382.2085	Q	***973.5061***	487.2567	956.4796	478.7434	955.4956	478.2514	9
8	896.4472	448.7272	879.4207	440.2140	878.4367	439.7220	D	***845.4476***	423.2274	828.4210	414.7141	827.4370	414.2221	8
9	995.5156	498.2615	978.4891	489.7482	977.5051	489.2562	V	***730.4206***	365.7139	713.3941	357.2007	712.4100	356.7087	7
10	**1066.5528**	533.7800	1049.5262	525.2667	1048.5422	524.7747	A	***631.3522***	316.1797	614.3257	307.6665	613.3416	307.1745	6
11	1137.5899	569.2986	1120.5633	560.7853	1119.5793	560.2933	A	***560.3151***	280.6612	543.2885	272.1479	542.3045	271.6559	5
12	1251.6328	626.3200	1234.6062	617.8068	1233.6222	617.3148	N	***489.2780***	245.1426	472.2514	236.6293	471.2674	236.1373	4
13	1364.7169	682.8621	1347.6903	674.3488	1346.7063	673.8568	I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
14	**1451.7489**	726.3781	1434.7223	717.8648	1433.7383	717.3728	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QSLNPLQDVAANISR

AT2G35490.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.0	1624.8533	-0.0015	QSLNPLQDVAANISR
5.1	1624.8494	0.0023	LKSLESLFLSNCSK
4.3	1624.8469	0.0048	MLLTPKMFSSWLR
2.0	1624.8533	-0.0015	NVDNVPSPPKTRSSK

AT2G35630.1

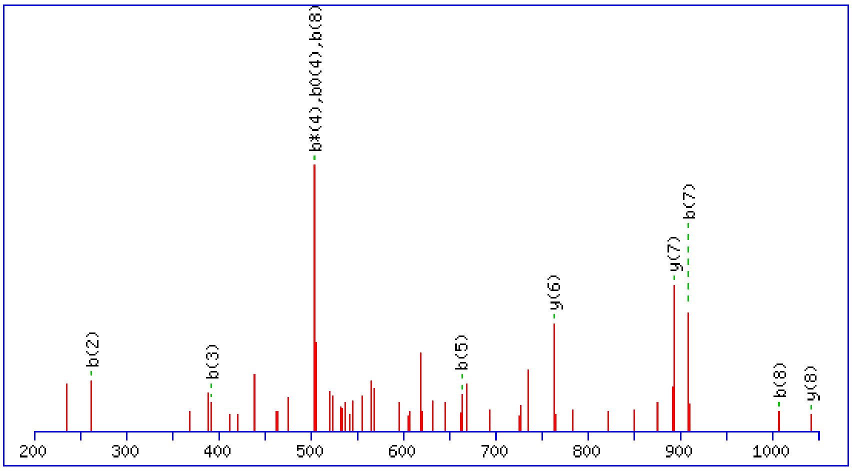
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMKEHKNPK**
Found in **AT2G35630.1** in **TAIR_Arabidopsis**, Symbols: GEM1, MOR1 | MOR1 (MICROTUBULE ORGANIZATION 1) | chr2:14973907-14987440 FORWARD

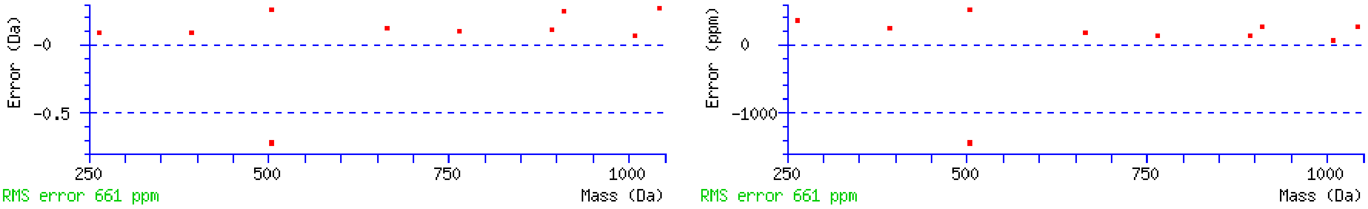
Match to Query 4047: 1154.566758 from(578.290655,2+) index(7376)
Title: Elution from: 64.751 to 64.751 scan no 9496 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.5677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.0047
Matches : 11/118 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							9
2	***263.1208***	132.0640					M	**1041.4938**	521.2505	1023.4702	512.2388	1023.4833	512.2453	8
3	***393.2098***	197.1086	375.1863	188.0968			K	**893.4614**	447.2343	875.4378	438.2225	875.4508	438.2290	7
4	523.2495	262.1284	505.2259	253.1166	505.2389	253.1231	E	**763.3723**	382.1898	745.3488	373.1780	745.3618	373.1845	6
5	***663.2995***	332.1534	645.2759	323.1416	645.2889	323.1481	H	633.3327	317.1700	615.3091	308.1582			5
6	793.3885	397.1979	775.3649	388.1861	775.3780	388.1926	K	493.2827	247.1450	475.2591	238.1332			4
7	***909.4255***	455.2164	891.4019	446.2046	891.4150	446.2111	N	363.1937	182.1005	345.1701	173.0887			3
8	***1007.4753***	504.2413	989.4517	495.2295	989.4648	495.2360	P	247.1567	124.0820	229.1331	115.0702			2
9							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of IMKEHKNPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G35630.1

Score	Mr(calc)	Delta	Sequence
30.5	1154.5677	-0.0009	IMKEHKNPK
25.6	1154.5638	0.0029	LFQVEYAFK
17.3	1154.5699	-0.0031	LMHFGAPQIK
8.8	1154.5676	-0.0009	FIQSKSMKR
8.8	1154.5676	-0.0009	GEHPKMGKLK
8.6	1154.5650	0.0018	SKMSYASILK
6.6	1154.5672	-0.0004	IFDKAIMYK
6.4	1154.5650	0.0018	KMQEDGLLPL
2.1	1154.5699	-0.0031	FGLMRNYIK
1.8	1154.5638	0.0029	APSFYYVGLK

AT2G35760.1

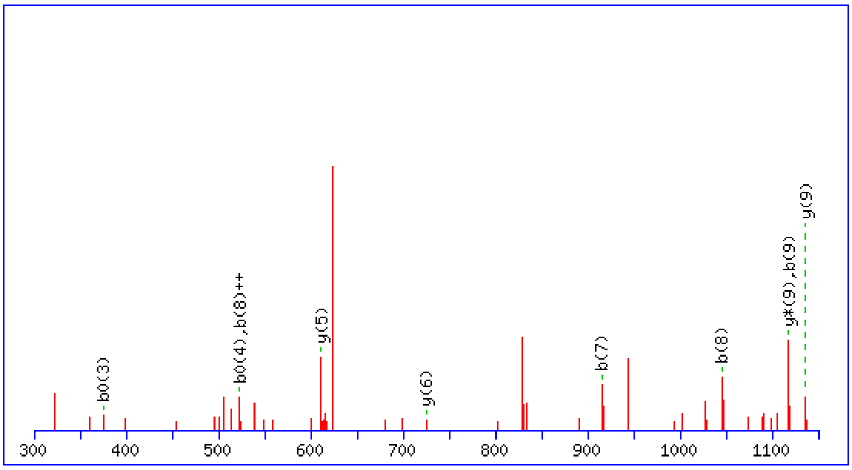
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIFMIQKKAK**
Found in **AT2G35760.1** in **TAIR_Arabidopsis**, Symbols: | integral membrane family protein | chr2:15039138-15040173 FORWARD

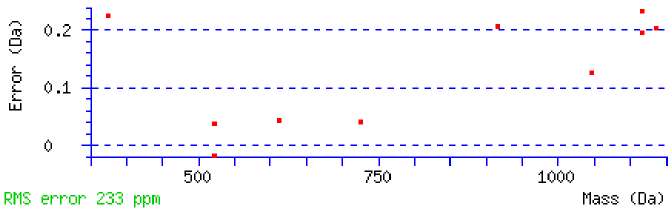
Match to Query 4881: 1264.664926 from(633.339739,2+) index(1900)
Title: Elution from: 22.693 to 22.693 scan no 2465 cid35.00 polarity:+
Data file D6h-1_1.mgf

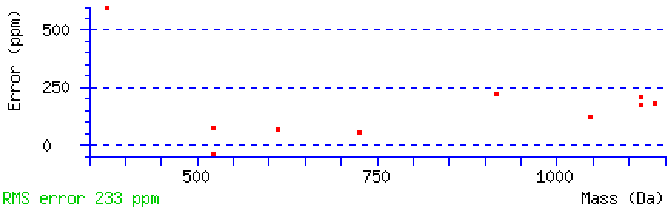
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1264.6642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.038
Matches : 10/124 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	131.0469	66.0271			113.0363	57.0218	E					10
2	245.1280	123.0676			227.1174	114.0624	I	***1135.6318***	568.3195	1117.6082	559.3078	9
3	393.1935	197.1004			375.1829	188.0951	F	1021.5507	511.2790	1003.5271	502.2672	8
4	541.2259	271.1166			523.2153	262.1113	M	873.4853	437.2463	855.4617	428.2345	7
5	655.3070	328.1571			637.2964	319.1518	I	***725.4528***	363.2301	707.4293	354.2183	6
6	785.3596	393.1835	767.3360	384.1717	767.3491	384.1782	Q	***611.3717***	306.1895	593.3482	297.1777	5
7	***915.4487***	458.2280	897.4251	449.2162	897.4381	449.2227	K	481.3191	241.1632	463.2955	232.1514	4
8	***1045.5377***	523.2725	1027.5141	514.2607	1027.5271	514.2672	K	351.2301	176.1187	333.2065	167.1069	3
9	***1117.5718***	559.2896	1099.5483	550.2778	1099.5613	550.2843	A	221.1410	111.0741	203.1174	102.0624	2
10							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of EIFMIQKKAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G35760.1

Score	Mr(calc)	Delta	Sequence
20.3	1264.6642	0.0008	EIFMIQKKAK
12.1	1264.6612	0.0037	KGFVAVASRGGAK
10.4	1264.6612	0.0037	KQNFNTVRLK
6.5	1264.6642	0.0008	MVTELFRVLK
0.5	1264.6668	-0.0019	MRGLLFNIIR
0.5	1264.6635	0.0015	YISIKRFHGK
0.5	1264.6661	-0.0012	KGLHVPPWRR
0.4	1264.6612	0.0037	QEFIASLRRK
0.2	1264.6664	-0.0015	KTIPFMQFIK
0.1	1264.6612	0.0037	SRFGILNKNAK

AT2G35840.1

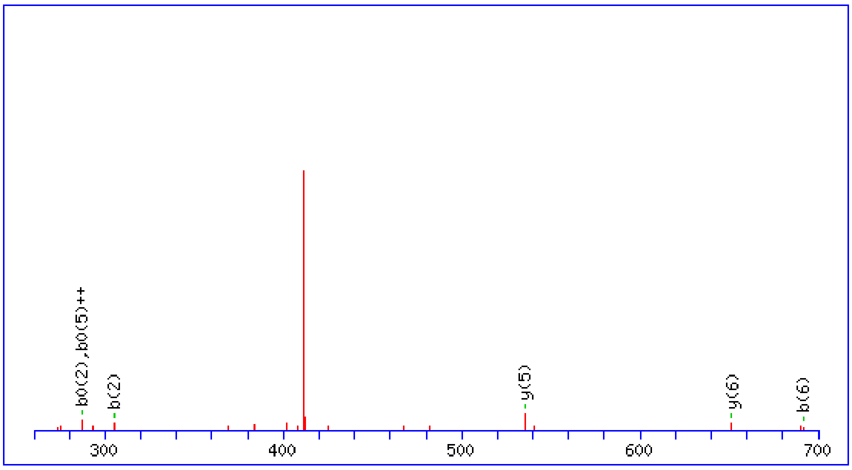
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDLGIVK**
Found in **AT2G35840.1** in **TAIR_Arabidopsis**, Symbols: | sucrose-phosphatase 1 (SPP1) | chr2:15061031-15062855 FORWARD

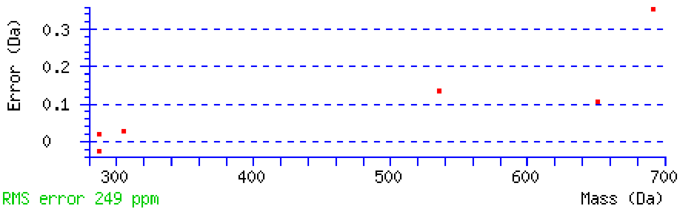
Match to Query 1184: 838.443556 from(420.229054,2+) index(6310)
Title: Elution from: 55.683 to 55.683 scan no 8111 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 260 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

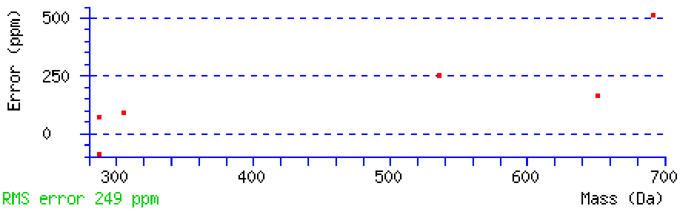


Monoisotopic mass of neutral peptide Mr(calc): 838.4431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.047
Matches : 6/48 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440			W							7
2	***305.1046***	153.0560	287.0941	144.0507	D	***651.3770***	326.1921	633.3534	317.1803	633.3664	317.1869	6
3	419.1857	210.0965	401.1752	201.0912	L	***535.3530***	268.1801	517.3294	259.1684			5
4	477.2042	239.1058	459.1937	230.1005	G	421.2719	211.1396	403.2483	202.1278			4
5	591.2853	296.1463	573.2748	287.1410	I	363.2534	182.1303	345.2298	173.1186			3
6	***691.3508***	346.1790	673.3402	337.1737	V	249.1723	125.0898	231.1487	116.0780			2
7					K	149.1069	75.0571	131.0833	66.0453			1



RMS error 249 ppm



RMS error 249 ppm

NCBI **BLAST** search of WDLGIVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.0	838.4431	0.0005	WDLGIVK
5.6	838.4431	0.0005	DWVVALK
5.1	838.4431	0.0004	VPLPNYK

AT2G35840.1

3.0	838.4435	0.0000	RLPDGIR

Mascot: http://www.matrixscience.com/

AT2G36160.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADRDESSPYAAMLAAQDVAQR**
Found in **AT2G36160.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S14 (RPS14A) | chr2:15177004-15178238 FORWARD

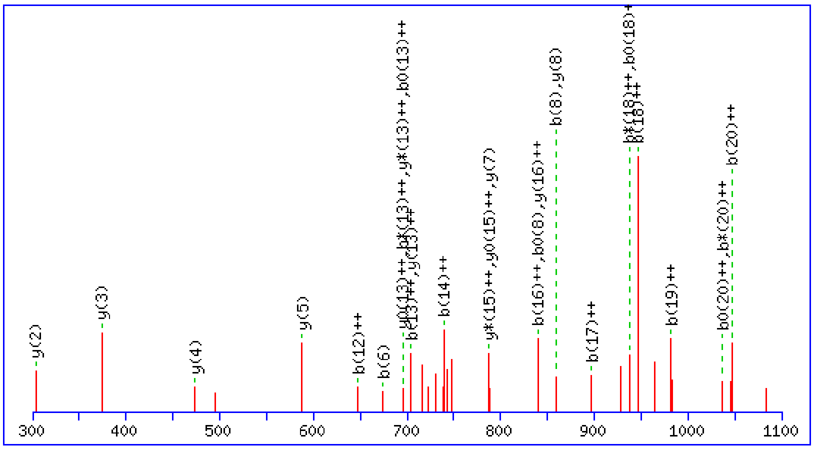
Match to Query 9804: 2264.053053 from(755.691627,3+) index(6650)
Title: Elution from: 58.511 to 58.511 scan no 8581 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●

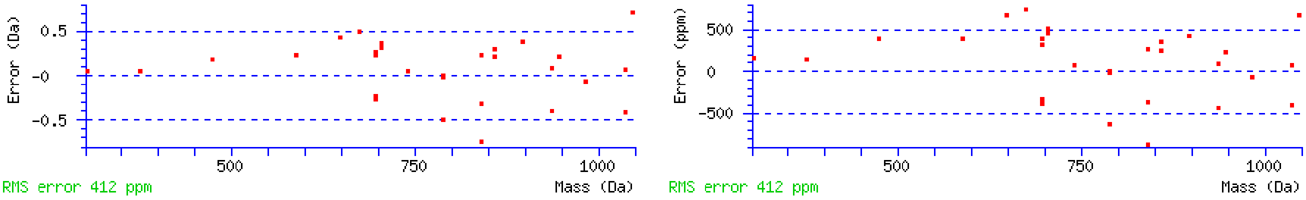
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2264.0491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 1.6e-007
Matches : 29/226 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**21**
2	187.0713	94.0393			169.0608	85.0340	**D**	2194.0193	1097.5133	2176.9928	1089.0000	2176.0088	1088.5080	**20**
3	343.1724	172.0899	326.1459	163.5766	325.1619	163.0846	**R**	2078.9924	1039.9998	2061.9658	1031.4866	2060.9818	1030.9945	**19**
4	458.1994	229.6033	441.1728	221.0901	440.1888	220.5980	**D**	1922.8913	961.9493	1905.8647	953.4360	1904.8807	952.9440	**18**
5	587.2420	294.1246	570.2154	285.6114	569.2314	285.1193	**E**	1807.8643	904.4358	1790.8378	895.9225	1789.8538	895.4305	**17**
6	**674.2740**	337.6406	657.2475	329.1274	656.2634	328.6354	**S**	1678.8217	839.9145	1661.7952	831.4012	1660.8112	830.9092	**16**
7	761.3060	381.1567	744.2795	372.6434	743.2955	372.1514	**S**	1591.7897	796.3985	1574.7632	787.8852	1573.7791	787.3932	**15**
8	**858.3588**	429.6830	841.3323	421.1698	840.3482	420.6778	**P**	1504.7577	752.8825	1487.7311	744.3692	1486.7471	743.8772	**14**
9	1021.4221	511.2147	1004.3956	502.7014	1003.4116	502.2094	**Y**	1407.7049	704.3561	1390.6784	695.8428	1389.6943	695.3508	**13**
10	1092.4592	546.7333	1075.4327	538.2200	1074.4487	537.7280	**A**	1244.6416	622.8244	1227.6150	614.3112	1226.6310	613.8191	**12**
11	1163.4964	582.2518	1146.4698	573.7385	1145.4858	573.2465	**A**	1173.6045	587.3059	1156.5779	578.7926	1155.5939	578.3006	**11**
12	1294.5368	***647.7721***	1277.5103	639.2588	1276.5263	638.7668	**M**	1102.5674	551.7873	1085.5408	543.2740	1084.5568	542.7820	**10**
13	1407.6209	***704.3141***	1390.5944	695.8008	1389.6103	695.3088	**L**	971.5269	486.2671	954.5003	477.7538	953.5163	477.2618	**9**
14	1478.6580	***739.8326***	1461.6315	731.3194	1460.6475	730.8274	**A**	**858.4428**	429.7250	841.4163	421.2118	840.4322	420.7198	**8**
15	1549.6951	775.3512	1532.6686	766.8379	1531.6846	766.3459	**A**	**787.4057**	394.2065	770.3791	385.6932	769.3951	385.2012	**7**
16	1677.7537	***839.3805***	1660.7272	830.8672	1659.7431	830.3752	**Q**	716.3686	358.6879	699.3420	350.1747	698.3580	349.6826	**6**
17	1792.7807	***896.8940***	1775.7541	888.3807	1774.7701	887.8887	**D**	**588.3100**	294.6586	571.2835	286.1454	570.2994	285.6534	**5**
18	1891.8491	***946.4282***	1874.8225	937.9149	1873.8385	937.4229	**V**	**473.2831**	237.1452	456.2565	228.6319			**4**
19	1962.8862	***981.9467***	1945.8596	973.4335	1944.8756	972.9414	**A**	**374.2146**	187.6110	357.1881	179.0977			**3**
20	2090.9448	***1045.9760***	2073.9182	1037.4627	2072.9342	1036.9707	**Q**	**303.1775**	152.0924	286.1510	143.5791			**2**
21							**R**	175.1190	88.0631	158.0924	79.5498			**1**

AT2G36160.1



NCBI **BLAST** search of ADRDESSPYAAMLAAQDVAQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.8	2264.0491	0.0039	ADRDESSPYAAMLAAQDVAQR
6.2	2264.0565	-0.0034	RSYEIPPPKGESLEMCAER

Mascot: http://www.matrixscience.com/

AT2G36250.1

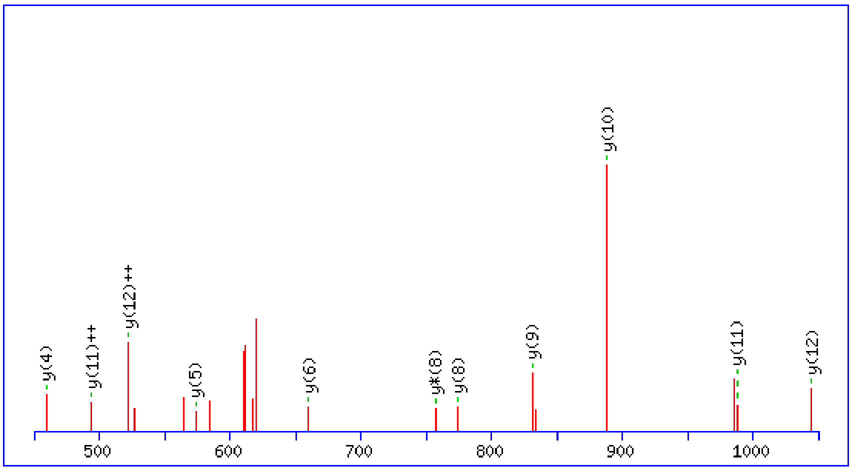
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIGVGGGGSNAVNR**
Found in **AT2G36250.1** in **TAIR_Arabidopsis**, Symbols: ATFTSZ2-1, FTSZ2-1 | FTSZ2-1 (FtsZ homolog 2-1); structural molecule | chr2:15204740-15207011 REVERSE

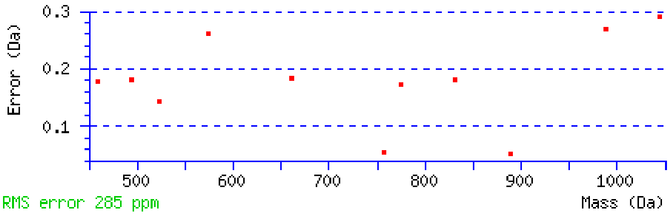
Match to Query 4534: 1255.659668 from(628.837110,2+) index(1464)
Title: Elution from: 19.702 to 19.702 scan no 1973 cid35.00 polarity:+
Data file C7-2_2.mgf

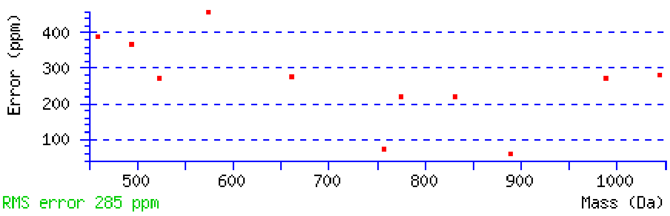
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1255.6633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 1.1e-005
Matches : 11/112 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**14**
2	213.1598	107.0835					**I**	1157.6022	579.3047	1140.5756	570.7914	1139.5916	570.2994	**13**
3	270.1812	135.5942					**G**	***1044.5181***	522.7627	1027.4915	514.2494	1026.5075	513.7574	**12**
4	369.2496	185.1285					**V**	***987.4966***	494.2520	970.4701	485.7387	969.4861	485.2467	**11**
5	426.2711	213.6392					**G**	***888.4282***	444.7177	871.4017	436.2045	870.4177	435.7125	**10**
6	483.2926	242.1499					**G**	***831.4068***	416.2070	814.3802	407.6937	813.3962	407.2017	**9**
7	540.3140	270.6607					**G**	***774.3853***	387.6963	757.3587	379.1830	756.3747	378.6910	**8**
8	597.3355	299.1714					**G**	717.3638	359.1856	700.3373	350.6723	699.3533	350.1803	**7**
9	684.3675	342.6874			666.3570	333.6821	**S**	***660.3424***	330.6748	643.3158	322.1615	642.3318	321.6695	**6**
10	798.4104	399.7089	781.3839	391.1956	780.3999	390.7036	**N**	***573.3103***	287.1588	556.2838	278.6455			**5**
11	869.4476	435.2274	852.4210	426.7141	851.4370	426.2221	**A**	***459.2674***	230.1373	442.2409	221.6241			**4**
12	968.5160	484.7616	951.4894	476.2483	950.5054	475.7563	**V**	388.2303	194.6188	371.2037	186.1055			**3**
13	1082.5589	541.7831	1065.5323	533.2698	1064.5483	532.7778	**N**	289.1619	145.0846	272.1353	136.5713			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VIGVGGGGSNAVNR

AT2G36250.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.3	1255.6633	-0.0036	VIGVGGGGSNAVNR
8.2	1255.6633	-0.0036	GALLAGNGENGKR

Mascot: http://www.matrixscience.com/

AT2G36460.1

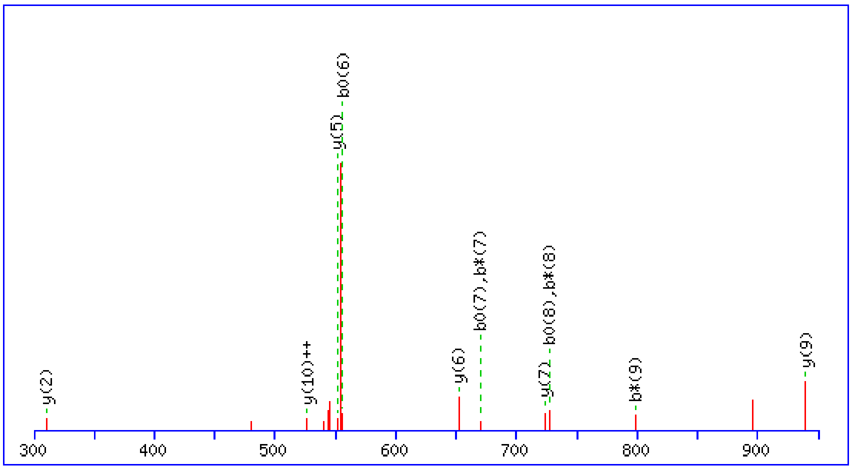
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANSEATLGAYK**
Found in **AT2G36460.1** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr2:15304008-15305466 REVERSE

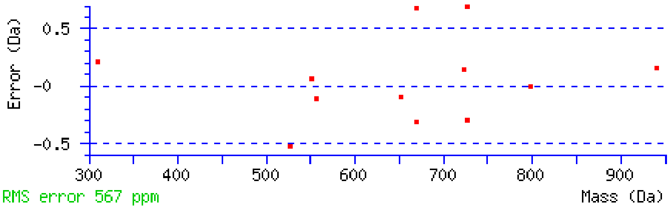
Match to Query 3756: 1123.549752 from(562.782152,2+) index(1518)
Title: Elution from: 19.168 to 19.168 scan no 1993 cid35.00 polarity:+
Data file D1d-3_2.mgf

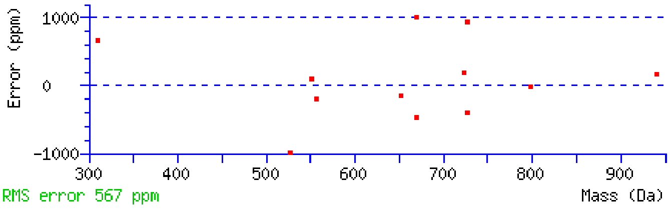
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1123.5509
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.007
Matches : 12/104 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							11
2	186.0873	93.5473	169.0608	85.0340			N	1053.5211	527.2642	1036.4946	518.7509	1035.5106	518.2589	10
3	273.1193	137.0633	256.0928	128.5500	255.1088	128.0580	S	***939.4782***	470.2427	922.4516	461.7295	921.4676	461.2375	9
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	E	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	8
5	473.1991	237.1032	456.1725	228.5899	455.1885	228.0979	A	***723.4036***	362.2054	706.3770	353.6921	705.3930	353.2001	7
6	574.2467	287.6270	557.2202	279.1137	556.2362	278.6217	T	***652.3665***	326.6869	635.3399	318.1736	634.3559	317.6816	6
7	687.3308	344.1690	670.3042	335.6558	669.3202	335.1638	L	***551.3188***	276.1630	534.2922	267.6498			5
8	744.3523	372.6798	727.3257	364.1665	726.3417	363.6745	G	438.2347	219.6210	421.2082	211.1077			4
9	815.3894	408.1983	798.3628	399.6851	797.3788	399.1930	A	381.2132	191.1103	364.1867	182.5970			3
10	978.4527	489.7300	961.4262	481.2167	960.4421	480.7247	Y	***310.1761***	155.5917	293.1496	147.0784			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ANSEATLGAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G36460.1

Score	Mr(calc)	Delta	Sequence
26.7	1123.5509	-0.0012	ANSEATLGAYK
14.5	1123.5509	-0.0012	TANDAATSVFK

AT2G36530.1

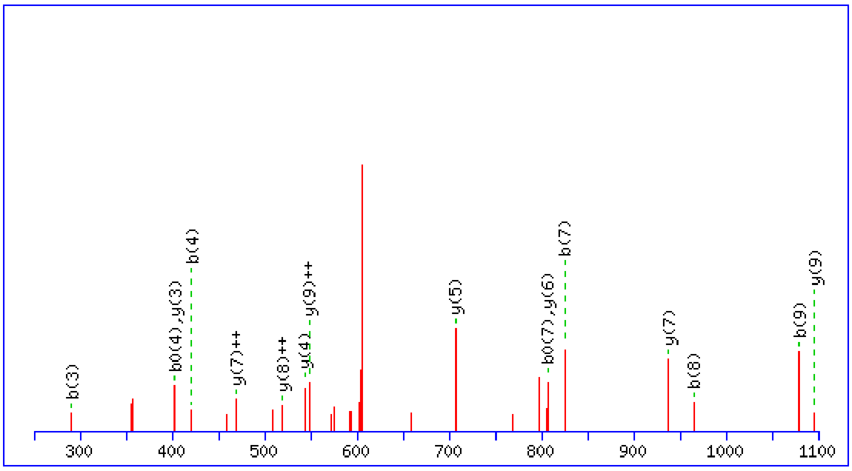
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGVEVYHHLK**
Found in **AT2G36530.1** in **TAIR_Arabidopsis**, Symbols: LOS2 | LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase | chr2:15328160-15330865 REVERSE

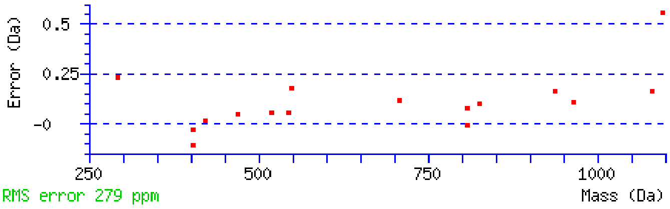
Match to Query 4561: 1226.565034 from(614.289793,2+) index(1812)
Title: Elution from: 22.770 to 22.770 scan no 2406 cid35.00 polarity:+
Data file D12h-1_1.mgf

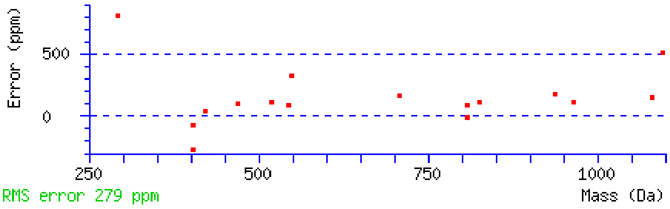
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1226.5676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 3.9e-005
Matches : 16/72 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260			**M**							**10**
2	191.0633	96.0353			**G**	***1095.5374***	548.2723	1077.5138	539.2605	1077.5268	539.2671	**9**
3	***291.1287***	146.0680			**V**	1037.5189	519.2631	1019.4953	510.2513	1019.5083	510.2578	**8**
4	***421.1684***	211.0878	403.1578	202.0825	**E**	***937.4534***	469.2304	919.4299	460.2186	919.4429	460.2251	**7**
5	521.2338	261.1205	503.2233	252.1153	**V**	***807.4138***	404.2105	789.3902	395.1988			**6**
6	685.2942	343.1507	667.2836	334.1454	**Y**	***707.3484***	354.1778	689.3248	345.1660			**5**
7	***825.3442***	413.1757	807.3336	404.1705	**H**	***543.2880***	272.1476	525.2644	263.1358			**4**
8	***965.3942***	483.2007	947.3837	474.1955	**H**	***403.2380***	202.1226	385.2144	193.1108			**3**
9	***1079.4753***	540.2413	1061.4648	531.2360	**L**	263.1880	132.0976	245.1644	123.0858			**2**
10					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MGVEVYHHLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G36530.1

Score	Mr(calc)	Delta	Sequence
52.2	1226.5676	-0.0026	MGVEVYHHLK
14.8	1226.5650	0.0001	MGVDYYNILK
9.6	1226.5620	0.0030	DEHSKAFLHK
6.1	1226.5650	0.0001	LMATVFENYK
3.4	1226.5675	-0.0024	EATPEGEELIK
1.6	1226.5649	0.0001	LFMTQGEVYK
1.4	1226.5676	-0.0026	QRWIAMYTK
0.7	1226.5627	0.0023	KCSYTEVSLK
0.6	1226.5620	0.0030	SQTQPFYGRK
0.6	1226.5643	0.0008	ATHSLSFFFR

AT2G36620.1

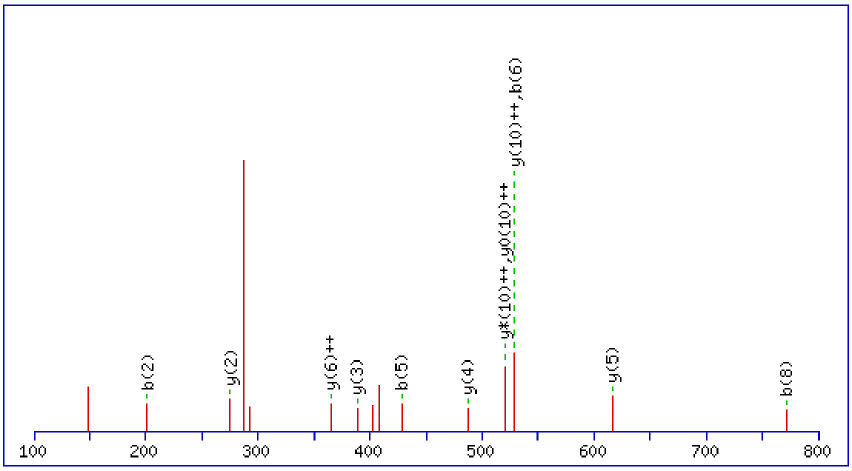
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIVGATLEVIQK**
Found in **AT2G36620.1** in **TAIR_Arabidopsis**, Symbols: RPL24A | RPL24A (RIBOSOMAL PROTEIN L24); structural constituent of ribosome | chr2:15357627-15358898 REVERSE

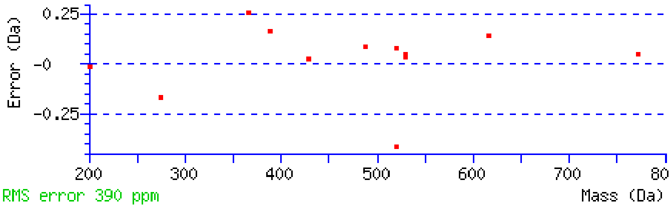
Match to Query 4255: 1256.733639 from(419.918489,3+) index(7137)
Title: Elution from: 63.547 to 63.547 scan no 9293 cid35.00 polarity:+
Data file C7-1_3.mgf

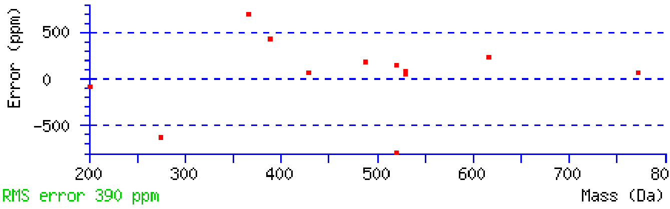
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1256.7340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0011
Matches : 12/104 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	***201.1234***	101.0653			183.1128	92.0600	I	1170.7093	585.8583	1153.6827	577.3450	1152.6987	576.8530	11
3	300.1918	150.5995			282.1812	141.5942	V	1057.6252	529.3162	1040.5986	520.8030	1039.6146	520.3109	10
4	357.2132	179.1103			339.2027	170.1050	G	958.5568	479.7820	941.5302	471.2688	940.5462	470.7767	9
5	***428.2504***	214.6288			410.2398	205.6235	A	901.5353	451.2713	884.5088	442.7580	883.5247	442.2660	8
6	***529.2980***	265.1527			511.2875	256.1474	T	830.4982	415.7527	813.4716	407.2395	812.4876	406.7475	7
7	642.3821	321.6947			624.3715	312.6894	L	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	6
8	***771.4247***	386.2160			753.4141	377.2107	E	***616.3665***	308.6869	599.3399	300.1736	598.3559	299.6816	5
9	870.4931	435.7502			852.4825	426.7449	V	***487.3239***	244.1656	470.2973	235.6523			4
10	983.5772	492.2922			965.5666	483.2869	I	***388.2554***	194.6314	371.2289	186.1181			3
11	1111.6358	556.3215	1094.6092	547.8082	1093.6252	547.3162	Q	***275.1714***	138.0893	258.1448	129.5761			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SIVGATLEVIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G36620.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.5	1256.7340	-0.0004	SIVGATLEVIQK
11.9	1256.7340	-0.0004	LGLTADIGLSVAK
4.5	1256.7340	-0.0003	ISIIGDSSKLPK
4.3	1256.7313	0.0023	AITKNTGARGLR
4.0	1256.7313	0.0023	VTNTVVARRNK
3.6	1256.7339	-0.0003	EIISKNEIALK
3.6	1256.7340	-0.0003	IKLSEDKIPSK
0.8	1256.7340	-0.0003	KPSSLEEVKLK
0.5	1256.7340	-0.0004	TLSSTPLALVGAK

AT2G36680.1

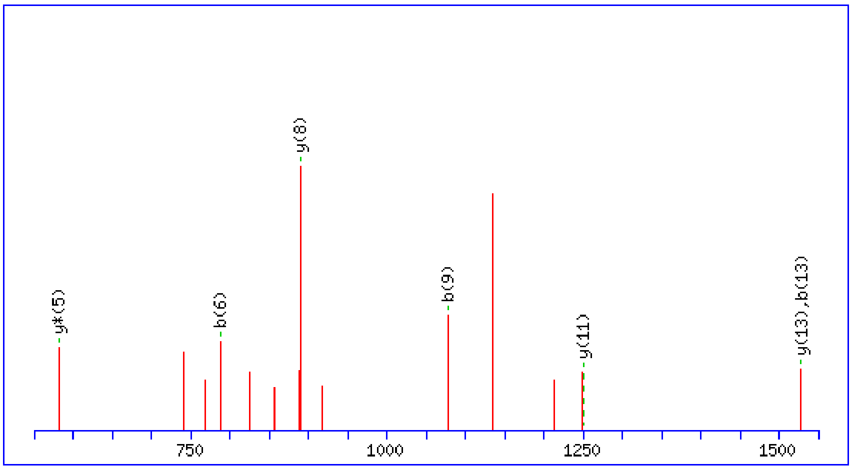
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FMEKDIDTAAFVQK**
Found in **AT2G36680.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G53120.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62968.1); contains InterPro domain Modifier of rudimentary, Modr (InterPro:IPR009851) | chr2:15376059-15377

Match to Query 7882: 1674.749154 from(838.381853,2+) index(10722)
Title: Elution from: 107.897 to 107.897 scan no 15637 cid35.00 polarity:+
Data file D6h-1_2.mgf

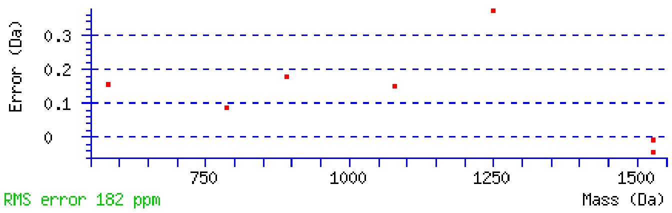
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1550 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

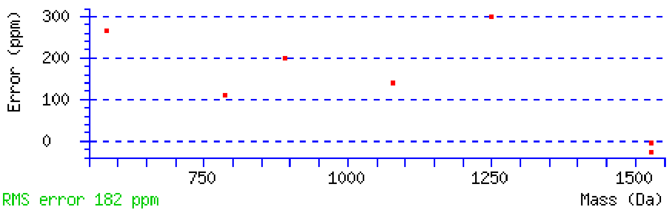


Monoisotopic mass of neutral peptide Mr(calc): 1674.7517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.043
Matches : 7/206 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	149.0727	75.0400					F							14
2	297.1052	149.0562					M	***1527.6936***	764.3504	1509.6700	755.3386	1509.6830	755.3451	13
3	427.1448	214.0760			409.1342	205.0707	E	1379.6611	690.3342	1361.6376	681.3224	1361.6506	681.3289	12
4	557.2338	279.1205	539.2102	270.1088	539.2233	270.1153	K	***1249.6215***	625.3144	1231.5979	616.3026	1231.6110	616.3091	11
5	673.2578	337.1325	655.2342	328.1207	655.2472	328.1273	D	1119.5325	560.2699	1101.5089	551.2581	1101.5219	551.2646	10
6	***787.3389***	394.1731	769.3153	385.1613	769.3283	385.1678	I	1003.5085	502.2579	985.4849	493.2461	985.4979	493.2526	9
7	903.3629	452.1851	885.3393	443.1733	885.3523	443.1798	D	***889.4274***	445.2173	871.4038	436.2056	871.4168	436.2121	8
8	1005.4076	503.2074	987.3840	494.1956	987.3970	494.2021	T	773.4034	387.2054	755.3798	378.1936	755.3929	378.2001	7
9	***1077.4417***	539.2245	1059.4182	530.2127	1059.4312	530.2192	A	671.3587	336.1830	653.3351	327.1712			6
10	1149.4759	575.2416	1131.4523	566.2298	1131.4653	566.2363	A	599.3246	300.1659	581.3010	291.1541			5
11	1297.5413	649.2743	1279.5178	640.2625	1279.5308	640.2690	F	527.2904	264.1488	509.2668	255.1371			4
12	1397.6068	699.3070	1379.5832	690.2952	1379.5962	690.3017	V	379.2250	190.1161	361.2014	181.1043			3
13	***1527.6594***	764.3334	1509.6358	755.3216	1509.6489	755.3281	Q	279.1595	140.0834	261.1359	131.0716			2
14							K	149.1069	75.0571	131.0833	66.0453			1

AT2G36680.1





NCBI **BLAST** search of FMEKDIDTAAFVQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.3	1674.7517	-0.0026	FMEKDIDTAAFVQK
20.2	1674.7504	-0.0012	VIRMDYTMLCDIK
9.9	1674.7519	-0.0027	NRGRNFQQNGTVTR
9.7	1674.7533	-0.0041	SNWFFPSYPIDRK
8.8	1674.7519	-0.0028	MWWEIFRCVKGK
2.0	1674.7510	-0.0019	FKTRSWISDWDSK
1.4	1674.7473	0.0019	MASLSVSSSSTIIDSR
1.4	1674.7448	0.0044	VYRTQKDMMDELK
0.7	1674.7492	-0.0001	GLGLHLGDAGDGGREAR
0.7	1674.7519	-0.0028	SPPHNGSRVRSGSPGR

Mascot: http://www.matrixscience.com/

AT2G36830.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIAIGRPDEATRPDALK**
Found in **AT2G36830.1** in **TAIR_Arabidopsis**, Symbols: TIP1;1, GAMMA-TIP1, GAMMA-TIP | GAMMA-TIP (Tonoplast intrinsic protein (TIP) gamma); water channel | chr2:15452569-15453415 FORWARD

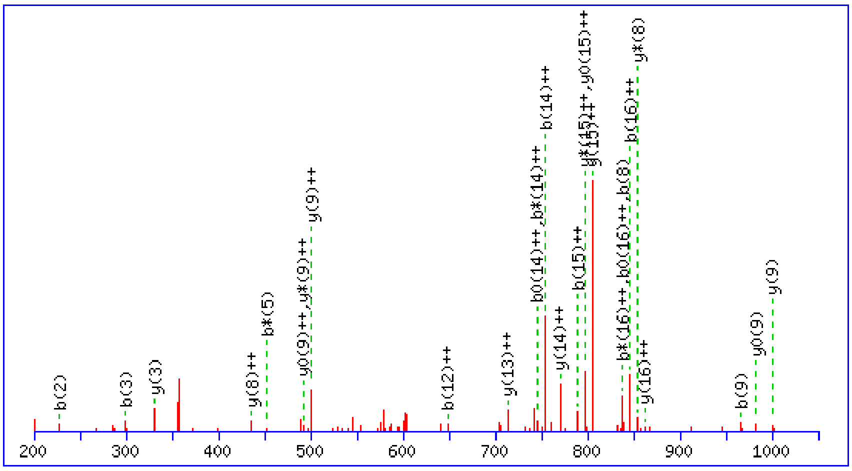
Match to Query 8917: 1835.982801 from(613.001543,3+) index(3289)
Title: Elution from: 33.900 to 33.900 scan no 4156 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

Label all possible matches ○ Label matches used for scoring ●

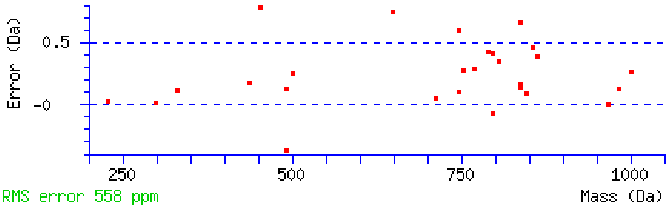
Show Y-axis ☐

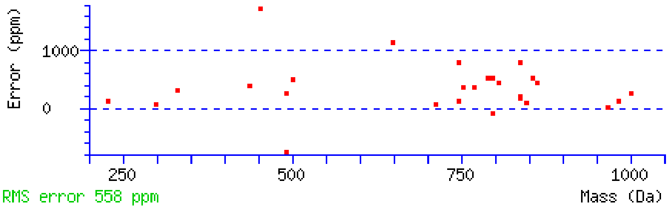


Monoisotopic mass of neutral peptide Mr(calc): 1835.9853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.027
Matches : 27/172 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							17
2	**228.1343**	114.5708	211.1077	106.0575			I	1722.9497	861.9785	1705.9232	853.4652	1704.9391	852.9732	16
3	**299.1714**	150.0893	282.1448	141.5761			A	1609.8656	805.4365	1592.8391	796.9232	1591.8551	796.4312	15
4	412.2554	206.6314	395.2289	198.1181			I	1538.8285	769.9179	1521.8020	761.4046	1520.8180	760.9126	14
5	469.2769	235.1421	452.2504	226.6288			G	1425.7445	713.3759	1408.7179	704.8626	1407.7339	704.3706	13
6	625.3780	313.1926	608.3515	304.6794			R	1368.7230	684.8651	1351.6965	676.3519	1350.7124	675.8599	12
7	722.4308	361.7190	705.4042	353.2058			P	1212.6219	606.8146	1195.5953	598.3013	1194.6113	597.8093	11
8	**837.4577**	419.2325	820.4312	410.7192	819.4472	410.2272	D	1115.5691	558.2882	1098.5426	549.7749	1097.5586	549.2829	10
9	**966.5003**	483.7538	949.4738	475.2405	948.4898	474.7485	E	1000.5422	500.7747	983.5156	492.2615	982.5316	491.7694	9
10	1037.5374	519.2724	1020.5109	510.7591	1019.5269	510.2671	A	871.4996	436.2534	854.4730	427.7402	853.4890	427.2482	8
11	1138.5851	569.7962	1121.5586	561.2829	1120.5745	560.7909	T	800.4625	400.7349	783.4359	392.2216	782.4519	391.7296	7
12	1294.6862	***647.8468***	1277.6597	639.3335	1276.6757	638.8415	R	699.4148	350.2110	682.3883	341.6978	681.4042	341.2058	6
13	1391.7390	696.3731	1374.7124	687.8599	1373.7284	687.3678	P	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	5
14	1506.7659	***753.8866***	1489.7394	745.3733	1488.7554	744.8813	D	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
15	1577.8030	***789.4052***	1560.7765	780.8919	1559.7925	780.3999	A	331.2340	166.1206	314.2074	157.6074			3
16	1690.8871	***845.9472***	1673.8606	837.4339	1672.8765	836.9419	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT2G36830.1





NCBI **BLAST** search of NIAIGRPDEATRPDALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.4	1835.9853	-0.0025	NIAIGRPDEATRPDALK
0.4	1835.9781	0.0047	LIIDIDFRSEFEIAR

Mascot: http://www.matrixscience.com/

AT2G36880.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNMVMVFGEITTAAK**
Found in **AT2G36880.1** in **TAIR_Arabidopsis**, Symbols: MAT3 | MAT3 (METHIONINE ADENOSYLTRANSFERASE 3); methionine adenosyltransferase | chr2:15486800-15487972 REVERSE

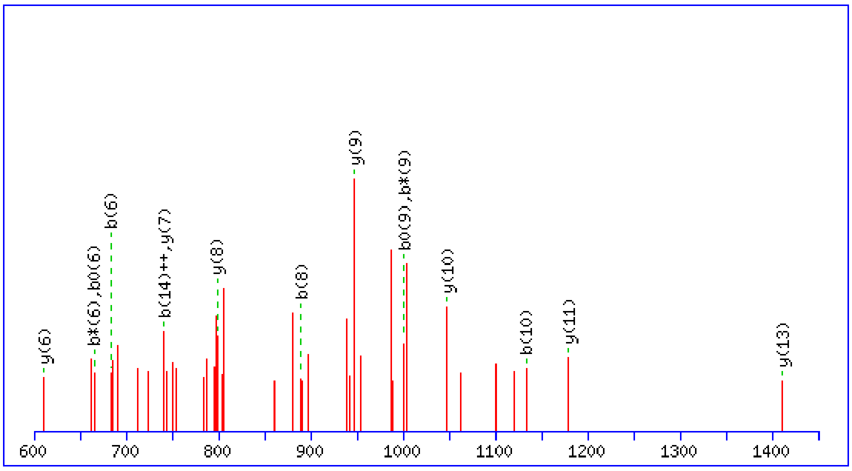
Match to Query 7362: 1628.746960 from(815.380756,2+) index(9270)
Title: Elution from: 84.263 to 84.263 scan no 12503 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 600 to 1450 Da Full range

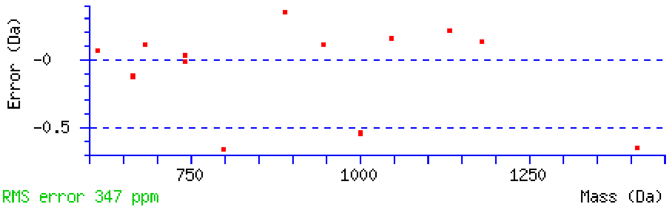
Label all possible matches ○ Label matches used for scoring ●

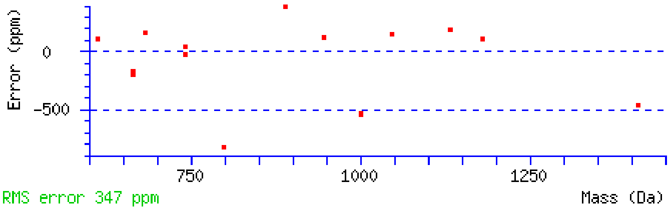
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1628.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0082
Matches : 15/160 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							15
2	219.0890	110.0481	201.0654	101.0363	201.0784	101.0428	N	1527.7122	764.3597	1509.6886	755.3480	1509.7016	755.3545	14
3	351.1265	176.0669	333.1029	167.0551	333.1159	167.0616	M	***1411.6752***	706.3412	1393.6516	697.3295	1393.6646	697.3360	13
4	451.1920	226.0996	433.1684	217.0878	433.1814	217.0943	V	1279.6377	640.3225	1261.6141	631.3107	1261.6271	631.3172	12
5	583.2295	292.1184	565.2059	283.1066	565.2189	283.1131	M	***1179.5722***	590.2898	1161.5487	581.2780	1161.5617	581.2845	11
6	**683.2949**	342.1511	665.2713	333.1393	665.2844	333.1458	V	***1047.5347***	524.2710	1029.5111	515.2592	1029.5242	515.2657	10
7	831.3604	416.1838	813.3368	407.1720	813.3498	407.1785	F	***947.4693***	474.2383	929.4457	465.2265	929.4587	465.2330	9
8	**889.3789**	445.1931	871.3553	436.1813	871.3683	436.1878	G	***799.4038***	400.2056	781.3802	391.1938	781.3933	391.2003	8
9	1019.4185	510.2129	1001.3949	501.2011	1001.4079	501.2076	E	***741.3853***	371.1963	723.3617	362.1845	723.3748	362.1910	7
10	**1133.4996**	567.2534	1115.4760	558.2416	1115.4890	558.2482	I	***611.3457***	306.1765	593.3221	297.1647	593.3351	297.1712	6
11	1235.5443	618.2758	1217.5207	609.2640	1217.5337	609.2705	T	497.2646	249.1359	479.2410	240.1241	479.2540	240.1307	5
12	1337.5890	669.2982	1319.5654	660.2864	1319.5785	660.2929	T	395.2199	198.1136	377.1963	189.1018	377.2093	189.1083	4
13	1409.6232	705.3152	1391.5996	696.3034	1391.6126	696.3099	A	293.1752	147.0912	275.1516	138.0794			3
14	1481.6573	741.3323	1463.6337	732.3205	1463.6468	732.3270	A	221.1410	111.0741	203.1174	102.0624			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT2G36880.1

NCBI **BLAST** search of TNMVMVFGEITTAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	1628.7496	-0.0027	TNMVMVFGEITTAAK
3.2	1628.7516	-0.0046	GQWVMNLKHGHGVK

AT2G37040.1

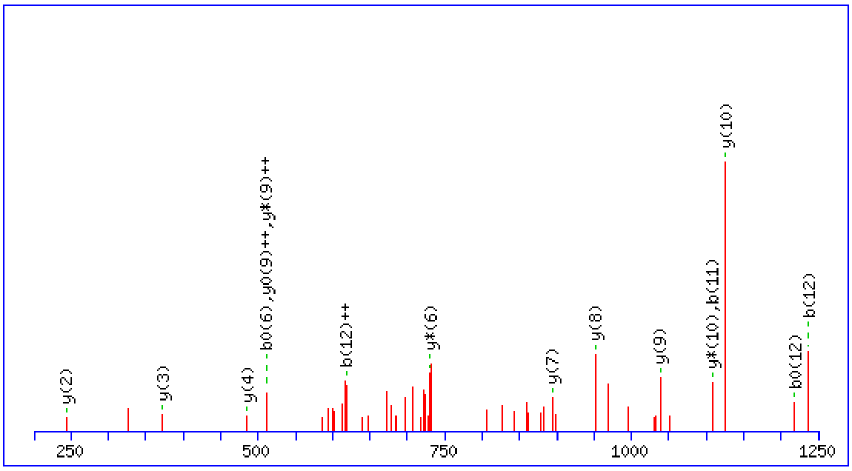
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGISSGFFDLQPK**
Found in **AT2G37040.1** in **TAIR_Arabidopsis**, Symbols: PAL1 | PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase | chr2:15564681-15567316 REVERSE

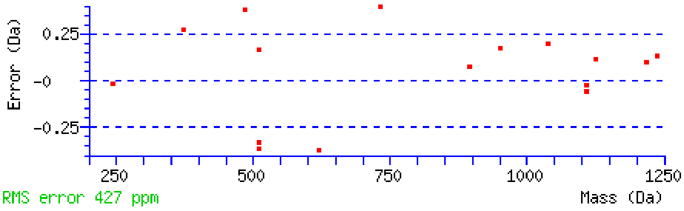
Match to Query 6454: 1478.773720 from(740.394136,2+) index(9287)
Title: Elution from: 81.114 to 81.114 scan no 12295 cid35.00 polarity:+
Data file C7-1_1.mgf

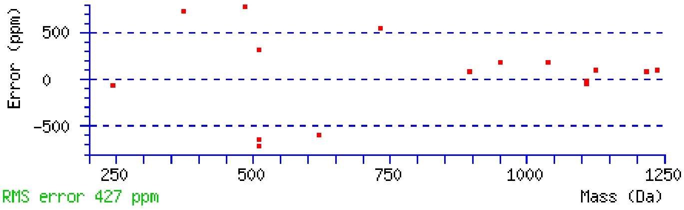
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1478.7769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 6e-005
Matches : 16/118 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	185.1285	93.0679					A	1366.7001	683.8537	1349.6736	675.3404	1348.6896	674.8484	13
3	242.1499	121.5786					G	1295.6630	648.3352	1278.6365	639.8219	1277.6525	639.3299	12
4	355.2340	178.1206					I	1238.6416	619.8244	1221.6150	611.3111	1220.6310	610.8191	11
5	442.2660	221.6366			424.2554	212.6314	S	***1125.5575***	563.2824	1108.5310	554.7691	1107.5469	554.2771	10
6	529.2980	265.1527			511.2875	256.1474	S	***1038.5255***	519.7664	1021.4989	511.2531	1020.5149	510.7611	9
7	586.3195	293.6634			568.3089	284.6581	G	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	8
8	733.3879	367.1976			715.3774	358.1923	F	***894.4720***	447.7396	877.4454	439.2264	876.4614	438.7343	7
9	880.4563	440.7318			862.4458	431.7265	F	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	6
10	995.4833	498.2453			977.4727	489.2400	D	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	5
11	**1108.5673**	554.7873			1090.5568	545.7820	L	***485.3082***	243.1577	468.2817	234.6445			4
12	**1236.6259**	618.8166	1219.5994	610.3033	1218.6153	609.8113	Q	***372.2241***	186.6157	355.1976	178.1024			3
13	1333.6787	667.3430	1316.6521	658.8297	1315.6681	658.3377	P	***244.1656***	122.5864	227.1390	114.0731			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LAGISSGFFDLQPK

AT2G37040.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.4	1478.7769	-0.0032	LAGISSGFFDLQPK
7.5	1478.7729	0.0009	IIKEHEEDPNKK

AT2G37080.1

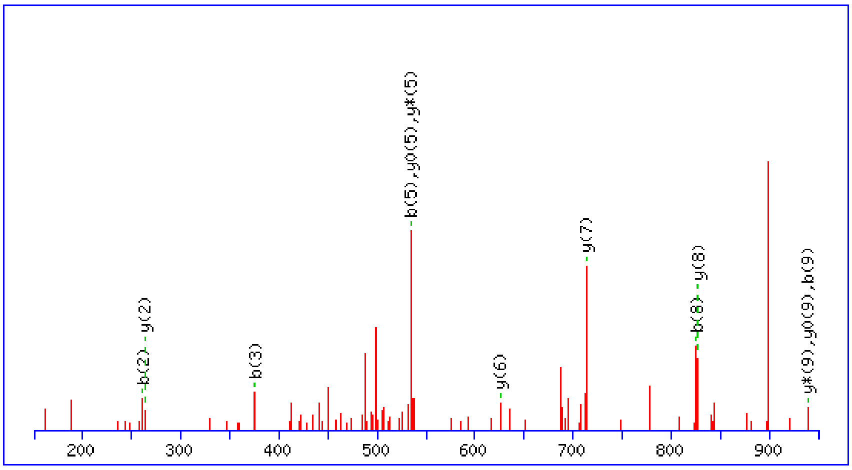
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQLSASEALK**
Found in **AT2G37080.1** in **TAIR_Arabidopsis**, Symbols: | myosin heavy chain-related | chr2:15588644-15591136 REVERSE

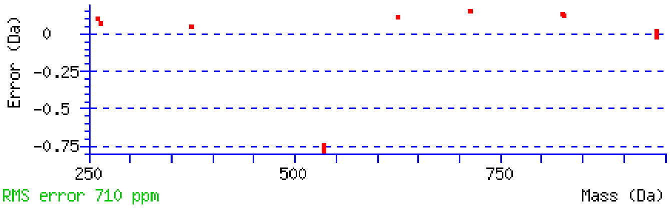
Match to Query 3189: 1086.519862 from(544.267207,2+) index(2414)
Title: Elution from: 25.287 to 25.287 scan no 3028 cid35.00 polarity:+
Data file D12h-3_3.mgf

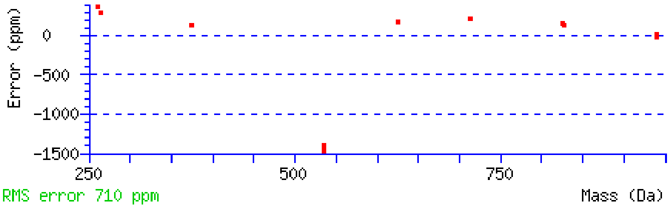
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1086.5201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0047
Matches : 13/100 fragment ions using 16 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							10
2	***261.0996***	131.0534	243.0760	122.0416	243.0890	122.0481	Q	957.4878	479.2475	939.4642	470.2357	939.4772	470.2422	9
3	***375.1806***	188.0940	357.1571	179.0822	357.1701	179.0887	L	***827.4351***	414.2212	809.4115	405.2094	809.4246	405.2159	8
4	463.2097	232.1085	445.1861	223.0967	445.1991	223.1032	S	***713.3540***	357.1807	695.3304	348.1689	695.3435	348.1754	7
5	***535.2439***	268.1256	517.2203	259.1138	517.2333	259.1203	A	***625.3250***	313.1661	607.3014	304.1543	607.3144	304.1608	6
6	623.2729	312.1401	605.2493	303.1283	605.2624	303.1348	S	553.2908	277.1490	535.2672	268.1373	535.2802	268.1438	5
7	753.3126	377.1599	735.2890	368.1481	735.3020	368.1546	E	465.2618	233.1345	447.2382	224.1227	447.2512	224.1292	4
8	***825.3467***	413.1770	807.3231	404.1652	807.3361	404.1717	A	335.2221	168.1147	317.1985	159.1029			3
9	***939.4278***	470.2175	921.4042	461.2057	921.4172	461.2123	L	***263.1880***	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EQLSASEALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G37080.1

32.7	1086.5201	-0.0003	EQLSASEALK
22.2	1086.5201	-0.0003	VSAVNESEIK
21.8	1086.5176	0.0023	WCLTGTPIK
12.7	1086.5201	-0.0002	SVKDVVDDAK
6.3	1086.5228	-0.0029	RVLTSPDER
5.3	1086.5201	-0.0003	SLISEDNGLK
4.5	1086.5201	-0.0002	LEEEKGKDK
4.5	1086.5201	-0.0002	ATVVEEGKDK
3.8	1086.5201	-0.0003	NGEDISSILK
3.1	1086.5228	-0.0029	QKAQAELER

Mascot: http://www.matrixscience.com/

AT2G37190.1

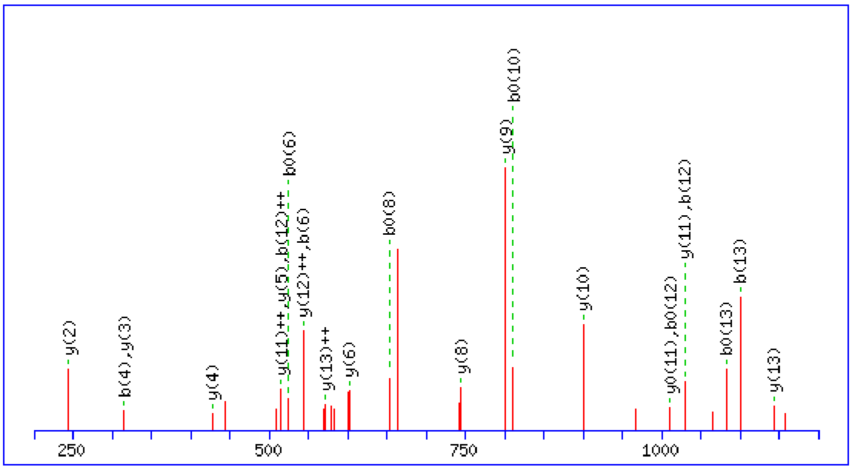
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTGGEVGAASSLAPK**
Found in **AT2G37190.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L12 (RPL12A) | chr2:15626638-15627138 REVERSE

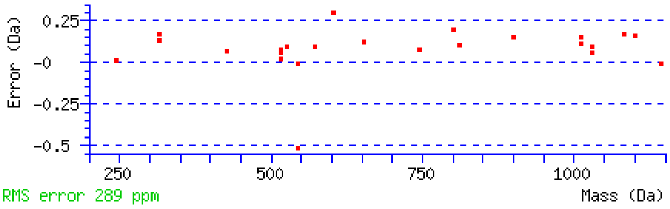
Match to Query 5434: 1342.708242 from(672.361397,2+) index(3088)
Title: Elution from: 30.679 to 30.679 scan no 3842 cid35.00 polarity:+
Data file D6h-1_1.mgf

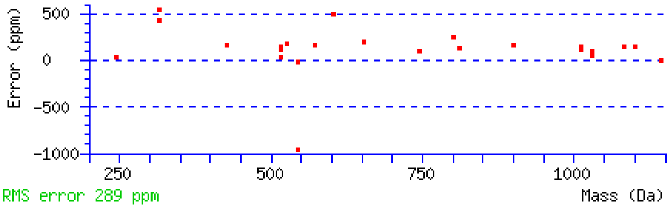
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1342.7092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 3.8e-010
Matches : 24/130 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							15
2	201.1234	101.0653	183.1128	92.0600	T	1244.6481	622.8277	1227.6216	614.3144	1226.6375	613.8224	14
3	258.1448	129.5761	240.1343	120.5708	G	***1143.6004***	572.3039	1126.5739	563.7906	1125.5899	563.2986	13
4	**315.1663**	158.0868	297.1557	149.0815	G	1086.5790	543.7931	1069.5524	535.2798	1068.5684	534.7878	12
5	444.2089	222.6081	426.1983	213.6028	E	***1029.5575***	515.2824	1012.5310	506.7691	1011.5469	506.2771	11
6	**543.2773**	272.1423	525.2667	263.1370	V	***900.5149***	450.7611	883.4884	442.2478	882.5043	441.7558	10
7	600.2988	300.6530	582.2882	291.6477	G	***801.4465***	401.2269	784.4199	392.7136	783.4359	392.2216	9
8	671.3359	336.1716	653.3253	327.1663	A	***744.4250***	372.7162	727.3985	364.2029	726.4145	363.7109	8
9	742.3730	371.6901	724.3624	362.6849	A	673.3879	337.1976	656.3614	328.6843	655.3774	328.1923	7
10	829.4050	415.2062	811.3945	406.2009	S	***602.3508***	301.6790	585.3243	293.1658	584.3402	292.6738	6
11	916.4371	458.7222	898.4265	449.7169	S	***515.3188***	258.1630	498.2922	249.6498	497.3082	249.1577	5
12	**1029.5211**	515.2642	1011.5106	506.2589	L	***428.2867***	214.6470	411.2602	206.1337			4
13	**1100.5582**	550.7828	1082.5477	541.7775	A	***315.2027***	158.1050	298.1761	149.5917			3
14	1197.6110	599.3091	1179.6004	590.3039	P	***244.1656***	122.5864	227.1390	114.0731			2
15					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VTGGEVGAASSLAPK

AT2G37190.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.2	1342.7092	-0.0010	VTGGEVGAASSLAPK
14.6	1342.7067	0.0015	WGLQMGQSVLPK
7.4	1342.7092	-0.0010	ALDAENKIDNLK
1.0	1342.7092	-0.0010	TRTDEVGIDLPK
0.4	1342.7092	-0.0010	DVSGEGVQQALLK

AT2G37220.1

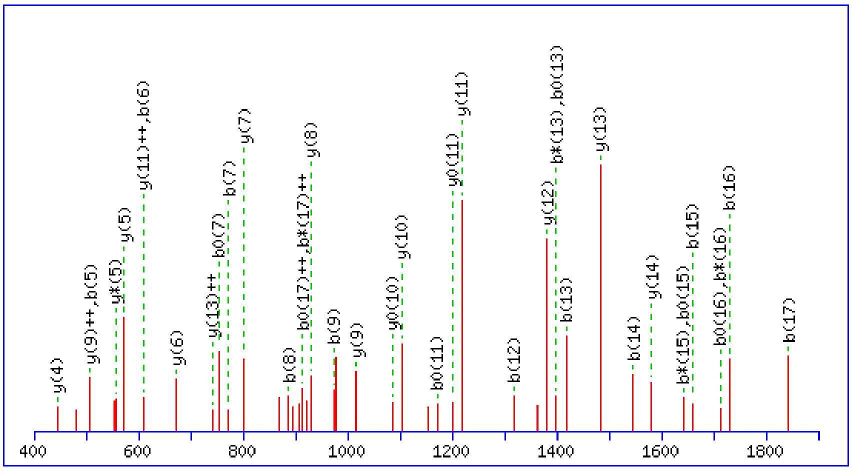
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGFVTYDSSQEVQNAIK**
Found in **AT2G37220.1** in **TAIR_Arabidopsis**, Symbols: | 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative | chr2:15642059-15643410 REVERSE

Match to Query 8930: 1988.947138 from(995.480845,2+) index(7722)
Title: Elution from: 68.155 to 68.155 scan no 10207 cid35.00 polarity:+
Data file 0-3_3.mgf

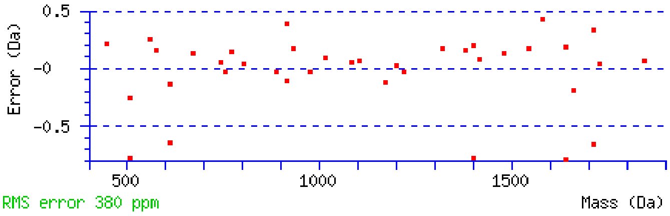
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

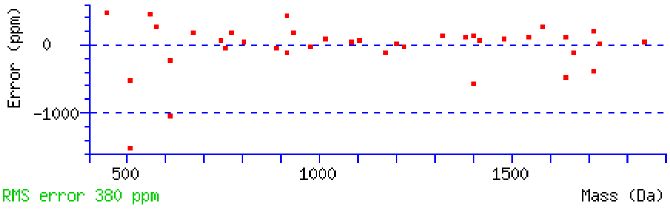


Monoisotopic mass of neutral peptide Mr(calc): 1988.9480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 135 **Expect:** 1.3e-013
Matches : 38/162 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							18
2	205.0972	103.0522					F	1932.9338	966.9705	1915.9072	958.4573	1914.9232	957.9652	17
3	262.1186	131.5629					G	1785.8654	893.4363	1768.8388	884.9230	1767.8548	884.4310	16
4	409.1870	205.0972					F	1728.8439	864.9256	1711.8174	856.4123	1710.8333	855.9203	15
5	***508.2554***	254.6314					V	***1581.7755***	791.3914	1564.7489	782.8781	1563.7649	782.3861	14
6	***609.3031***	305.1552			591.2926	296.1499	T	***1482.7071***	741.8572	1465.6805	733.3439	1464.6965	732.8519	13
7	***772.3665***	386.6869			754.3559	377.6816	Y	***1381.6594***	691.3333	1364.6329	682.8201	1363.6488	682.3281	12
8	***887.3934***	444.2003			869.3828	435.1951	D	***1218.5961***	609.8017	1201.5695	601.2884	1200.5855	600.7964	11
9	***974.4254***	487.7164			956.4149	478.7111	S	***1103.5691***	552.2882	1086.5426	543.7749	1085.5586	543.2829	10
10	1061.4575	531.2324			1043.4469	522.2271	S	***1016.5371***	508.7722	999.5106	500.2589	998.5265	499.7669	9
11	1189.5160	595.2617	1172.4895	586.7484	1171.5055	586.2564	Q	***929.5051***	465.2562	912.4785	456.7429	911.4945	456.2509	8
12	***1318.5586***	659.7830	1301.5321	651.2697	1300.5481	650.7777	E	***801.4465***	401.2269	784.4199	392.7136	783.4359	392.2216	7
13	***1417.6270***	709.3172	1400.6005	700.8039	1399.6165	700.3119	V	***672.4039***	336.7056	655.3774	328.1923			6
14	***1545.6856***	773.3464	1528.6591	764.8332	1527.6751	764.3412	Q	***573.3355***	287.1714	556.3089	278.6581			5
15	***1659.7285***	830.3679	1642.7020	821.8546	1641.7180	821.3626	N	***445.2769***	223.1421	428.2504	214.6288			4
16	***1730.7657***	865.8865	1713.7391	857.3732	1712.7551	856.8812	A	331.2340	166.1206	314.2074	157.6074			3
17	***1843.8497***	922.4285	1826.8232	913.9152	1825.8392	913.4232	I	260.1969	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT2G37220.1





NCBI **BLAST** search of GFGFVTYDSSQEVQNAIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
134.6	1988.9480	-0.0008	GFGFVTYDSSQEVQNAIK
8.9	1988.9482	-0.0010	LPDTMREQMLAHMQLK
2.6	1988.9488	-0.0017	MDWDVLEHMIKNWIK
0.3	1988.9522	-0.0051	EFHCDMALCTVPLGVLK

Mascot: http://www.matrixscience.com/

AT2G37270.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAVDISPLR**
Found in **AT2G37270.1** in **TAIR_Arabidopsis**, Symbols: ATRPS5B | ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome | chr2:15654962-15656121 REVERSE

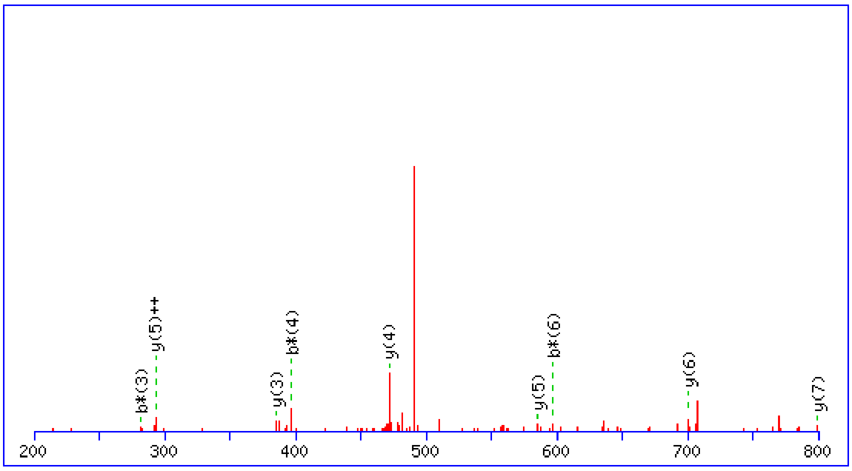
Match to Query 2592: 997.555002 from(499.784777,2+) index(3871)
Title: Elution from: 36.917 to 36.917 scan no 4793 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 800 Da Full range

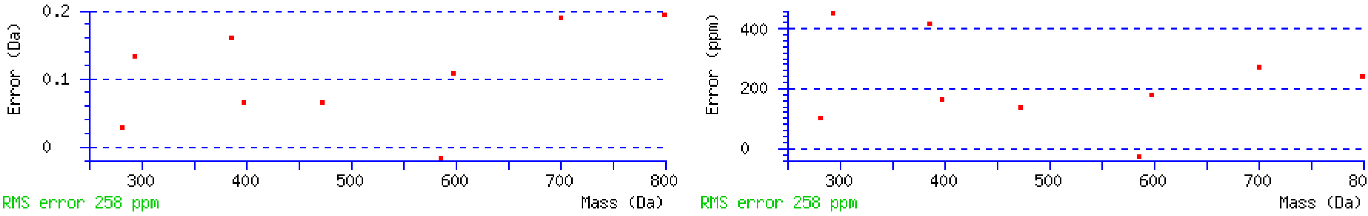
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 997.5556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.016
Matches : 9/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							9
2	200.1030	100.5551	183.0764	92.0418			A	870.5043	435.7558	853.4778	427.2425	852.4938	426.7505	8
3	299.1714	150.0893	282.1448	141.5761			V	***799.4672***	400.2373	782.4407	391.7240	781.4567	391.2320	7
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	D	***700.3988***	350.7030	683.3723	342.1898	682.3883	341.6978	6
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1396	I	***585.3719***	293.1896	568.3453	284.6763	567.3613	284.1843	5
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	S	***472.2878***	236.6475	455.2613	228.1343	454.2772	227.6423	4
7	711.3672	356.1872	694.3406	347.6740	693.3566	347.1819	P	***385.2558***	193.1315	368.2292	184.6183			3
8	824.4512	412.7293	807.4247	404.2160	806.4407	403.7240	L	288.2030	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of QAVDISPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G37270.1

23.2	997.5556	-0.0006	QAVDISPLR
3.9	997.5556	-0.0006	EAPVEARVK
3.8	997.5556	-0.0006	TQVSPTPIR
2.7	997.5556	-0.0006	LVGAEGSPIR
1.6	997.5556	-0.0006	VNISPVDVR
1.3	997.5556	-0.0006	VNLAEPSLR
0.4	997.5556	-0.0006	DGDIPVRVK
0.3	997.5556	-0.0006	ILEGGSGIPR

AT2G37390.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSGRAIDRHNPIIK**
Found in **AT2G37390.1** in **TAIR_Arabidopsis**, Symbols: | heavy-metal-associated domain-containing protein | chr2:15701379-15702540 FORWARD

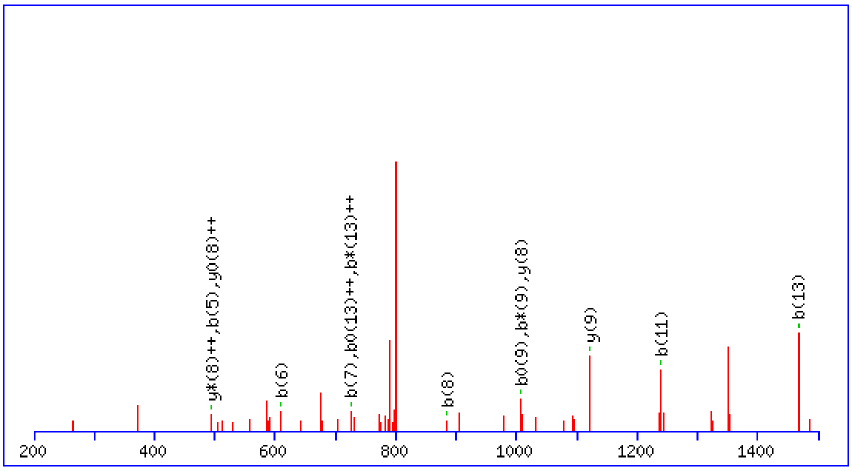
Match to Query 7012: 1614.798812 from(808.406682,2+) index(4285)
Title: Elution from: 39.148 to 39.148 scan no 5378 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

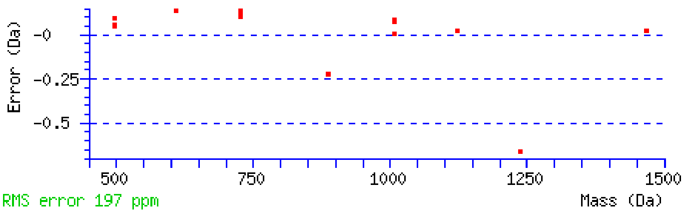
Label all possible matches ○ Label matches used for scoring ●

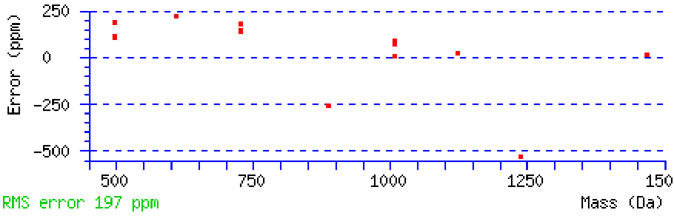
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1614.8009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.012
Matches : 14/140 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							14
2	205.0733	103.0403	187.0498	94.0285	187.0628	94.0350	S	1499.7712	750.3892	1481.7476	741.3774	1481.7606	741.3839	13
3	263.0918	132.0496	245.0683	123.0378	245.0813	123.0443	G	1411.7421	706.3747	1393.7185	697.3629	1393.7315	697.3694	12
4	423.1811	212.0942	405.1575	203.0824	405.1705	203.0889	R	1353.7236	677.3654	1335.7000	668.3537	1335.7130	668.3602	11
5	***495.2152***	248.1113	477.1917	239.0995	477.2047	239.1060	A	1193.6344	597.3208	1175.6108	588.3090	1175.6238	588.3155	10
6	***609.2963***	305.1518	591.2728	296.1400	591.2858	296.1465	I	**1121.6002**	561.3037	1103.5766	552.2920	1103.5896	552.2985	9
7	***725.3203***	363.1638	707.2967	354.1520	707.3097	354.1585	D	**1007.5191**	504.2632	989.4955	495.2514	989.5085	495.2579	8
8	***885.4096***	443.2084	867.3860	434.1966	867.3990	434.2031	R	891.4951	446.2512	873.4716	437.2394			7
9	1025.4596	513.2334	1007.4360	504.2216	1007.4490	504.2281	H	731.4059	366.2066	713.3823	357.1948			6
10	1141.4966	571.2519	1123.4730	562.2401	1123.4860	562.2466	N	591.3559	296.1816	573.3323	287.1698			5
11	***1239.5464***	620.2768	1221.5228	611.2650	1221.5358	611.2715	P	475.3189	238.1631	457.2953	229.1513			4
12	1353.6275	677.3174	1335.6039	668.3056	1335.6169	668.3121	I	377.2691	189.1382	359.2455	180.1264			3
13	***1467.7086***	734.3579	1449.6850	725.3461	1449.6980	725.3526	I	263.1880	132.0976	245.1644	123.0858			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NSGRAIDRHNPIIK

AT2G37390.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	1614.8009	-0.0021	NSGRAIDRHNPIIK
6.2	1614.7955	0.0033	IEQQQLLNPASEVK
6.0	1614.8005	-0.0016	NFISGRNYGINVLK
5.7	1614.8034	-0.0046	GKIYFLMPATKSDK
4.5	1614.7955	0.0033	KIAKEDHVTEALDK
3.8	1614.8004	-0.0016	SRVKFYNVLDPTR
1.4	1614.7964	0.0024	MVRGLMKFPGISTK
1.3	1614.8005	-0.0016	RESPHISKWVDLK
0.7	1614.7955	0.0033	HVSGLEKEVQETIK
0.4	1614.7977	0.0011	KVYVGQGDSGVVYVK

AT2G37660.1

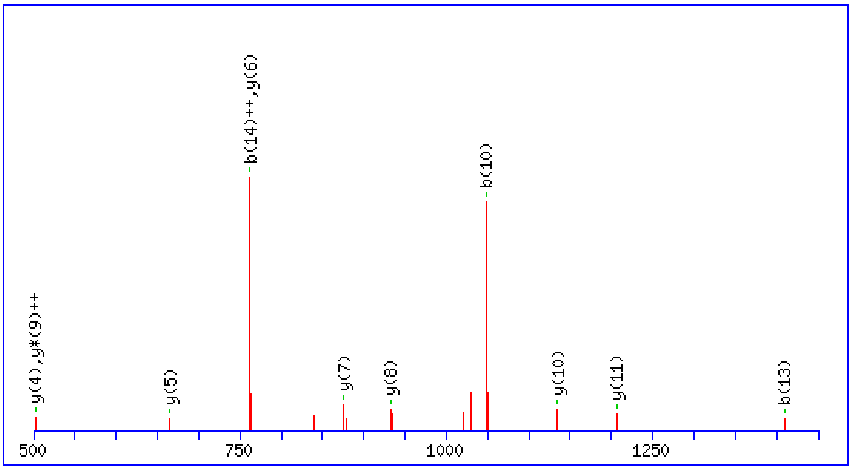
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEQYLADSGIPYTIIR**
Found in **AT2G37660.1** in **TAIR_Arabidopsis**, Symbols: | binding / catalytic/ coenzyme binding | chr2:15802559-15804055 REVERSE

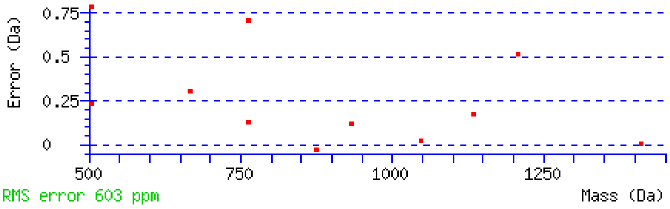
Match to Query 8164: 1808.934066 from(905.474309,2+) index(7955)
Title: Elution from: 74.650 to 74.650 scan no 10734 cid35.00 polarity:+
Data file D1d-1-2.mgf

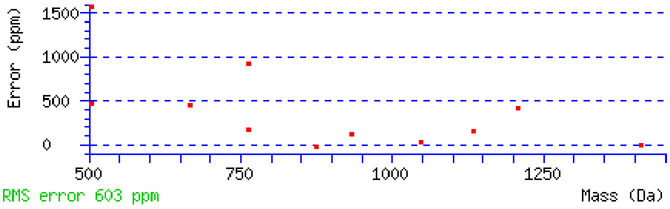
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1808.9308
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 4.6e-007
Matches : 11/168 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							16
2	201.0870	101.0471			183.0764	92.0418	E	1738.9010	869.9542	1721.8745	861.4409	1720.8905	860.9489	15
3	329.1456	165.0764	312.1190	156.5631	311.1350	156.0711	Q	1609.8584	805.4329	1592.8319	796.9196	1591.8479	796.4276	14
4	492.2089	246.6081	475.1823	238.0948	474.1983	237.6028	Y	1481.7999	741.4036	1464.7733	732.8903	1463.7893	732.3983	13
5	605.2930	303.1501	588.2664	294.6368	587.2824	294.1448	L	1318.7365	659.8719	1301.7100	651.3586	1300.7260	650.8666	12
6	676.3301	338.6687	659.3035	330.1554	658.3195	329.6634	A	***1205.6525***	603.3299	1188.6259	594.8166	1187.6419	594.3246	11
7	791.3570	396.1821	774.3305	387.6689	773.3464	387.1769	D	***1134.6154***	567.8113	1117.5888	559.2980	1116.6048	558.8060	10
8	878.3890	439.6982	861.3625	431.1849	860.3785	430.6929	S	1019.5884	510.2978	1002.5619	501.7846	1001.5778	501.2926	9
9	935.4105	468.2089	918.3840	459.6956	917.3999	459.2036	G	***932.5564***	466.7818	915.5298	458.2686	914.5458	457.7765	8
10	**1048.4946**	524.7509	1031.4680	516.2376	1030.4840	515.7456	I	***875.5349***	438.2711	858.5084	429.7578	857.5244	429.2658	7
11	1145.5473	573.2773	1128.5208	564.7640	1127.5368	564.2720	P	***762.4509***	381.7291	745.4243	373.2158	744.4403	372.7238	6
12	1308.6107	654.8090	1291.5841	646.2957	1290.6001	645.8037	Y	***665.3981***	333.2027	648.3715	324.6894	647.3875	324.1974	5
13	**1409.6583**	705.3328	1392.6318	696.8195	1391.6478	696.3275	T	***502.3348***	251.6710	485.3082	243.1577	484.3242	242.6657	4
14	1522.7424	761.8748	1505.7159	753.3616	1504.7318	752.8696	I	401.2871	201.1472	384.2605	192.6339			3
15	1635.8265	818.4169	1618.7999	809.9036	1617.8159	809.4116	I	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1





AT2G37660.1

NCBI **BLAST** search of AEQYLADSGIPYTIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.5	1808.9308	0.0032	AEQYLADSGIPYTIIR
1.2	1808.9308	0.0032	EGVYEETVRVPFEKK

AT2G38040.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAINENMNEFGK**
Found in **AT2G38040.1** in **TAIR_Arabidopsis**, Symbols: CAC3 | CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit); acetyl-CoA carboxylase | chr2:15924690-15927827 FORWARD

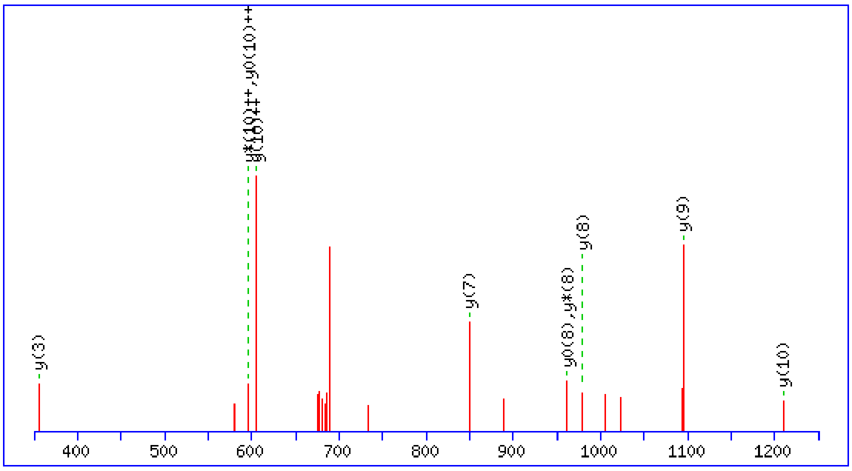
Match to Query 4861: 1394.608990 from(698.311771,2+) index(4667)
Title: Elution from: 45.130 to 45.130 scan no 5945 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1250 Da Full range

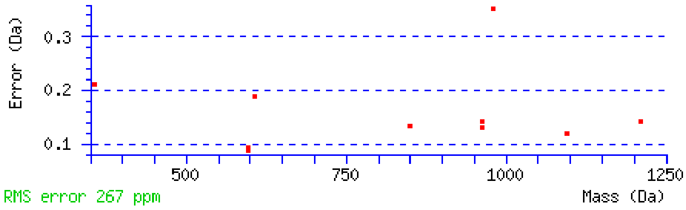
Label all possible matches ○ Label matches used for scoring ●

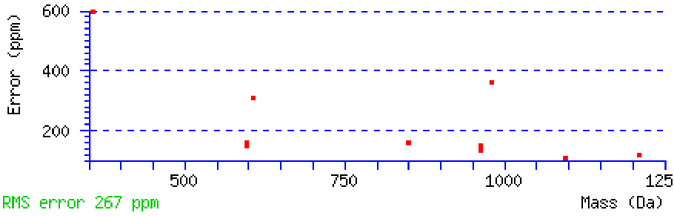
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1394.6077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00083
Matches : 10/112 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**I**							**12**
2	187.1225	94.0649					**A**	1281.5338	641.2706	1263.5103	632.2588	1263.5233	632.2653	**11**
3	301.2036	151.1054					**I**	***1209.4997***	605.2535	1191.4761	596.2417	1191.4891	596.2482	**10**
4	417.2406	209.1239	399.2170	200.1122			**N**	***1095.4186***	548.2129	1077.3950	539.2011	1077.4080	539.2076	**9**
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	**E**	***979.3816***	490.1944	961.3580	481.1826	961.3710	481.1892	**8**
6	663.3172	332.1623	645.2937	323.1505	645.3067	323.1570	**N**	***849.3420***	425.1746	831.3184	416.1628	831.3314	416.1693	**7**
7	795.3548	398.1810	777.3312	389.1692	777.3442	389.1757	**M**	733.3050	367.1561	715.2814	358.1443	715.2944	358.1508	**6**
8	911.3918	456.1995	893.3682	447.1877	893.3812	447.1942	**N**	601.2674	301.1374	583.2439	292.1256	583.2569	292.1321	**5**
9	1041.4314	521.2193	1023.4078	512.2075	1023.4208	512.2141	**E**	485.2304	243.1189	467.2069	234.1071	467.2199	234.1136	**4**
10	1189.4968	595.2521	1171.4733	586.2403	1171.4863	586.2468	**F**	***355.1908***	178.0990	337.1672	169.0873			**3**
11	1247.5153	624.2613	1229.4918	615.2495	1229.5048	615.2560	**G**	207.1254	104.0663	189.1018	95.0545			**2**
12							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of IAINENMNEFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G38040.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.2	1394.6077	0.0013	IAINENMNEFGK
3.3	1394.6110	-0.0020	SMVLSLAMSPDGR
1.7	1394.6070	0.0020	LAFDHNNLYNR
0.8	1394.6108	-0.0018	GRGIMHSRESSR
0.8	1394.6124	-0.0034	LGSKPDTFESDGK

AT2G38230.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGVIMDVVNAEQAR**
Found in **AT2G38230.1** in **TAIR_Arabidopsis**, Symbols: ATPDX1.1 | ATPDX1.1 (PYRIDOXINE BIOSYNTHESIS 1.1); protein heterodimerization | chr2:16018553-16019482 FORWARD

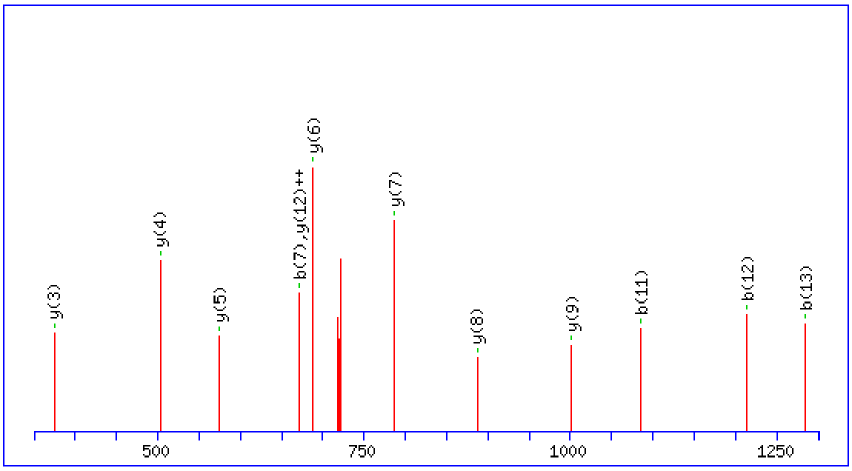
Match to Query 5866: 1457.730780 from(729.872666,2+) index(6350)
Title: Elution from: 56.773 to 56.773 scan no 8185 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1300 Da Full range

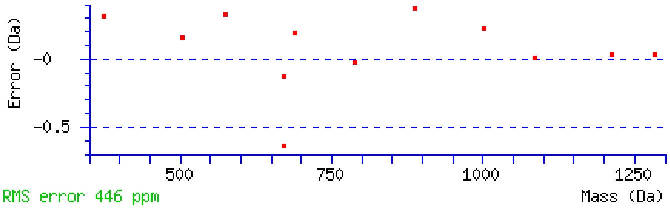
Label all possible matches ○ Label matches used for scoring ●

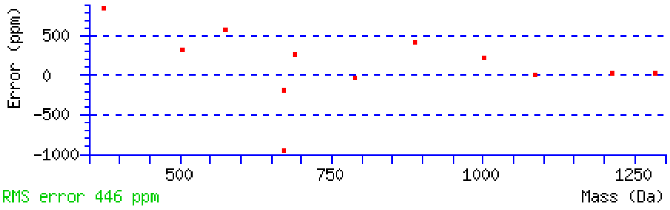
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1457.7297
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 8.3e-008
Matches : 12/124 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**14**
2	115.0502	58.0287					**G**	1401.7155	701.3614	1384.6889	692.8481	1383.7049	692.3561	**13**
3	214.1186	107.5629					**V**	1344.6940	672.8506	1327.6675	664.3374	1326.6834	663.8454	**12**
4	327.2027	164.1050					**I**	1245.6256	623.3164	1228.5990	614.8032	1227.6150	614.3112	**11**
5	458.2432	229.6252					**M**	1132.5415	566.7744	1115.5150	558.2611	1114.5310	557.7691	**10**
6	573.2701	287.1387			555.2595	278.1334	**D**	***1001.5010***	501.2542	984.4745	492.7409	983.4905	492.2489	**9**
7	***672.3385***	336.6729			654.3280	327.6676	**V**	***886.4741***	443.7407	869.4476	435.2274	868.4635	434.7354	**8**
8	771.4069	386.2071			753.3964	377.2018	**V**	***787.4057***	394.2065	770.3791	385.6932	769.3951	385.2012	**7**
9	885.4499	443.2286	868.4233	434.7153	867.4393	434.2233	**N**	***688.3373***	344.6723	671.3107	336.1590	670.3267	335.6670	**6**
10	956.4870	478.7471	939.4604	470.2339	938.4764	469.7418	**A**	***574.2944***	287.6508	557.2678	279.1375	556.2838	278.6455	**5**
11	***1085.5296***	543.2684	1068.5030	534.7551	1067.5190	534.2631	**E**	***503.2572***	252.1323	486.2307	243.6190	485.2467	243.1270	**4**
12	***1213.5881***	607.2977	1196.5616	598.7844	1195.5776	598.2924	**Q**	***374.2146***	187.6110	357.1881	179.0977			**3**
13	***1284.6253***	642.8163	1267.5987	634.3030	1266.6147	633.8110	**A**	246.1561	123.5817	229.1295	115.0684			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GGVIMDVVNAEQAR

AT2G38230.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.4	1457.7297	0.0011	GGVIMDVVNAEQAR

Mascot: http://www.matrixscience.com/

AT2G38240.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMQALGGGDK**
Found in **AT2G38240.1** in **TAIR_Arabidopsis**, Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr2:16019801-16021744 REVERSE

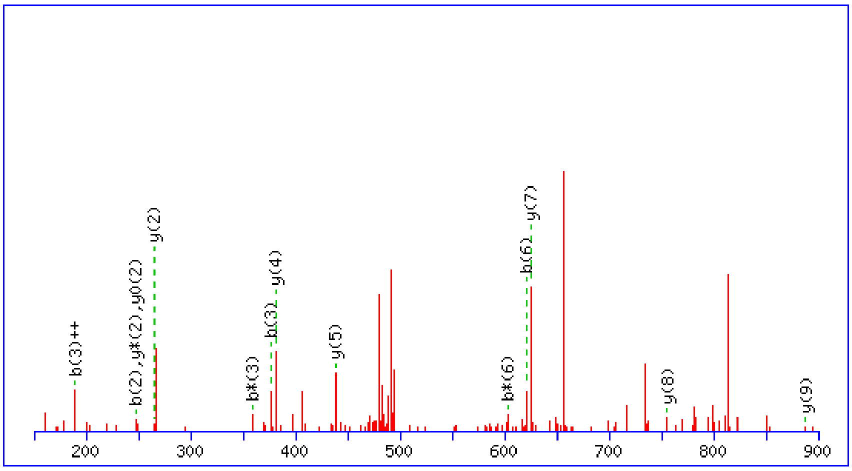
Match to Query 2467: 1000.463258 from(501.238905,2+) index(2535)
Title: Elution from: 26.758 to 26.758 scan no 3178 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

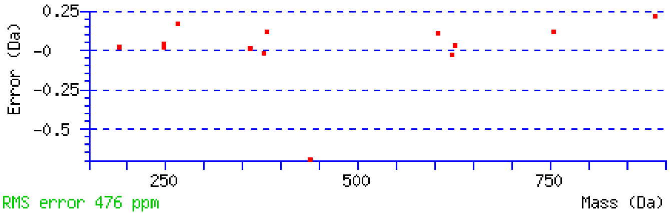
Label all possible matches ○ Label matches used for scoring ●

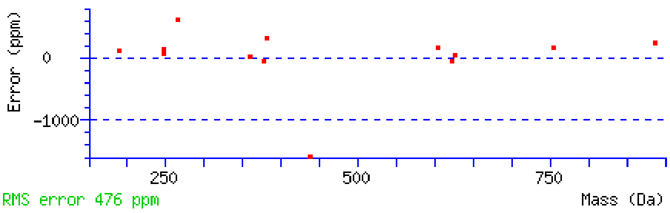
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1000.4656
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.014
Matches : 14/86 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							10
2	**247.1259**	124.0666					M	***887.3918***	444.1995	869.3682	435.1877	869.3812	435.1942	9
3	**377.1785**	189.0929	359.1550	180.0811			Q	***755.3542***	378.1808	737.3307	369.1690	737.3437	369.1755	8
4	449.2127	225.1100	431.1891	216.0982			A	***625.3016***	313.1544	607.2780	304.1426	607.2910	304.1492	7
5	563.2938	282.1505	545.2702	273.1387			L	553.2674	277.1374	535.2439	268.1256	535.2569	268.1321	6
6	**621.3123**	311.1598	603.2887	302.1480			G	***439.1863***	220.0968	421.1628	211.0850	421.1758	211.0915	5
7	679.3308	340.1690	661.3072	331.1572			G	***381.1679***	191.0876	363.1443	182.0758	363.1573	182.0823	4
8	737.3493	369.1783	719.3257	360.1665			G	323.1494	162.0783	305.1258	153.0665	305.1388	153.0730	3
9	853.3733	427.1903	835.3497	418.1785	835.3627	418.1850	D	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LMQALGGGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G38240.1

Score	Mr(calc)	Delta	Sequence
28.2	1000.4656	-0.0023	LMQALGGGDK
8.6	1000.4656	-0.0023	QIMPELSR
8.3	1000.4622	0.0011	ELLEWGSR
5.5	1000.4656	-0.0023	LMLDQVDR
5.3	1000.4644	-0.0012	ITYQFYR
5.3	1000.4653	-0.0021	SRSPRHSR
4.7	1000.4622	0.0011	IWGLSEER
4.6	1000.4656	-0.0023	ISGMTTHVK
4.4	1000.4626	0.0006	NAAGNTGRPK
4.3	1000.4626	0.0006	SQHASKATR

AT2G38270.1

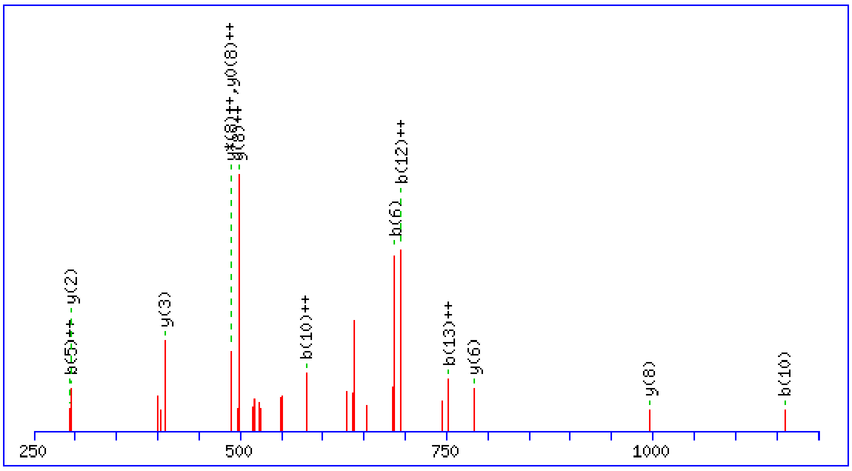
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVELTVPLEELIDR**
Found in **AT2G38270.1** in **TAIR_Arabidopsis**, Symbols: CXIP2 | CXIP2 (CAX-INTERACTING PROTEIN 2); electron carrier/ protein disulfide oxidoreductase | chr2:16038425-16040132 REVERSE

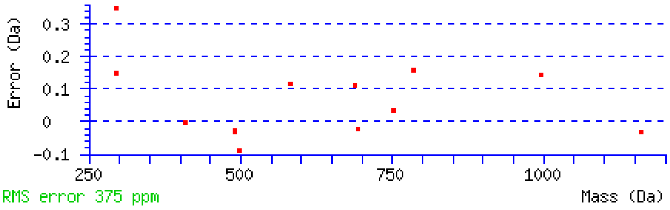
Match to Query 7865: 1680.841896 from(561.287908,3+) index(9130)
Title: Elution from: 82.504 to 82.504 scan no 12432 cid35.00 polarity:+
Data file 0-1_3.mgf

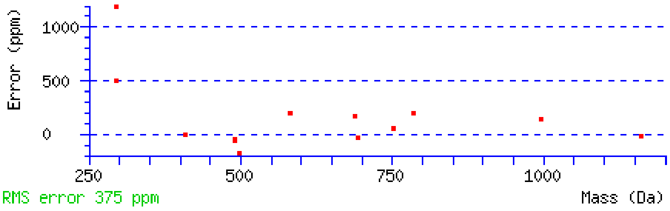
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1680.8425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00028
Matches : 13/124 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	141.0573	71.0323			H							14
2	241.1227	121.0650			V	1541.7998	771.4035	1523.7762	762.3917	1523.7892	762.3982	13
3	371.1624	186.0848	353.1518	177.0795	E	1441.7343	721.3708	1423.7107	712.3590	1423.7237	712.3655	12
4	485.2435	243.1254	467.2329	234.1201	L	1311.6947	656.3510	1293.6711	647.3392	1293.6841	647.3457	11
5	587.2882	***294.1477***	569.2776	285.1424	T	1197.6136	599.3104	1179.5900	590.2986	1179.6030	590.3051	10
6	**687.3536**	344.1805	669.3431	335.1752	V	1095.5689	548.2881	1077.5453	539.2763	1077.5583	539.2828	9
7	785.4034	393.2054	767.3929	384.2001	P	***995.5034***	498.2553	977.4798	489.2436	977.4929	489.2501	8
8	899.4845	450.2459	881.4740	441.2406	L	897.4536	449.2304	879.4300	440.2187	879.4431	440.2252	7
9	1029.5242	515.2657	1011.5136	506.2604	E	***783.3725***	392.1899	765.3489	383.1781	765.3620	383.1846	6
10	**1159.5638**	***580.2855***	1141.5532	571.2802	E	653.3329	327.1701	635.3093	318.1583	635.3223	318.1648	5
11	1273.6449	637.3261	1255.6343	628.3208	L	523.2933	262.1503	505.2697	253.1385	505.2827	253.1450	4
12	1387.7260	***694.3666***	1369.7154	685.3613	I	***409.2122***	205.1097	391.1886	196.0979	391.2016	196.1044	3
13	1503.7500	***752.3786***	1485.7394	743.3733	D	***295.1311***	148.0692	277.1075	139.0574	277.1205	139.0639	2
14					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of HVELTVPLEELIDR

AT2G38270.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.0	1680.8425	-0.0006	HVELTVPLEELIDR
9.2	1680.8429	-0.0010	SIQRLKDQISSLDR
8.3	1680.8452	-0.0033	NRLQIFGANKLEEK
4.0	1680.8378	0.0041	QIVNFPLLGMLSSAR
1.1	1680.8459	-0.0040	LMSEELKVSVEVKR

AT2G38540.1

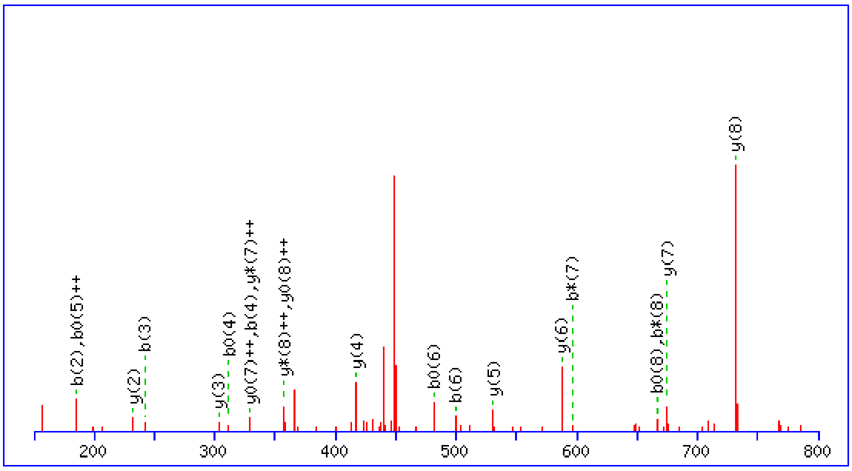
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGSGLNAGR**
Found in **AT2G38540.1** in **TAIR_Arabidopsis**, Symbols: LTP1, ATLTP1, LP1 | LP1 (nonspecific lipid transfer protein 1) | chr2:16137496-16137971 FORWARD

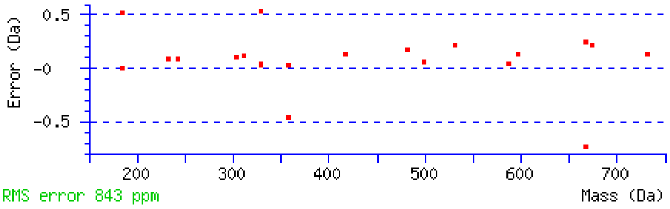
Match to Query 1892: 914.493920 from(458.254236,2+) index(1293)
Title: Elution from: 19.133 to 19.133 scan no 1820 cid35.00 polarity:+
Data file D12h-1_1.mgf

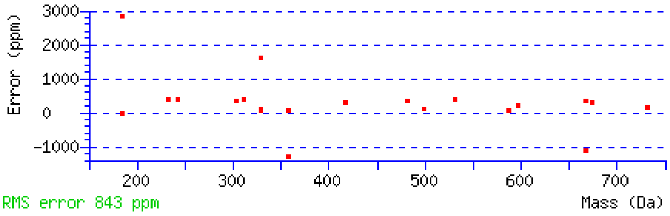
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 914.4934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 1.8e-005
Matches : 21/78 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							10
2	**185.1285**	93.0679					L	844.4635	422.7354	827.4370	414.2221	826.4530	413.7301	9
3	**242.1499**	121.5786					G	***731.3795***	366.1934	714.3529	357.6801	713.3689	357.1881	8
4	**329.1819**	165.0946			311.1714	156.0893	S	***674.3580***	337.6826	657.3315	329.1694	656.3474	328.6774	7
5	386.2034	193.6053			368.1928	184.6001	G	***587.3260***	294.1666	570.2994	285.6534			6
6	**499.2875**	250.1474			481.2769	241.1421	L	***530.3045***	265.6559	513.2780	257.1426			5
7	613.3304	307.1688	596.3039	298.6556	595.3198	298.1636	N	***417.2205***	209.1139	400.1939	200.6006			4
8	684.3675	342.6874	667.3410	334.1741	666.3569	333.6821	A	***303.1775***	152.0924	286.1510	143.5791			3
9	741.3890	371.1981	724.3624	362.6849	723.3784	362.1928	G	***232.1404***	116.5738	215.1139	108.0606			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALGSGLNAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G38540.1

Score	Mr(calc)	Delta	Sequence
53.8	914.4934	0.0006	ALGSGLNAGR
12.4	914.4934	0.0006	RGDGLIER
5.4	914.4947	-0.0008	GVHHRPGR
1.5	914.4933	0.0006	ALEQRNGK

Mascot: http://www.matrixscience.com/

AT2G39010.1

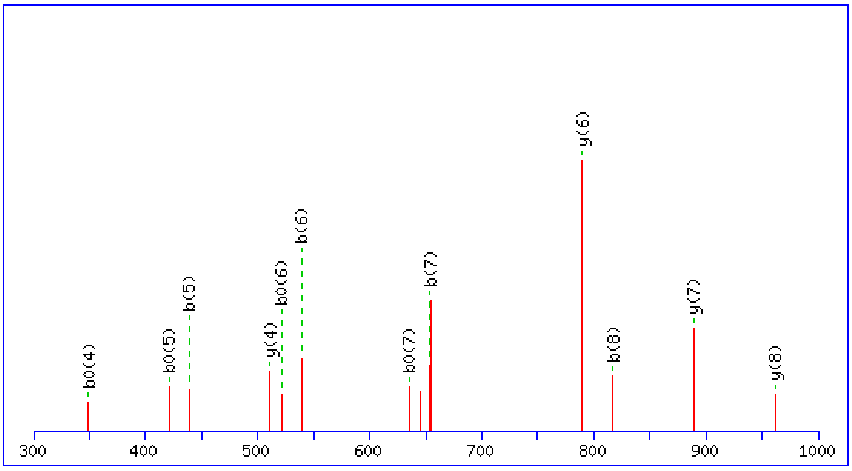
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFGAAVIYNNQK**
Found in **AT2G39010.1** in **TAIR_Arabidopsis**, Symbols: PIP2E, PIP2;6 | PIP2;6/PIP2E (plasma membrane intrinsic protein 2;6); water channel | chr2:16298642-16300824 FORWARD

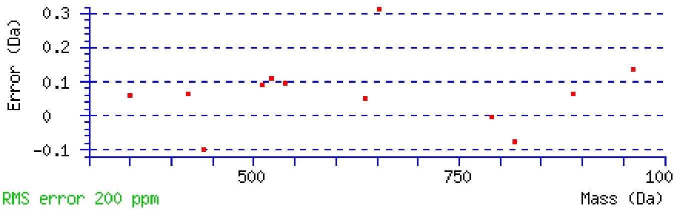
Match to Query 4753: 1326.613480 from(664.314016,2+) index(3868)
Title: Elution from: 35.652 to 35.652 scan no 4841 cid35.00 polarity:+
Data file 0-2_3.mgf

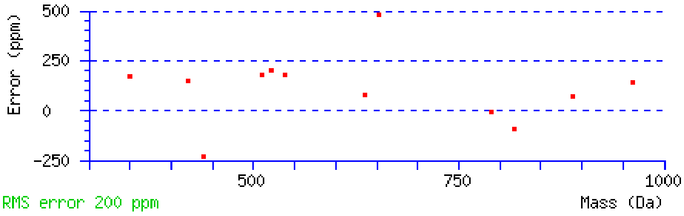
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1326.6145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.0002
Matches : 12/94 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	89.0363	45.0218			71.0258	36.0165	S					12
2	237.1018	119.0545			219.0912	110.0492	F	1239.5927	620.3000	1221.5691	611.2882	11
3	295.1203	148.0638			277.1097	139.0585	G	1091.5272	546.2673	1073.5036	537.2555	10
4	367.1544	184.0809			349.1439	175.0756	A	1033.5087	517.2580	1015.4851	508.2462	9
5	***439.1886***	220.0979			421.1780	211.0926	A	***961.4746***	481.2409	943.4510	472.2291	8
6	***539.2540***	270.1307			521.2435	261.1254	V	***889.4404***	445.2239	871.4168	436.2121	7
7	***653.3351***	327.1712			635.3246	318.1659	I	***789.3750***	395.1911	771.3514	386.1793	6
8	***817.3955***	409.2014			799.3849	400.1961	Y	675.2939	338.1506	657.2703	329.1388	5
9	933.4325	467.2199	915.4089	458.2081	915.4219	458.2146	N	***511.2335***	256.1204	493.2099	247.1086	4
10	1049.4695	525.2384	1031.4459	516.2266	1031.4589	516.2331	N	395.1965	198.1019	377.1729	189.0901	3
11	1179.5221	590.2647	1161.4986	581.2529	1161.5116	581.2594	Q	279.1595	140.0834	261.1359	131.0716	2
12							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of SFGAAVIYNNQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G39010.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.5	1326.6145	-0.0010	SFGAAVIYNNQK
31.5	1326.6144	-0.0010	DFIRQFAAESK
15.4	1326.6144	-0.0010	YVDKDFIAANR
3.6	1326.6122	0.0013	NQNGVQIPPDTK
1.8	1326.6109	0.0026	LVMMSNTGRIR
1.2	1326.6138	-0.0003	KMMVLTQMSTK

AT2G39280.1

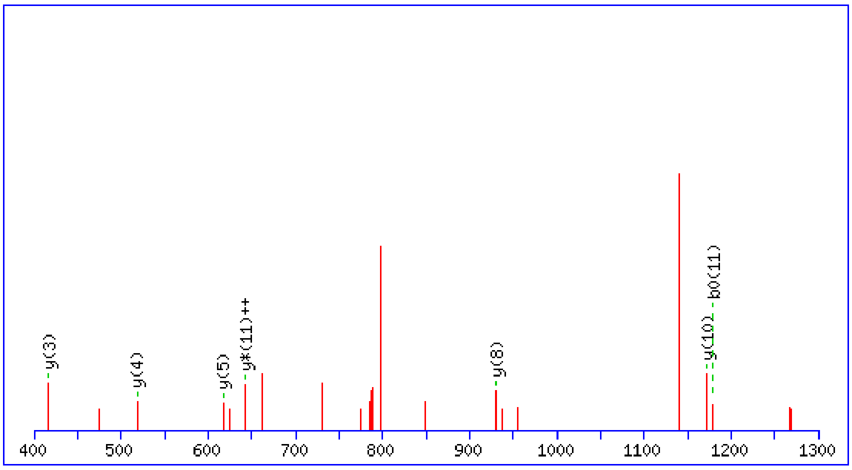
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKIEQLEQGVTELR**
Found in **AT2G39280.1** in **TAIR_Arabidopsis**, Symbols: | RAB GTPase activator | chr2:16409079-16413728 REVERSE

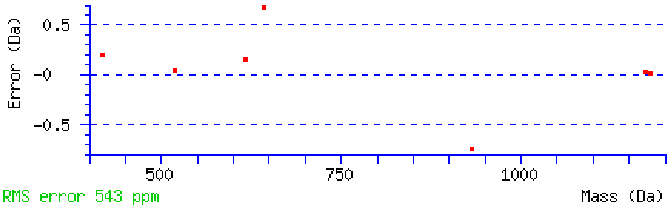
Match to Query 7255: 1612.876228 from(807.445390,2+) index(7377)
Title: Elution from: 67.405 to 67.405 scan no 9718 cid35.00 polarity:+
Data file D1d-2_1.mgf

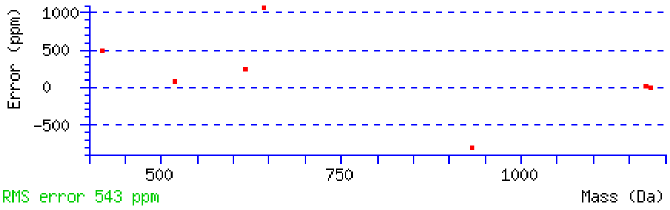
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1612.8784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.041
Matches : 7/144 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							14
2	200.1394	100.5733	183.1128	92.0600			K	1542.8486	771.9279	1525.8221	763.4147	1524.8380	762.9227	13
3	313.2234	157.1153	296.1969	148.6021			I	1414.7536	707.8805	1397.7271	699.3672	1396.7431	698.8752	12
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	E	1301.6696	651.3384	1284.6430	642.8251	1283.6590	642.3331	11
5	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	Q	***1172.6270***	586.8171	1155.6004	578.3039	1154.6164	577.8118	10
6	683.4087	342.2080	666.3821	333.6947	665.3981	333.2027	L	1044.5684	522.7878	1027.5419	514.2746	1026.5578	513.7826	9
7	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	E	***931.4843***	466.2458	914.4578	457.7325	913.4738	457.2405	8
8	940.5098	470.7585	923.4833	462.2453	922.4993	461.7533	Q	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	7
9	997.5313	499.2693	980.5047	490.7560	979.5207	490.2640	G	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
10	1096.5997	548.8035	1079.5732	540.2902	1078.5891	539.7982	V	***617.3617***	309.1845	600.3352	300.6712	599.3511	300.1792	5
11	1197.6474	599.3273	1180.6208	590.8141	1179.6368	590.3220	T	***518.2933***	259.6503	501.2667	251.1370	500.2827	250.6450	4
12	1326.6900	663.8486	1309.6634	655.3354	1308.6794	654.8433	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
13	1439.7740	720.3907	1422.7475	711.8774	1421.7635	711.3854	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AKIEQLEQGVTELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G39280.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.5	1612.8784	-0.0022	AKIEQLEQGVTELR
7.6	1612.8719	0.0043	RAGSHLLTAKPTSMK
0.8	1612.8784	-0.0021	LPSASAKASSPKAAAEK
0.6	1612.8766	-0.0003	SPFWKLLYERFK

AT2G39460.1

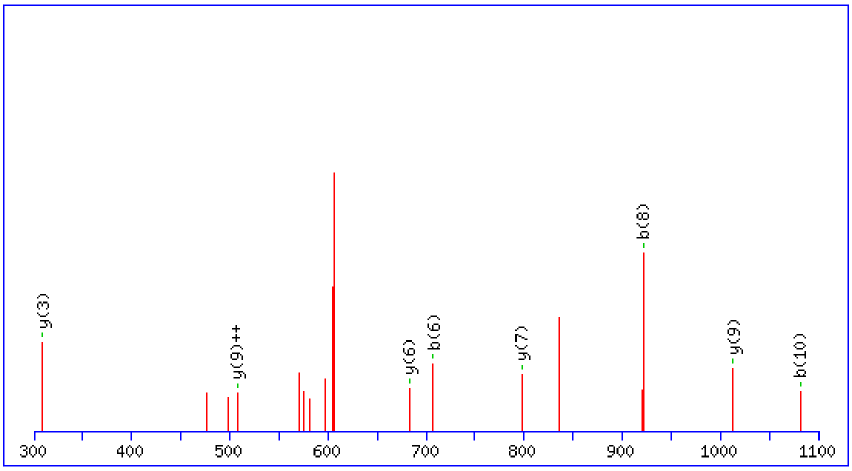
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNTLIRPDGTK**
Found in **AT2G39460.1** in **TAIR_Arabidopsis**, Symbols: RPL23A, ATRPL23A | ATRPL23A (RIBOSOMAL PROTEIN L23A); RNA binding / structural constituent of ribosome | chr2:16482127-16482982 FORWARD

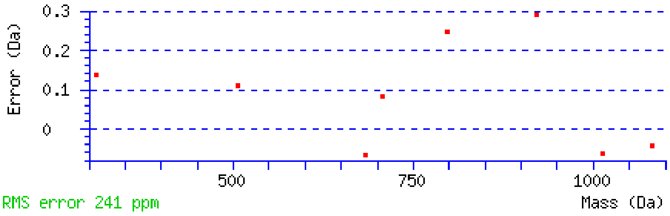
Match to Query 4600: 1228.634914 from(615.324733,2+) index(1453)
Title: Elution from: 19.742 to 19.742 scan no 1969 cid35.00 polarity:+
Data file D6h-1_1.mgf

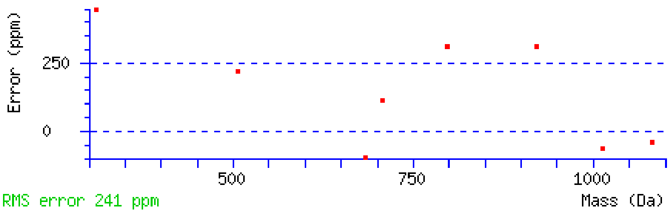
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1228.6352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0063
Matches : 8/112 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							11
2	217.1097	109.0585	199.0861	100.0467			N	1129.5770	565.2921	1111.5534	556.2804	1111.5665	556.2869	10
3	319.1544	160.0809	301.1309	151.0691	301.1439	151.0756	T	***1013.5400***	507.2737	995.5164	498.2619	995.5295	498.2684	9
4	433.2355	217.1214	415.2120	208.1096	415.2250	208.1161	L	911.4953	456.2513	893.4717	447.2395	893.4847	447.2460	8
5	547.3166	274.1620	529.2930	265.1502	529.3061	265.1567	I	***797.4142***	399.2107	779.3906	390.1990	779.4036	390.2055	7
6	***707.4059***	354.2066	689.3823	345.1948	689.3953	345.2013	R	***683.3331***	342.1702	665.3095	333.1584	665.3225	333.1649	6
7	805.4557	403.2315	787.4321	394.2197	787.4451	394.2262	P	523.2439	262.1256	505.2203	253.1138	505.2333	253.1203	5
8	***921.4797***	461.2435	903.4561	452.2317	903.4691	452.2382	D	425.1941	213.1007	407.1705	204.0889	407.1835	204.0954	4
9	979.4982	490.2527	961.4746	481.2409	961.4876	481.2474	G	***309.1701***	155.0887	291.1465	146.0769	291.1595	146.0834	3
10	***1081.5429***	541.2751	1063.5193	532.2633	1063.5323	532.2698	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VNTLIRPDGTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G39460.1

Score	Mr(calc)	Delta	Sequence
30.9	1228.6352	-0.0003	VNTLIRPDGTK
15.1	1228.6379	-0.0029	SSEHRVVLRK
5.1	1228.6352	-0.0003	LVQKELEAQR
4.3	1228.6381	-0.0032	MTEVLLLPGTK
4.2	1228.6374	-0.0025	IYGAPPAERLK
3.4	1228.6352	-0.0003	RPTIEKGSPTK
2.7	1228.6381	-0.0032	ILDEVKMLEK
2.0	1228.6325	0.0024	EKIGIDDLSVK
1.8	1228.6352	-0.0003	ALEENQILRK
1.8	1228.6352	-0.0003	ESQEVIKPRK

Mascot: http://www.matrixscience.com/

AT2G39730.1

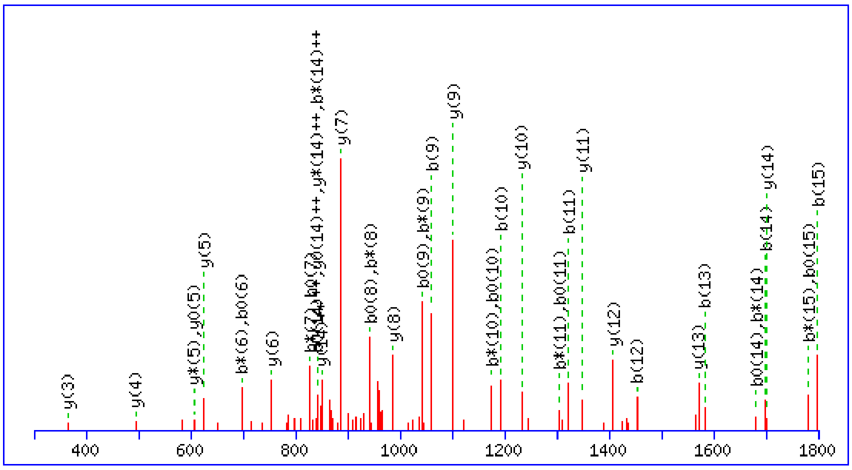
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMEYGNMLVMEQENVK**
Found in **AT2G39730.1** in **TAIR_Arabidopsis**, Symbols: RCA | RCA (RUBISCO ACTIVASE) | chr2:16578029-16580423 REVERSE

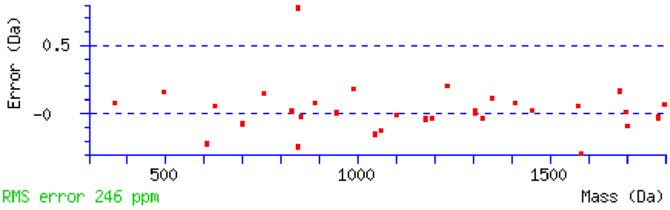
Match to Query 8978: 1946.830714 from(974.422633,2+) index(7688)
Title: Elution from: 68.505 to 68.505 scan no 10135 cid35.00 polarity:+
Data file D6h-1_3.mgf

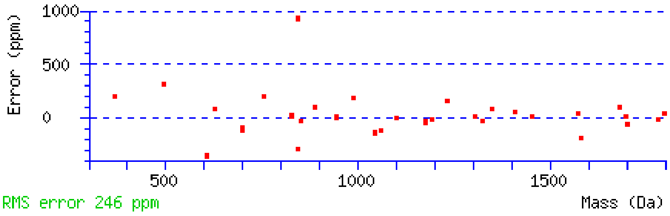
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1946.8296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 1.1e-011
Matches : 42/160 fragment ions using 37 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							16
2	247.1259	124.0666					M	1833.7558	917.3815	1815.7322	908.3698	1815.7453	908.3763	15
3	377.1655	189.0864			359.1550	180.0811	E	***1701.7183***	851.3628	1683.6947	842.3510	1683.7077	842.3575	14
4	541.2259	271.1166			523.2153	262.1113	Y	***1571.6787***	786.3430	1553.6551	777.3312	1553.6681	777.3377	13
5	599.2444	300.1258			581.2338	291.1205	G	***1407.6183***	704.3128	1389.5947	695.3010	1389.6077	695.3075	12
6	715.2814	358.1443	697.2578	349.1325	697.2708	349.1390	N	***1349.5998***	675.3035	1331.5762	666.2917	1331.5892	666.2983	11
7	847.3189	424.1631	829.2953	415.1513	829.3083	415.1578	M	***1233.5628***	617.2850	1215.5392	608.2733	1215.5522	608.2798	10
8	961.4000	481.2036	943.3764	472.1918	943.3894	472.1984	L	***1101.5253***	551.2663	1083.5017	542.2545	1083.5147	542.2610	9
9	**1061.4655**	531.2364	1043.4419	522.2246	1043.4549	522.2311	V	***987.4442***	494.2257	969.4206	485.2139	969.4336	485.2205	8
10	**1193.5030**	597.2551	1175.4794	588.2433	1175.4924	588.2498	M	***887.3787***	444.1930	869.3552	435.1812	869.3682	435.1877	7
11	**1323.5426**	662.2749	1305.5190	653.2631	1305.5320	653.2697	E	***755.3412***	378.1742	737.3176	369.1625	737.3307	369.1690	6
12	**1453.5952**	727.3013	1435.5717	718.2895	1435.5847	718.2960	Q	***625.3016***	313.1544	607.2780	304.1426	607.2910	304.1492	5
13	**1583.6349**	792.3211	1565.6113	783.3093	1565.6243	783.3158	E	***495.2489***	248.1281	477.2254	239.1163	477.2384	239.1228	4
14	**1699.6719**	850.3396	1681.6483	841.3278	1681.6613	841.3343	N	***365.2093***	183.1083	347.1857	174.0965			3
15	**1799.7373**	900.3723	1781.7137	891.3605	1781.7268	891.3670	V	249.1723	125.0898	231.1487	116.0780			2
16							K	149.1069	75.0571	131.0833	66.0453			1





AT2G39730.1

NCBI **BLAST** search of LMEYGNMLVMEQENVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
117.3	1946.8296	0.0011	LMEYGNMLVMEQENVK
10.4	1946.8341	-0.0034	QIRCNWATKGATSGEDK
10.2	1946.8255	0.0052	DTAAWNSMVHGYLQFGK
8.6	1946.8255	0.0052	DYSDHMALVRAFEGWK
4.3	1946.8265	0.0042	LCKSQDLTESLSDESSK

AT2G40010.1

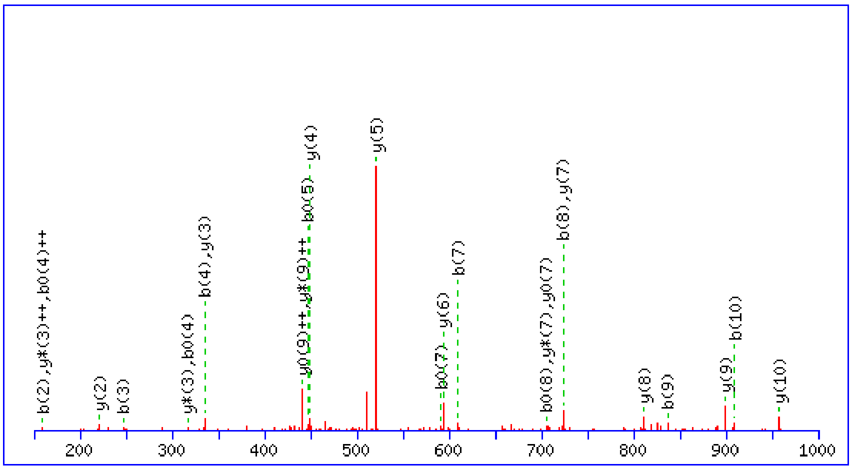
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSSEAALLAK**
Found in **AT2G40010.1** in **TAIR_Arabidopsis**, Symbols: | 60S acidic ribosomal protein P0 (RPP0A) | chr2:16715656-16717526 REVERSE

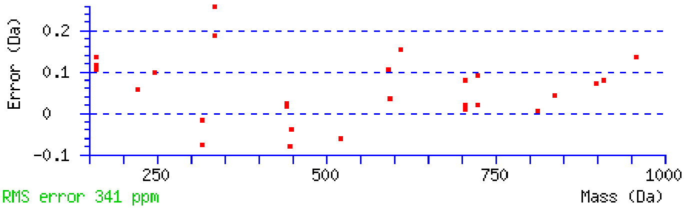
Match to Query 2996: 1056.546884 from(529.280718,2+) index(2382)
Title: Elution from: 25.735 to 25.735 scan no 2999 cid35.00 polarity:+
Data file 0-1_3.mgf

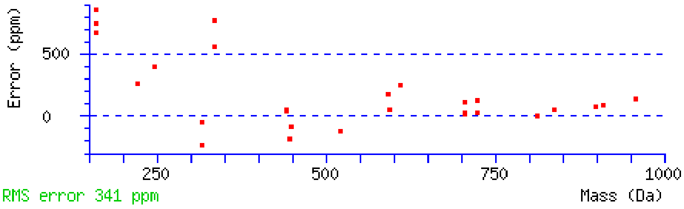
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.5459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 96 **Expect:** 2.5e-009
Matches : 27/84 fragment ions using 24 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400			V							11
2	**159.0912**	80.0492			G	***957.4878***	479.2475	939.4642	470.2357	939.4772	470.2422	10
3	**247.1203**	124.0638	229.1097	115.0585	S	***899.4693***	450.2383	881.4457	441.2265	881.4587	441.2330	9
4	**335.1493**	168.0783	317.1388	159.0730	S	***811.4402***	406.2237	793.4166	397.2120	793.4296	397.2185	8
5	465.1890	233.0981	447.1784	224.0928	E	***723.4111***	362.2092	705.3876	353.1974	705.4006	353.2039	7
6	537.2231	269.1152	519.2126	260.1099	A	***593.3715***	297.1894	575.3479	288.1776			6
7	**609.2573**	305.1323	591.2467	296.1270	A	***521.3374***	261.1723	503.3138	252.1605			5
8	**723.3384**	362.1728	705.3278	353.1675	L	***449.3032***	225.1552	431.2796	216.1435			4
9	**837.4195**	419.2134	819.4089	410.2081	L	***335.2221***	168.1147	317.1985	159.1029			3
10	**909.4536**	455.2304	891.4431	446.2252	A	***221.1410***	111.0741	203.1174	102.0624			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VGSSEAALLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G40010.1

Score	Mr(calc)	Delta	Sequence
95.9	1056.5459	0.0009	VGSSEAALLAK
17.8	1056.5482	-0.0013	LFALDDKPK
16.6	1056.5459	0.0009	VSAEEKAALK
11.7	1056.5459	0.0010	GSTLQDLALK
10.0	1056.5482	-0.0013	LPGGDLYLAK
8.5	1056.5482	-0.0013	VFITDNLPK
8.5	1056.5482	-0.0013	VNLFLSEPK
8.3	1056.5459	0.0010	GVKSVDVDVK
6.6	1056.5459	0.0009	LSSEVLAGAAK
6.0	1056.5459	0.0009	QLAEEKLSK

AT2G40290.1

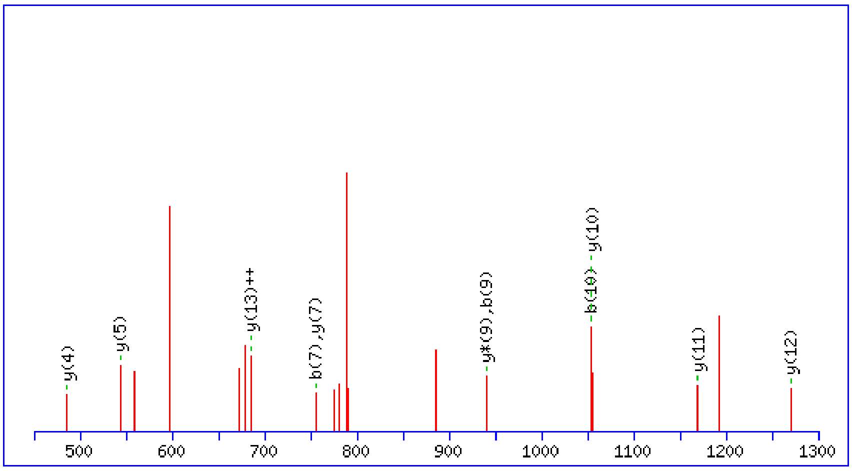
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILVTDPDSVLGPLTR**
Found in **AT2G40290.1** in **TAIR_Arabidopsis**, Symbols: | eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative | chr2:16836108-16837967 REVERSE

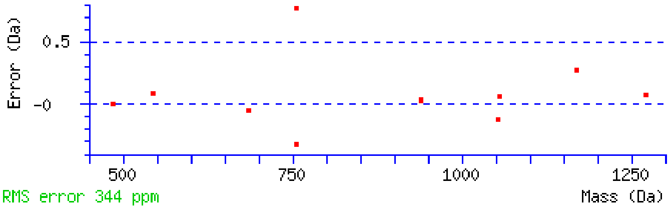
Match to Query 7257: 1594.890686 from(798.452619,2+) index(8926)
Title: Elution from: 78.454 to 78.454 scan no 11917 cid35.00 polarity:+
Data file D1d-3_2.mgf

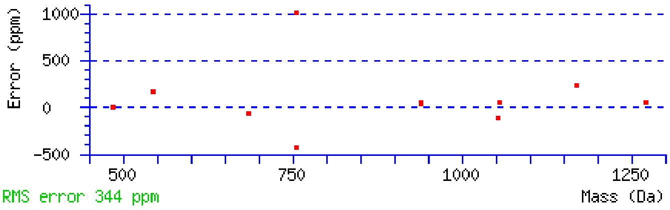
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1594.8930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0011
Matches : 11/132 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			I							15
2	227.1754	114.0913			L	1482.8162	741.9118	1465.7897	733.3985	1464.8057	732.9065	14
3	326.2438	163.6255			V	1369.7322	685.3697	1352.7056	676.8564	1351.7216	676.3644	13
4	427.2915	214.1494	409.2809	205.1441	T	***1270.6638***	635.8355	1253.6372	627.3222	1252.6532	626.8302	12
5	542.3184	271.6629	524.3079	262.6576	D	***1169.6161***	585.3117	1152.5895	576.7984	1151.6055	576.3064	11
6	639.3712	320.1892	621.3606	311.1840	P	***1054.5891***	527.7982	1037.5626	519.2849	1036.5786	518.7929	10
7	**754.3981**	377.7027	736.3876	368.6974	D	957.5364	479.2718	940.5098	470.7585	939.5258	470.2665	9
8	841.4302	421.2187	823.4196	412.2134	S	842.5094	421.7584	825.4829	413.2451	824.4989	412.7531	8
9	**940.4986**	470.7529	922.4880	461.7476	V	***755.4774***	378.2423	738.4509	369.7291	737.4668	369.2371	7
10	**1053.5827**	527.2950	1035.5721	518.2897	L	656.4090	328.7081	639.3824	320.1949	638.3984	319.7028	6
11	1110.6041	555.8057	1092.5936	546.8004	G	***543.3249***	272.1661	526.2984	263.6528	525.3144	263.1608	5
12	1207.6569	604.3321	1189.6463	595.3268	P	***486.3035***	243.6554	469.2769	235.1421	468.2929	234.6501	4
13	1320.7409	660.8741	1302.7304	651.8688	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
14	1421.7886	711.3979	1403.7781	702.3927	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
15					R	175.1190	88.0631	158.0924	79.5498			1





AT2G40290.1

NCBI **BLAST** search of ILVTDPDSVLGPLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.8	1594.8930	-0.0024	ILVTDPDSVLGPLTR
0.3	1594.8912	-0.0005	KLYLVYSFFFLR
0.3	1594.8939	-0.0032	KLCLAFSAMGKIIK
0.1	1594.8885	0.0022	HIPHIRFYKAWK

AT2G40490.1

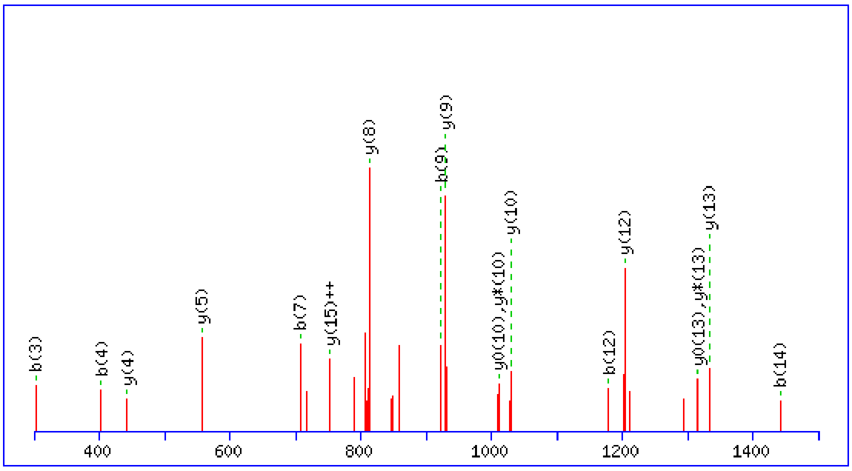
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIAVQGNVDPGVLFGSK**
Found in **AT2G40490.1** in **TAIR_Arabidopsis**, Symbols: HEME2 | HEME2; uroporphyrinogen decarboxylase | chr2:16920039-16922066 FORWARD

Match to Query 8000: 1734.824672 from(868.419612,2+) index(8081)
Title: Elution from: 71.490 to 71.490 scan no 10796 cid35.00 polarity:+
Data file 0-2_3.mgf

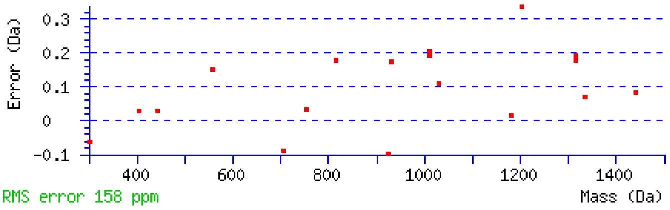
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

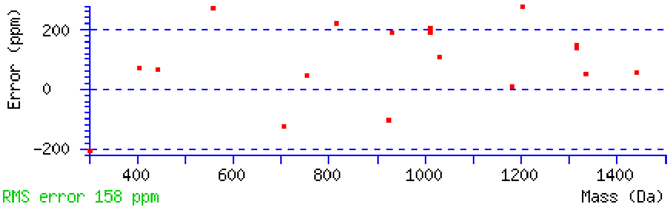


Monoisotopic mass of neutral peptide Mr(calc): 1734.8297
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.4e-006
Matches : 18/182 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							17
2	231.1124	116.0598			213.1018	107.0545	I	1619.8130	810.4101	1601.7894	801.3983	1601.8024	801.4049	16
3	***303.1465***	152.0769			285.1359	143.0716	A	1505.7319	753.3696	1487.7083	744.3578	1487.7213	744.3643	15
4	***403.2120***	202.1096			385.2014	193.1043	V	1433.6977	717.3525	1415.6742	708.3407	1415.6872	708.3472	14
5	533.2646	267.1359	515.2410	258.1241	515.2540	258.1307	Q	***1333.6323***	667.3198	1315.6087	658.3080	1315.6217	658.3145	13
6	591.2831	296.1452	573.2595	287.1334	573.2725	287.1399	G	***1203.5797***	602.2935	1185.5561	593.2817	1185.5691	593.2882	12
7	***707.3201***	354.1637	689.2965	345.1519	689.3095	345.1584	N	1145.5612	573.2842	1127.5376	564.2724	1127.5506	564.2789	11
8	807.3855	404.1964	789.3620	395.1846	789.3750	395.1911	V	***1029.5242***	515.2657	1011.5006	506.2539	1011.5136	506.2604	10
9	***923.4095***	462.2084	905.3859	453.1966	905.3990	453.2031	D	***929.4587***	465.2330	911.4351	456.2212	911.4481	456.2277	9
10	1021.4593	511.2333	1003.4357	502.2215	1003.4488	502.2280	P	***813.4347***	407.2210	795.4111	398.2092	795.4242	398.2157	8
11	1079.4778	540.2425	1061.4542	531.2308	1061.4673	531.2373	G	715.3849	358.1961	697.3613	349.1843	697.3744	349.1908	7
12	***1179.5433***	590.2753	1161.5197	581.2635	1161.5327	581.2700	V	657.3664	329.1869	639.3428	320.1751	639.3559	320.1816	6
13	1293.6244	647.3158	1275.6008	638.3040	1275.6138	638.3105	L	***557.3010***	279.1541	539.2774	270.1423	539.2904	270.1488	5
14	***1441.6898***	721.3485	1423.6662	712.3368	1423.6793	712.3433	F	***443.2199***	222.1136	425.1963	213.1018	425.2093	213.1083	4
15	1499.7083	750.3578	1481.6847	741.3460	1481.6977	741.3525	G	295.1544	148.0809	277.1309	139.0691	277.1439	139.0756	3
16	1587.7374	794.3723	1569.7138	785.3605	1569.7268	785.3670	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT2G40490.1





NCBI **BLAST** search of DIAVQGNVDPGVLFGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.0	1734.8297	-0.0050	DIAVQGNVDPGVLFGSK
0.9	1734.8274	-0.0028	VEVEDKNVLQISGER

Mascot: http://www.matrixscience.com/

AT2G40510.1

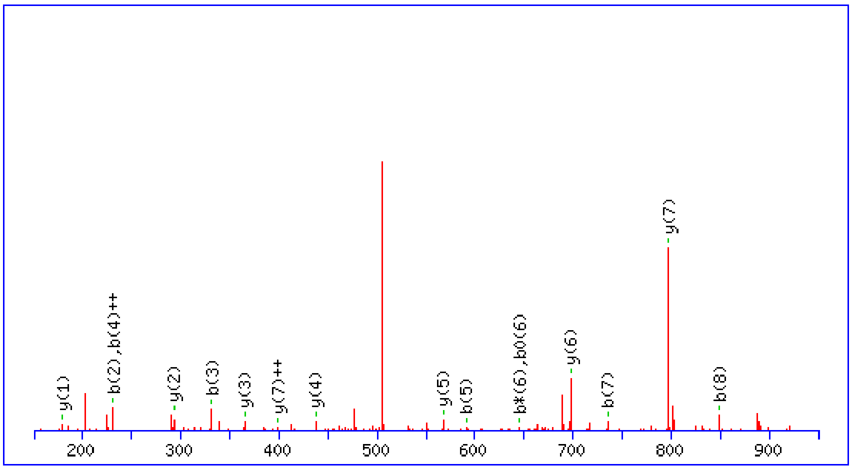
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIVEQAAIR**
Found in **AT2G40510.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S26 (RPS26A) | chr2:16925584-16926701 FORWARD

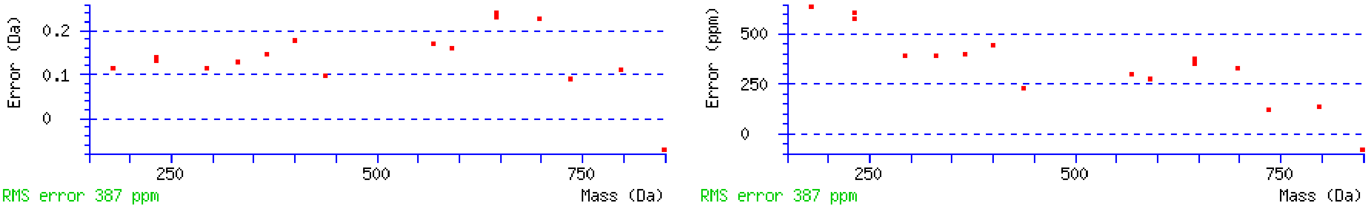
Match to Query 2880: 1026.525782 from(514.270167,2+) index(2771)
Title: Elution from: 29.232 to 29.232 scan no 3473 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1026.5250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00037
Matches : 16/80 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	**231.1254**	116.0663	213.1018	107.0545			I	911.4953	456.2513	893.4717	447.2395	893.4847	447.2460	8
3	**331.1908**	166.0990	313.1672	157.0873			V	***797.4142***	399.2107	779.3906	390.1990	779.4036	390.2055	7
4	461.2304	231.1189	443.2069	222.1071	443.2199	222.1136	E	***697.3488***	349.1780	679.3252	340.1662	679.3382	340.1727	6
5	**591.2831**	296.1452	573.2595	287.1334	573.2725	287.1399	Q	***567.3091***	284.1582	549.2856	275.1464			5
6	663.3172	332.1623	645.2937	323.1505	645.3067	323.1570	A	***437.2565***	219.1319	419.2329	210.1201			4
7	**735.3514**	368.1793	717.3278	359.1675	717.3408	359.1741	A	***365.2223***	183.1148	347.1988	174.1030			3
8	**849.4325**	425.2199	831.4089	416.2081	831.4219	416.2146	I	***293.1882***	147.0977	275.1646	138.0859			2
9							R	***179.1071***	90.0572	161.0835	81.0454			1



NCBI **BLAST** search of NIVEQAAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.8	1026.5250	0.0008	NIVEQAAIR

AT2G40510.1

8.5	1026.5277	-0.0019	NLNQPRIR
7.1	1026.5250	0.0008	GGLTVPSNLR
6.9	1026.5250	0.0007	NLDASKPLR
6.9	1026.5250	0.0008	VKVNSVDPR
4.1	1026.5250	0.0008	EQLLNQLR
3.3	1026.5273	-0.0015	NLEIWLAR
3.3	1026.5250	0.0008	VEQGLQLAR
2.8	1026.5250	0.0008	QQLQDIIR
0.3	1026.5250	0.0008	NGELQLALR

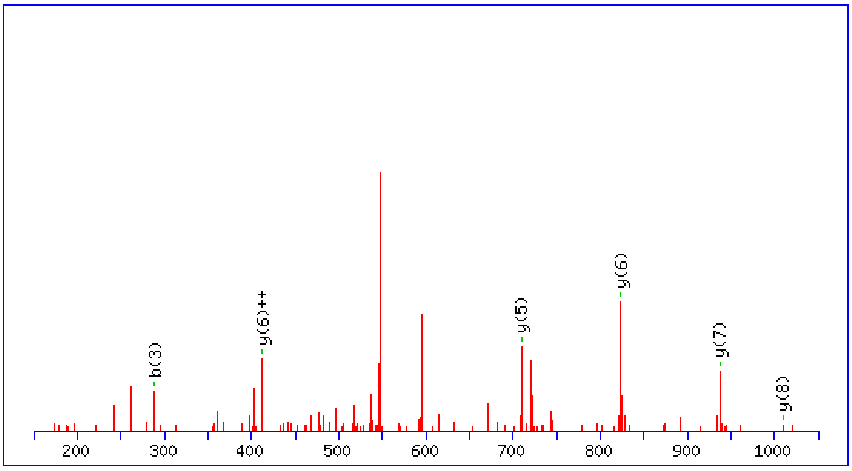
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TALIDMYFK**
Found in **AT2G40720.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:16994347-16996929 FORWARD

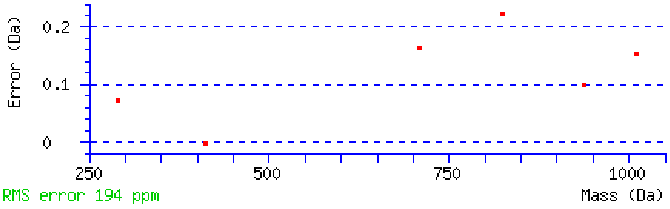
Match to Query 3136: 1110.530516 from(556.272534,2+) index(3641)
Title: Elution from: 37.759 to 37.759 scan no 4675 cid35.00 polarity:+
Data file D12h-2_1.mgf

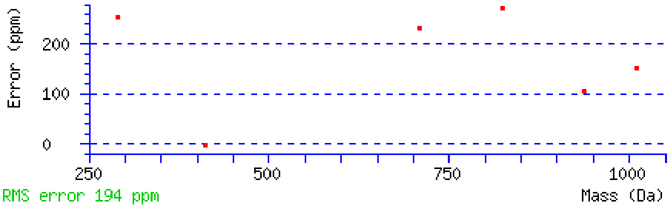
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1110.5280
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.039
Matches : 6/72 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							9
2	175.0861	88.0467	157.0756	79.0414	A	***1009.4905***	505.2489	991.4669	496.2371	991.4800	496.2436	8
3	289.1672	145.0873	271.1567	136.0820	L	***937.4564***	469.2318	919.4328	460.2200	919.4458	460.2265	7
4	403.2483	202.1278	385.2378	193.1225	I	***823.3753***	412.1913	805.3517	403.1795	805.3647	403.1860	6
5	519.2723	260.1398	501.2617	251.1345	D	***709.2942***	355.1507	691.2706	346.1389	691.2836	346.1454	5
6	651.3098	326.1586	633.2993	317.1533	M	593.2702	297.1387	575.2466	288.1269			4
7	815.3702	408.1887	797.3596	399.1835	Y	461.2327	231.1200	443.2091	222.1082			3
8	963.4356	482.2215	945.4251	473.2162	F	297.1723	149.0898	279.1487	140.0780			2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TALIDMYFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G40720.1

21.9	1110.5280	0.0026	TALIDMYFK
8.1	1110.5331	-0.0026	EDLKEVTHK
5.0	1110.5331	-0.0026	GDIAEILDPR
2.4	1110.5306	-0.0001	VMFNTAFIR
1.2	1110.5284	0.0021	ATLCSRYVK
0.8	1110.5331	-0.0026	TGDVVTIEHK
0.3	1110.5284	0.0021	MHPSALAQVK

AT2G41530.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLSENFSQLDTTK**
Found in **AT2G41530.1** in **TAIR_Arabidopsis**, Symbols: ATSFGH | ATSFGH (ARABIDOPSIS THALIANA S-FORMYLGLUTATHIONE HYDROLASE); S-formylglutathione hydrolase/ hydrolase, acting on ester bonds | chr2:17330734-17332508 REVERSE

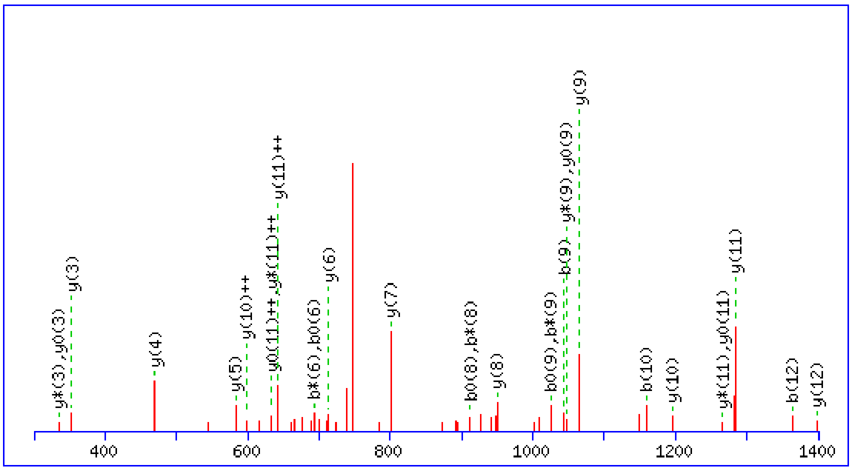
Match to Query 6269: 1510.706390 from(756.360471,2+) index(5556)
Title: Elution from: 49.568 to 49.568 scan no 7044 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1400 Da Full range

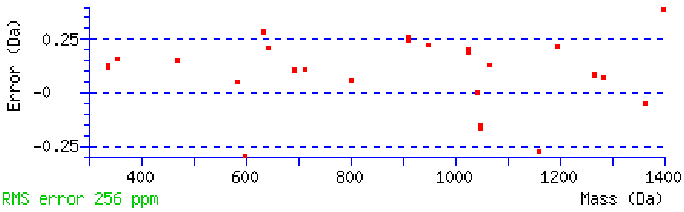
Label all possible matches ○ Label matches used for scoring ●

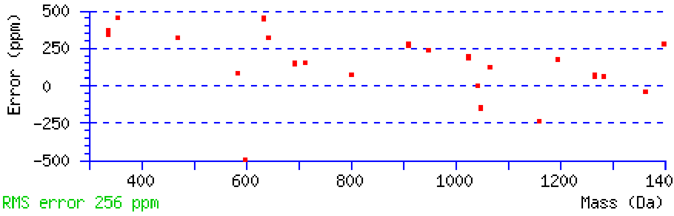
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1510.7091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 95 **Expect:** 2.7e-009
Matches : 29/130 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							13
2	229.1695	115.0884					L	***1397.6353***	699.3213	1379.6117	690.3095	1379.6248	690.3160	12
3	317.1985	159.1029			299.1880	150.0976	S	***1283.5542***	642.2808	1265.5306	633.2690	1265.5437	633.2755	11
4	447.2382	224.1227			429.2276	215.1174	E	***1195.5252***	598.2662	1177.5016	589.2544	1177.5146	589.2609	10
5	563.2752	282.1412	545.2516	273.1294	545.2646	273.1359	N	***1065.4855***	533.2464	1047.4619	524.2346	1047.4750	524.2411	9
6	711.3406	356.1739	693.3170	347.1622	693.3300	347.1687	F	***949.4485***	475.2279	931.4250	466.2161	931.4380	466.2226	8
7	799.3697	400.1885	781.3461	391.1767	781.3591	391.1832	S	***801.3831***	401.1952	783.3595	392.1834	783.3725	392.1899	7
8	929.4223	465.2148	911.3987	456.2030	911.4118	456.2095	Q	***713.3540***	357.1807	695.3304	348.1689	695.3435	348.1754	6
9	**1043.5034**	522.2553	1025.4798	513.2436	1025.4929	513.2501	L	***583.3014***	292.1543	565.2778	283.1425	565.2908	283.1490	5
10	**1159.5274**	580.2673	1141.5038	571.2555	1141.5168	571.2621	D	***469.2203***	235.1138	451.1967	226.1020	451.2097	226.1085	4
11	1261.5721	631.2897	1243.5485	622.2779	1243.5615	622.2844	T	***353.1963***	177.1018	335.1727	168.0900	335.1857	168.0965	3
12	**1363.6168**	682.3121	1345.5932	673.3003	1345.6063	673.3068	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LLSENFSQLDTTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G41530.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.4	1510.7091	-0.0027	LLSENFSQLDTTK
7.3	1510.7044	0.0020	MLEDQVAYLLQR
7.1	1510.7053	0.0011	KIEWACLMKMGK
5.8	1510.7100	-0.0036	LLEVACSMLGAFGK
3.9	1510.7044	0.0020	YSSVGLLAPNMQAK
3.6	1510.7048	0.0016	QCSSLVERLRDK
3.4	1510.7048	0.0016	VTCRQVAVAGTNSK
1.2	1510.7044	0.0020	ACSTNGVTTFLVPK
0.4	1510.7077	-0.0014	VTMEDMSTVVVKR
0.2	1510.7100	-0.0036	MKMEGISIKEWK

AT2G41550.1

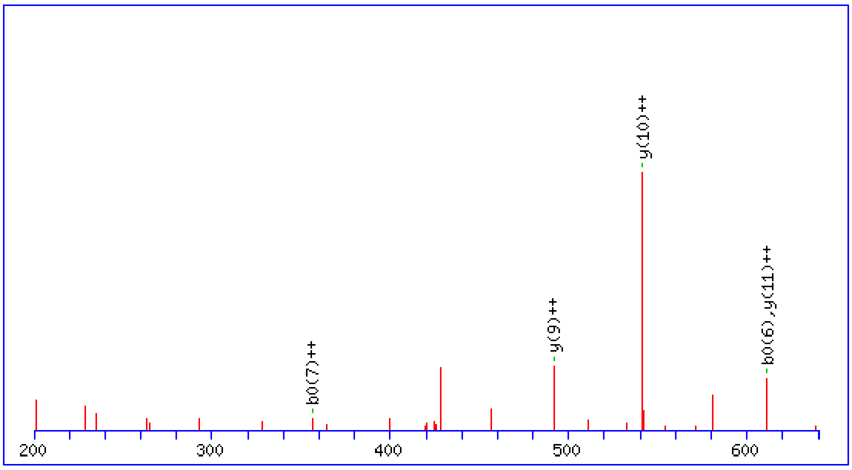
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHPEAVVKTVVK**
Found in **AT2G41550.1** in **TAIR_Arabidopsis**, Symbols: | transcription termination factor | chr2:17336164-17337908 REVERSE

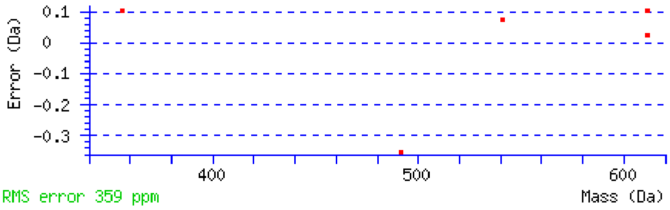
Match to Query 4732: 1308.696888 from(437.239572,3+) index(4485)
Title: Elution from: 41.163 to 41.163 scan no 5621 cid35.00 polarity:+
Data file D12h-3_2.mgf

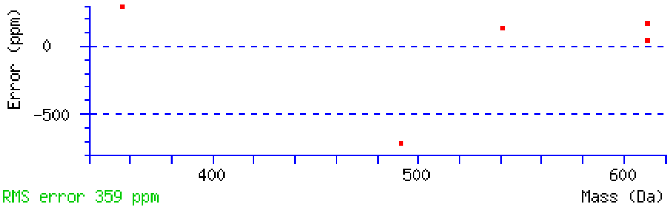
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 640 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1308.6978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.046
Matches : 5/112 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	229.0864	115.0468			211.0758	106.0415	H	1221.6760	611.3416	1203.6524	602.3299	1203.6654	602.3364	11
3	327.1362	164.0717			309.1256	155.0664	P	1081.6260	541.3166	1063.6024	532.3048	1063.6154	532.3114	10
4	457.1758	229.0915			439.1652	220.0862	E	983.5762	492.2917	965.5526	483.2799	965.5656	483.2865	9
5	529.2099	265.1086			511.1994	256.1033	A	853.5366	427.2719	835.5130	418.2601	835.5260	418.2666	8
6	629.2754	315.1413			611.2648	306.1360	V	781.5024	391.2548	763.4788	382.2431	763.4919	382.2496	7
7	729.3408	365.1741			711.3303	356.1688	V	681.4370	341.2221	663.4134	332.2103	663.4264	332.2168	6
8	859.4299	430.2186	841.4063	421.2068	841.4193	421.2133	K	581.3715	291.1894	563.3479	282.1776	563.3610	282.1841	5
9	961.4746	481.2409	943.4510	472.2291	943.4640	472.2356	T	451.2825	226.1449	433.2589	217.1331	433.2719	217.1396	4
10	1061.5400	531.2737	1043.5164	522.2619	1043.5295	522.2684	V	349.2378	175.1225	331.2142	166.1107			3
11	1161.6055	581.3064	1143.5819	572.2946	1143.5949	572.3011	V	249.1723	125.0898	231.1487	116.0780			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SHPEAVVKTVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G41550.1

Score	Mr(calc)	Delta	Sequence
17.7	1308.6978	-0.0009	SHPEAVVKTVVK
2.5	1308.6931	0.0038	ILGPRGLMPNPK
1.9	1308.6964	0.0004	MLKMLSILRR
0.4	1308.6974	-0.0005	AVELYSVIYIK
0.2	1308.7000	-0.0031	IIFSLFAAIGSR

AT2G41560.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQERQEGSK**
Found in **AT2G41560.1** in **TAIR_Arabidopsis**, Symbols: ACA4 | ACA4 (AUTO-INHIBITED CA(2+)-ATPASE, ISOFORM 4); calcium-transporting ATPase/ calmodulin binding | chr2:17339334-17344257 REVERSE

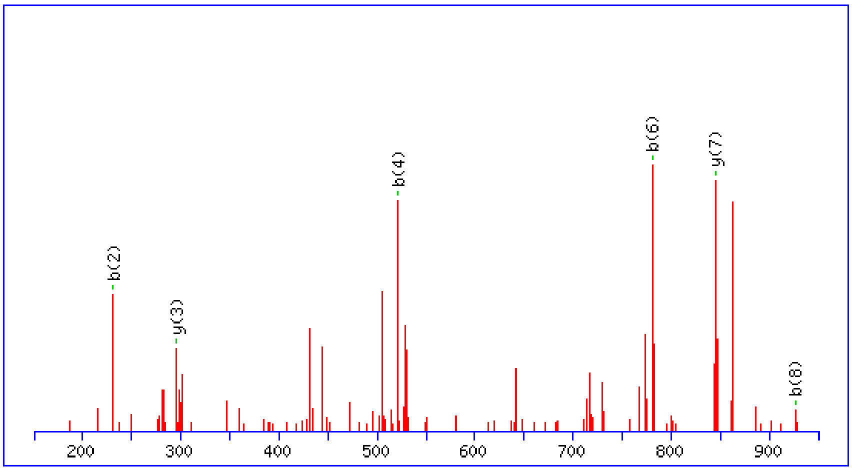
Match to Query 3027: 1074.487944 from(538.251248,2+) index(5488)
Title: Elution from: 49.396 to 49.396 scan no 6958 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

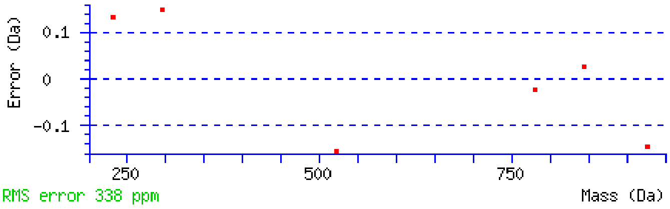
Label all possible matches ○ Label matches used for scoring ●

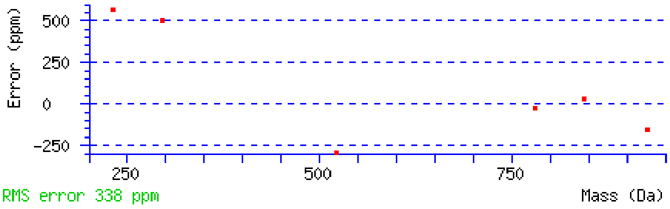
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1074.4864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.019
Matches : 6/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							9
2	***231.1254***	116.0663	213.1018	107.0545			Q	975.4282	488.2178	957.4047	479.2060	957.4177	479.2125	8
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	E	**845.3756**	423.1914	827.3520	414.1796	827.3650	414.1862	7
4	***521.2543***	261.1308	503.2307	252.1190	503.2437	252.1255	R	715.3360	358.1716	697.3124	349.1598	697.3254	349.1663	6
5	651.3069	326.1571	633.2833	317.1453	633.2963	317.1518	Q	555.2467	278.1270	537.2231	269.1152	537.2361	269.1217	5
6	***781.3465***	391.1769	763.3229	382.1651	763.3360	382.1716	E	425.1941	213.1007	407.1705	204.0889	407.1835	204.0954	4
7	839.3650	420.1862	821.3414	411.1744	821.3545	411.1809	G	**295.1544**	148.0809	277.1309	139.0691	277.1439	139.0756	3
8	***927.3941***	464.2007	909.3705	455.1889	909.3835	455.1954	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VQERQEGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G41560.1

27.1	1074.4864	0.0016	VQERQEGSK
8.6	1074.4861	0.0018	MPTWWGRK
3.1	1074.4893	-0.0014	IDDVEKSMK

Mascot: http://www.matrixscience.com/

AT2G41680.1

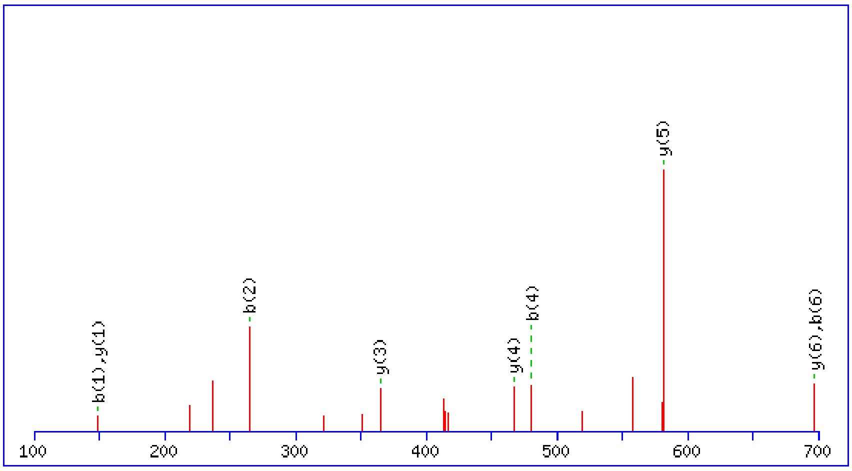
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDITLTK**
Found in **AT2G41680.1** in **TAIR_Arabidopsis**, Symbols: | thioredoxin reductase, putative / NADPH-dependent thioredoxin reductase, putative | chr2:17383427-17386106 REVERSE

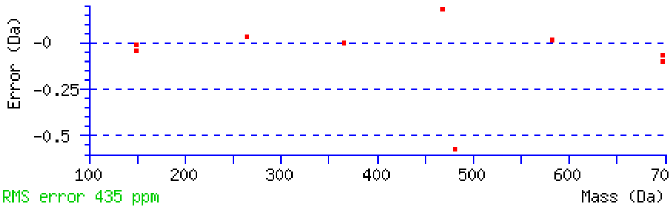
Match to Query 1278: 844.440738 from(423.227645,2+) index(4579)
Title: Elution from: 41.782 to 41.782 scan no 5761 cid35.00 polarity:+
Data file C7-3_3.mgf

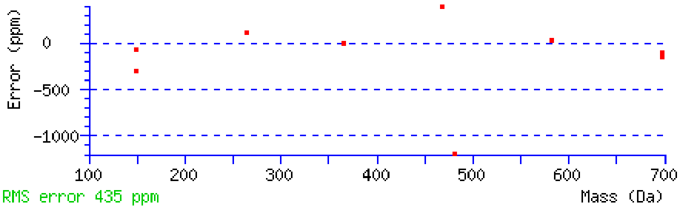
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 844.4406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0022
Matches : 9/56 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**149.0727**	75.0400			F							7
2	**265.0967**	133.0520	247.0861	124.0467	D	***697.3825***	349.1949	679.3589	340.1831	679.3719	340.1896	6
3	379.1778	190.0925	361.1672	181.0873	I	***581.3585***	291.1829	563.3349	282.1711	563.3479	282.1776	5
4	**481.2225**	241.1149	463.2120	232.1096	T	***467.2774***	234.1423	449.2538	225.1305	449.2668	225.1371	4
5	595.3036	298.1554	577.2930	289.1502	L	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
6	**697.3483**	349.1778	679.3378	340.1725	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
7					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FDITLTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.0	844.4406	0.0001	FDITLTK
24.1	844.4393	0.0015	MMVKVTK

AT2G41680.1

24.1	844.4384	0.0023	SSSTLTIK
24.1	844.4406	0.0001	TVYLVDK
19.1	844.4406	0.0001	SFLEITK
19.1	844.4406	0.0001	SFLETIK
18.8	844.4406	0.0001	FSEILTK
14.4	844.4411	-0.0003	QSRTLTK
11.4	844.4411	-0.0003	DRSIKSK
11.4	844.4406	0.0001	TFLLESK

AT2G41840.1

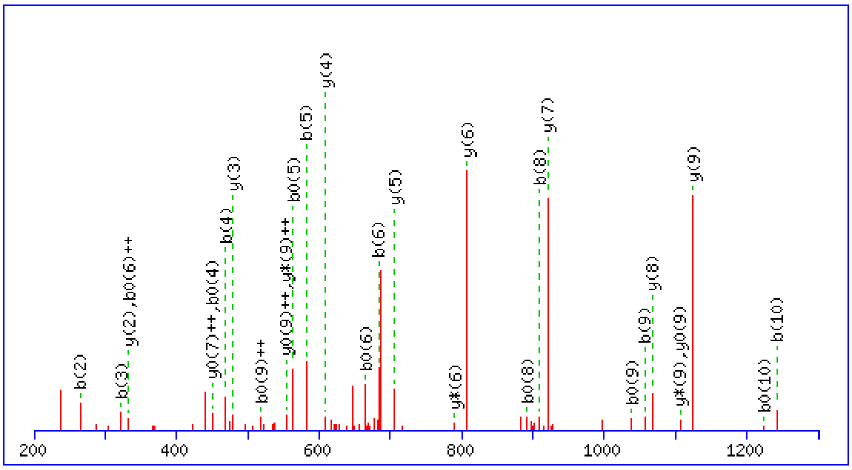
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYGFLTPEFWK**
Found in **AT2G41840.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S2 (RPS2C) | chr2:17467094-17468476 REVERSE

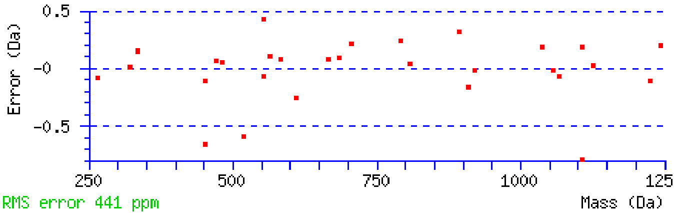
Match to Query 5098: 1387.679708 from(694.847130,2+) index(9410)
Title: Elution from: 86.518 to 86.518 scan no 13122 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

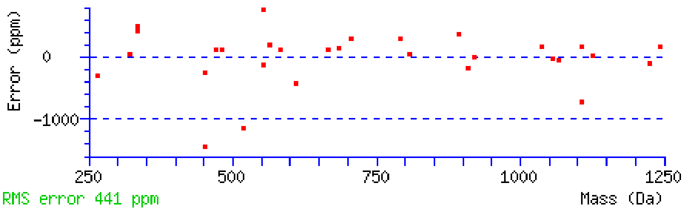


Monoisotopic mass of neutral peptide Mr(calc): 1387.6812
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 1.4e-006
Matches : 30/94 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							11
2	***265.1183***	133.0628	247.1077	124.0575	Y	1287.6408	644.3241	1270.6143	635.8108	1269.6303	635.3188	10
3	***322.1397***	161.5735	304.1292	152.5682	G	***1124.5775***	562.7924	1107.5510	554.2791	1106.5669	553.7871	9
4	***469.2082***	235.1077	451.1976	226.1024	F	***1067.5560***	534.2817	1050.5295	525.7684	1049.5455	525.2764	8
5	***582.2922***	291.6498	564.2817	282.6445	L	***920.4876***	460.7475	903.4611	452.2342	902.4771	451.7422	7
6	***683.3399***	342.1736	665.3293	333.1683	T	***807.4036***	404.2054	790.3770	395.6921	789.3930	395.2001	6
7	780.3927	390.7000	762.3821	381.6947	P	***706.3559***	353.6816	689.3293	345.1683	688.3453	344.6763	5
8	***909.4353***	455.2213	891.4247	446.2160	E	***609.3031***	305.1552	592.2766	296.6419	591.2926	296.1499	4
9	***1056.5037***	528.7555	1038.4931	519.7502	F	***480.2605***	240.6339	463.2340	232.1206			3
10	***1242.5830***	621.7951	1224.5724	612.7899	W	***333.1921***	167.0997	316.1656	158.5864			2
11					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 441 ppm



RMS error 441 ppm

NCBI **BLAST** search of TYGFLTPEFWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G41840.1

Score	Mr(calc)	Delta	Sequence
63.7	1387.6812	-0.0015	TYGFLTPEFWK
3.3	1387.6765	0.0032	AMVNGEEEKPLR

Mascot: http://www.matrixscience.com/

AT2G42130.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SALGQAATTLQQLPALIK**
Found in **AT2G42130.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Probable plastid-lipid-associated protein 13, chloroplast precursor (PAP13) [Arabidopsis Thaliana] (GB:Q8S9M1;GB:O48521;GB:Q84X37;GB:Q84X38;GB:Q84X39;GB:Q8GY49); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G

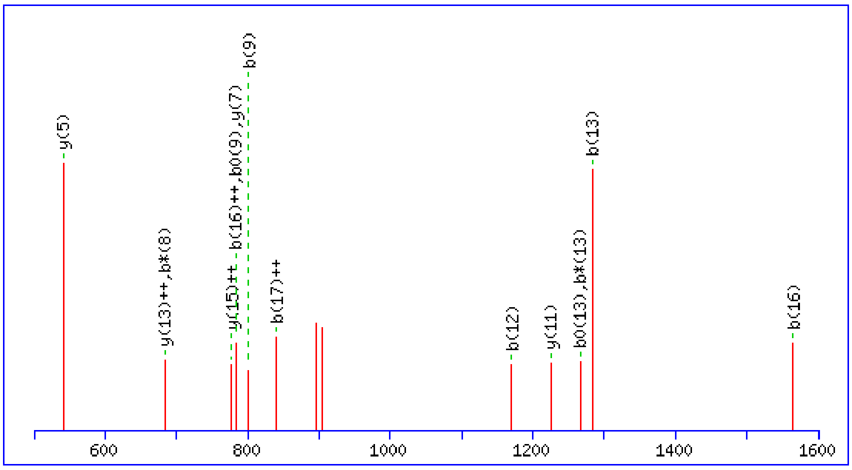
Match to Query 8242: 1823.056060 from(912.535306,2+) index(9650)
Title: Elution from: 94.247 to 94.247 scan no 13790 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

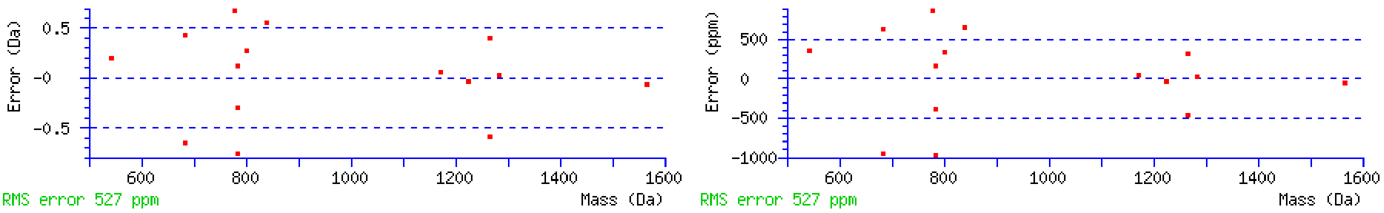
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1823.0516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00015
Matches : 15/178 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							18
2	159.0764	80.0418			141.0659	71.0366	A	1737.0269	869.0171	1720.0004	860.5038	1719.0163	860.0118	17
3	272.1605	136.5839			254.1499	127.5786	L	1665.9898	833.4985	1648.9632	824.9853	1647.9792	824.4932	16
4	329.1819	165.0946			311.1714	156.0893	G	1552.9057	776.9565	1535.8792	768.4432	1534.8952	767.9512	15
5	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	Q	1495.8843	748.4458	1478.8577	739.9325	1477.8737	739.4405	14
6	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	A	1367.8257	684.4165	1350.7991	675.9032	1349.8151	675.4112	13
7	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	A	1296.7886	648.8979	1279.7620	640.3846	1278.7780	639.8926	12
8	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	T	***1225.7515***	613.3794	1208.7249	604.8661	1207.7409	604.3741	11
9	***801.4101***	401.2087	784.3836	392.6954	783.3995	392.2034	T	1124.7038	562.8555	1107.6772	554.3422	1106.6932	553.8502	10
10	914.4942	457.7507	897.4676	449.2375	896.4836	448.7454	L	1023.6561	512.3317	1006.6295	503.8184			9
11	1042.5528	521.7800	1025.5262	513.2667	1024.5422	512.7747	Q	910.5720	455.7897	893.5455	447.2764			8
12	***1170.6113***	585.8093	1153.5848	577.2960	1152.6008	576.8040	Q	***782.5135***	391.7604	765.4869	383.2471			7
13	***1283.6954***	642.3513	1266.6688	633.8381	1265.6848	633.3461	L	654.4549	327.7311	637.4283	319.2178			6
14	1380.7482	690.8777	1363.7216	682.3644	1362.7376	681.8724	P	***541.3708***	271.1890	524.3443	262.6758			5
15	1451.7853	726.3963	1434.7587	717.8830	1433.7747	717.3910	A	444.3180	222.6627	427.2915	214.1494			4
16	***1564.8693***	**782.9383**	1547.8428	774.4250	1546.8588	773.9330	L	373.2809	187.1441	356.2544	178.6308			3
17	1677.9534	**839.4803**	1660.9269	830.9671	1659.9428	830.4751	I	260.1969	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT2G42130.1



NCBI **BLAST** search of SALGQAATTLQQLPALIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.1	1823.0516	0.0044	SALGQAATTLQQLPALIK
7.3	1823.0603	-0.0043	TGLLVAKAHSLRMWLK
3.2	1823.0516	0.0045	DVKPTNILINEKLQAK
3.2	1823.0516	0.0045	DVKPTNILLNEKLQAK

Mascot: http://www.matrixscience.com/

AT2G42370.1

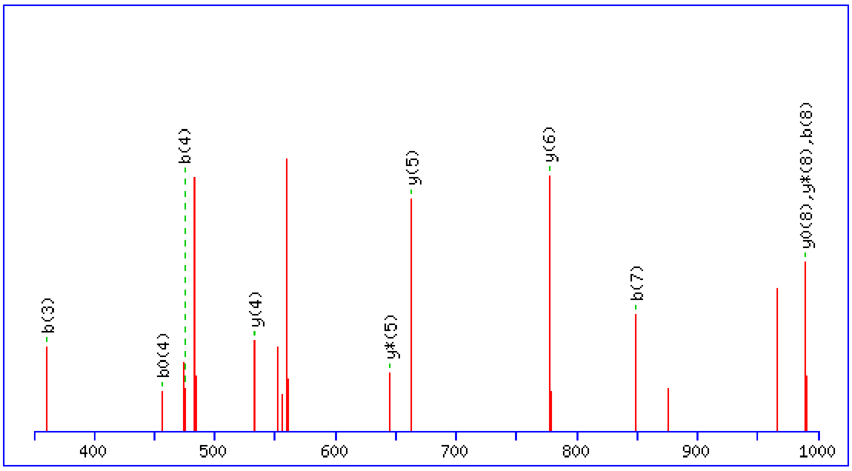
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDIIQQLHK**
Found in **AT2G42370.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58110.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63361.1) | chr2:17650412-17652611 FORWARD

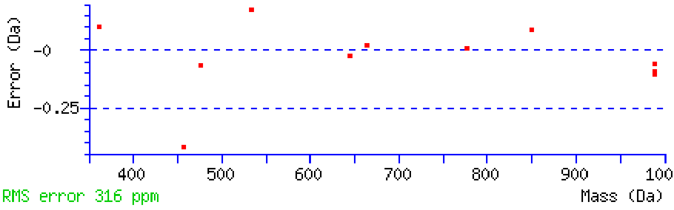
Match to Query 3186: 1136.560388 from(569.287470,2+) index(1235)
Title: Elution from: 20.814 to 20.814 scan no 1804 cid35.00 polarity:+
Data file D12h-2_2.mgf

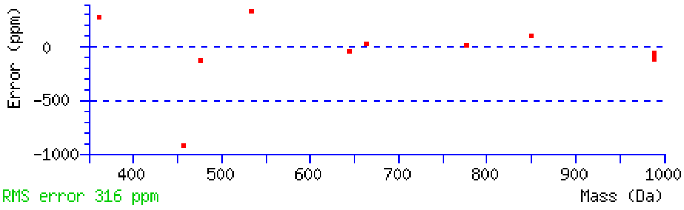
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1136.5618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.03
Matches : 11/74 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							9
2	247.0709	124.0391			229.0603	115.0338	D	1007.5295	504.2684	989.5059	495.2566	989.5189	495.2631	8
3	***361.1520***	181.0796			343.1414	172.0743	I	891.5055	446.2564	873.4819	437.2446			7
4	***475.2331***	238.1202			457.2225	229.1149	I	***777.4244***	389.2158	759.4008	380.2040			6
5	605.2857	303.1465	587.2621	294.1347	587.2752	294.1412	Q	***663.3433***	332.1753	645.3197	323.1635			5
6	735.3384	368.1728	717.3148	359.1610	717.3278	359.1675	Q	***533.2906***	267.1490	515.2671	258.1372			4
7	***849.4195***	425.2134	831.3959	416.2016	831.4089	416.2081	L	403.2380	202.1226	385.2144	193.1108			3
8	***989.4695***	495.2384	971.4459	486.2266	971.4589	486.2331	H	289.1569	145.0821	271.1333	136.0703			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EDIIQQLHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G42370.1

22.7	1136.5618	-0.0014	EDIIQQLHK
2.2	1136.5618	-0.0014	KKVNDAASYK
2.2	1136.5571	0.0033	LMLGNGRFSK
2.1	1136.5571	0.0033	RTPTMVYVR
1.5	1136.5578	0.0026	MATTMKGLLK
0.8	1136.5571	0.0033	FLSKQNVMR
0.6	1136.5618	-0.0014	DGLAKTIYSR
0.5	1136.5578	0.0026	VIEMKSKMK
0.4	1136.5618	-0.0014	FVTSITSVNR
0.2	1136.5618	-0.0014	EEHNLIGALK

AT2G42530.1

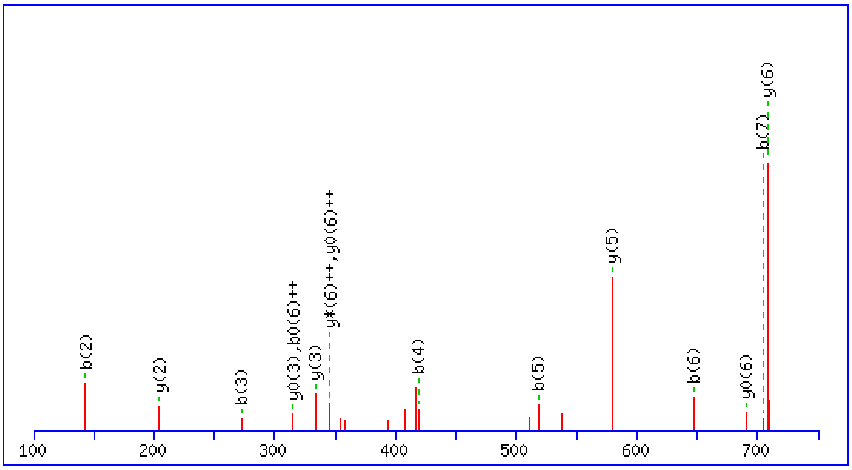
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAEFVEGK**
Found in **AT2G42530.1** in **TAIR_Arabidopsis**, Symbols: COR15B | COR15B | chr2:17716269-17716951 REVERSE

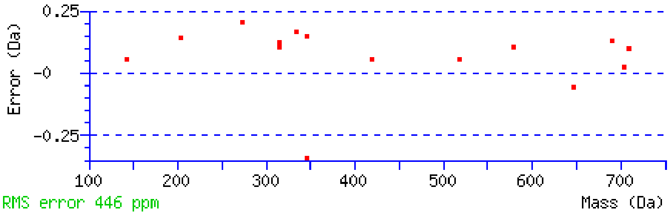
Match to Query 1314: 849.422786 from(425.718669,2+) index(782)
Title: Elution from: 13.626 to 13.626 scan no 1136 cid35.00 polarity:+
Data file D12h-1_2.mgf

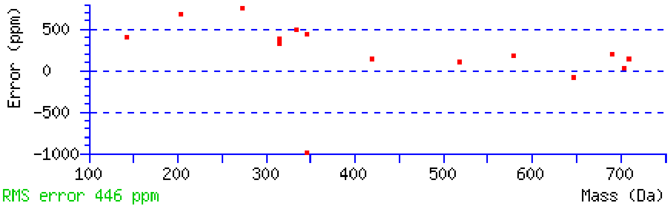
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 849.4232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 5.5e-006
Matches : 15/62 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							8
2	***143.0815***	72.0444			A	779.3934	390.2003	762.3668	381.6871	761.3828	381.1951	7
3	***272.1241***	136.5657	254.1135	127.5604	E	**708.3563**	354.6818	691.3297	346.1685	690.3457	345.6765	6
4	***419.1925***	210.0999	401.1819	201.0946	F	**579.3137**	290.1605	562.2871	281.6472	561.3031	281.1552	5
5	***518.2609***	259.6341	500.2504	250.6288	V	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
6	***647.3035***	324.1554	629.2930	315.1501	E	**333.1769**	167.0921	316.1503	158.5788	315.1663	158.0868	3
7	***704.3250***	352.6661	686.3144	343.6608	G	**204.1343**	102.5708	187.1077	94.0575			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AAEFVEGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.1	849.4232	-0.0004	AAEFVEGK

AT2G42530.1

Mascot: http://www.matrixscience.com/

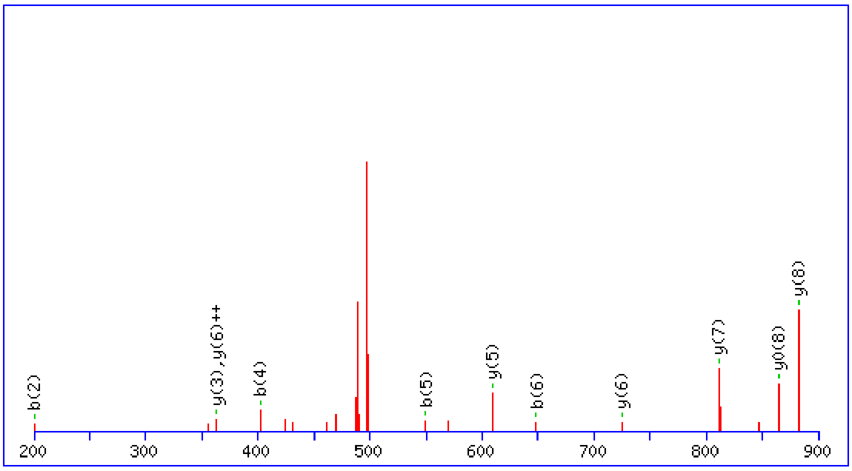
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KASDFVTDK**
Found in **AT2G42540.1** in **TAIR_Arabidopsis**, Symbols: COR15, COR15A | COR15A (COLD-REGULATED 15A) | chr2:17718319-17719008 REVERSE

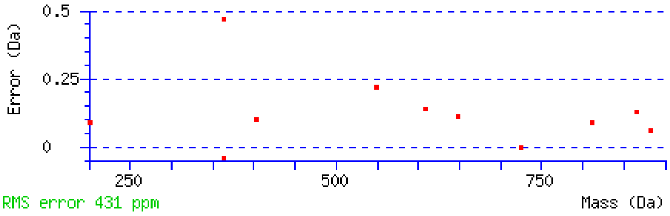
Match to Query 2456: 1009.507524 from(505.761038,2+) index(480)
Title: Elution from: 10.205 to 10.205 scan no 746 cid35.00 polarity:+
Data file C7-3_3.mgf

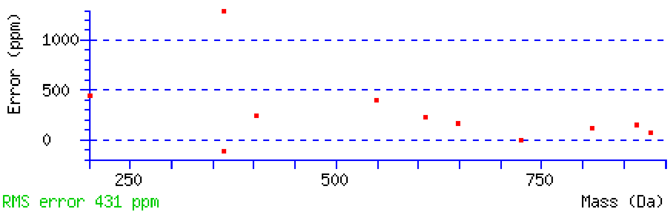
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1009.5080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 4.5e-005
Matches : 12/90 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**9**
2	***200.1394***	100.5733	183.1128	92.0600			**A**	***882.4203***	441.7138	865.3938	433.2005	864.4098	432.7085	**8**
3	287.1714	144.0893	270.1448	135.5761	269.1608	135.0840	**S**	***811.3832***	406.1953	794.3567	397.6820	793.3727	397.1900	**7**
4	***402.1983***	201.6028	385.1718	193.0895	384.1878	192.5975	**D**	***724.3512***	362.6792	707.3246	354.1660	706.3406	353.6740	**6**
5	***549.2667***	275.1370	532.2402	266.6237	531.2562	266.1317	**F**	***609.3243***	305.1658	592.2977	296.6525	591.3137	296.1605	**5**
6	***648.3352***	324.6712	631.3086	316.1579	630.3246	315.6659	**V**	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	**4**
7	749.3828	375.1951	732.3563	366.6818	731.3723	366.1898	**T**	***363.1874***	182.0974	346.1609	173.5841	345.1769	173.0921	**3**
8	***864.4098***	432.7085	847.3832	424.1953	846.3992	423.7032	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
9							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of KASDFVTDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G42540.1

49.4	1009.5080	-0.0005	KASDFVTDK
7.5	1009.5049	0.0027	MSNLMKVR
6.0	1009.5080	-0.0005	YEKEAKDK
1.4	1009.5049	0.0027	MTNMTLRK
1.3	1009.5080	-0.0005	GKDTDSFIK
1.3	1009.5048	0.0027	REMATMKK
1.3	1009.5080	-0.0005	FSSLDQVSK
1.3	1009.5080	-0.0005	TVSVYEQGK
0.9	1009.5080	-0.0005	YETELSLR
0.7	1009.5048	0.0027	AAKKACSMK

AT2G42590.1

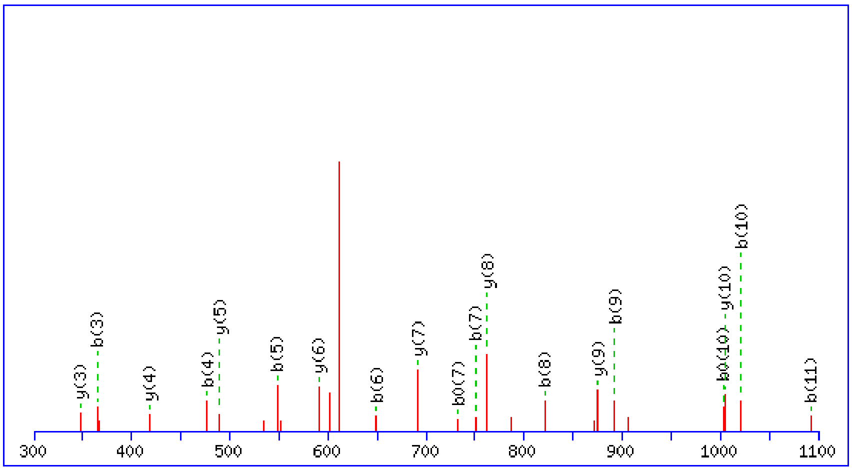
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYEIATTAAEAK**
Found in **AT2G42590.1** in **TAIR_Arabidopsis**, Symbols: GF14 MU, GRF9 | GRF9 (GENERAL REGULATORY FACTOR 9); protein phosphorylated amino acid binding | chr2:17739196-17740853 REVERSE

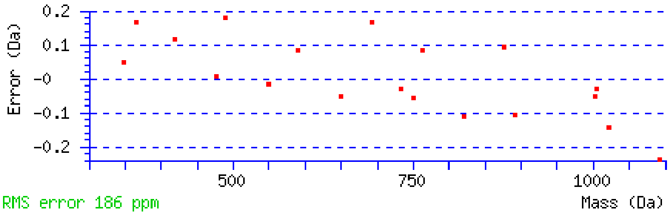
Match to Query 3843: 1237.619290 from(619.816921,2+) index(2168)
Title: Elution from: 25.331 to 25.331 scan no 2806 cid35.00 polarity:+
Data file D12h-2_3.mgf

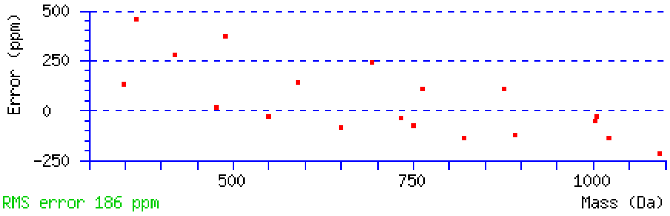
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1237.6190
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 97 **Expect:** 8.9e-010
Matches : 19/102 fragment ions using 22 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258			A							12
2	235.1077	118.0575			Y	1167.5892	584.2982	1150.5626	575.7850	1149.5786	575.2930	11
3	***364.1503***	182.5788	346.1397	173.5735	E	***1004.5259***	502.7666	987.4993	494.2533	986.5153	493.7613	10
4	***477.2344***	239.1208	459.2238	230.1155	I	***875.4833***	438.2453	858.4567	429.7320	857.4727	429.2400	9
5	***548.2715***	274.6394	530.2609	265.6341	A	***762.3992***	381.7032	745.3727	373.1900	744.3886	372.6980	8
6	***649.3192***	325.1632	631.3086	316.1579	T	***691.3621***	346.1847	674.3355	337.6714	673.3515	337.1794	7
7	***750.3668***	375.6871	732.3563	366.6818	T	***590.3144***	295.6608	573.2879	287.1476	572.3039	286.6556	6
8	***821.4040***	411.2056	803.3934	402.2003	A	***489.2667***	245.1370	472.2402	236.6237	471.2562	236.1317	5
9	***892.4411***	446.7242	874.4305	437.7189	A	***418.2296***	209.6185	401.2031	201.1052	400.2191	200.6132	4
10	***1021.4837***	511.2455	1003.4731	502.2402	E	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
11	***1092.5208***	546.7640	1074.5102	537.7587	A	218.1499	109.5786	201.1234	101.0653			2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AYEIATTAAEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G42590.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.7	1237.6190	0.0003	AYEIATTAAEAK
11.7	1237.6190	0.0003	DYTAEKAIEAK
9.1	1237.6159	0.0034	MAVTCAKNLSK
2.3	1237.6204	-0.0011	GRFGNFLDNAK
2.0	1237.6190	0.0002	FSPGTTVEVSSK
2.0	1237.6159	0.0034	MSTKQMDLIR
1.9	1237.6203	-0.0011	IRDYRSDWK
1.0	1237.6204	-0.0011	DGNFLGRNAFK
0.9	1237.6159	0.0034	RLKDVMMADK
0.8	1237.6224	-0.0031	EKDSLAMTVTK

Mascot: http://www.matrixscience.com/

AT2G42590.3

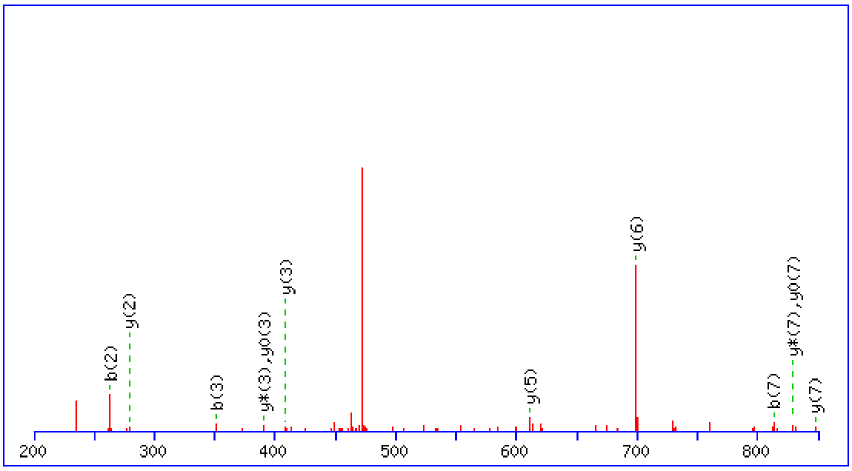
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFSSIEQK**
Found in **AT2G42590.3** in **TAIR_Arabidopsis**, Symbols: GF14 MU, GRF9 | GRF9 (GENERAL REGULATORY FACTOR 9); protein phosphorylated amino acid binding | chr2:17739242-17740853 REVERSE

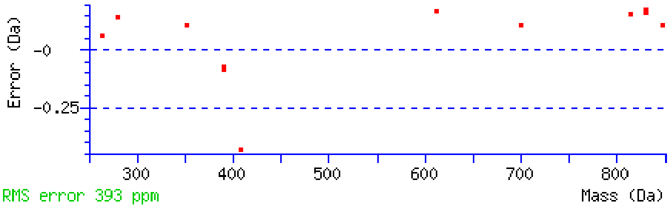
Match to Query 2255: 960.476048 from(481.245300,2+) index(2221)
Title: Elution from: 25.625 to 25.625 scan no 2850 cid35.00 polarity:+
Data file 0-1_1.mgf

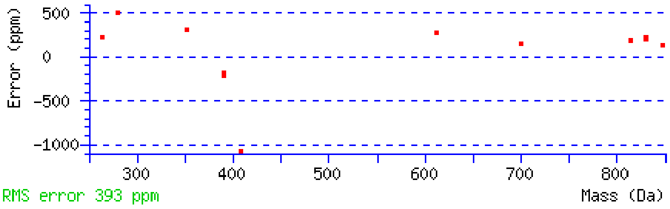
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 960.4776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0024
Matches : 12/64 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							8
2	**263.1538**	132.0805					F	***847.4038***	424.2055	829.3802	415.1938	829.3933	415.2003	7
3	**351.1829**	176.0951			333.1723	167.0898	S	***699.3384***	350.1728	681.3148	341.1610	681.3278	341.1675	6
4	439.2120	220.1096			421.2014	211.1043	S	***611.3093***	306.1583	593.2857	297.1465	593.2987	297.1530	5
5	553.2930	277.1502			535.2825	268.1449	I	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	4
6	683.3327	342.1700			665.3221	333.1647	E	***409.1991***	205.1032	391.1756	196.0914	391.1886	196.0979	3
7	**813.3853**	407.1963	795.3617	398.1845	795.3748	398.1910	Q	***279.1595***	140.0834	261.1359	131.0716			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IFSSIEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.4	960.4776	-0.0016	IFSSIEQK

AT2G42590.3

19.6	960.4781	-0.0020	RTTVGSAQK
19.0	960.4777	-0.0016	SYKEPSLK
17.3	960.4776	-0.0016	AEEFKSLK
15.4	960.4763	-0.0002	MIMNGKLK
13.9	960.4733	0.0027	MAARNKQK
13.6	960.4733	0.0027	QMREKVR
12.9	960.4776	-0.0016	VFTSIQEK
12.9	960.4776	-0.0016	VFTSLQEK
11.4	960.4776	-0.0016	LFDQLTSK

AT2G42600.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFSIEWYR**
Found in **AT2G42600.1** in **TAIR_Arabidopsis**, Symbols: ATPPC2 | ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXYLASE 2); phosphoenolpyruvate carboxylase | chr2:17742234-17745756 REVERSE

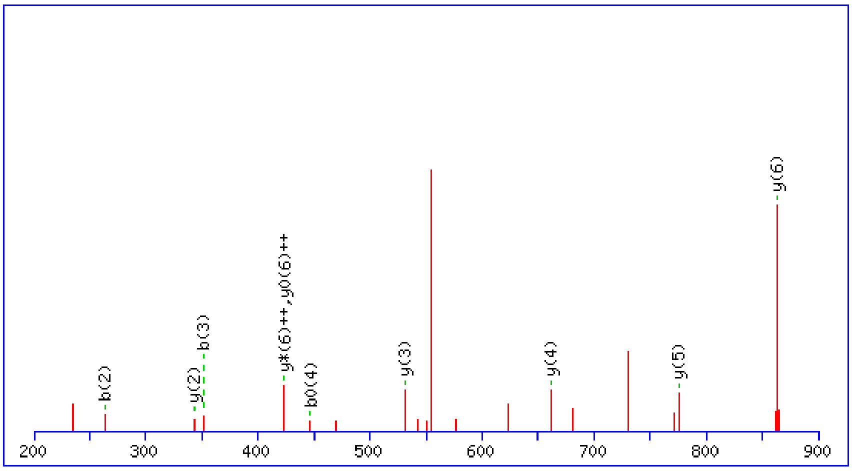
Match to Query 3580: 1124.529892 from(563.272222,2+) index(8750)
Title: Elution from: 77.803 to 77.803 scan no 11662 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

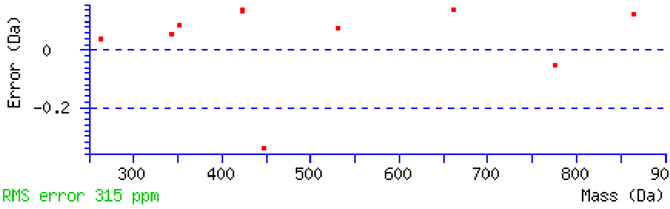
Label all possible matches ○ Label matches used for scoring ●

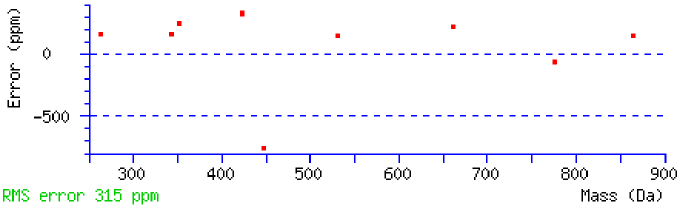
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1124.5299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0062
Matches : 10/60 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	**263.1538**	132.0805			F	1011.4561	506.2317	993.4325	497.2199	993.4455	497.2264	7
3	**351.1829**	176.0951	333.1723	167.0898	S	***863.3906***	432.1990	845.3670	423.1872	845.3801	423.1937	6
4	465.2640	233.1356	447.2534	224.1303	I	***775.3616***	388.1844	757.3380	379.1726	757.3510	379.1791	5
5	595.3036	298.1554	577.2930	289.1502	E	***661.2805***	331.1439	643.2569	322.1321	643.2699	322.1386	4
6	783.3770	392.1921	765.3664	383.1869	W	***531.2408***	266.1241	513.2173	257.1123			3
7	947.4374	474.2223	929.4268	465.2170	Y	***343.1675***	172.0874	325.1439	163.0756			2
8					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LFSIEWYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.1	1124.5299	0.0000	LFSIEWYR

AT2G42600.1

22.3	1124.5288	0.0011	MISSSSRSLK
11.7	1124.5333	-0.0034	FISALQCFK
2.5	1124.5276	0.0022	IFIDYTANR
2.2	1124.5276	0.0023	RGFTFDELK
1.8	1124.5310	-0.0011	MTTTSVFLGR
1.7	1124.5330	-0.0031	RTRGQFWR
1.7	1124.5276	0.0022	LPEWTPDVR

AT2G42650.1

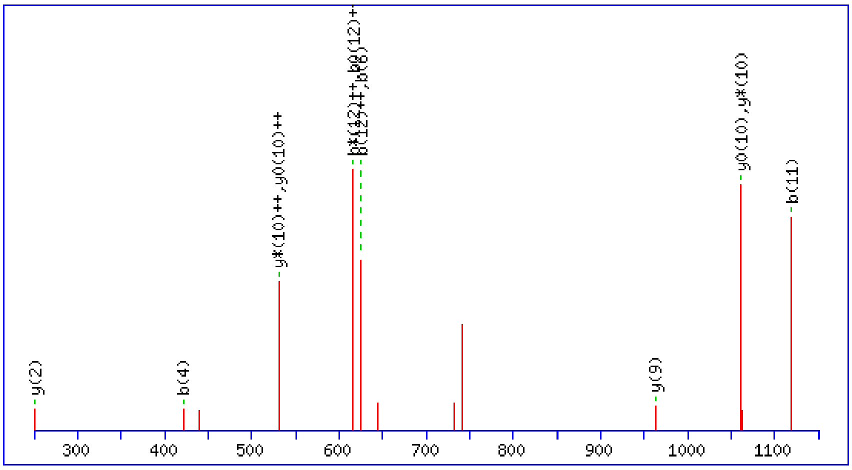
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDVDDSSSKSVKTK**
Found in **AT2G42650.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein-related | chr2:17772607-17773725 FORWARD

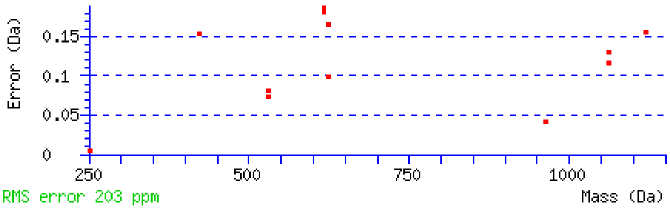
Match to Query 6172: 1498.668408 from(750.341480,2+) index(4750)
Title: Elution from: 43.190 to 43.190 scan no 5966 cid35.00 polarity:+
Data file D12h-3_2.mgf

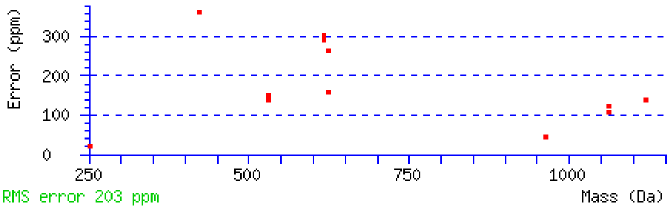
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1498.6705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.01
Matches : 12/138 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							14
2	205.0603	103.0338			187.0498	94.0285	D	1411.6487	706.3280	1393.6252	697.3162	1393.6382	697.3227	13
3	305.1258	153.0665			287.1152	144.0612	V	1295.6248	648.3160	1277.6012	639.3042	1277.6142	639.3107	12
4	***421.1497***	211.0785			403.1392	202.0732	D	1195.5593	598.2833	1177.5357	589.2715	1177.5487	589.2780	11
5	537.1737	269.0905			519.1632	260.0852	D	1079.5353	540.2713	1061.5117	531.2595	1061.5248	531.2660	10
6	***625.2028***	313.1050			607.1922	304.0997	S	***963.5114***	482.2593	945.4878	473.2475	945.5008	473.2540	9
7	713.2318	357.1196			695.2213	348.1143	S	875.4823	438.2448	857.4587	429.2330	857.4717	429.2395	8
8	801.2609	401.1341			783.2503	392.1288	S	787.4532	394.2303	769.4296	385.2185	769.4427	385.2250	7
9	931.3499	466.1786	913.3264	457.1668	913.3394	457.1733	K	699.4242	350.2157	681.4006	341.2039	681.4136	341.2104	6
10	1019.3790	510.1931	1001.3554	501.1813	1001.3684	501.1879	S	569.3351	285.1712	551.3115	276.1594	551.3246	276.1659	5
11	***1119.4445***	560.2259	1101.4209	551.2141	1101.4339	551.2206	V	481.3061	241.1567	463.2825	232.1449	463.2955	232.1514	4
12	1249.5335	625.2704	1231.5099	616.2586	1231.5229	616.2651	K	381.2406	191.1239	363.2170	182.1122	363.2301	182.1187	3
13	1351.5782	676.2927	1333.5546	667.2809	1333.5676	667.2875	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SDVDDSSSKSVKTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G42650.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.1	1498.6705	-0.0021	SDVDDSSSKSVKTK
3.3	1498.6669	0.0015	SEFALAISHGFFSA
3.0	1498.6707	-0.0023	DAFSLCVQQGAKR
2.9	1498.6651	0.0033	HHVGKESASNDAVK
2.1	1498.6680	0.0004	ITVGGEDVRMFDK
1.6	1498.6680	0.0004	TFTMSGPRDLTEK

AT2G42740.1

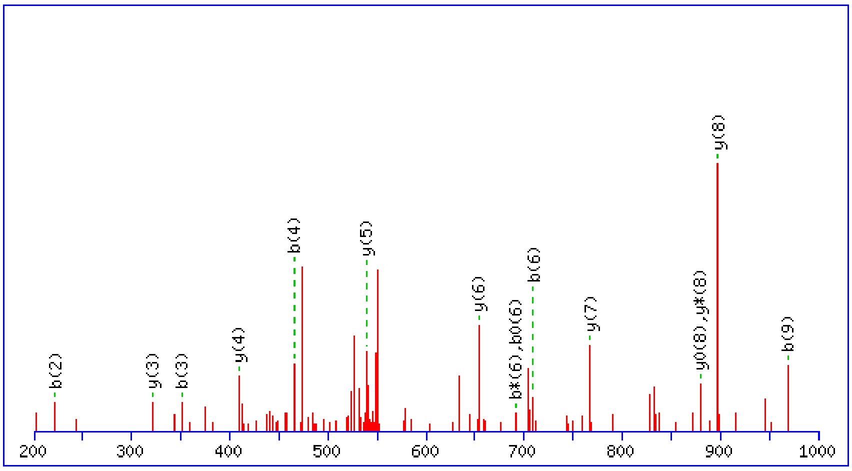
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMQLLESGLK**
Found in **AT2G42740.1** in **TAIR_Arabidopsis**, Symbols: RPL16A | RPL16A (ribosomal protein large subunit 16A); structural constituent of ribosome | chr2:17798871-17800023 FORWARD

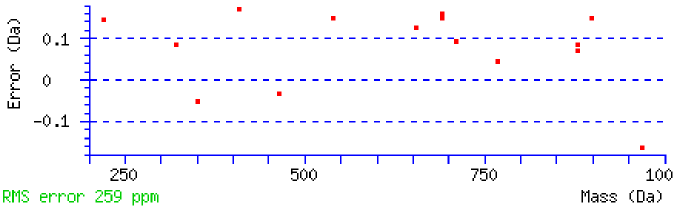
Match to Query 3552: 1116.547444 from(559.280998,2+) index(3203)
Title: Elution from: 31.496 to 31.496 scan no 3961 cid35.00 polarity:+
Data file D12h-1_2.mgf

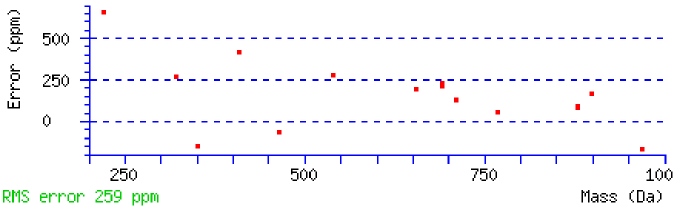
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5493
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 41 **Expect:** 0.00096
Matches : 15/132 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							10
2	***221.0739***	111.0406					M	1045.5224	523.2649	1027.4989	514.2531	1027.5119	514.2596	9
3	***351.1265***	176.0669	333.1029	167.0551			Q	***897.4900***	449.2486	879.4664	440.2369	879.4794	440.2434	8
4	***465.2076***	233.1074	447.1840	224.0956			L	***767.4374***	384.2223	749.4138	375.2105	749.4268	375.2170	7
5	579.2887	290.1480	561.2651	281.1362			L	***653.3563***	327.1818	635.3327	318.1700	635.3457	318.1765	6
6	***709.3283***	355.1678	691.3047	346.1560	691.3178	346.1625	E	***539.2752***	270.1412	521.2516	261.1294	521.2646	261.1359	5
7	797.3574	399.1823	779.3338	390.1705	779.3468	390.1771	S	***409.2355***	205.1214	391.2120	196.1096	391.2250	196.1161	4
8	855.3759	428.1916	837.3523	419.1798	837.3653	419.1863	G	***321.2065***	161.1069	303.1829	152.0951			3
9	***969.4570***	485.2321	951.4334	476.2203	951.4464	476.2269	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AMQLLESGLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G42740.1

Score	Mr(calc)	Delta	Sequence
41.3	1116.5493	-0.0019	AMQLLESGLK
27.7	1116.5493	-0.0019	AKEMVSLAEK
25.2	1116.5493	-0.0019	AMQIEEKLK
21.2	1116.5459	0.0015	FASGIPESAVK
19.7	1116.5459	0.0015	AEFVLDNVAK
18.5	1116.5493	-0.0019	MIEKLQEAK
16.2	1116.5459	0.0015	IAVFEAQEAK
12.3	1116.5493	-0.0019	KLSMADIAEK
8.1	1116.5493	-0.0019	DMIVNGITVK
8.0	1116.5493	-0.0019	TVIQMEKEK

AT2G43030.1

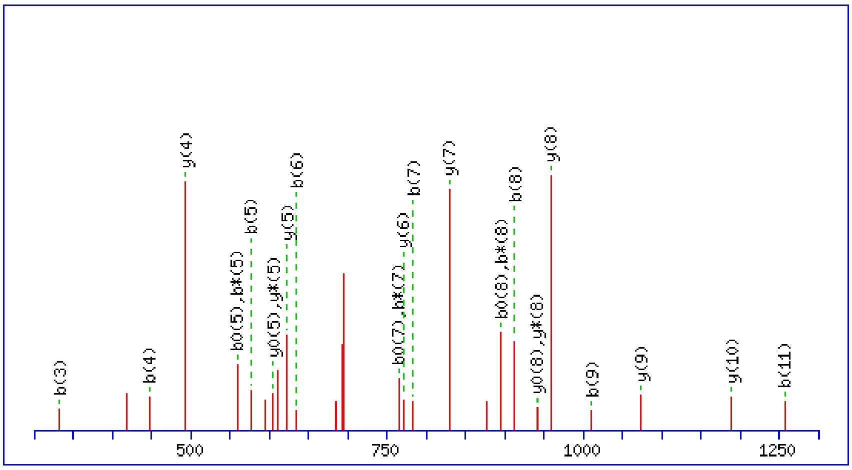
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTNIEGFEPNQK**
Found in **AT2G43030.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L3 family protein | chr2:17901975-17902790 FORWARD

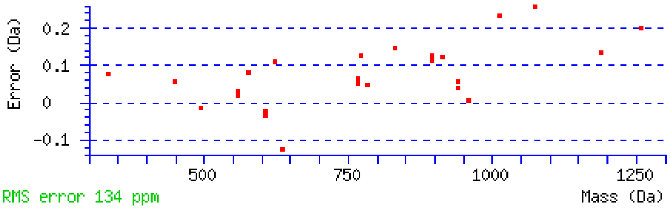
Match to Query 5580: 1404.645570 from(703.330061,2+) index(4201)
Title: Elution from: 38.077 to 38.077 scan no 5233 cid35.00 polarity:+
Data file D1d-3_2.mgf

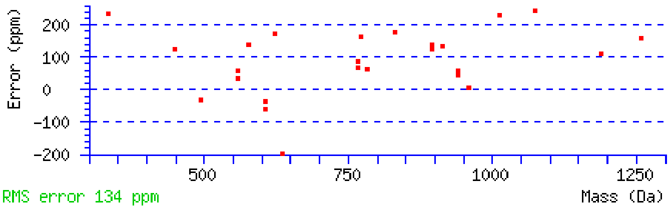
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1404.6461
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 1.6e-007
Matches : 25/118 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							12
2	217.1331	109.0702			199.1225	100.0649	T	1291.5723	646.2898	1273.5487	637.2780	1273.5618	637.2845	11
3	***333.1701***	167.0887	315.1465	158.0769	315.1595	158.0834	N	***1189.5276***	595.2674	1171.5040	586.2557	1171.5171	586.2622	10
4	***447.2512***	224.1292	429.2276	215.1174	429.2406	215.1239	I	***1073.4906***	537.2489	1055.4670	528.2372	1055.4801	528.2437	9
5	***577.2908***	289.1490	559.2672	280.1373	559.2802	280.1438	E	***959.4095***	480.2084	941.3859	471.1966	941.3990	471.2031	8
6	***635.3093***	318.1583	617.2857	309.1465	617.2987	309.1530	G	***829.3699***	415.1886	811.3463	406.1768	811.3593	406.1833	7
7	***783.3748***	392.1910	765.3512	383.1792	765.3642	383.1857	F	***771.3514***	386.1793	753.3278	377.1675	753.3408	377.1741	6
8	***913.4144***	457.2108	895.3908	448.1990	895.4038	448.2055	E	***623.2859***	312.1466	605.2624	303.1348	605.2754	303.1413	5
9	***1011.4642***	506.2357	993.4406	497.2239	993.4536	497.2304	P	***493.2463***	247.1268	475.2227	238.1150			4
10	1127.5012	564.2542	1109.4776	555.2424	1109.4906	555.2489	N	395.1965	198.1019	377.1729	189.0901			3
11	***1257.5538***	629.2806	1239.5302	620.2688	1239.5433	620.2753	Q	279.1595	140.0834	261.1359	131.0716			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LTNIEGFEPNQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G43030.1

Score	Mr(calc)	Delta	Sequence
77.7	1404.6461	-0.0006	LTNIEGFEPNQK
15.0	1404.6495	-0.0040	LSDSHSMKEVLK
13.7	1404.6439	0.0016	KLAEENNGADSIK
13.7	1404.6414	0.0042	QSPQELMWKNK
10.4	1404.6469	-0.0013	EIEVMASLDELK
6.6	1404.6495	-0.0039	VQELTGVCENLK
5.5	1404.6495	-0.0040	NLKNVGMEEEVK
5.5	1404.6436	0.0019	ILFQNFDMHPK
3.6	1404.6495	-0.0040	AKEALNNAEGLLM
3.5	1404.6468	-0.0013	LDTDIAILEDMK

AT2G43090.1

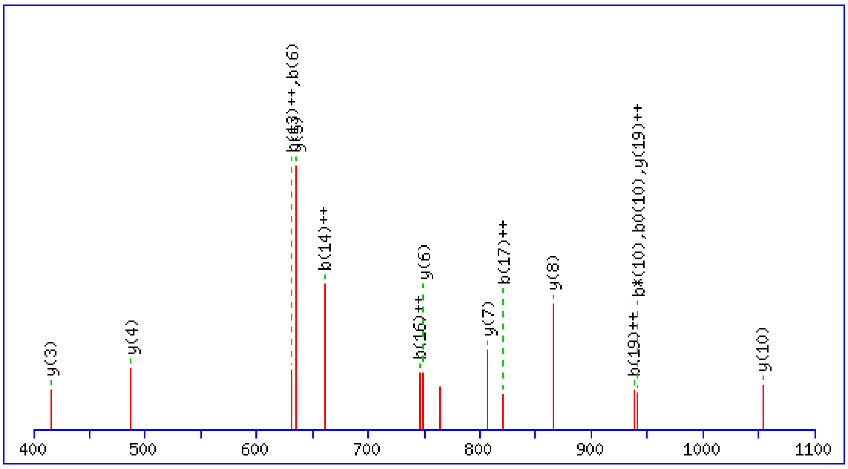
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKPIGDAGPVIDAGGIFAYAR**
Found in **AT2G43090.1** in **TAIR_Arabidopsis**, Symbols: | aconitase C-terminal domain-containing protein | chr2:17926034-17926789 FORWARD

Match to Query 9861: 2125.066392 from(709.362740,3+) index(9074)
Title: Elution from: 83.189 to 83.189 scan no 12220 cid35.00 polarity:+
Data file D12h-2_1.mgf

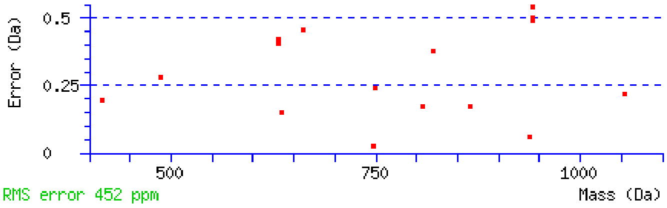
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

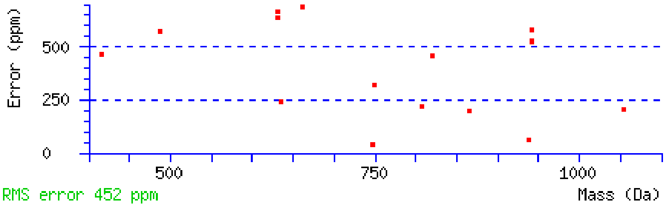


```
Monoisotopic mass of neutral peptide Mr(calc): 2125.0626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 3e-006
Matches : 16/210 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							21
2	245.1774	123.0923	227.1538	114.0805			K	2011.9888	1006.4981	1993.9652	997.4863	1993.9783	997.4928	20
3	343.2272	172.1172	325.2036	163.1054			P	1881.8998	941.4535	1863.8762	932.4417	1863.8892	932.4483	19
4	457.3083	229.1578	439.2847	220.1460			I	1783.8500	892.4286	1765.8264	883.4168	1765.8394	883.4234	18
5	515.3268	258.1670	497.3032	249.1552			G	1669.7689	835.3881	1651.7453	826.3763	1651.7583	826.3828	17
6	631.3508	316.1790	613.3272	307.1672	613.3402	307.1737	D	1611.7504	806.3788	1593.7268	797.3670	1593.7398	797.3736	16
7	703.3849	352.1961	685.3613	343.1843	685.3744	343.1908	A	1495.7264	748.3668	1477.7028	739.3551	1477.7159	739.3616	15
8	761.4034	381.2054	743.3798	372.1936	743.3929	372.2001	G	1423.6923	712.3498	1405.6687	703.3380	1405.6817	703.3445	14
9	859.4532	430.2303	841.4296	421.2185	841.4427	421.2250	P	1365.6738	683.3405	1347.6502	674.3287	1347.6632	674.3352	13
10	959.5187	480.2630	941.4951	471.2512	941.5081	471.2577	V	1267.6240	634.3156	1249.6004	625.3038	1249.6134	625.3103	12
11	1073.5998	537.3035	1055.5762	528.2917	1055.5892	528.2982	I	1167.5585	584.2829	1149.5349	575.2711	1149.5480	575.2776	11
12	1189.6238	595.3155	1171.6002	586.3037	1171.6132	586.3102	D	***1053.4774***	527.2424	1035.4538	518.2306	1035.4669	518.2371	10
13	1261.6579	***631.3326***	1243.6343	622.3208	1243.6473	622.3273	A	937.4534	469.2304	919.4299	460.2186			9
14	1319.6764	***660.3418***	1301.6528	651.3300	1301.6658	651.3366	G	***865.4193***	433.2133	847.3957	424.2015			8
15	1377.6949	689.3511	1359.6713	680.3393	1359.6843	680.3458	G	***807.4008***	404.2040	789.3772	395.1922			7
16	1491.7760	***746.3916***	1473.7524	737.3798	1473.7654	737.3864	I	***749.3823***	375.1948	731.3587	366.1830			6
17	1639.8415	***820.4244***	1621.8179	811.4126	1621.8309	811.4191	F	***635.3012***	318.1542	617.2776	309.1424			5
18	1711.8756	856.4414	1693.8520	847.4296	1693.8650	847.4362	A	***487.2358***	244.1215	469.2122	235.1097			4
19	1875.9360	***938.4716***	1857.9124	929.4598	1857.9254	929.4663	Y	***415.2016***	208.1044	397.1780	199.0926			3
20	1947.9701	974.4887	1929.9465	965.4769	1929.9595	965.4834	A	251.1412	126.0743	233.1177	117.0625			2
21							R	179.1071	90.0572	161.0835	81.0454			1

AT2G43090.1





NCBI **BLAST** search of LKPIGDAGPVIDAGGIFAYAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.4	2125.0626	0.0038	LKPIGDAGPVIDAGGIFAYAR
62.4	2125.0626	0.0038	LKPLGDAGPVIDAGGIFAYAR
2.8	2125.0653	0.0011	FLDNHIPRQRILTEAFK
0.2	2125.0712	-0.0048	VEIIPSSKQAIQKATNNTR

Mascot: http://www.matrixscience.com/

AT2G43280.1

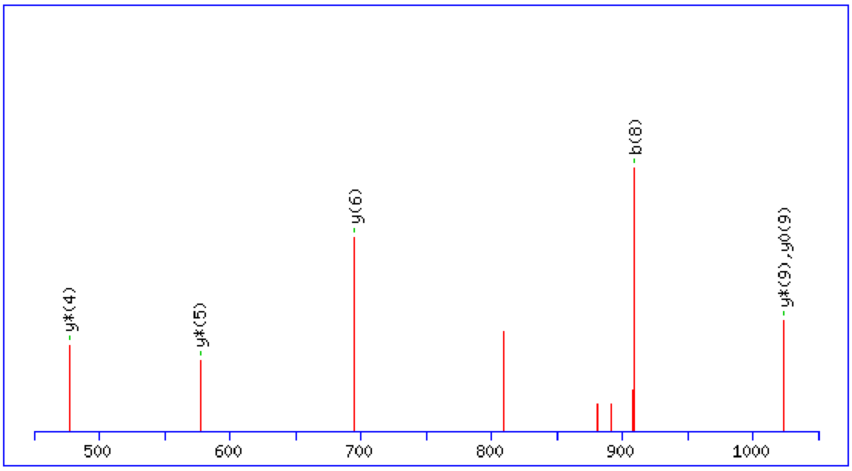
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVENVVNNLK**
Found in **AT2G43280.1** in **TAIR_Arabidopsis**, Symbols: | far-red impaired responsive family protein / FAR1 family protein | chr2:17996816-17997938 FORWARD

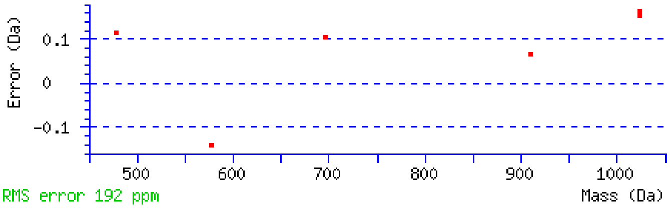
Match to Query 3931: 1170.615744 from(586.315148,2+) index(4462)
Title: Elution from: 40.884 to 40.884 scan no 5598 cid35.00 polarity:+
Data file 0-1_3.mgf

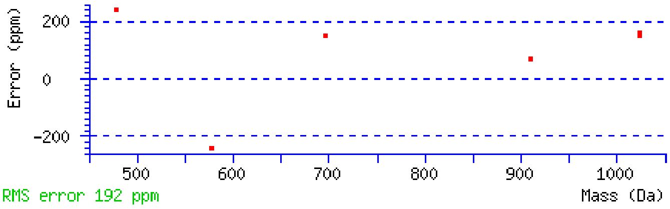
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1170.6167
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0049
Matches : 9/90 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							10
2	231.1618	116.0845	213.1382	107.0727			V	1041.5349	521.2711	1023.5114	512.2593	1023.5244	512.2658	9
3	361.2014	181.1043	343.1778	172.0925	343.1908	172.0990	E	941.4695	471.2384	923.4459	462.2266	923.4589	462.2331	8
4	***477.2384***	239.1228	459.2148	230.1110	459.2278	230.1175	N	811.4299	406.2186	793.4063	397.2068			7
5	***577.3038***	289.1556	559.2802	280.1438	559.2933	280.1503	V	695.3929	348.2001	677.3693	339.1883			6
6	677.3693	339.1883	659.3457	330.1765	659.3587	330.1830	V	595.3274	298.1673	577.3038	289.1556			5
7	793.4063	397.2068	775.3827	388.1950	775.3957	388.2015	N	495.2620	248.1346	477.2384	239.1228			4
8	***909.4433***	455.2253	891.4197	446.2135	891.4327	446.2200	N	379.2250	190.1161	361.2014	181.1043			3
9	***1023.5244***	512.2658	1005.5008	503.2540	1005.5138	503.2605	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KVENVVNNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G43280.1

Score	Mr(calc)	Delta	Sequence
30.9	1170.6167	-0.0010	KVENVVNNLK
30.4	1170.6167	-0.0009	TRVLSLDQPK
30.0	1170.6167	-0.0010	QPSRIESVLK
17.1	1170.6167	-0.0009	RLDAIEAQIK
4.8	1170.6140	0.0017	SELKAELELK
4.5	1170.6167	-0.0009	GDVSLALNVLR
4.2	1170.6189	-0.0032	AQAHLYTIIK
4.2	1170.6167	-0.0010	ASKTANNPLLK
4.2	1170.6140	0.0017	ELEADKLTIK
4.2	1170.6167	-0.0009	ELIQQERIK

AT2G43410.1

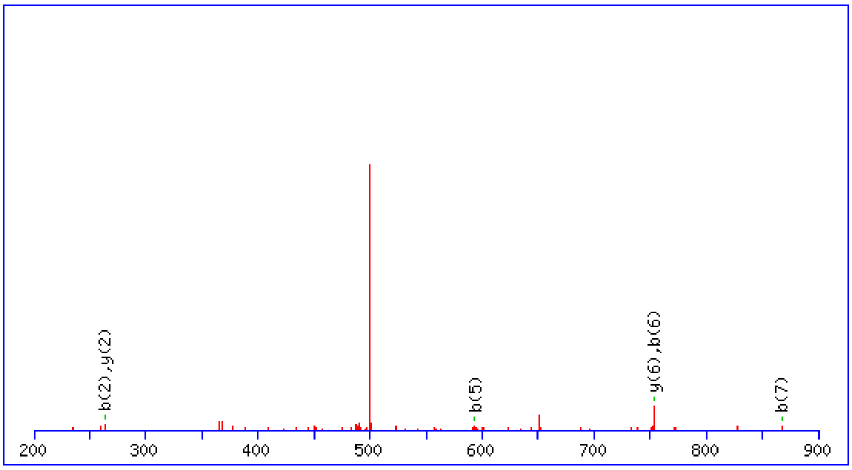
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFNNPRIK**
Found in **AT2G43410.1** in **TAIR_Arabidopsis**, Symbols: FPA | FPA; RNA binding | chr2:18033474-18038066 REVERSE

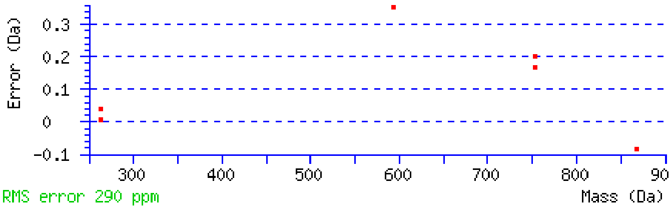
Match to Query 2659: 1014.539688 from(508.277120,2+) index(4013)
Title: Elution from: 38.304 to 38.304 scan no 5030 cid35.00 polarity:+
Data file D12h-3_1.mgf

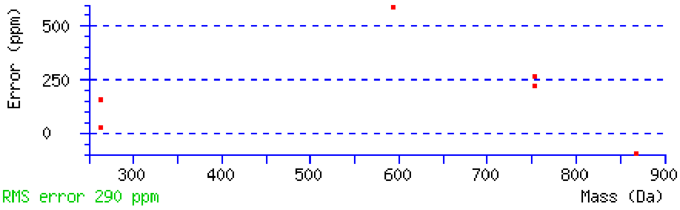
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1014.5403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.011
Matches : 6/52 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	115.0884	58.0478			L					8
2	***263.1538***	132.0805			F	901.4665	451.2369	883.4429	442.2251	7
3	379.1908	190.0990	361.1672	181.0873	N	**753.4010**	377.2041	735.3774	368.1924	6
4	495.2278	248.1175	477.2042	239.1058	N	637.3640	319.1856	619.3404	310.1739	5
5	***593.2776***	297.1424	575.2540	288.1307	P	521.3270	261.1671	503.3034	252.1554	4
6	***753.3669***	377.1871	735.3433	368.1753	R	423.2772	212.1422	405.2536	203.1305	3
7	***867.4480***	434.2276	849.4244	425.2158	I	**263.1880**	132.0976	245.1644	123.0858	2
8					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LFNNPRIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1014.5403	-0.0006	LFNNPRIK
23.9	1014.5410	-0.0013	IMLSGAATLK

AT2G43410.1

23.9	1014.5376	0.0021	LFTPSLAQK
18.2	1014.5376	0.0021	LFQLNELK
18.2	1014.5403	-0.0006	RTFLSHIK
15.7	1014.5403	-0.0006	TFLSHLRK
15.3	1014.5410	-0.0013	MIVLEKQK
13.9	1014.5380	0.0016	SDGIRLALR
13.5	1014.5403	-0.0006	GQWKKNLK
13.0	1014.5376	0.0021	EIFKDPKK

AT2G43460.1

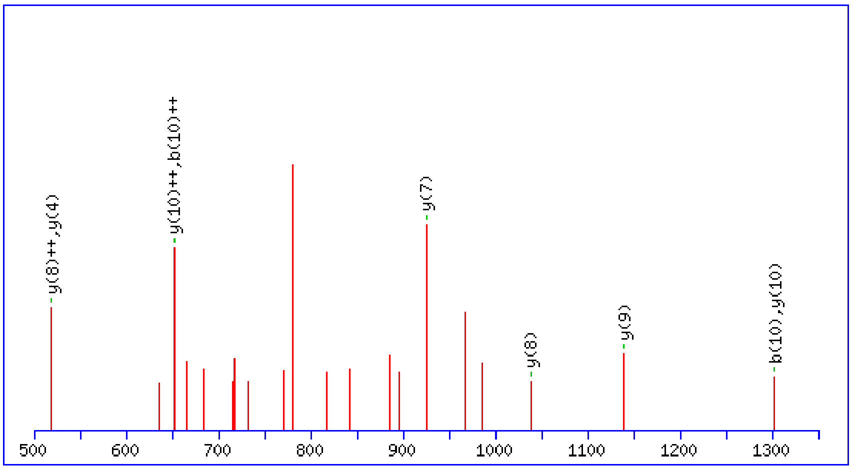
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLYTLCVFDQEK**
Found in **AT2G43460.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L38 (RPL38A) | chr2:18053362-18054369 REVERSE

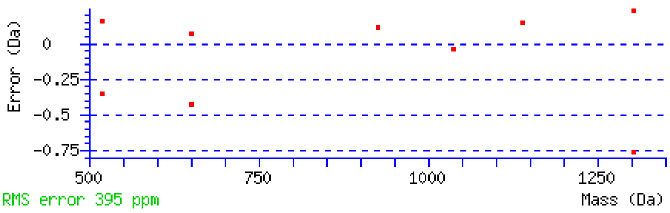
Match to Query 6418: 1577.746768 from(789.880660,2+) index(7814)
Title: Elution from: 71.463 to 71.463 scan no 10433 cid35.00 polarity:+
Data file D1d-1_3.mgf

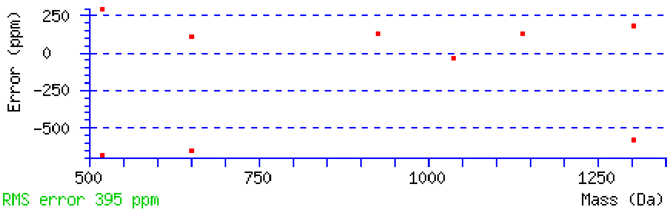
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1577.7436
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0003
Matches : 9/106 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							12
2	277.1547	139.0810					L	1415.6875	708.3474	1398.6610	699.8341	1397.6770	699.3421	11
3	440.2180	220.6126					Y	***1302.6035***	651.8054	1285.5769	643.2921	1284.5929	642.8001	10
4	541.2657	271.1365			523.2551	262.1312	T	***1139.5401***	570.2737	1122.5136	561.7604	1121.5296	561.2684	9
5	654.3497	327.6785			636.3392	318.6732	L	***1038.4925***	519.7499	1021.4659	511.2366	1020.4819	510.7446	8
6	814.3804	407.6938			796.3698	398.6886	C	***925.4084***	463.2078	908.3818	454.6946	907.3978	454.2026	7
7	913.4488	457.2280			895.4382	448.2228	V	765.3777	383.1925	748.3512	374.6792	747.3672	374.1872	6
8	1060.5172	530.7622			1042.5067	521.7570	F	666.3093	333.6583	649.2828	325.1450	648.2988	324.6530	5
9	1175.5442	588.2757			1157.5336	579.2704	D	***519.2409***	260.1241	502.2144	251.6108	501.2304	251.1188	4
10	1303.6027	652.3050	1286.5762	643.7917	1285.5922	643.2997	Q	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
11	1432.6453	716.8263	1415.6188	708.3130	1414.6348	707.8210	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YLYTLCVFDQEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G43460.1

Score	Mr(calc)	Delta	Sequence
40.1	1577.7436	0.0032	YLYTLCVFDQEK
7.5	1577.7467	0.0000	LSMGNGARNVSEAEK
4.2	1577.7508	-0.0040	LEIYDHGSEMRTK
2.9	1577.7481	-0.0013	NAHQSGVNCLHVSR
0.9	1577.7481	-0.0013	GGPENSRCSFRGVR
0.7	1577.7436	0.0032	DFFETYEQKLMK
0.2	1577.7468	0.0000	ERMDRTPVSTNEK
0.2	1577.7494	-0.0027	EVEELTSCLELEK

AT2G43560.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLDEGILSMK**
Found in **AT2G43560.1** in **TAIR_Arabidopsis**, Symbols: | immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein | chr2:18081072-18082462 REVERSE

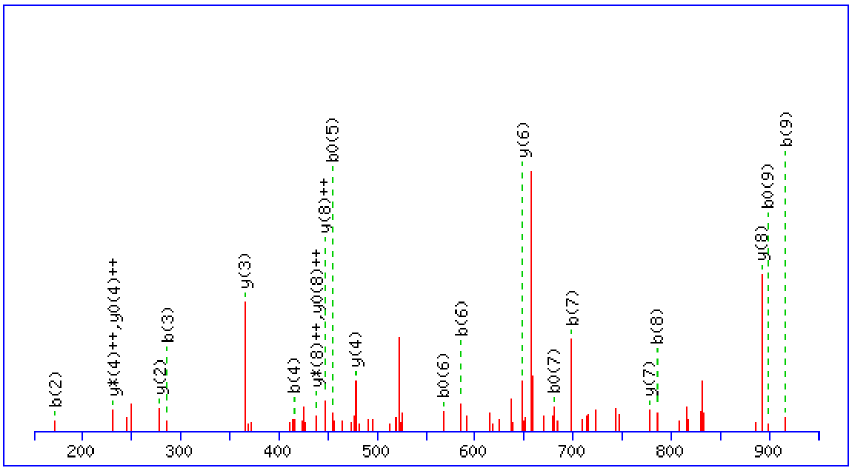
Match to Query 3000: 1061.544442 from(531.779497,2+) index(5976)
Title: Elution from: 52.432 to 52.432 scan no 7674 cid35.00 polarity:+
Data file 0-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

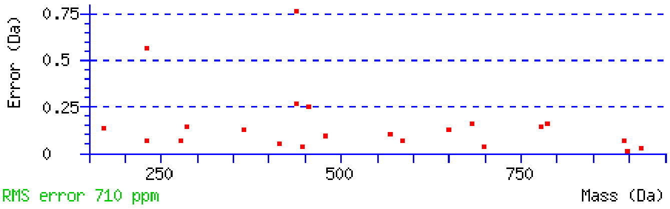
Label all possible matches ○ Label matches used for scoring ●

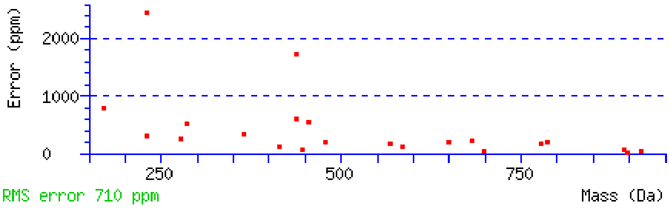
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1061.5427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00025
Matches : 22/82 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							10
2	***171.1128***	86.0600			L	1005.5285	503.2679	988.5020	494.7546	987.5179	494.2626	9
3	***286.1397***	143.5735	268.1292	134.5682	D	**892.4444**	446.7259	875.4179	438.2126	874.4339	437.7206	8
4	***415.1823***	208.0948	397.1718	199.0895	E	**777.4175**	389.2124	760.3910	380.6991	759.4069	380.2071	7
5	472.2038	236.6055	454.1932	227.6003	G	**648.3749**	324.6911	631.3484	316.1778	630.3643	315.6858	6
6	***585.2879***	293.1476	567.2773	284.1423	I	591.3534	296.1804	574.3269	287.6671	573.3429	287.1751	5
7	***698.3719***	349.6896	680.3614	340.6843	L	**478.2694**	239.6383	461.2428	231.1251	460.2588	230.6330	4
8	***785.4040***	393.2056	767.3934	384.2003	S	**365.1853**	183.0963	348.1588	174.5830	347.1748	174.0910	3
9	***916.4444***	458.7259	898.4339	449.7206	M	**278.1533**	139.5803	261.1267	131.0670			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GLDEGILSMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G43560.1

Score	Mr(calc)	Delta	Sequence
42.2	1061.5427	0.0018	GLDEGILSMK

Mascot: http://www.matrixscience.com/

AT2G43710.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQDLTGLSGEGNK**
Found in **AT2G43710.1** in **TAIR_Arabidopsis**, Symbols: FAB2, SSI2 | SSI2 (fatty acid biosynthesis 2); acyl-[acyl-carrier-protein] desaturase | chr2:18127184-18129572 FORWARD

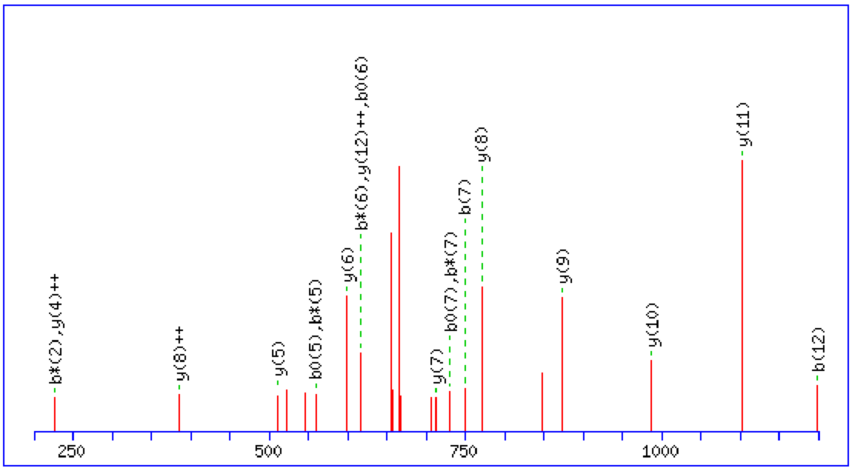
Match to Query 5446: 1346.621492 from(674.318022,2+) index(3742)
Title: Elution from: 35.595 to 35.595 scan no 4606 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1200 Da Full range

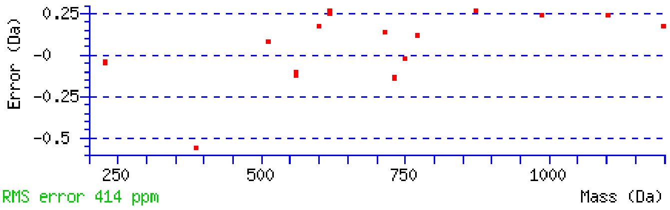
Label all possible matches ○ Label matches used for scoring ●

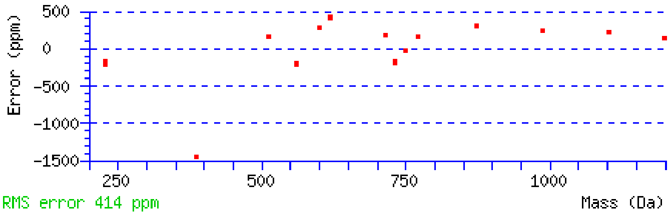
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1346.6254
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 8.2e-006
Matches : 19/132 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							13
2	245.1410	123.0741	227.1174	114.0624			Q	1233.5516	617.2794	1215.5280	608.2676	1215.5410	608.2742	12
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	D	***1103.4989***	552.2531	1085.4754	543.2413	1085.4884	543.2478	11
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	L	***987.4750***	494.2411	969.4514	485.2293	969.4644	485.2358	10
5	577.2908	289.1490	559.2672	280.1373	559.2802	280.1438	T	***873.3939***	437.2006	855.3703	428.1888	855.3833	428.1953	9
6	635.3093	318.1583	617.2857	309.1465	617.2987	309.1530	G	***771.3492***	386.1782	753.3256	377.1664	753.3386	377.1729	8
7	**749.3904**	375.1988	731.3668	366.1871	731.3798	366.1936	L	***713.3307***	357.1690	695.3071	348.1572	695.3201	348.1637	7
8	837.4195	419.2134	819.3959	410.2016	819.4089	410.2081	S	***599.2496***	300.1284	581.2260	291.1166	581.2390	291.1231	6
9	895.4380	448.2226	877.4144	439.2108	877.4274	439.2173	G	***511.2205***	256.1139	493.1969	247.1021	493.2099	247.1086	5
10	1025.4776	513.2424	1007.4540	504.2306	1007.4670	504.2372	E	453.2020	227.1046	435.1784	218.0928	435.1914	218.0994	4
11	1083.4961	542.2517	1065.4725	533.2399	1065.4855	533.2464	G	323.1624	162.0848	305.1388	153.0730			3
12	**1199.5331**	600.2702	1181.5095	591.2584	1181.5225	591.2649	N	265.1439	133.0756	247.1203	124.0638			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IQDLTGLSGEGNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G43710.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.0	1346.6254	-0.0039	IQDLTGLSGEGNK
11.9	1346.6254	-0.0039	DGQTILLDGNTGK
8.2	1346.6254	-0.0039	LEDESRNLLDK
6.9	1346.6180	0.0035	LESIENMLSKGP
3.3	1346.6229	-0.0014	ACSGQSWLPVVK
2.9	1346.6180	0.0035	MSTDQAIVEPVK
1.9	1346.6254	-0.0039	ELGPSSEISEKR
1.4	1346.6180	0.0035	IEDNMQVIVEK
1.0	1346.6207	0.0008	MTGHSIISSLER
0.3	1346.6180	0.0035	CLALLSGELDDK

AT2G43750.1

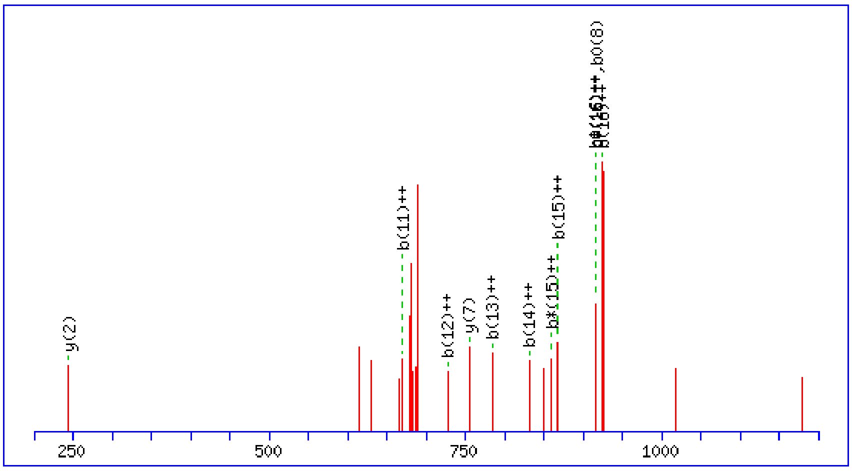
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KTPNSYMLQQFDNPANPK**
Found in **AT2G43750.1** in **TAIR_Arabidopsis**, Symbols: ACS1, CPACS1, ATCS-B, OASB | OASB (O-ACETYLSERINE (THIOL) LYASE B); cysteine synthase | chr2:18136681-18139399 REVERSE

Match to Query 9214: 2092.005984 from(698.342604,3+) index(4957)
Title: Elution from: 43.405 to 43.405 scan no 6207 cid35.00 polarity:+
Data file D1d-3_3.mgf

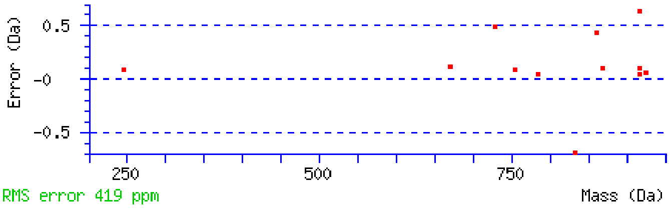
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

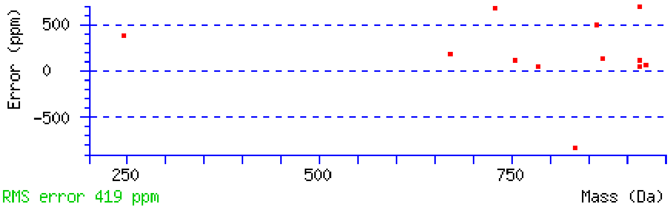


Monoisotopic mass of neutral peptide Mr(calc): 2092.0047
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.025
Matches : 12/190 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**18**
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	**T**	1964.9171	982.9622	1947.8905	974.4489	1946.9065	973.9569	**17**
3	327.2027	164.1050	310.1761	155.5917	309.1921	155.0997	**P**	1863.8694	932.4383	1846.8429	923.9251	1845.8588	923.4331	**16**
4	441.2456	221.1264	424.2191	212.6132	423.2350	212.1212	**N**	1766.8166	883.9120	1749.7901	875.3987	1748.8061	874.9067	**15**
5	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	**S**	1652.7737	826.8905	1635.7472	818.3772	1634.7632	817.8852	**14**
6	691.3410	346.1741	674.3144	337.6608	673.3304	337.1688	**Y**	1565.7417	783.3745	1548.7151	774.8612	1547.7311	774.3692	**13**
7	822.3815	411.6944	805.3549	403.1811	804.3709	402.6891	**M**	1402.6784	701.8428	1385.6518	693.3295	1384.6678	692.8375	**12**
8	935.4655	468.2364	918.4390	459.7231	917.4550	459.2311	**L**	1271.6379	636.3226	1254.6113	627.8093	1253.6273	627.3173	**11**
9	1063.5241	532.2657	1046.4975	523.7524	1045.5135	523.2604	**Q**	1158.5538	579.7805	1141.5273	571.2673	1140.5432	570.7753	**10**
10	1191.5827	596.2950	1174.5561	587.7817	1173.5721	587.2897	**Q**	1030.4952	515.7513	1013.4687	507.2380	1012.4847	506.7460	**9**
11	1338.6511	***669.8292***	1321.6245	661.3159	1320.6405	660.8239	**F**	902.4367	451.7220	885.4101	443.2087	884.4261	442.7167	**8**
12	1453.6780	***727.3427***	1436.6515	718.8294	1435.6675	718.3374	**D**	**755.3682**	378.1878	738.3417	369.6745	737.3577	369.1825	**7**
13	1567.7210	***784.3641***	1550.6944	775.8508	1549.7104	775.3588	**N**	640.3413	320.6743	623.3148	312.1610			**6**
14	1664.7737	***832.8905***	1647.7472	824.3772	1646.7632	823.8852	**P**	526.2984	263.6528	509.2718	255.1395			**5**
15	1735.8108	***868.4091***	1718.7843	859.8958	1717.8003	859.4038	**A**	429.2456	215.1264	412.2191	206.6132			**4**
16	1849.8538	***925.4305***	1832.8272	916.9172	1831.8432	916.4252	**N**	358.2085	179.6079	341.1819	171.0946			**3**
17	1946.9065	973.9569	1929.8800	965.4436	1928.8960	964.9516	**P**	**244.1656**	122.5864	227.1390	114.0731			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT2G43750.1





NCBI **BLAST** search of KTPNSYMLQQFDNPANPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.6	2092.0047	0.0012	KTPNSYMLQQFDNPANPK
7.8	2092.0054	0.0006	GWWAEDIAELGIDLYWR
7.0	2092.0081	-0.0021	NPIYVMEAASRMIEPSPR
5.9	2092.0106	-0.0047	KSSKGKPENSVDTTCNDII
2.5	2092.0081	-0.0021	MGGCTSKPSSSVKPNPYAPK
0.4	2092.0048	0.0012	YLDSLAGLWCTALGGNEPR
0.2	2092.0113	-0.0053	QDGSKDFEGYTTNLKYVK
0.1	2092.0047	0.0012	ECINLGAFGWAASLLEDAR

AT2G43910.1

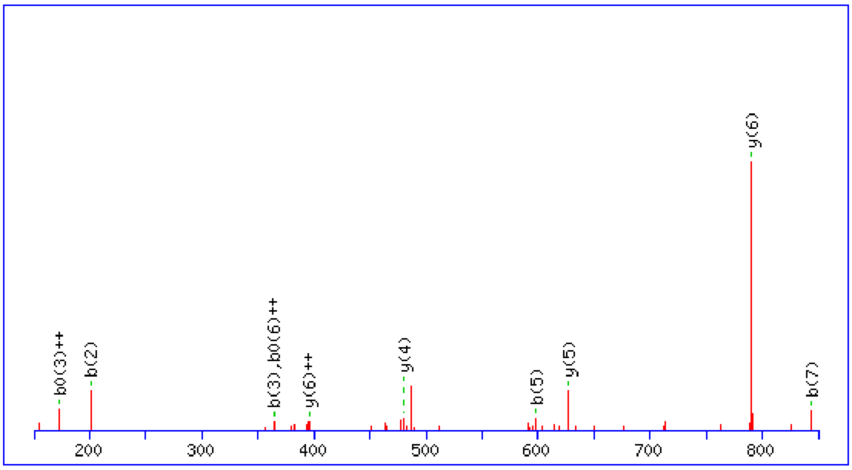
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEYFSFVK**
Found in **AT2G43910.1** in **TAIR_Arabidopsis**, Symbols: | thiol methyltransferase, putative | chr2:18191734-18194027 REVERSE

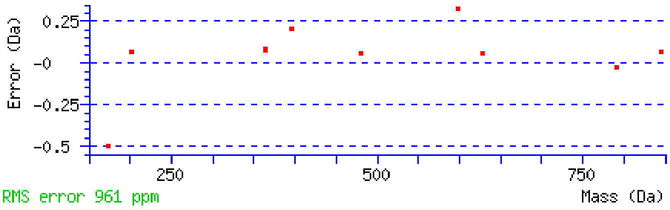
Match to Query 2338: 989.485828 from(495.750190,2+) index(5826)
Title: Elution from: 52.169 to 52.169 scan no 7444 cid35.00 polarity:+
Data file D6h-1_3.mgf

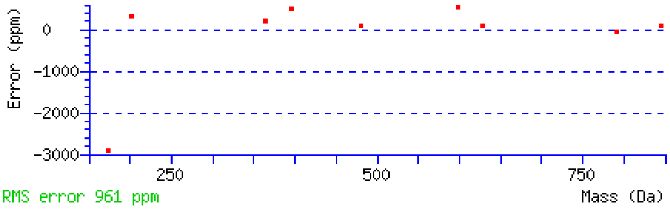
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 989.4858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0018
Matches : 10/62 fragment ions using 12 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258			A							8
2	***201.0870***	101.0471	183.0764	92.0418	E	919.4560	460.2316	902.4294	451.7184	901.4454	451.2264	7
3	***364.1503***	182.5788	346.1397	173.5735	Y	***790.4134***	395.7103	773.3869	387.1971	772.4028	386.7051	6
4	511.2187	256.1130	493.2082	247.1077	F	***627.3501***	314.1787	610.3235	305.6654	609.3395	305.1734	5
5	***598.2508***	299.6290	580.2402	290.6237	S	***480.2817***	240.6445	463.2551	232.1312	462.2711	231.6392	4
6	745.3192	373.1632	727.3086	364.1579	F	393.2496	197.1285	376.2231	188.6152			3
7	***844.3876***	422.6974	826.3770	413.6921	V	246.1812	123.5942	229.1547	115.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AEYFSFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.4	989.4858	0.0000	AEYFSFVK
5.6	989.4852	0.0007	DGLVQEAMK

AT2G43910.1

5.2	989.4852	0.0006	VGNVEVDMK
0.6	989.4852	0.0007	EQEVMNLK

Mascot: http://www.matrixscience.com/

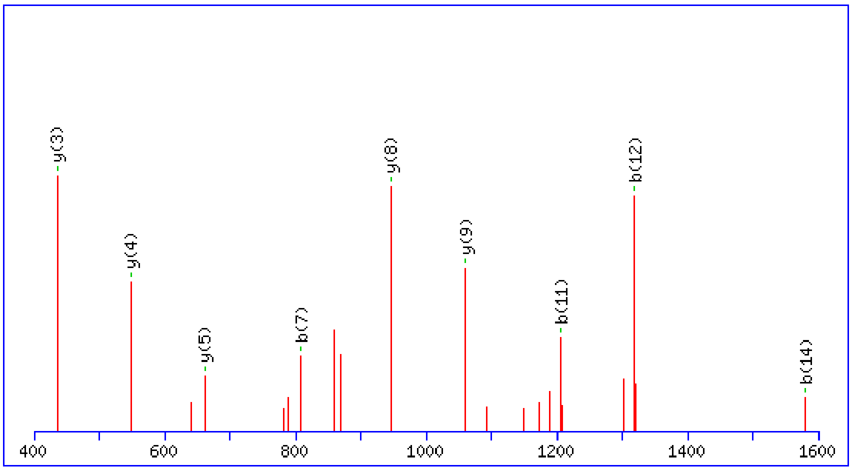
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STYNDINPGMIIPYR**
Found in **AT2G44060.1** in **TAIR_Arabidopsis**, Symbols: | late embryogenesis abundant family protein / LEA family protein | chr2:18233998-18235064 FORWARD

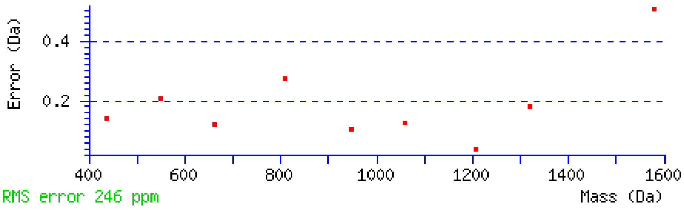
Match to Query 8238: 1752.850826 from(877.432689,2+) index(7987)
Title: Elution from: 73.391 to 73.391 scan no 10597 cid35.00 polarity:+
Data file D1d-1_1.mgf

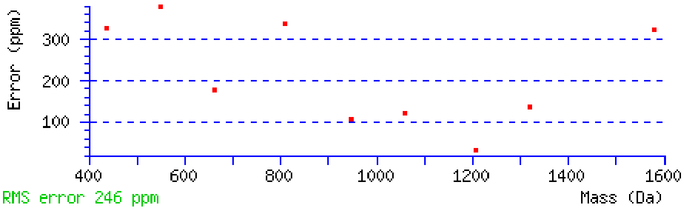
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1752.8505
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 3.6e-005
Matches : 9/142 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	189.0870	95.0471			171.0764	86.0418	T	1666.8258	833.9165	1649.7992	825.4032	1648.8152	824.9112	14
3	352.1503	176.5788			334.1397	167.5735	Y	1565.7781	783.3927	1548.7515	774.8794	1547.7675	774.3874	13
4	466.1932	233.6003	449.1667	225.0870	448.1827	224.5950	N	1402.7147	701.8610	1385.6882	693.3477	1384.7042	692.8557	12
5	581.2202	291.1137	564.1936	282.6005	563.2096	282.1084	D	1288.6718	644.8395	1271.6453	636.3263	1270.6613	635.8343	11
6	694.3042	347.6558	677.2777	339.1425	676.2937	338.6505	I	1173.6449	587.3261	1156.6183	578.8128			10
7	***808.3472***	404.6772	791.3206	396.1640	790.3366	395.6719	N	***1060.5608***	530.7840	1043.5343	522.2708			9
8	905.3999	453.2036	888.3734	444.6903	887.3894	444.1983	P	***946.5179***	473.7626	929.4913	465.2493			8
9	962.4214	481.7143	945.3949	473.2011	944.4108	472.7091	G	849.4651	425.2362	832.4386	416.7229			7
10	1093.4619	547.2346	1076.4353	538.7213	1075.4513	538.2293	M	792.4437	396.7255	775.4171	388.2122			6
11	***1206.5459***	603.7766	1189.5194	595.2633	1188.5354	594.7713	I	***661.4032***	331.2052	644.3766	322.6919			5
12	***1319.6300***	660.3186	1302.6035	651.8054	1301.6194	651.3134	I	***548.3191***	274.6632	531.2926	266.1499			4
13	1416.6828	708.8450	1399.6562	700.3318	1398.6722	699.8397	P	***435.2350***	218.1212	418.2085	209.6079			3
14	***1579.7461***	790.3767	1562.7196	781.8634	1561.7355	781.3714	Y	338.1823	169.5948	321.1557	161.0815			2
15							R	175.1190	88.0631	158.0924	79.5498			1





AT2G44060.1

NCBI **BLAST** search of STYNDINPGMIIPYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.6	1752.8505	0.0003	STYNDINPGMIIPYR
3.0	1752.8465	0.0043	ATINFTQNGISVEGMR
2.3	1752.8539	-0.0031	STFVPNVLMGMQELR
1.4	1752.8505	0.0003	YKFLLPGNCLRDEE
1.0	1752.8460	0.0049	SLMEEEKMELVLMR

AT2G44120.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

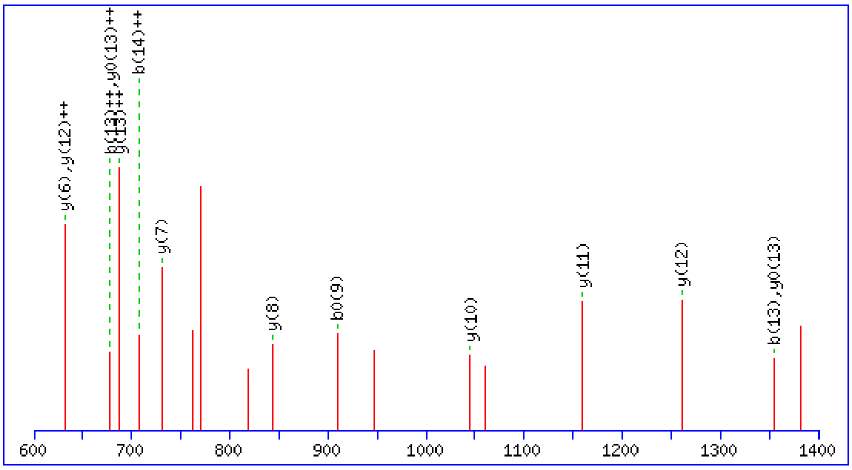
MS/MS Fragmentation of **IALTDNSIVDQALGK**
Found in **AT2G44120.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L7 (RPL7C) | chr2:18256303-18257478 REVERSE

Match to Query 6785: 1556.843340 from(779.428946,2+) index(8143)
Title: Elution from: 72.821 to 72.821 scan no 10862 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

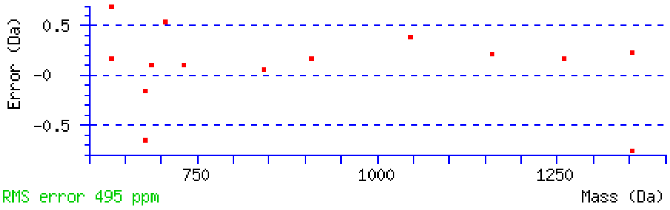
Or, Plot from 600 to 1400 Da Full range

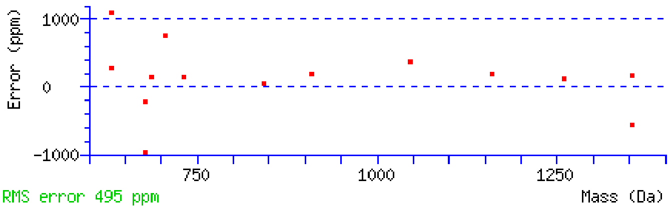
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1556.8410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00049
Matches : 14/142 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							15
2	185.1285	93.0679					A	1444.7642	722.8857	1427.7377	714.3725	1426.7536	713.8805	14
3	298.2125	149.6099					L	1373.7271	687.3672	1356.7005	678.8539	1355.7165	678.3619	13
4	399.2602	200.1337			381.2496	191.1285	T	***1260.6430***	630.8251	1243.6165	622.3119	1242.6325	621.8199	12
5	514.2871	257.6472			496.2766	248.6419	D	***1159.5953***	580.3013	1142.5688	571.7880	1141.5848	571.2960	11
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	N	***1044.5684***	522.7878	1027.5419	514.2746	1026.5578	513.7826	10
7	715.3621	358.1847	698.3355	349.6714	697.3515	349.1794	S	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	9
8	828.4462	414.7267	811.4196	406.2134	810.4356	405.7214	I	***843.4934***	422.2504	826.4669	413.7371	825.4829	413.2451	8
9	927.5146	464.2609	910.4880	455.7476	909.5040	455.2556	V	***730.4094***	365.7083	713.3828	357.1951	712.3988	356.7030	7
10	1042.5415	521.7744	1025.5150	513.2611	1024.5310	512.7691	D	***631.3410***	316.1741	614.3144	307.6608	613.3304	307.1688	6
11	1170.6001	585.8037	1153.5735	577.2904	1152.5895	576.7984	Q	516.3140	258.6607	499.2875	250.1474			5
12	1241.6372	621.3222	1224.6107	612.8090	1223.6266	612.3170	A	388.2554	194.6314	371.2289	186.1181			4
13	1354.7213	**677.8643**	1337.6947	669.3510	1336.7107	668.8590	L	317.2183	159.1128	300.1918	150.5995			3
14	1411.7427	**706.3750**	1394.7162	697.8617	1393.7322	697.3697	G	204.1343	102.5708	187.1077	94.0575			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IALTDNSIVDQALGK

AT2G44120.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.1	1556.8410	0.0024	IALTDNSIVDQALGK
9.4	1556.8457	-0.0023	IVREQMAVREAAGK
3.5	1556.8410	0.0024	AGLEKEAEVASQVVK
0.2	1556.8457	-0.0023	DVLDLMRIGQKNR

AT2G44350.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGLALERPK**
Found in **AT2G44350.1** in **TAIR_Arabidopsis**, Symbols: CSY4, ATCS | ATCS (CITRATE SYNTHASE 4); citrate (SI)-synthase | chr2:18323749-18327600 FORWARD

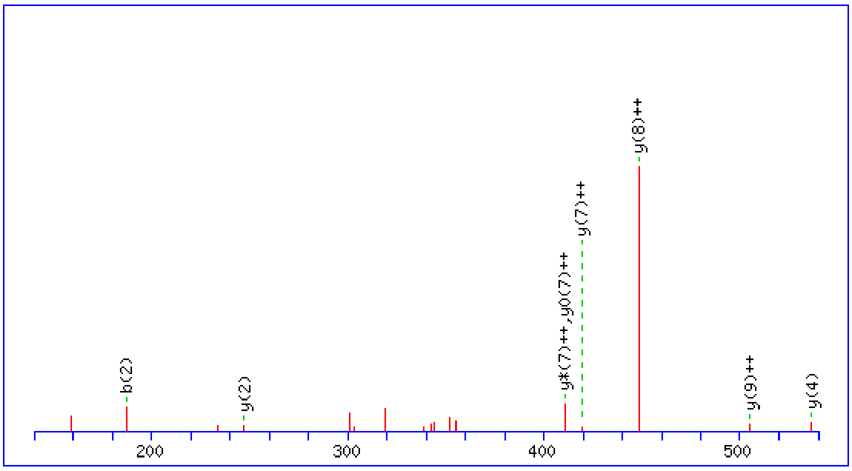
Match to Query 2783: 1080.608658 from(361.210162,3+) index(2957)
Title: Elution from: 30.502 to 30.502 scan no 3739 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 140 to 540 Da Full range

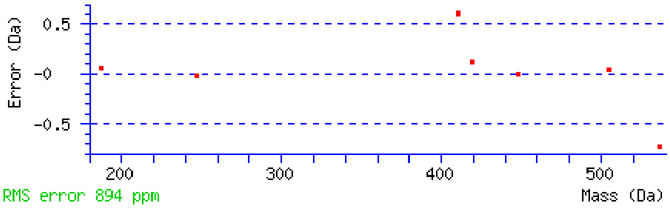
Label all possible matches ○ Label matches used for scoring ●

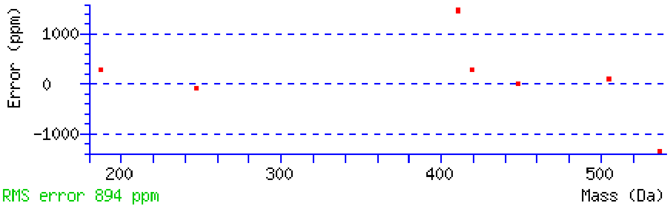
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1080.6084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.028
Matches : 8/76 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							10
2	187.1225	94.0649					L	1009.5815	505.2944	991.5579	496.2826	991.5709	496.2891	9
3	245.1410	123.0741					G	895.5004	448.2538	877.4768	439.2420	877.4898	439.2486	8
4	359.2221	180.1147					L	837.4819	419.2446	819.4583	410.2328	819.4713	410.2393	7
5	431.2563	216.1318					A	723.4008	362.2040	705.3772	353.1922	705.3902	353.1988	6
6	545.3374	273.1723					L	651.3667	326.1870	633.3431	317.1752	633.3561	317.1817	5
7	675.3770	338.1921			657.3664	329.1869	E	***537.2856***	269.1464	519.2620	260.1346	519.2750	260.1411	4
8	835.4662	418.2368	817.4427	409.2250	817.4557	409.2315	R	407.2459	204.1266	389.2223	195.1148			3
9	933.5160	467.2617	915.4925	458.2499	915.5055	458.2564	P	***247.1567***	124.0820	229.1331	115.0702			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ALGLALERPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G44350.1

Score	Mr(calc)	Delta	Sequence
20.5	1080.6084	0.0003	ALGLALERPK
4.8	1080.6084	0.0003	LRIPSSVAPK
4.8	1080.6057	0.0030	IAIELIGDVK
4.7	1080.6111	-0.0024	IAIKPRPNR
4.5	1080.6084	0.0003	AIVVDAKPVR

AT2G44920.1

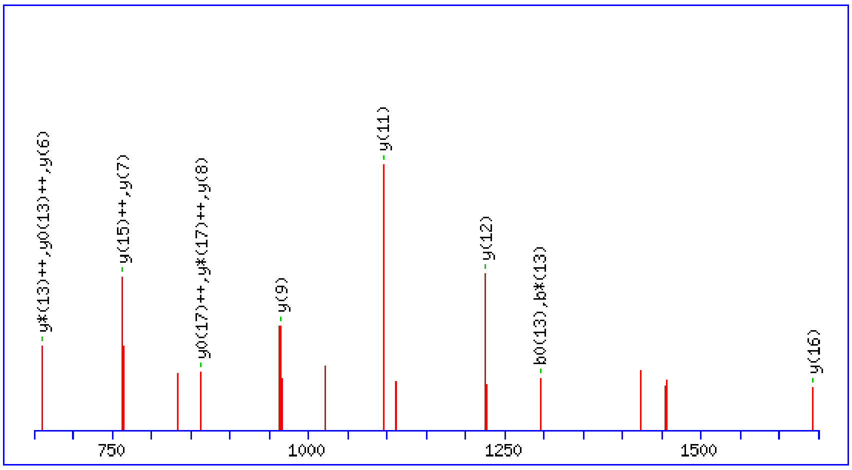
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNLTNANLEGATVTGNTSFK**
Found in **AT2G44920.1** in **TAIR_Arabidopsis**, Symbols: | thylakoid lumenal 15 kDa protein, chloroplast | chr2:18531494-18533311 FORWARD

Match to Query 9454: 2074.960058 from(1038.487305,2+) index(6005)
Title: Elution from: 53.153 to 53.153 scan no 7651 cid35.00 polarity:+
Data file 0-3_2.mgf

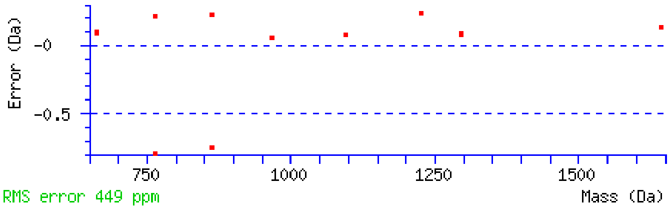
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

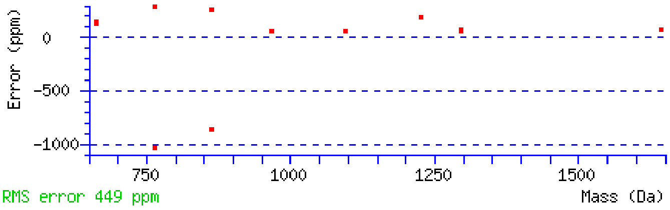


Monoisotopic mass of neutral peptide Mr(calc): 2074.9590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 4.3e-005
Matches : 14/216 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							20
2	217.1097	109.0585	199.0861	100.0467			N	1975.9008	988.4540	1957.8772	979.4422	1957.8902	979.4488	19
3	331.1908	166.0990	313.1672	157.0873			L	1859.8638	930.4355	1841.8402	921.4237	1841.8532	921.4303	18
4	433.2355	217.1214	415.2120	208.1096	415.2250	208.1161	T	1745.7827	873.3950	1727.7591	864.3832	1727.7721	864.3897	17
5	549.2725	275.1399	531.2489	266.1281	531.2620	266.1346	N	***1643.7380***	822.3726	1625.7144	813.3608	1625.7274	813.3673	16
6	621.3067	311.1570	603.2831	302.1452	603.2961	302.1517	A	1527.7010	764.3541	1509.6774	755.3423	1509.6904	755.3489	15
7	737.3437	369.1755	719.3201	360.1637	719.3331	360.1702	N	1455.6668	728.3371	1437.6433	719.3253	1437.6563	719.3318	14
8	851.4248	426.2160	833.4012	417.2042	833.4142	417.2107	L	1339.6298	670.3186	1321.6063	661.3068	1321.6193	661.3133	13
9	981.4644	491.2358	963.4408	482.2240	963.4538	482.2306	E	***1225.5487***	613.2780	1207.5252	604.2662	1207.5382	604.2727	12
10	1039.4829	520.2451	1021.4593	511.2333	1021.4723	511.2398	G	***1095.5091***	548.2582	1077.4855	539.2464	1077.4986	539.2529	11
11	1111.5171	556.2622	1093.4935	547.2504	1093.5065	547.2569	A	1037.4906	519.2489	1019.4670	510.2372	1019.4801	510.2437	10
12	1213.5618	607.2845	1195.5382	598.2727	1195.5512	598.2792	T	***965.4565***	483.2319	947.4329	474.2201	947.4459	474.2266	9
13	1313.6272	657.3172	1295.6036	648.3055	1295.6166	648.3120	V	***863.4118***	432.2095	845.3882	423.1977	845.4012	423.2042	8
14	1415.6719	708.3396	1397.6483	699.3278	1397.6614	699.3343	T	***763.3463***	382.1768	745.3227	373.1650	745.3357	373.1715	7
15	1473.6904	737.3489	1455.6668	728.3371	1455.6799	728.3436	G	***661.3016***	331.1544	643.2780	322.1426	643.2910	322.1492	6
16	1589.7274	795.3673	1571.7038	786.3556	1571.7169	786.3621	N	603.2831	302.1452	585.2595	293.1334	585.2725	293.1399	5
17	1691.7721	846.3897	1673.7486	837.3779	1673.7616	837.3844	T	487.2461	244.1267	469.2225	235.1149	469.2355	235.1214	4
18	1779.8012	890.4042	1761.7776	881.3924	1761.7906	881.3990	S	385.2014	193.1043	367.1778	184.0925	367.1908	184.0990	3
19	1927.8666	964.4370	1909.8431	955.4252	1909.8561	955.4317	F	297.1723	149.0898	279.1487	140.0780			2
20							K	149.1069	75.0571	131.0833	66.0453			1

AT2G44920.1





NCBI **BLAST** search of VNLTNANLEGATVTGNTSFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.3	2074.9590	0.0011	VNLTNANLEGATVTGNTSFK
1.4	2074.9549	0.0051	NIELSREVAEMKTEMIK
1.2	2074.9542	0.0058	CAVSPTLIKTFDSDPSRR

Mascot: http://www.matrixscience.com/

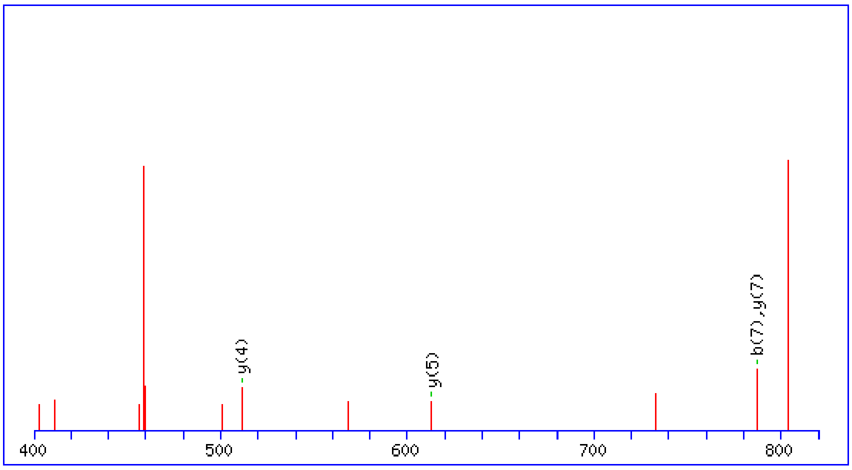
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGNTKVMK**
Found in **AT2G44990.1** in **TAIR_Arabidopsis**, Symbols: MAX3, CCD7 | CCD7 (more axillary growth 3) | chr2:18566013-18568408 FORWARD

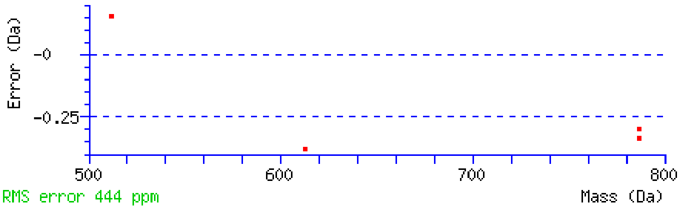
Match to Query 1860: 934.458382 from(468.236467,2+) index(7877)
Title: Elution from: 70.585 to 70.585 scan no 10311 cid35.00 polarity:+
Data file D6h-2_2.mgf

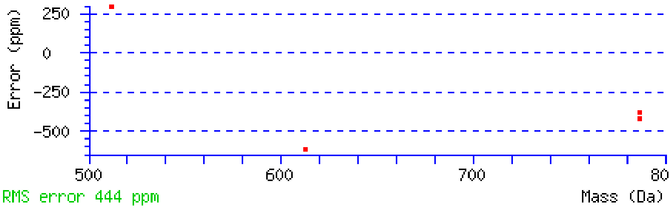
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 820 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 934.4572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.036
Matches : 4/66 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							8
2	207.0912	104.0492					G	***787.3991***	394.2032	769.3755	385.1914	769.3885	385.1979	7
3	323.1282	162.0677	305.1046	153.0560			N	729.3806	365.1939	711.3570	356.1821	711.3700	356.1886	6
4	425.1729	213.0901	407.1494	204.0783	407.1624	204.0848	T	***613.3436***	307.1754	595.3200	298.1636	595.3330	298.1702	5
5	555.2620	278.1346	537.2384	269.1228	537.2514	269.1293	K	***511.2989***	256.1531	493.2753	247.1413			4
6	655.3274	328.1673	637.3038	319.1556	637.3169	319.1621	V	381.2098	191.1086	363.1863	182.0968			3
7	787.3649	394.1861	769.3414	385.1743	769.3544	385.1808	M	281.1444	141.0758	263.1208	132.0640			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FGNTKVMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.9	934.4572	0.0011	FGNTKVMK
9.6	934.4572	0.0011	FDRIMVK

AT2G44990.1

9.6	934.4577	0.0007	MGRGSLRK
9.6	934.4577	0.0007	MRNTVRK
4.2	934.4577	0.0007	ARARMATK
3.9	934.4573	0.0011	HAMLPEVK
3.4	934.4573	0.0011	FKKNMEK

AT2G45080.1

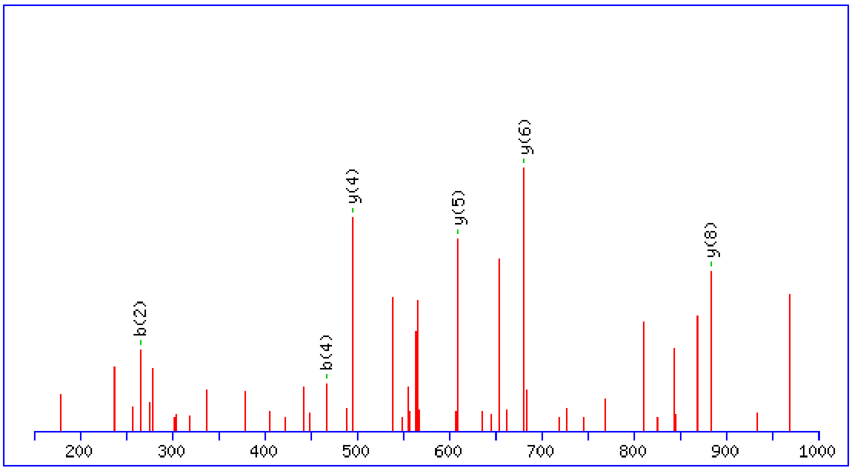
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDSLAISPRK**
Found in **AT2G45080.1** in **TAIR_Arabidopsis**, Symbols: CYCP3;1 | CYCP3;1 (cyclin p3;1); cyclin-dependent protein kinase | chr2:18598763-18599518 FORWARD

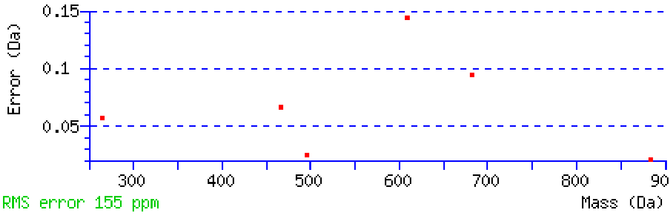
Match to Query 3597: 1146.552176 from(574.283364,2+) index(6539)
Title: Elution from: 57.153 to 57.153 scan no 8448 cid35.00 polarity:+
Data file D6h-3_3.mgf

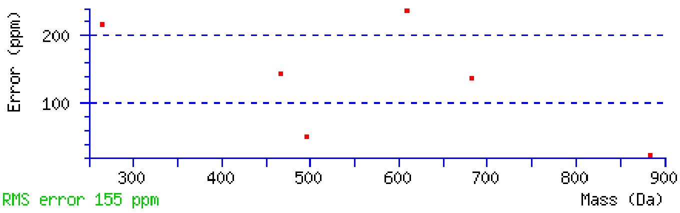
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1146.5495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.023
Matches : 6/120 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	149.0397	75.0235					M							10
2	**265.0637**	133.0355			247.0531	124.0302	D	999.5244	500.2658	981.5008	491.2540	981.5138	491.2605	9
3	353.0928	177.0500			335.0822	168.0447	S	***883.5004***	442.2538	865.4768	433.2420	865.4898	433.2486	8
4	**467.1739**	234.0906			449.1633	225.0853	L	795.4713	398.2393	777.4478	389.2275	777.4608	389.2340	7
5	539.2080	270.1076			521.1974	261.1024	A	***681.3902***	341.1988	663.3667	332.1870	663.3797	332.1935	6
6	653.2891	327.1482			635.2785	318.1429	I	***609.3561***	305.1817	591.3325	296.1699	591.3455	296.1764	5
7	741.3182	371.1627			723.3076	362.1574	S	***495.2750***	248.1411	477.2514	239.1293	477.2644	239.1358	4
8	839.3680	420.1876			821.3574	411.1823	P	407.2459	204.1266	389.2223	195.1148			3
9	999.4572	500.2322	981.4336	491.2205	981.4466	491.2270	R	309.1961	155.1017	291.1725	146.0899			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MDSLAISPRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G45080.1

Score	Mr(calc)	Delta	Sequence
26.8	1146.5495	0.0026	MDSLAISPRK
13.5	1146.5495	0.0026	IMRDLNVEK
11.9	1146.5518	0.0004	KVFDLMPER
10.6	1146.5495	0.0026	IMQAAAASNLK
9.0	1146.5549	-0.0027	TRHAIARMR
6.7	1146.5495	0.0026	GESMEILAKR
6.3	1146.5522	-0.0000	KCNQLKPSR
6.3	1146.5522	-0.0000	MRKGGLTPDR
5.3	1146.5488	0.0034	AYRVDGHGKK
5.0	1146.5542	-0.0021	ATEGKDVTVSK

AT2G45290.1

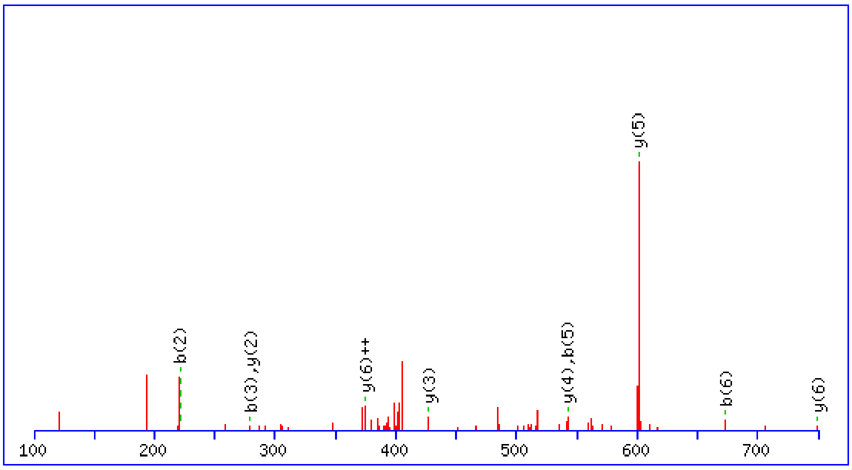
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFGNFQK**
Found in **AT2G45290.1** in **TAIR_Arabidopsis**, Symbols: | transketolase, putative | chr2:18679811-18682663 FORWARD

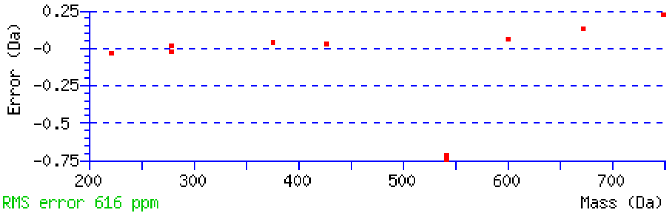
Match to Query 1083: 820.372478 from(411.193515,2+) index(2261)
Title: Elution from: 25.130 to 25.130 scan no 2866 cid35.00 polarity:+
Data file D12h-3_2.mgf

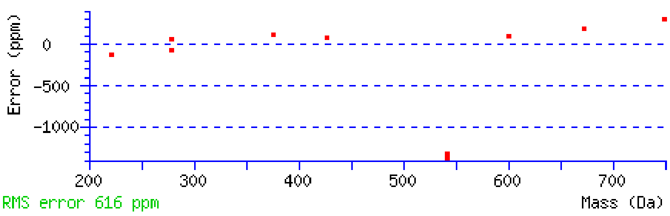
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 820.3728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.015
Matches : 10/42 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	73.0414	37.0244			A					7
2	***221.1069***	111.0571			F	***749.3459***	375.1766	731.3223	366.1648	6
3	***279.1254***	140.0663			G	***601.2805***	301.1439	583.2569	292.1321	5
4	395.1624	198.0848	377.1388	189.0730	N	***543.2620***	272.1346	525.2384	263.1228	4
5	***543.2278***	272.1175	525.2042	263.1058	F	***427.2250***	214.1161	409.2014	205.1043	3
6	***673.2805***	337.1439	655.2569	328.1321	Q	***279.1595***	140.0834	261.1359	131.0716	2
7					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of AFGNFQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.9	820.3728	-0.0003	AFGNFQK
12.0	820.3739	-0.0014	AMSRTTK
8.6	820.3739	-0.0014	MASRTTK

AT2G45290.1

8.0	820.3739	-0.0014	MATTRSK
3.2	820.3721	0.0003	MIMMKK
2.6	820.3705	0.0019	EGRSYAK
2.6	820.3705	0.0019	RADSYAK
1.9	820.3705	0.0019	GYERSAK
1.8	820.3728	-0.0003	AFPSSFR
1.8	820.3705	0.0019	AFSDKSR

Mascot: http://www.matrixscience.com/

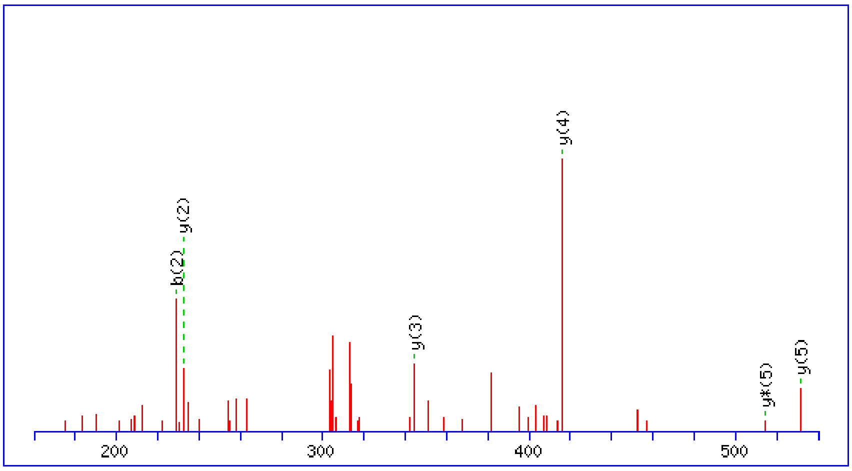
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDALGR**
Found in **AT2G45330.1** in **TAIR_Arabidopsis**, Symbols: EMB1067 | EMB1067 (EMBRYO DEFECTIVE 1067); tRNA 2'-phosphotransferase | chr2:18693414-18694948 FORWARD

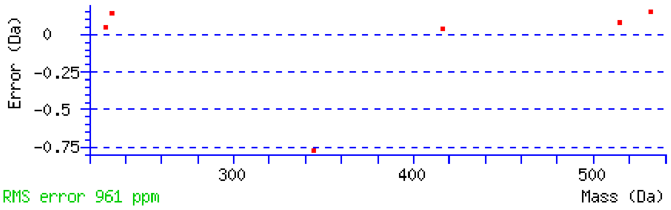
Match to Query 563: 643.366262 from(322.690407,2+) index(1243)
Title: Elution from: 18.012 to 18.012 scan no 1715 cid35.00 polarity:+
Data file C7-2_2.mgf

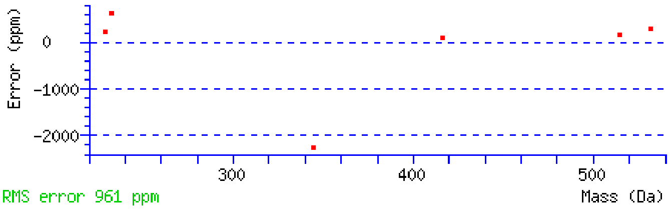
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 540 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 643.3653
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.03
Matches : 6/40 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							6
2	229.1183	115.0628	211.1077	106.0575	D	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	5
3	300.1554	150.5813	282.1448	141.5761	A	***416.2616***	208.6344	399.2350	200.1212			4
4	413.2395	207.1234	395.2289	198.1181	L	***345.2245***	173.1159	328.1979	164.6026			3
5	470.2609	235.6341	452.2504	226.6288	G	***232.1404***	116.5738	215.1139	108.0606			2
6					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IDALGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.7	643.3653	0.0010	IDALGR
25.9	643.3653	0.0010	LDLAGR
11.1	643.3653	0.0010	LEGGLR

AT2G45330.1

10.0	643.3653	0.0010	IEVQR
9.4	643.3653	0.0010	EIGIGR
9.3	643.3653	0.0010	IDQLR
9.3	643.3653	0.0010	LDQIR
9.3	643.3653	0.0010	LDQLR
8.4	643.3653	0.0010	LGAVER
8.0	643.3653	0.0010	DLAVAR

AT2G45470.1

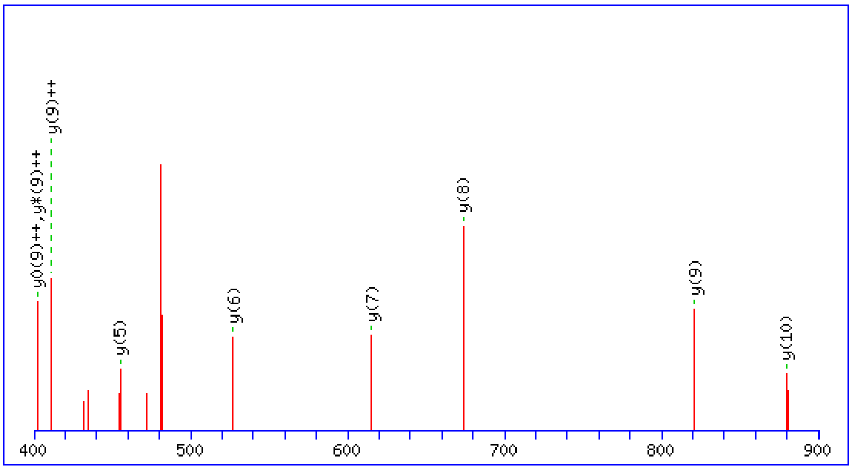
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGFGSAASGSK**
Found in **AT2G45470.1** in **TAIR_Arabidopsis**, Symbols: AGP8, FLA8 | FLA8 (Arabinogalactan protein 8) | chr2:18749871-18751133 REVERSE

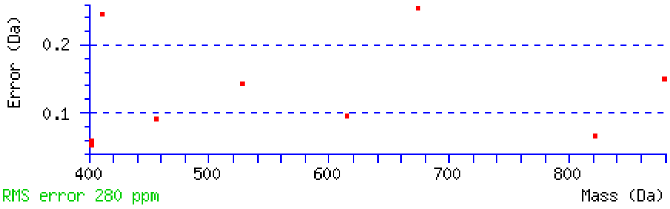
Match to Query 2265: 978.441156 from(490.227854,2+) index(759)
Title: Elution from: 13.337 to 13.337 scan no 1098 cid35.00 polarity:+
Data file D6h-3_1.mgf

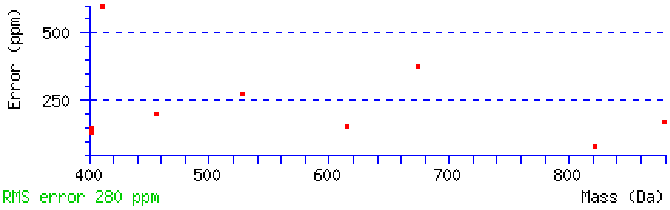
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 978.4415
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 4.9e-005
Matches : 9/90 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400			**V**							11
2	159.0912	80.0492			**G**	***879.3833***	440.1953	861.3597	431.1835	861.3727	431.1900	10
3	307.1567	154.0820			**F**	***821.3648***	411.1860	803.3412	402.1743	803.3542	402.1808	9
4	365.1752	183.0912			**G**	***673.2994***	337.1533	655.2758	328.1415	655.2888	328.1480	8
5	453.2042	227.1058	435.1937	218.1005	**S**	***615.2809***	308.1441	597.2573	299.1323	597.2703	299.1388	7
6	525.2384	263.1228	507.2278	254.1175	**A**	***527.2518***	264.1295	509.2282	255.1177	509.2412	255.1243	6
7	597.2725	299.1399	579.2620	290.1346	**A**	***455.2176***	228.1125	437.1941	219.1007	437.2071	219.1072	5
8	685.3016	343.1544	667.2910	334.1492	**S**	383.1835	192.0954	365.1599	183.0836	365.1729	183.0901	4
9	743.3201	372.1637	725.3095	363.1584	**G**	295.1544	148.0809	277.1309	139.0691	277.1439	139.0756	3
10	831.3492	416.1782	813.3386	407.1729	**S**	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
11					**K**	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VGFGSAASGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G45470.1

Score	Mr(calc)	Delta	Sequence
50.1	978.4415	-0.0003	VGFGSAASGSK
3.7	978.4415	-0.0003	VGSAYGSAQK
2.0	978.4393	0.0019	SSAGKSSQSK
0.1	978.4428	-0.0016	CKARCIR

AT2G45510.1

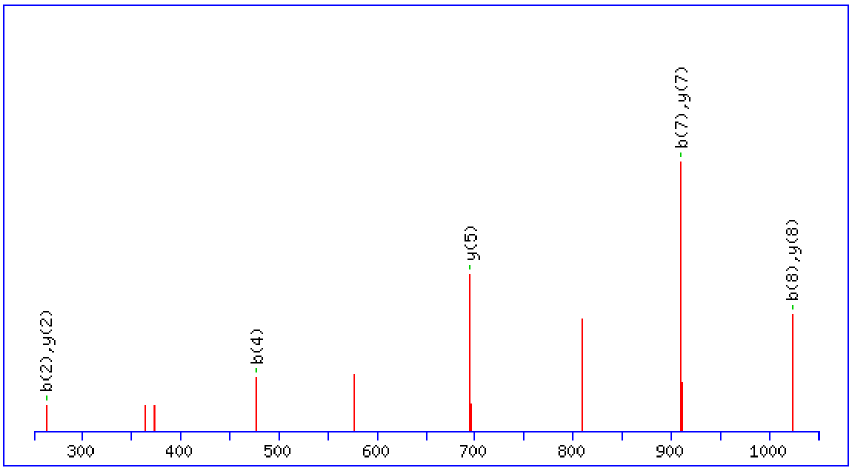
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FIDPLWKLK**
Found in **AT2G45510.1** in **TAIR_Arabidopsis**, Symbols: CYP704A2 | CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding | chr2:18760159-18762018 FORWARD

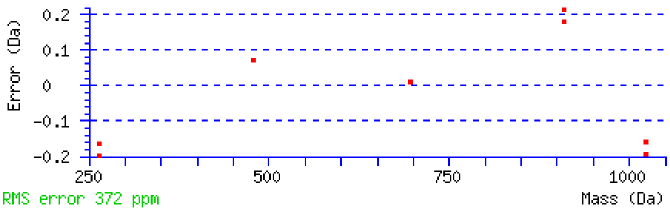
Match to Query 3870: 1170.642132 from(586.328342,2+) index(4485)
Title: Elution from: 41.193 to 41.193 scan no 5668 cid35.00 polarity:+
Data file D6h-3_2.mgf

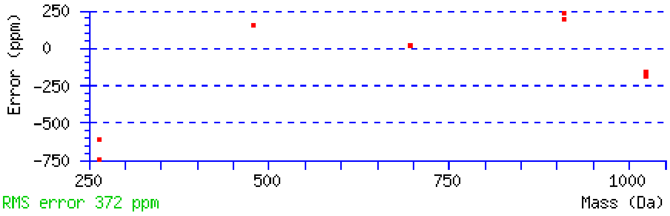
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1170.6445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.003
Matches : 8/68 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0727	75.0400					**F**							**9**
2	***263.1538***	132.0805					**I**	***1023.5864***	512.2968	1005.5628	503.2850	1005.5758	503.2915	**8**
3	379.1778	190.0925			361.1672	181.0873	**D**	***909.5053***	455.2563	891.4817	446.2445	891.4947	446.2510	**7**
4	***477.2276***	239.1174			459.2170	230.1122	**P**	793.4813	397.2443	775.4577	388.2325			**6**
5	591.3087	296.1580			573.2981	287.1527	**L**	***695.4315***	348.2194	677.4079	339.2076			**5**
6	779.3821	390.1947			761.3715	381.1894	**W**	581.3504	291.1788	563.3268	282.1670			**4**
7	***909.4711***	455.2392	891.4475	446.2274	891.4606	446.2339	**K**	393.2770	197.1421	375.2534	188.1303			**3**
8	***1023.5522***	512.2797	1005.5286	503.2680	1005.5417	503.2745	**L**	***263.1880***	132.0976	245.1644	123.0858			**2**
9							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of FIDPLWKLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT2G45510.1

33.0	1170.6445	-0.0024	FIDPLWKLK
15.1	1170.6401	0.0021	LAEEIRSVIK
15.1	1170.6401	0.0021	LRSAIEDLIK
15.1	1170.6401	0.0021	STAVPVINTKK
15.1	1170.6427	-0.0006	LGSVNVPRGKK
12.7	1170.6400	0.0021	LRDAITELVK
4.8	1170.6423	-0.0002	YNVLLAQPLK
4.2	1170.6423	-0.0002	VADFGLAKPLK
3.2	1170.6400	0.0021	GVIDGGTKVAIK
3.2	1170.6400	0.0021	KLQGEVDKLK

AT2G45680.1

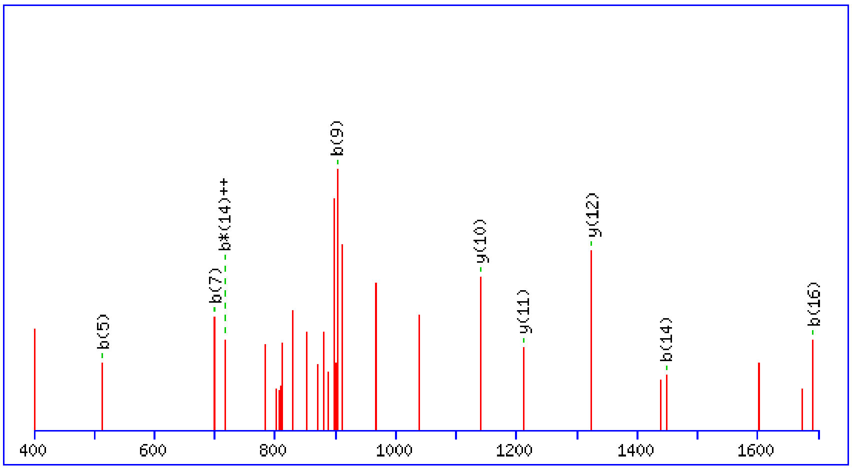
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPTTTNADSDMGENLMK**
Found in **AT2G45680.1** in **TAIR_Arabidopsis**, Symbols: | TCP family transcription factor, putative | chr2:18827791-18828861 REVERSE

Match to Query 8301: 1836.827830 from(919.421191,2+) index(4619)
Title: Elution from: 45.802 to 45.802 scan no 5953 cid35.00 polarity:+
Data file D1d-1-2.mgf

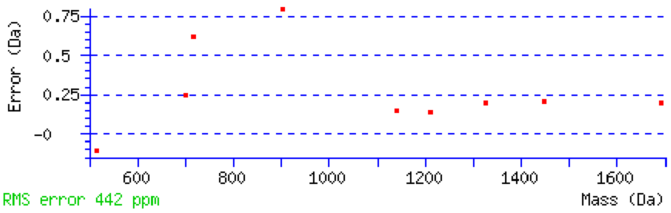
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

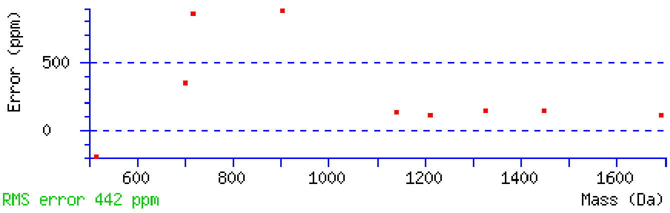


Monoisotopic mass of neutral peptide Mr(calc): 1836.8233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0013
Matches : 9/170 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							17
2	211.1441	106.0757					P	1724.7466	862.8769	1707.7200	854.3637	1706.7360	853.8716	16
3	312.1918	156.5995			294.1812	147.5942	T	1627.6938	814.3505	1610.6673	805.8373	1609.6832	805.3453	15
4	413.2395	207.1234			395.2289	198.1181	T	1526.6461	763.8267	1509.6196	755.3134	1508.6356	754.8214	14
5	***514.2871***	257.6472			496.2766	248.6419	T	1425.5985	713.3029	1408.5719	704.7896	1407.5879	704.2976	13
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	N	**1324.5508**	662.7790	1307.5242	654.2658	1306.5402	653.7737	12
7	***699.3672***	350.1872	682.3406	341.6740	681.3566	341.1819	A	**1210.5079**	605.7576	1193.4813	597.2443	1192.4973	596.7523	11
8	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	D	**1139.4707**	570.2390	1122.4442	561.7257	1121.4602	561.2337	10
9	***901.4262***	451.2167	884.3996	442.7034	883.4156	442.2114	S	1024.4438	512.7255	1007.4172	504.2123	1006.4332	503.7203	9
10	1016.4531	508.7302	999.4265	500.2169	998.4425	499.7249	D	937.4118	469.2095	920.3852	460.6962	919.4012	460.2042	8
11	1147.4936	574.2504	1130.4670	565.7372	1129.4830	565.2451	M	822.3848	411.6960	805.3583	403.1828	804.3743	402.6908	7
12	1204.5150	602.7612	1187.4885	594.2479	1186.5045	593.7559	G	691.3443	346.1758	674.3178	337.6625	673.3338	337.1705	6
13	1333.5576	667.2825	1316.5311	658.7692	1315.5471	658.2772	E	634.3229	317.6651	617.2963	309.1518	616.3123	308.6598	5
14	***1447.6006***	724.3039	1430.5740	715.7906	1429.5900	715.2986	N	505.2803	253.1438	488.2537	244.6305			4
15	1560.6846	780.8460	1543.6581	772.3327	1542.6741	771.8407	L	391.2374	196.1223	374.2108	187.6090			3
16	***1691.7251***	846.3662	1674.6986	837.8529	1673.7145	837.3609	M	278.1533	139.5803	261.1267	131.0670			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT2G45680.1





NCBI **BLAST** search of IPTTTNADSDMGENLMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.3	1836.8233	0.0045	IPTTTNADSDMGENLMK

Mascot: http://www.matrixscience.com/

AT2G45710.1

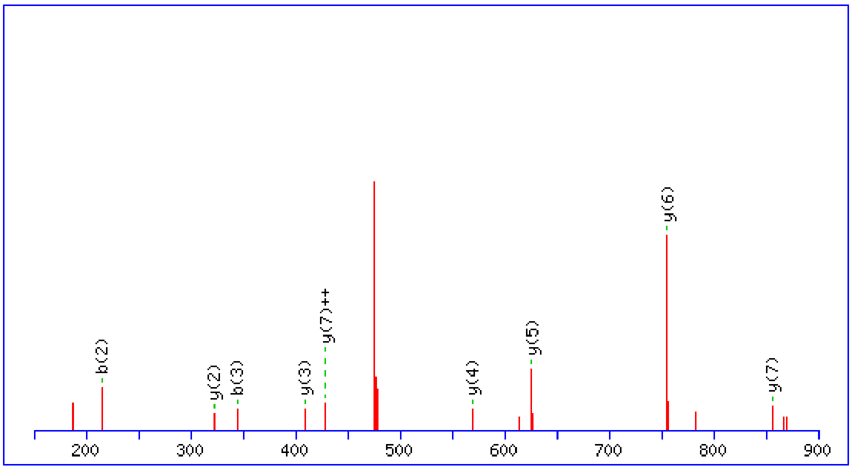
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTEGCSFR**
Found in **AT2G45710.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S27 (RPS27A) | chr2:18838317-18839073 FORWARD

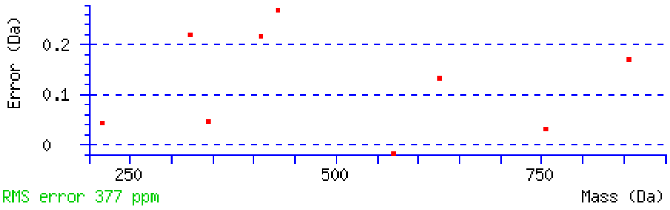
Match to Query 2235: 968.438958 from(485.226755,2+) index(1068)
Title: Elution from: 17.107 to 17.107 scan no 1518 cid35.00 polarity:+
Data file D12h-3_1.mgf

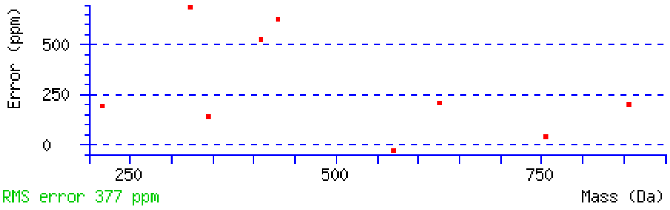
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.4386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00022
Matches : 9/64 fragment ions using 19 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493			L							8
2	**215.1390**	108.0731	197.1285	99.0679	T	***856.3618***	428.6845	839.3352	420.1713	838.3512	419.6792	7
3	**344.1816**	172.5944	326.1710	163.5892	E	***755.3141***	378.1607	738.2876	369.6474	737.3035	369.1554	6
4	401.2031	201.1052	383.1925	192.0999	G	***626.2715***	313.6394	609.2450	305.1261	608.2609	304.6341	5
5	561.2337	281.1205	543.2232	272.1152	C	***569.2500***	285.1287	552.2235	276.6154	551.2395	276.1234	4
6	648.2658	324.6365	630.2552	315.6312	S	***409.2194***	205.1133	392.1928	196.6001	391.2088	196.1081	3
7	795.3342	398.1707	777.3236	389.1654	F	***322.1874***	161.5973	305.1608	153.0840			2
8					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LTEGCSFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.4	968.4386	0.0004	LTEGCSFR
1.4	968.4386	0.0004	DINSFAMR

AT2G45710.1

Mascot: http://www.matrixscience.com/

AT2G45740.1

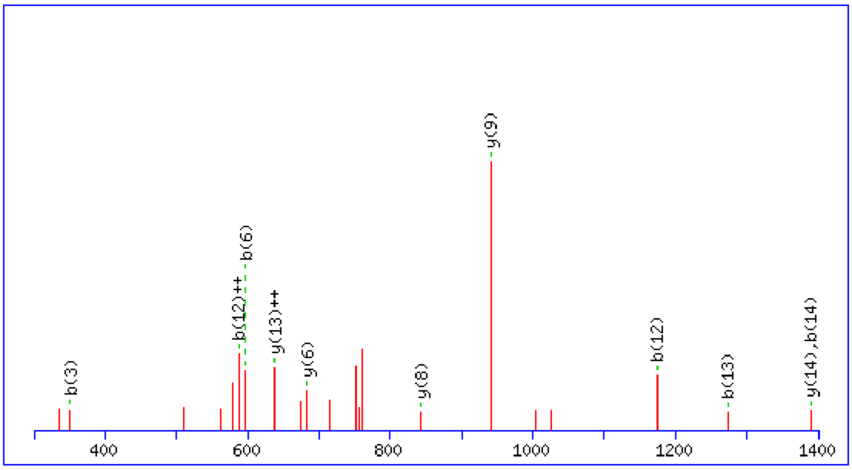
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLSGGQPGTAQNVDK**
Found in **AT2G45740.1** in **TAIR_Arabidopsis**, Symbols: PEX11D | PEX11D | chr2:18846939-18848176 FORWARD

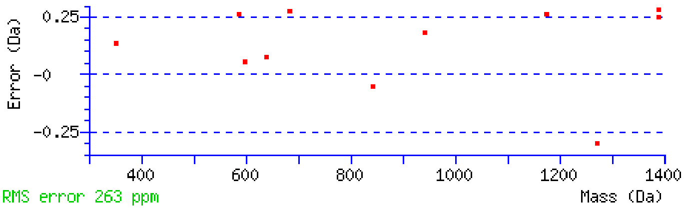
Match to Query 7036: 1536.690048 from(769.352300,2+) index(2119)
Title: Elution from: 24.738 to 24.738 scan no 2744 cid35.00 polarity:+
Data file D12h-1_1.mgf

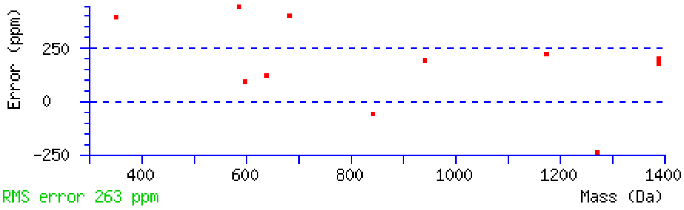
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1536.6911
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0031
Matches : 11/152 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							15
2	263.1538	132.0805					L	***1389.6329***	695.3201	1371.6093	686.3083	1371.6223	686.3148	14
3	***351.1829***	176.0951			333.1723	167.0898	S	1275.5518	638.2795	1257.5282	629.2678	1257.5412	629.2743	13
4	409.2014	205.1043			391.1908	196.0990	G	1187.5227	594.2650	1169.4992	585.2532	1169.5122	585.2597	12
5	467.2199	234.1136			449.2093	225.1083	G	1129.5043	565.2558	1111.4807	556.2440	1111.4937	556.2505	11
6	***597.2725***	299.1399	579.2489	290.1281	579.2620	290.1346	Q	1071.4858	536.2465	1053.4622	527.2347	1053.4752	527.2412	10
7	695.3223	348.1648	677.2987	339.1530	677.3118	339.1595	P	***941.4331***	471.2202	923.4095	462.2084	923.4225	462.2149	9
8	753.3408	377.1741	735.3172	368.1623	735.3303	368.1688	G	***843.3833***	422.1953	825.3597	413.1835	825.3727	413.1900	8
9	855.3855	428.1964	837.3620	419.1846	837.3750	419.1911	T	785.3648	393.1860	767.3412	384.1742	767.3542	384.1808	7
10	927.4197	464.2135	909.3961	455.2017	909.4091	455.2082	A	***683.3201***	342.1637	665.2965	333.1519	665.3095	333.1584	6
11	1057.4723	529.2398	1039.4488	520.2280	1039.4618	520.2345	Q	611.2859	306.1466	593.2624	297.1348	593.2754	297.1413	5
12	***1173.5093***	587.2583	1155.4858	578.2465	1155.4988	578.2530	N	481.2333	241.1203	463.2097	232.1085	463.2227	232.1150	4
13	***1273.5748***	637.2910	1255.5512	628.2792	1255.5642	628.2857	V	365.1963	183.1018	347.1727	174.0900	347.1857	174.0965	3
14	***1389.5988***	695.3030	1371.5752	686.2912	1371.5882	686.2977	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FLSGGQPGTAQNVDK

AT2G45740.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.0	1536.6911	-0.0010	FLSGGQPGTAQNVDK
10.9	1536.6884	0.0016	SAPSSVLAAFVDDDK
7.5	1536.6897	0.0003	TASTGYMSRRLMK
7.0	1536.6888	0.0012	DESRNDGSLANVLK
5.3	1536.6920	-0.0019	KWNVALMSMSAHK
4.6	1536.6897	0.0003	LRACLADTNVCPK
2.8	1536.6884	0.0017	EFLDEQSQLADVK
2.8	1536.6884	0.0017	LNDVESLDAFGVDK
1.6	1536.6897	0.0003	TASTGYMSRRLMK
0.9	1536.6933	-0.0033	NSIYISGFDYGRK

AT2G45790.1

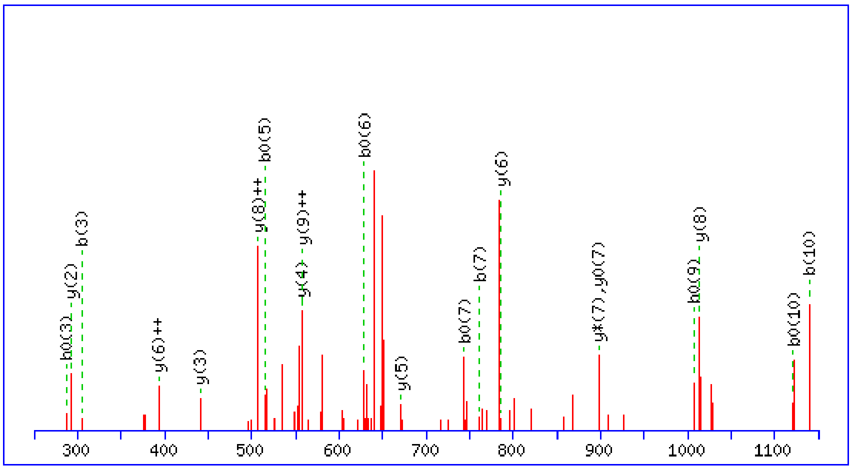
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EATPELLDFIR**
Found in **AT2G45790.1** in **TAIR_Arabidopsis**, Symbols: ATPMM | ATPMM; phosphomannomutase | chr2:18862950-18864827 FORWARD

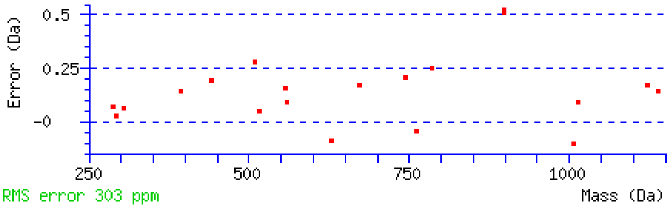
Match to Query 4796: 1316.637870 from(659.326211,2+) index(9444)
Title: Elution from: 86.824 to 86.824 scan no 13056 cid35.00 polarity:+
Data file 0-2_2.mgf

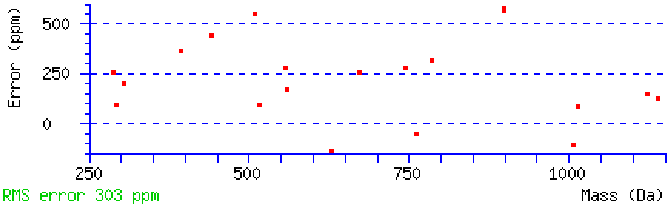
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1316.6404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.036
Matches : 20/94 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							11
2	203.0811	102.0442	185.0705	93.0389	A	1187.6081	594.3077	1169.5845	585.2959	1169.5975	585.3024	10
3	**305.1258**	153.0665	287.1152	144.0612	T	1115.5740	558.2906	1097.5504	549.2788	1097.5634	549.2853	9
4	403.1756	202.0914	385.1650	193.0861	P	***1013.5292***	507.2683	995.5057	498.2565	995.5187	498.2630	8
5	533.2152	267.1112	515.2046	258.1060	E	915.4794	458.2434	897.4559	449.2316	897.4689	449.2381	7
6	647.2963	324.1518	629.2857	315.1465	L	***785.4398***	393.2235	767.4162	384.2118	767.4293	384.2183	6
7	**761.3774**	381.1923	743.3668	372.1871	L	***671.3587***	336.1830	653.3351	327.1712	653.3482	327.1777	5
8	877.4014	439.2043	859.3908	430.1990	D	***557.2776***	279.1424	539.2540	270.1307	539.2671	270.1372	4
9	1025.4668	513.2370	1007.4563	504.2318	F	***441.2536***	221.1305	423.2301	212.1187			3
10	**1139.5479**	570.2776	1121.5374	561.2723	I	***293.1882***	147.0977	275.1646	138.0859			2
11					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EATPELLDFIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G45790.1

Score	Mr(calc)	Delta	Sequence
22.7	1316.6404	-0.0026	EATPELLDFIR
9.9	1316.6361	0.0017	HTMRDLVASIR
2.3	1316.6382	-0.0003	SNVLEQELAATK

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYQALGGGANTIAHGYTK**
Found in **AT2G45960.1** in **TAIR_Arabidopsis**, Symbols: TMP-A, ATHH2, PIP1;2, PIP1B | PIP1B (plasma membrane intrinsic protein 1;2); water channel | chr2:18917523-18918776 FORWARD

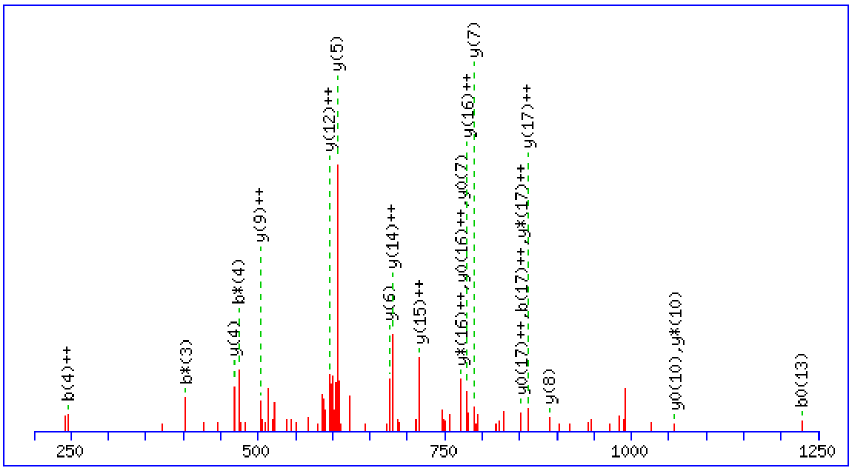
Match to Query 9393: 1848.908532 from(617.310120,3+) index(3525)
Title: Elution from: 34.321 to 34.321 scan no 4346 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1250 Da Full range

Label all possible matches ○ Label matches used for scoring ●

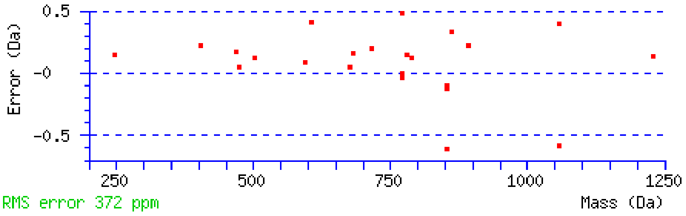
Show Y-axis ☐

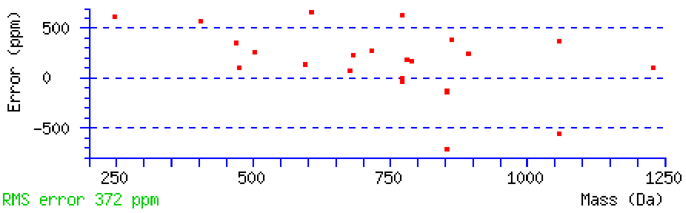


Monoisotopic mass of neutral peptide Mr(calc): 1848.9119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0014
Matches : 23/182 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			**Q**							**18**
2	292.1292	146.5682	275.1026	138.0550			**Y**	1721.8606	861.4339	1704.8340	852.9206	1703.8500	852.4286	**17**
3	420.1878	210.5975	403.1612	202.0842			**Q**	1558.7972	779.9023	1541.7707	771.3890	1540.7867	770.8970	**16**
4	491.2249	246.1161	474.1983	237.6028			**A**	1430.7387	715.8730	1413.7121	707.3597	1412.7281	706.8677	**15**
5	604.3089	302.6581	587.2824	294.1448			**L**	1359.7015	680.3544	1342.6750	671.8411	1341.6910	671.3491	**14**
6	661.3304	331.1688	644.3039	322.6556			**G**	1246.6175	623.8124	1229.5909	615.2991	1228.6069	614.8071	**13**
7	718.3519	359.6796	701.3253	351.1663			**G**	1189.5960	595.3016	1172.5695	586.7884	1171.5854	586.2964	**12**
8	775.3733	388.1903	758.3468	379.6770			**G**	1132.5746	566.7909	1115.5480	558.2776	1114.5640	557.7856	**11**
9	846.4104	423.7089	829.3839	415.1956			**A**	1075.5531	538.2802	1058.5265	529.7669	1057.5425	529.2749	**10**
10	960.4534	480.7303	943.4268	472.2170			**N**	1004.5160	502.7616	987.4894	494.2483	986.5054	493.7563	**9**
11	1061.5011	531.2542	1044.4745	522.7409	1043.4905	522.2489	**T**	***890.4730***	445.7402	873.4465	437.2269	872.4625	436.7349	**8**
12	1174.5851	587.7962	1157.5586	579.2829	1156.5746	578.7909	**I**	***789.4254***	395.2163	772.3988	386.7030	771.4148	386.2110	**7**
13	1245.6222	623.3148	1228.5957	614.8015	1227.6117	614.3095	**A**	***676.3413***	338.6743	659.3148	330.1610	658.3307	329.6690	**6**
14	1382.6811	691.8442	1365.6546	683.3309	1364.6706	682.8389	**H**	***605.3042***	303.1557	588.2776	294.6425	587.2936	294.1504	**5**
15	1439.7026	720.3549	1422.6761	711.8417	1421.6920	711.3497	**G**	***468.2453***	234.6263	451.2187	226.1130	450.2347	225.6210	**4**
16	1602.7659	801.8866	1585.7394	793.3733	1584.7554	792.8813	**Y**	411.2238	206.1155	394.1973	197.6023	393.2132	197.1103	**3**
17	1703.8136	852.4104	1686.7871	843.8972	1685.8030	843.4052	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT2G45960.1





NCBI **BLAST** search of QYQALGGGANTIAHGYTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.5	1848.9119	-0.0033	QYQALGGGANTIAHGYTK
4.4	1848.9047	0.0039	MGGAAVLLSNRSSDRCR
3.0	1848.9087	-0.0001	MASIRRTLSPMYHDR
0.6	1848.9078	0.0007	FRSDNNAGKPTSVEATR

Mascot: http://www.matrixscience.com/

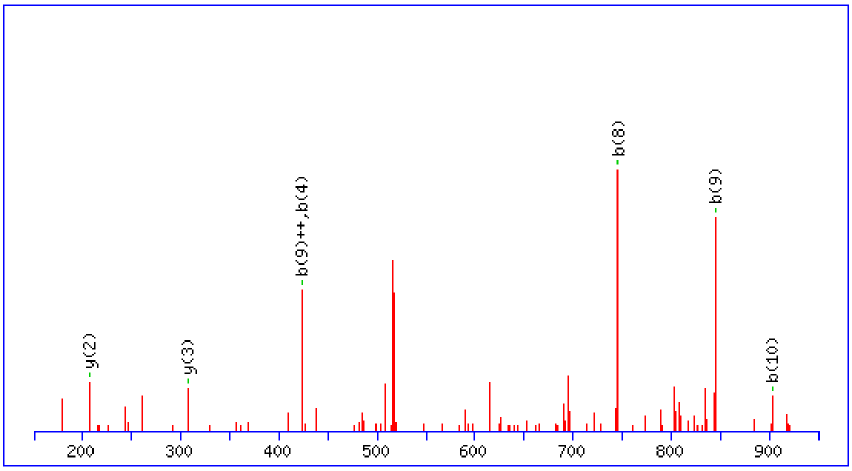
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGMVGSSSVGK**
Found in **AT2G46020.1** in **TAIR_Arabidopsis**, Symbols: ATBRM, CHR2, BRM | ATBRM/BRM/CHR2 (ARABIDOPSIS THALIANA BRAHMA); ATP binding / DNA binding / helicase/ transcription regulator | chr2:18930377-18938842 FORWARD

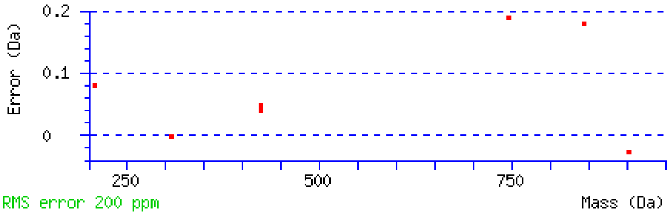
Match to Query 2474: 1050.450684 from(526.232618,2+) index(3877)
Title: Elution from: 37.666 to 37.666 scan no 4927 cid35.00 polarity:+
Data file D12h-2_3.mgf

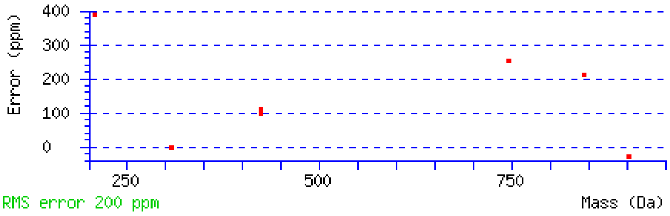
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1050.4482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0043
Matches : 7/84 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260			M							11
2	191.0633	96.0353			G	919.4180	460.2126	901.3944	451.2008	901.4074	451.2073	10
3	323.1008	162.0540			M	861.3995	431.2034	843.3759	422.1916	843.3889	422.1981	9
4	***423.1663***	212.0868			V	729.3620	365.1846	711.3384	356.1728	711.3514	356.1793	8
5	481.1848	241.0960			G	629.2965	315.1519	611.2729	306.1401	611.2859	306.1466	7
6	569.2138	285.1106	551.2033	276.1053	S	571.2780	286.1426	553.2544	277.1309	553.2674	277.1374	6
7	657.2429	329.1251	639.2323	320.1198	S	483.2489	242.1281	465.2254	233.1163	465.2384	233.1228	5
8	***745.2720***	373.1396	727.2614	364.1343	S	395.2199	198.1136	377.1963	189.1018	377.2093	189.1083	4
9	***845.3374***	423.1723	827.3268	414.1671	V	**307.1908**	154.0990	289.1672	145.0873			3
10	***903.3559***	452.1816	885.3453	443.1763	G	**207.1254**	104.0663	189.1018	95.0545			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MGMVGSSSVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G46020.1

Score	Mr(calc)	Delta	Sequence
31.8	1050.4482	0.0025	MGMVGSSSVGK
27.8	1050.4518	-0.0011	GFVEEDFAK
15.0	1050.4500	0.0007	TSGGKDSASAR
7.9	1050.4500	0.0007	GSTRTGEGSGK
4.4	1050.4522	-0.0015	GFTVNGETGR
3.1	1050.4482	0.0025	VQENMKMK
3.1	1050.4482	0.0025	VSAMVQCTK
2.8	1050.4518	-0.0011	FVENEFEK
1.5	1050.4530	-0.0023	IMSSSLSDGK
1.1	1050.4522	-0.0016	TLGQNYGER

AT2G46040.1

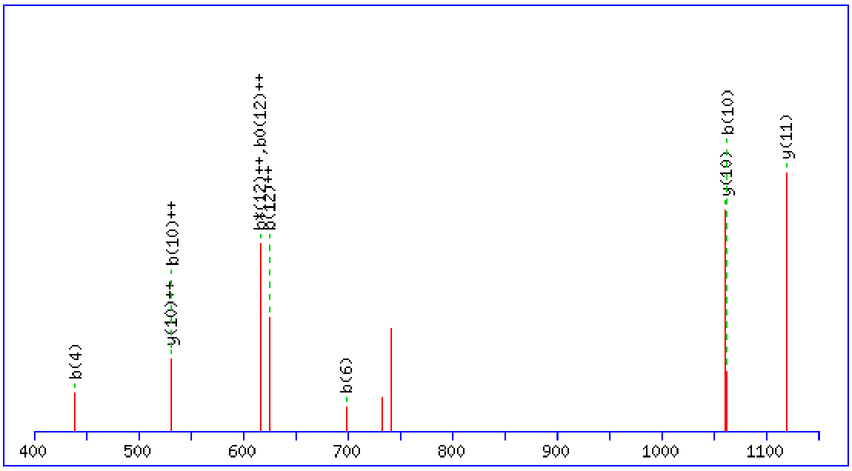
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HHVGKESASNDAVK**
Found in **AT2G46040.1** in **TAIR_Arabidopsis**, Symbols: | ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein | chr2:18942757-18944880 REVERSE

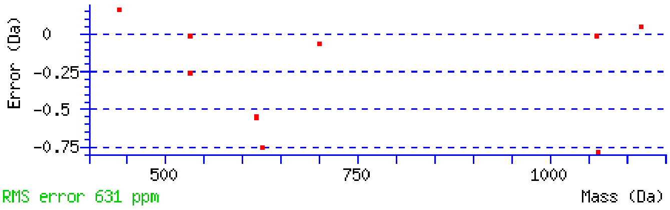
Match to Query 6239: 1498.667802 from(750.341177,2+) index(4842)
Title: Elution from: 45.053 to 45.053 scan no 6085 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

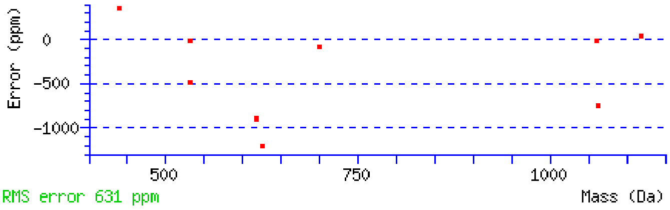


Monoisotopic mass of neutral peptide Mr(calc): 1498.6651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.015
Matches : 10/132 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	141.0573	71.0323					**H**							**14**
2	281.1073	141.0573					**H**	1359.6223	680.3148	1341.5988	671.3030	1341.6118	671.3095	**13**
3	381.1728	191.0900					**V**	1219.5723	610.2898	1201.5487	601.2780	1201.5618	601.2845	**12**
4	***439.1913***	220.0993					**G**	***1119.5069***	560.2571	1101.4833	551.2453	1101.4963	551.2518	**11**
5	569.2803	285.1438	551.2567	276.1320			**K**	***1061.4884***	531.2478	1043.4648	522.2360	1043.4778	522.2425	**10**
6	***699.3199***	350.1636	681.2963	341.1518	681.3094	341.1583	**E**	931.3993	466.2033	913.3758	457.1915	913.3888	457.1980	**9**
7	787.3490	394.1781	769.3254	385.1663	769.3384	385.1728	**S**	801.3597	401.1835	783.3361	392.1717	783.3492	392.1782	**8**
8	859.3831	430.1952	841.3595	421.1834	841.3726	421.1899	**A**	713.3307	357.1690	695.3071	348.1572	695.3201	348.1637	**7**
9	947.4122	474.2097	929.3886	465.1979	929.4016	465.2045	**S**	641.2965	321.1519	623.2729	312.1401	623.2859	312.1466	**6**
10	***1063.4492***	***532.2282***	1045.4256	523.2164	1045.4386	523.2230	**N**	553.2674	277.1374	535.2439	268.1256	535.2569	268.1321	**5**
11	1179.4732	590.2402	1161.4496	581.2284	1161.4626	581.2349	**D**	437.2304	219.1189	419.2069	210.1071	419.2199	210.1136	**4**
12	1251.5073	***626.2573***	1233.4837	617.2455	1233.4968	617.2520	**A**	321.2065	161.1069	303.1829	152.0951			**3**
13	1351.5728	676.2900	1333.5492	667.2782	1333.5622	667.2847	**V**	249.1723	125.0898	231.1487	116.0780			**2**
14							**K**	149.1069	75.0571	131.0833	66.0453			**1**



RMS error 631 ppm



RMS error 631 ppm

NCBI **BLAST** search of HHVGKESASNDAVK

AT2G46040.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.4	1498.6651	0.0027	HHVGKESASNDAVK
12.8	1498.6707	-0.0029	DAFSLCVQQGAKR
4.6	1498.6705	-0.0027	SDVDDSSSKSVKTK
3.2	1498.6669	0.0009	SEFALAISHGFFSA
3.0	1498.6680	-0.0002	NVVSWTTMISSNK
3.0	1498.6680	-0.0002	ITVGGEDVRMFDK
2.6	1498.6637	0.0041	MGGGNAQKSAMARAK
2.2	1498.6680	-0.0002	EFELEMEQKRK
2.2	1498.6680	-0.0002	MQRLVFEASEEK
2.1	1498.6680	-0.0002	TFTMSGPRDLTEK

Mascot: http://www.matrixscience.com/

AT2G46280.1

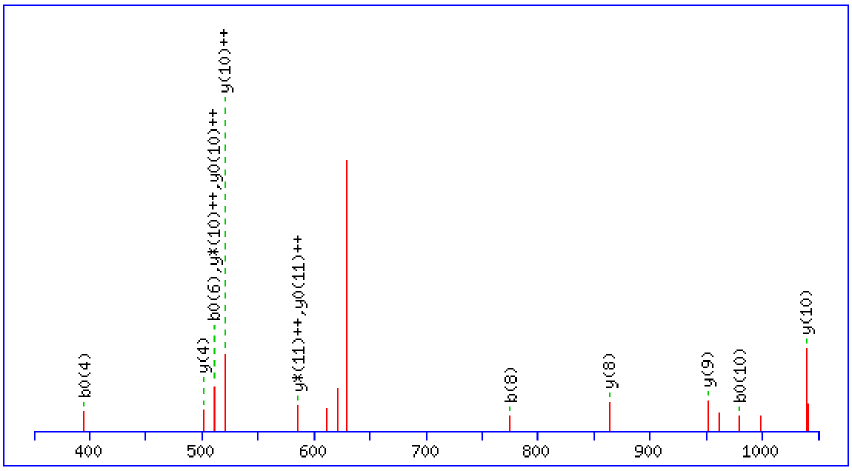
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFSSGGEDGYVR**
Found in **AT2G46280.1** in **TAIR_Arabidopsis**, Symbols: TIF3I1, TRIP-1 | TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); nucleotide binding / protein binding | chr2:19010729-19012466 REVERSE

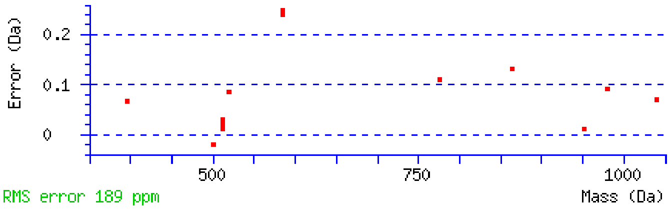
Match to Query 4575: 1274.500646 from(638.257599,2+) index(2107)
Title: Elution from: 23.831 to 23.831 scan no 2681 cid35.00 polarity:+
Data file D6h-3_2.mgf

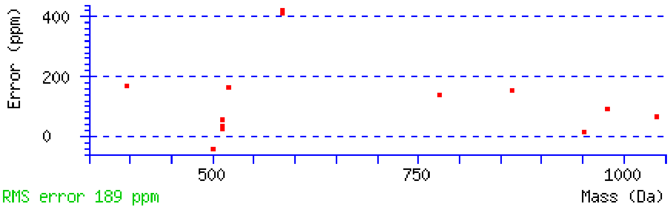
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1274.4973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.033
Matches : 13/102 fragment ions using 18 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218	71.0258	36.0165	S							12
2	237.1018	119.0545	219.0912	110.0492	F	1187.4756	594.2414	1169.4520	585.2296	1169.4650	585.2361	11
3	325.1309	163.0691	307.1203	154.0638	S	***1039.4101***	520.2087	1021.3866	511.1969	1021.3996	511.2034	10
4	413.1599	207.0836	395.1493	198.0783	S	***951.3811***	476.1942	933.3575	467.1824	933.3705	467.1889	9
5	471.1784	236.0928	453.1678	227.0876	G	***863.3520***	432.1796	845.3284	423.1679	845.3414	423.1744	8
6	529.1969	265.1021	511.1863	256.0968	G	805.3335	403.1704	787.3099	394.1586	787.3229	394.1651	7
7	659.2365	330.1219	641.2260	321.1166	E	747.3150	374.1611	729.2914	365.1494	729.3044	365.1559	6
8	775.2605	388.1339	757.2500	379.1286	D	617.2754	309.1413	599.2518	300.1295	599.2648	300.1360	5
9	833.2790	417.1431	815.2685	408.1379	G	***501.2514***	251.1293	483.2278	242.1175			4
10	997.3394	499.1733	979.3288	490.1680	Y	443.2329	222.1201	425.2093	213.1083			3
11	1097.4048	549.2061	1079.3943	540.2008	V	279.1725	140.0899	261.1490	131.0781			2
12					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SFSSGGEDGYVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G46280.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.0	1274.4973	0.0033	SFSSGGEDGYVR
8.3	1274.4969	0.0037	ADDDYDYLFK
4.5	1274.5030	-0.0023	MQYLFDESGR
4.5	1274.5030	-0.0023	MQYLYDESGR

AT2G46820.1

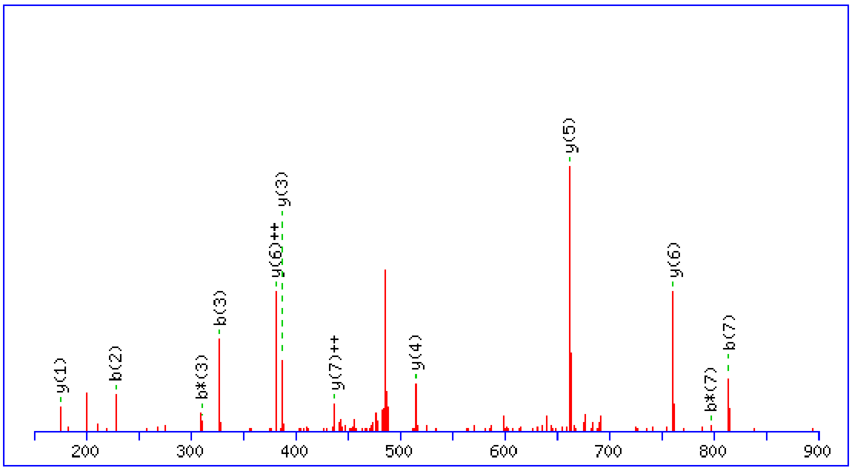
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLVFKPDR**
Found in **AT2G46820.1** in **TAIR_Arabidopsis**, Symbols: PTAC8, TMP14, PSAP, PSI-P | PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA); DNA binding | chr2:19250798-19251939 FORWARD

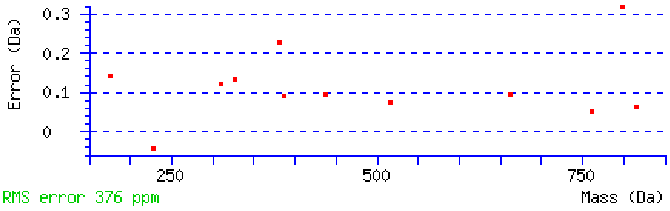
Match to Query 2348: 987.550290 from(494.782421,2+) index(1878)
Title: Elution from: 23.481 to 23.481 scan no 2482 cid35.00 polarity:+
Data file 0-1_2.mgf

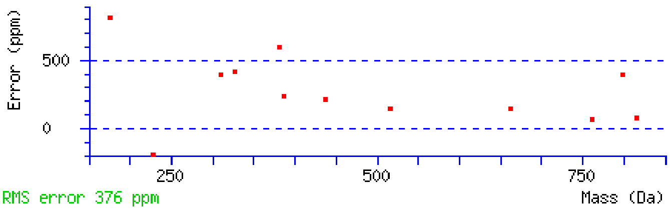
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 987.5502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0014
Matches : 12/70 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	**228.1343**	114.5708	211.1077	106.0575			L	874.5145	437.7609	857.4880	429.2476	856.5039	428.7556	7
3	**327.2027**	164.1050	310.1761	155.5917			V	***761.4305***	381.2189	744.4039	372.7056	743.4199	372.2136	6
4	474.2711	237.6392	457.2445	229.1259			F	***662.3620***	331.6847	645.3355	323.1714	644.3515	322.6794	5
5	602.3661	301.6867	585.3395	293.1734			K	***515.2936***	258.1504	498.2671	249.6372	497.2831	249.1452	4
6	699.4188	350.2130	682.3923	341.6998			P	***387.1987***	194.1030	370.1721	185.5897	369.1881	185.0977	3
7	**814.4458**	407.7265	797.4192	399.2132	796.4352	398.7212	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of NLVFKPDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.1	987.5502	0.0001	NLVFKPDR

AT2G46820.1

13.1	987.5502	0.0001	AGVVPVQYR
6.7	987.5501	0.0001	NLSSWLLR
2.2	987.5501	0.0001	SIINWSIR

Mascot: http://www.matrixscience.com/

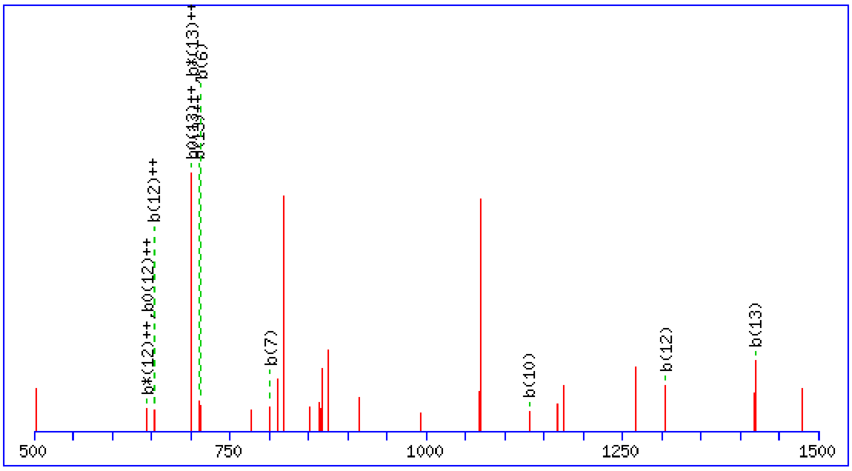
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YINVSKSDLVNGIVTK**
Found in **AT2G46915.1** in **TAIR_Arabidopsis**, Symbols: | similar to sodium:dicarboxylate symporter [Arabidopsis thaliana] (TAIR:AT3G19340.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24360.1) | chr2:19281087-19284776 REVERSE

Match to Query 8760: 1768.912368 from(885.463460,2+) index(7668)
Title: Elution from: 67.341 to 67.341 scan no 9915 cid35.00 polarity:+
Data file C7-2_1.mgf

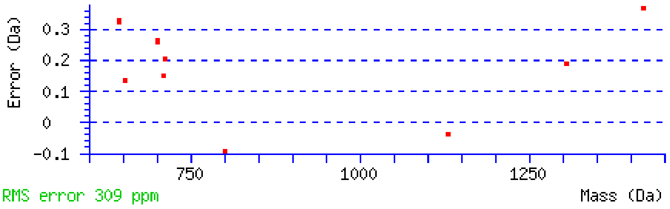
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

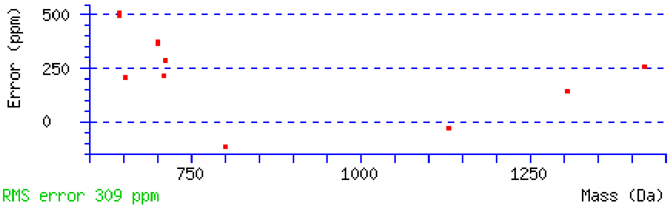


Monoisotopic mass of neutral peptide Mr(calc): 1768.9079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.041
Matches : 11/166 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							16
2	279.1487	140.0780					I	1605.8549	803.4311	1587.8313	794.4193	1587.8443	794.4258	15
3	395.1857	198.0965	377.1622	189.0847			N	1491.7738	746.3905	1473.7502	737.3787	1473.7632	737.3852	14
4	495.2512	248.1292	477.2276	239.1174			V	1375.7368	688.3720	1357.7132	679.3602	1357.7262	679.3667	13
5	583.2802	292.1438	565.2567	283.1320	565.2697	283.1385	S	1275.6713	638.3393	1257.6477	629.3275	1257.6608	629.3340	12
6	***713.3693***	357.1883	695.3457	348.1765	695.3587	348.1830	K	1187.6423	594.3248	1169.6187	585.3130	1169.6317	585.3195	11
7	***801.3983***	401.2028	783.3748	392.1910	783.3878	392.1975	S	1057.5532	529.2802	1039.5296	520.2685	1039.5427	520.2750	10
8	917.4223	459.2148	899.3987	450.2030	899.4118	450.2095	D	969.5242	485.2657	951.5006	476.2539	951.5136	476.2604	9
9	1031.5034	516.2553	1013.4798	507.2436	1013.4929	507.2501	L	853.5002	427.2537	835.4766	418.2419	835.4896	418.2484	8
10	***1131.5689***	566.2881	1113.5453	557.2763	1113.5583	557.2828	V	739.4191	370.2132	721.3955	361.2014	721.4085	361.2079	7
11	1247.6059	624.3066	1229.5823	615.2948	1229.5953	615.3013	N	639.3536	320.1805	621.3300	311.1687	621.3431	311.1752	6
12	***1305.6244***	**653.3158**	1287.6008	644.3040	1287.6138	644.3105	G	523.3166	262.1620	505.2930	253.1502	505.3061	253.1567	5
13	***1419.7055***	**710.3564**	1401.6819	701.3446	1401.6949	701.3511	I	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
14	1519.7709	760.3891	1501.7473	751.3773	1501.7603	751.3838	V	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
15	1621.8156	811.4115	1603.7920	802.3997	1603.8051	802.4062	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT2G46915.1





NCBI **BLAST** search of [YINVSKSDLVNGIVTK]

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways]

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	1768.9079	0.0044	YINVSKSDLVNGIVTK
1.5	1768.9079	0.0044	LSDFERLTAEIKSLK
1.5	1768.9162	-0.0038	MGARDLLALVATVVFR
1.5	1768.9106	0.0018	SIRPTTVGFTARLEAK
0.3	1768.9129	-0.0005	IPKRKPYQENFTVK

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFYDLLER**
Found in **AT2G47380.1** in **TAIR_Arabidopsis**, Symbols: | cytochrome c oxidase subunit Vc family protein / COX5C family protein | chr2:19448764-19448958 FORWARD

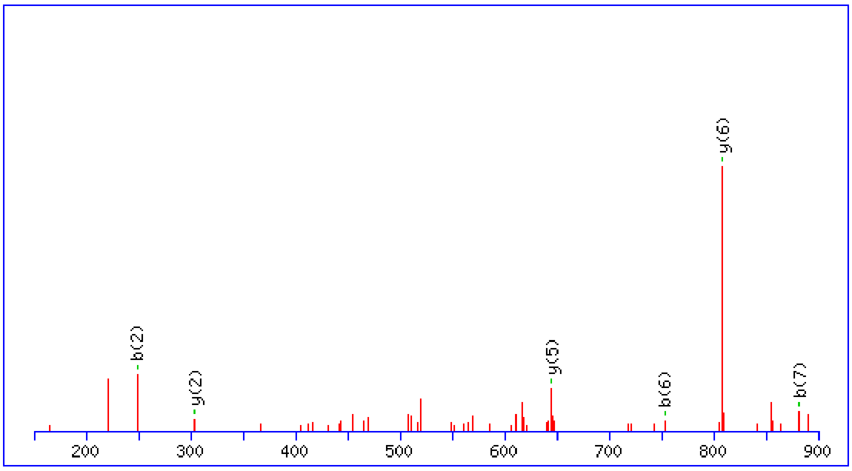
Match to Query 3153: 1055.529038 from(528.771795,2+) index(8104)
Title: Elution from: 70.430 to 70.430 scan no 10407 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

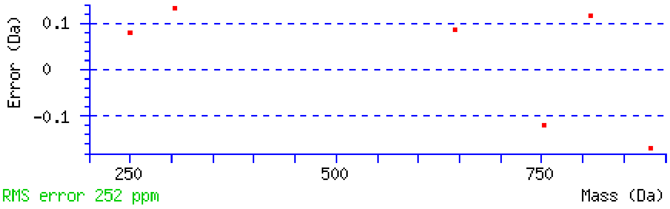
Label all possible matches ○ Label matches used for scoring ●

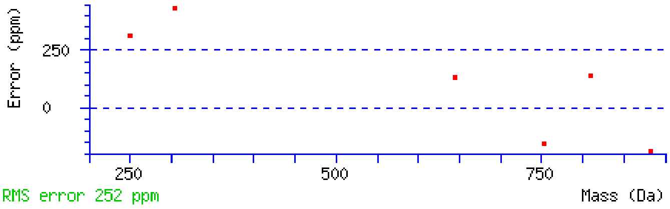
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1055.5287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0041
Matches : 6/68 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							8
2	***249.1234***	125.0653	231.1128	116.0600	F	955.4884	478.2478	938.4618	469.7345	937.4778	469.2425	7
3	412.1867	206.5970	394.1761	197.5917	Y	***808.4199***	404.7136	791.3934	396.2003	790.4094	395.7083	6
4	527.2136	264.1105	509.2031	255.1052	D	***645.3566***	323.1819	628.3301	314.6687	627.3461	314.1767	5
5	640.2977	320.6525	622.2871	311.6472	L	530.3297	265.6685	513.3031	257.1552	512.3191	256.6632	4
6	***753.3818***	377.1945	735.3712	368.1892	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
7	***882.4244***	441.7158	864.4138	432.7105	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
8					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TFYDLLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.7	1055.5287	0.0003	TFYDLLER

AT2G47380.1

2.8	1055.5288	0.0003	FTFTNIDAK

Mascot: http://www.matrixscience.com/

AT2G47390.1

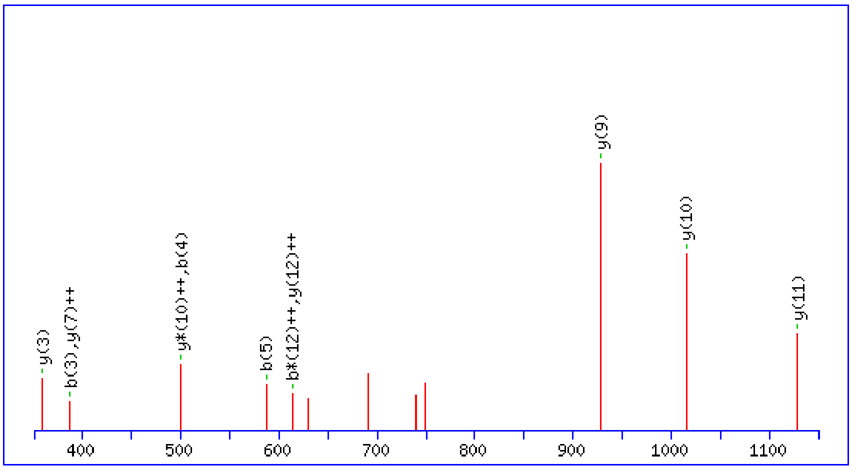
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWVISPGSNDVSPR**
Found in **AT2G47390.1** in **TAIR_Arabidopsis**, Symbols: | serine-type endopeptidase/ serine-type peptidase | chr2:19449348-19453323 REVERSE

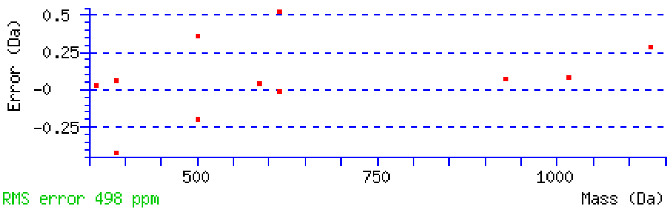
Match to Query 6316: 1513.754802 from(757.884677,2+) index(5020)
Title: Elution from: 45.562 to 45.562 scan no 6331 cid35.00 polarity:+
Data file D6h-1_3.mgf

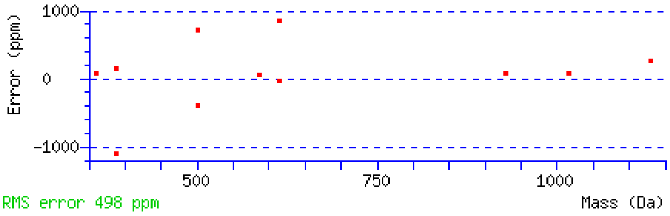
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1513.7525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0018
Matches : 11/136 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	288.1343	144.5708			270.1237	135.5655	W	1413.7121	707.3597	1396.6856	698.8464	1395.7015	698.3544	13
3	**387.2027**	194.1050			369.1921	185.0997	V	1227.6328	614.3200	1210.6062	605.8068	1209.6222	605.3148	12
4	**500.2867**	250.6470			482.2762	241.6417	I	***1128.5644***	564.7858	1111.5378	556.2726	1110.5538	555.7805	11
5	**587.3188**	294.1630			569.3082	285.1577	S	***1015.4803***	508.2438	998.4538	499.7305	997.4697	499.2385	10
6	684.3715	342.6894			666.3610	333.6841	P	***928.4483***	464.7278	911.4217	456.2145	910.4377	455.7225	9
7	741.3930	371.2001			723.3824	362.1949	G	831.3955	416.2014	814.3690	407.6881	813.3850	407.1961	8
8	828.4250	414.7162			810.4145	405.7109	S	774.3741	387.6907	757.3475	379.1774	756.3635	378.6854	7
9	942.4680	471.7376	925.4414	463.2243	924.4574	462.7323	N	687.3420	344.1747	670.3155	335.6614	669.3315	335.1694	6
10	1057.4949	529.2511	1040.4684	520.7378	1039.4843	520.2458	D	573.2991	287.1532	556.2726	278.6399	555.2885	278.1479	5
11	1156.5633	578.7853	1139.5368	570.2720	1138.5527	569.7800	V	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	4
12	1243.5953	622.3013	1226.5688	613.7880	1225.5848	613.2960	S	***359.2037***	180.1055	342.1772	171.5922	341.1932	171.1002	3
13	1340.6481	670.8277	1323.6216	662.3144	1322.6375	661.8224	P	272.1717	136.5895	255.1452	128.0762			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TWVISPGSNDVSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G47390.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.5	1513.7525	0.0023	TWVISPGSNDVSPR

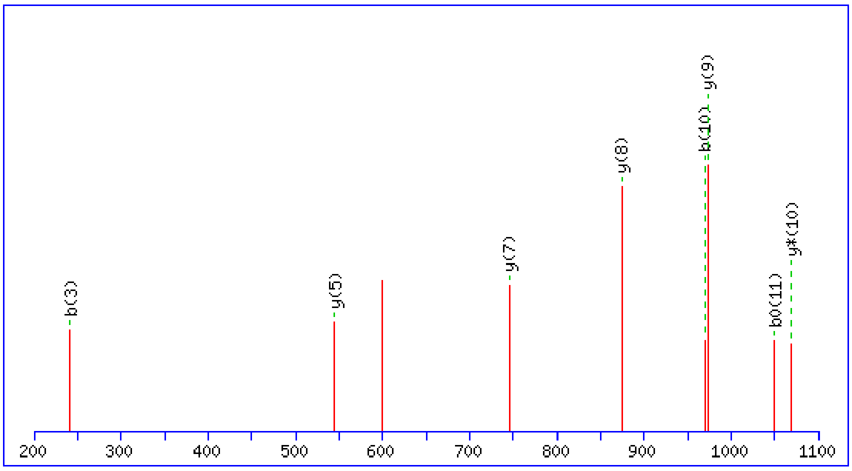
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGIVESLDALVK**
Found in **AT2G47470.1** in **TAIR_Arabidopsis**, Symbols: ATPDIL2-1, UNE5, MEE30 | ATPDIL2-1/MEE30/UNE5 (PDI-LIKE 2-1); thiol-disulfide exchange intermediate | chr2:19488573-19490753 FORWARD

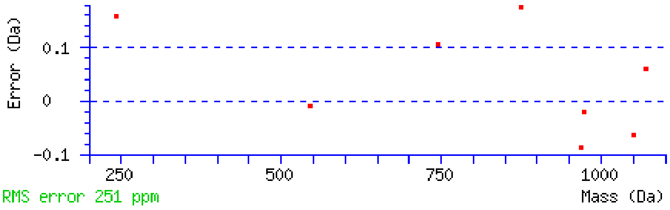
Match to Query 4131: 1213.690930 from(607.852741,2+) index(9047)
Title: Elution from: 80.189 to 80.189 scan no 12114 cid35.00 polarity:+
Data file D6h-3_2.mgf

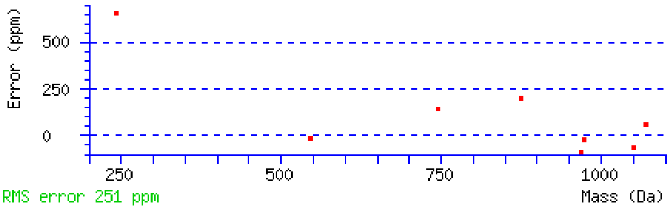
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1213.6918
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0015
Matches : 8/94 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			A							12
2	129.0659	65.0366			G	1143.6620	572.3346	1126.6354	563.8213	1125.6514	563.3293	11
3	**242.1499**	121.5786			I	1086.6405	543.8239	1069.6140	535.3106	1068.6299	534.8186	10
4	341.2183	171.1128			V	***973.5564***	487.2819	956.5299	478.7686	955.5459	478.2766	9
5	470.2609	235.6341	452.2504	226.6288	E	***874.4880***	437.7477	857.4615	429.2344	856.4775	428.7424	8
6	557.2930	279.1501	539.2824	270.1448	S	***745.4454***	373.2264	728.4189	364.7131	727.4349	364.2211	7
7	670.3770	335.6921	652.3665	326.6869	L	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
8	785.4040	393.2056	767.3934	384.2003	D	***545.3293***	273.1683	528.3028	264.6550	527.3188	264.1630	5
9	856.4411	428.7242	838.4305	419.7189	A	430.3024	215.6548	413.2758	207.1416			4
10	**969.5251**	485.2662	951.5146	476.2609	L	359.2653	180.1363	342.2387	171.6230			3
11	1068.5936	534.8004	1050.5830	525.7951	V	246.1812	123.5942	229.1547	115.0810			2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AGIVESLDALVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT2G47470.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.2	1213.6918	-0.0009	AGIVESLDALVK
12.4	1213.6918	-0.0009	IQLDSLEGVIK
8.9	1213.6931	-0.0022	RALQFNPLAGK
3.1	1213.6891	0.0018	IQNKNGAVKSR
2.9	1213.6918	-0.0008	KLEELDLQVK
2.4	1213.6918	-0.0008	LQKVLLDEEK
1.5	1213.6891	0.0018	RLAQTKVENR

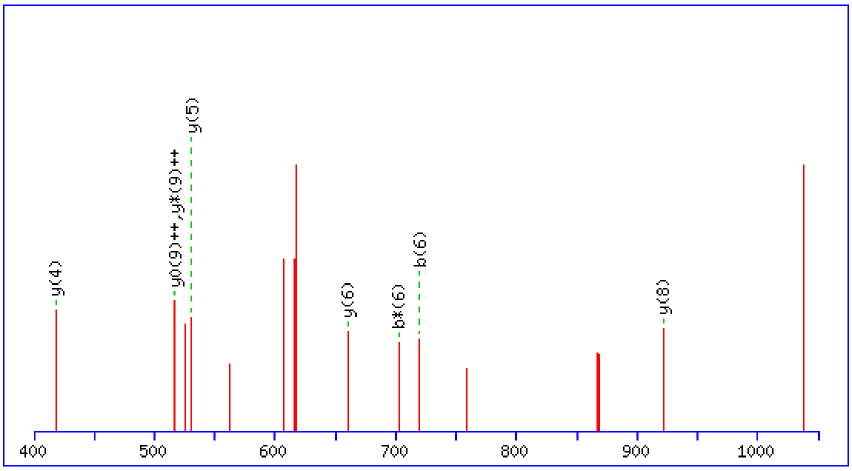
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLQNFEIGGER**
Found in **AT2G47510.1** in **TAIR_Arabidopsis**, Symbols: FUM1 | FUM1 (FUMARASE 1); fumarate hydratase | chr2:19505684-19509090 FORWARD

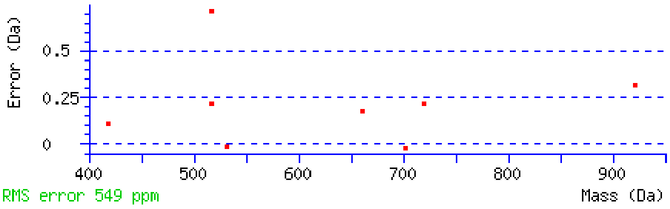
Match to Query 4031: 1248.609238 from(625.311895,2+) index(4451)
Title: Elution from: 44.114 to 44.114 scan no 5716 cid35.00 polarity:+
Data file D1d-1_1.mgf

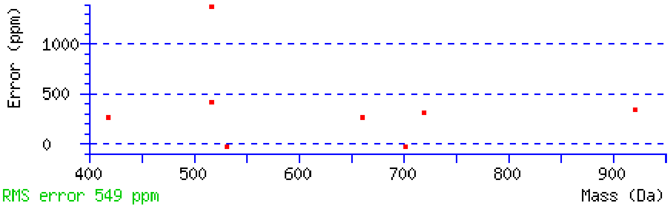
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1248.6098
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.036
Matches : 8/114 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	201.1234	101.0653			183.1128	92.0600	L	1162.5851	581.7962	1145.5586	573.2829	1144.5745	572.7909	10
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	1049.5010	525.2542	1032.4745	516.7409	1031.4905	516.2489	9
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	N	***921.4425***	461.2249	904.4159	452.7116	903.4319	452.2196	8
5	590.2933	295.6503	573.2667	287.1370	572.2827	286.6450	F	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	7
6	719.3359	360.1716	702.3093	351.6583	701.3253	351.1663	E	***660.3311***	330.6692	643.3046	322.1559	642.3206	321.6639	6
7	832.4199	416.7136	815.3934	408.2003	814.4094	407.7083	I	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	5
8	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	G	***418.2045***	209.6059	401.1779	201.0926	400.1939	200.6006	4
9	946.4629	473.7351	929.4363	465.2218	928.4523	464.7298	G	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
10	1075.5055	538.2564	1058.4789	529.7431	1057.4949	529.2511	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SLQNFEIGGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT2G47510.1

Score	Mr(calc)	Delta	Sequence
19.3	1248.6098	-0.0006	SLQNFEIGGER
0.7	1248.6098	-0.0006	GAATDPQSLYAR

Mascot: http://www.matrixscience.com/

AT2G47610.1

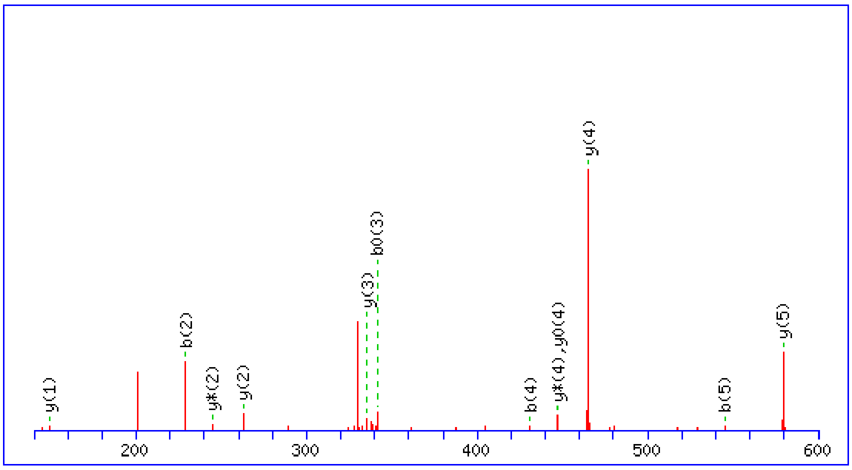
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILEAIK**
Found in **AT2G47610.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L7A (RPL7aA) | chr2:19536924-19538471 FORWARD

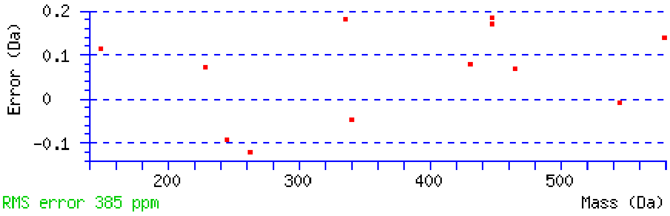
Match to Query 626: 692.417206 from(347.215879,2+) index(1943)
Title: Elution from: 23.735 to 23.735 scan no 2530 cid35.00 polarity:+
Data file D12h-3_1.mgf

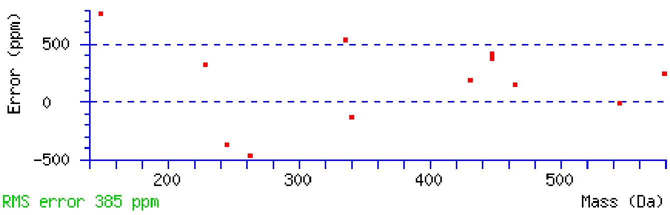
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 692.4167
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00039
Matches : 12/40 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							6
2	**229.1695**	115.0884			L	***579.3428***	290.1751	561.3193	281.1633	561.3323	281.1698	5
3	359.2091	180.1082	341.1985	171.1029	E	***465.2618***	233.1345	447.2382	224.1227	447.2512	224.1292	4
4	**431.2433**	216.1253	413.2327	207.1200	A	***335.2221***	168.1147	317.1985	159.1029			3
5	**545.3244**	273.1658	527.3138	264.1605	I	***263.1880***	132.0976	245.1644	123.0858			2
6					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ILEAIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.5	692.4167	0.0005	IIEALK
39.5	692.4167	0.0005	ILEAIK
39.5	692.4167	0.0005	ILEALK
39.5	692.4167	0.0005	LIEALK

AT2G47610.1

25.6	692.4167	0.0005	ILAEIK
25.6	692.4167	0.0005	ILAELK
24.5	692.4167	0.0005	LLEIAK
21.0	692.4167	0.0005	LEIAIK
19.6	692.4167	0.0006	LLVDVK
12.4	692.4167	0.0005	LLAVSAI

AT2G47730.1

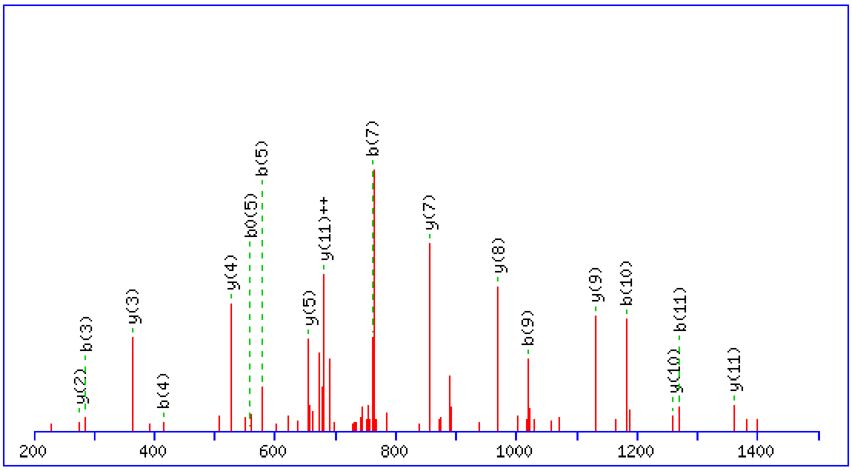
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AITQYLAEEYSEK**
Found in **AT2G47730.1** in **TAIR_Arabidopsis**, Symbols: GST6, ATGSTF5, GSTF8, ATGSTF8 | ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8); glutathione transferase | chr2:19565283-19566336 FORWARD

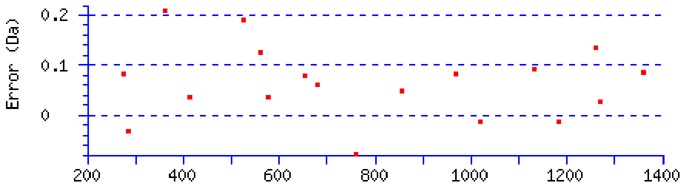
Match to Query 6792: 1543.739512 from(772.877032,2+) index(5893)
Title: Elution from: 51.152 to 51.152 scan no 7443 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

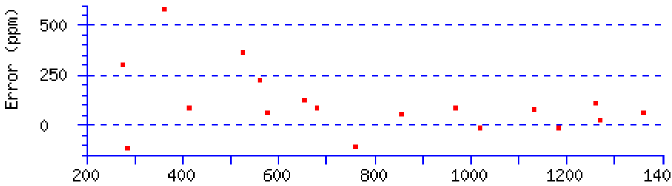


Monoisotopic mass of neutral peptide Mr(calc): 1543.7406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 8.9e-008
Matches : 18/132 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							13
2	185.1285	93.0679					I	1473.7108	737.3590	1456.6842	728.8457	1455.7002	728.3537	12
3	**286.1761**	143.5917			268.1656	134.5864	T	***1360.6267***	680.8170	1343.6002	672.3037	1342.6161	671.8117	11
4	**414.2347**	207.6210	397.2082	199.1077	396.2241	198.6157	Q	***1259.5790***	630.2932	1242.5525	621.7799	1241.5685	621.2879	10
5	**577.2980**	289.1527	560.2715	280.6394	559.2875	280.1474	Y	***1131.5204***	566.2639	1114.4939	557.7506	1113.5099	557.2586	9
6	690.3821	345.6947	673.3556	337.1814	672.3715	336.6894	L	***968.4571***	484.7322	951.4306	476.2189	950.4466	475.7269	8
7	**761.4192**	381.2132	744.3927	372.7000	743.4087	372.2080	A	***855.3731***	428.1902	838.3465	419.6769	837.3625	419.1849	7
8	890.4618	445.7345	873.4353	437.2213	872.4512	436.7293	E	784.3359	392.6716	767.3094	384.1583	766.3254	383.6663	6
9	**1019.5044**	510.2558	1002.4779	501.7426	1001.4938	501.2506	E	***655.2933***	328.1503	638.2668	319.6370	637.2828	319.1450	5
10	**1182.5677**	591.7875	1165.5412	583.2742	1164.5572	582.7822	Y	***526.2508***	263.6290	509.2242	255.1157	508.2402	254.6237	4
11	**1269.5998**	635.3035	1252.5732	626.7902	1251.5892	626.2982	S	***363.1874***	182.0974	346.1609	173.5841	345.1769	173.0921	3
12	1398.6424	699.8248	1381.6158	691.3115	1380.6318	690.8195	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 196 ppm



RMS error 196 ppm

NCBI **BLAST** search of AITQYLAEEYSEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT2G47730.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.9	1543.7406	-0.0010	AITQYLAEEYSEK

Mascot: http://www.matrixscience.com/

AT2G47970.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATMRALK**
Found in **AT2G47970.1** in **TAIR_Arabidopsis**, Symbols: | NPL4 family protein | chr2:19636595-19638043 FORWARD

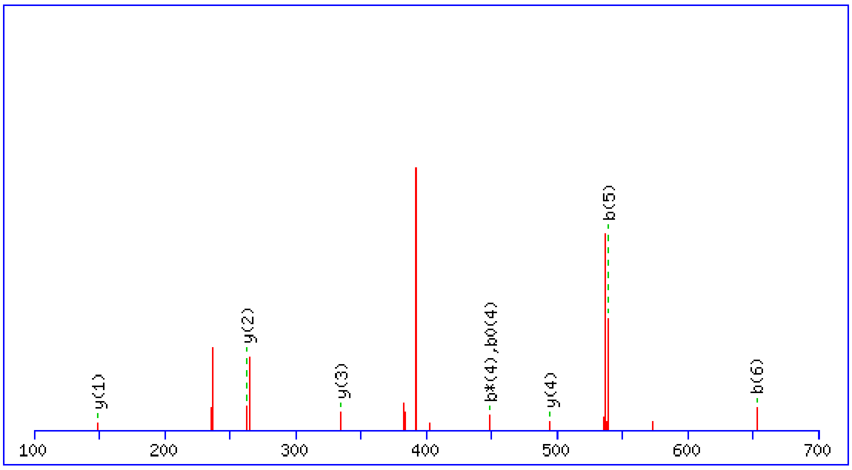
Match to Query 995: 800.420670 from(401.217611,2+) index(5656)
Title: Elution from: 50.637 to 50.637 scan no 7209 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

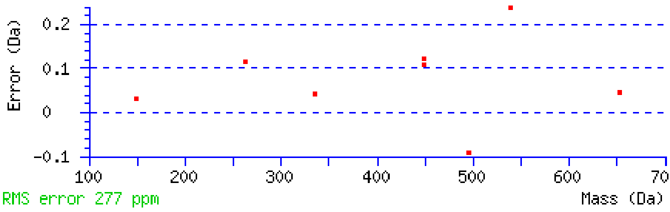
Label all possible matches ○ Label matches used for scoring ●

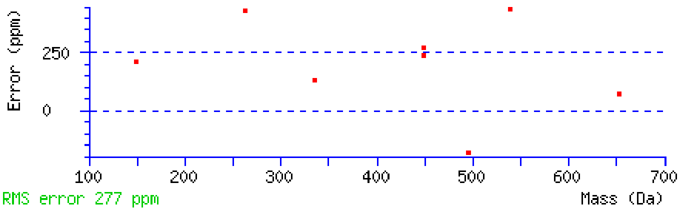
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 800.4205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.032
Matches : 8/54 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							7
2	175.0861	88.0467			157.0756	79.0414	T	729.3936	365.2004	711.3700	356.1886	711.3830	356.1952	6
3	307.1237	154.0655			289.1131	145.0602	M	627.3489	314.1781	609.3253	305.1663			5
4	467.2129	234.1101	449.1893	225.0983	449.2023	225.1048	R	***495.3114***	248.1593	477.2878	239.1475			4
5	**539.2471**	270.1272	521.2235	261.1154	521.2365	261.1219	A	***335.2221***	168.1147	317.1985	159.1029			3
6	**653.3282**	327.1677	635.3046	318.1559	635.3176	318.1624	L	***263.1880***	132.0976	245.1644	123.0858			2
7							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ATMRALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.0	800.4205	0.0002	ATMRALK
21.0	800.4205	0.0002	KMRLDK
21.0	800.4205	0.0002	NMRILK

AT2G47970.1

18.0	800.4205	0.0002	AMKKANK
16.3	800.4205	0.0002	LMRNLK
11.5	800.4205	0.0002	LMAVKGR
10.6	800.4205	0.0002	RLLMNK
10.6	800.4205	0.0002	RMLLNK
9.9	800.4205	0.0002	DKMRLK
8.6	800.4205	0.0002	LCRTLK

AT3G01120.1

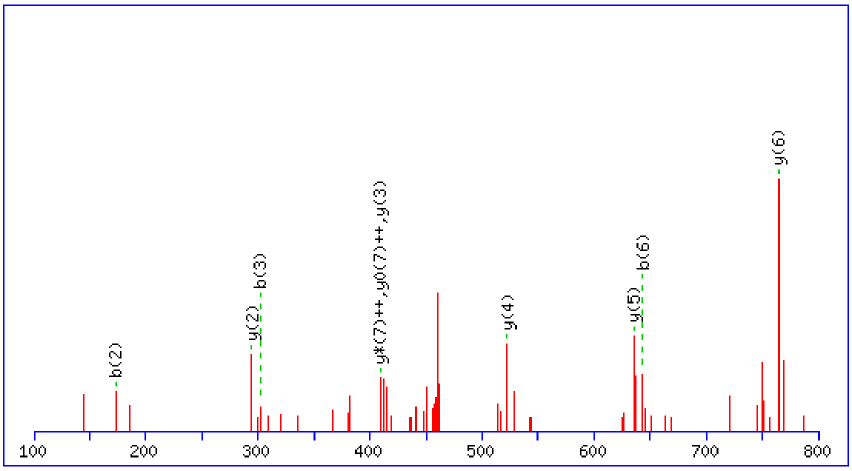
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAELIDFK**
Found in **AT3G01120.1** in **TAIR_Arabidopsis**, Symbols: CGS, ATCYS1, CGS1, MTO1 | MTO1 (METHIONINE OVERACCUMULATION 1) | chr3:39241-41872 REVERSE

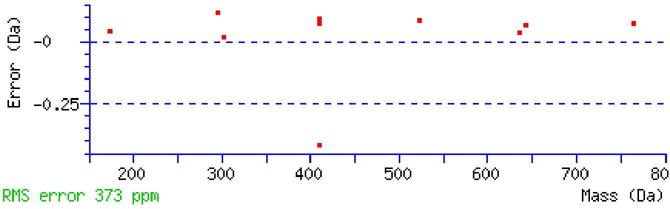
Match to Query 2087: 935.496106 from(468.755329,2+) index(5027)
Title: Elution from: 44.215 to 44.215 scan no 6273 cid35.00 polarity:+
Data file D1d-3_2.mgf

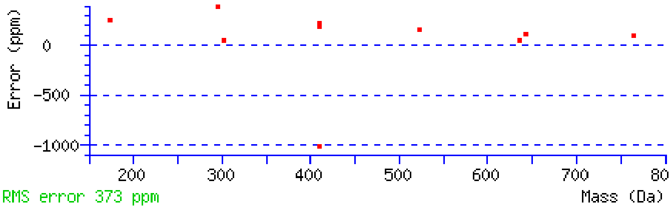
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 935.4964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0013
Matches : 10/66 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							8
2	**173.0921**	87.0497	155.0815	78.0444	A	835.4560	418.2316	818.4294	409.7184	817.4454	409.2264	7
3	**302.1347**	151.5710	284.1241	142.5657	E	***764.4189***	382.7131	747.3923	374.1998	746.4083	373.7078	6
4	415.2187	208.1130	397.2082	199.1077	L	***635.3763***	318.1918	618.3497	309.6785	617.3657	309.1865	5
5	528.3028	264.6550	510.2922	255.6498	I	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
6	**643.3297**	322.1685	625.3192	313.1632	D	***409.2082***	205.1077	392.1816	196.5944	391.1976	196.1024	3
7	790.3981	395.7027	772.3876	386.6974	F	***294.1812***	147.5942	277.1547	139.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TAELIDFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.6	935.4964	-0.0003	TAELIDFK

AT3G01120.1

Mascot: http://www.matrixscience.com/

AT3G01280.1

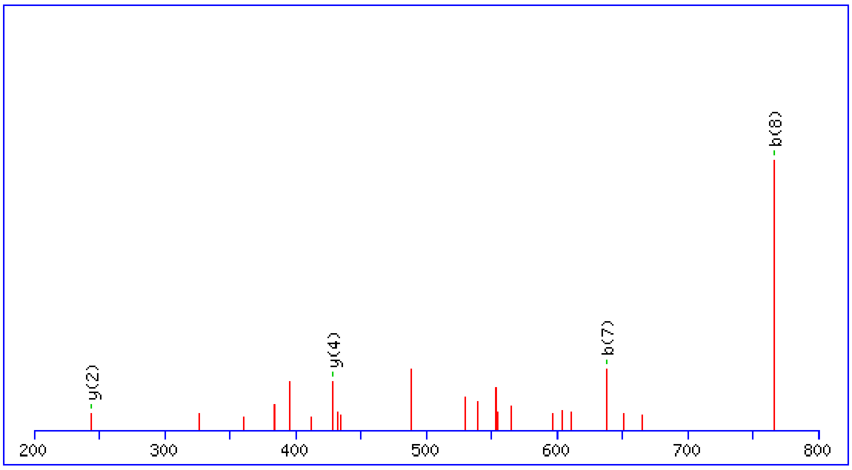
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGLALALKP**
Found in **AT3G01280.1** in **TAIR_Arabidopsis**, Symbols: | porin, putative | chr3:85761-87619 FORWARD

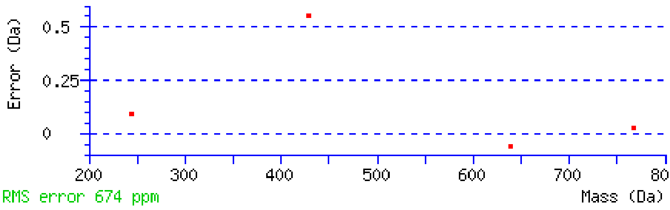
Match to Query 1469: 880.574154 from(441.294353,2+) index(5940)
Title: Elution from: 52.736 to 52.736 scan no 7575 cid35.00 polarity:+
Data file D12h-3_2.mgf

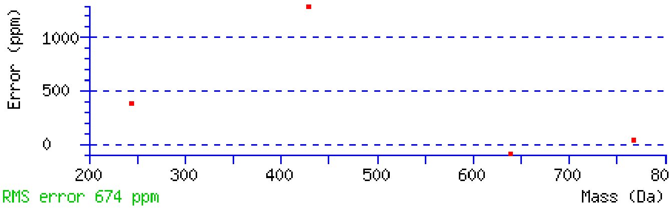
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 880.5746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.037
Matches : 4/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.0757	50.5415			V					9
2	157.0972	79.0522			G	782.5135	391.7604	765.4869	383.2471	8
3	270.1812	135.5942			L	725.4920	363.2496	708.4654	354.7364	7
4	341.2183	171.1128			A	612.4079	306.7076	595.3814	298.1943	6
5	454.3024	227.6548			L	541.3708	271.1890	524.3443	262.6758	5
6	525.3395	263.1734			A	***428.2867***	214.6470	411.2602	206.1337	4
7	***638.4236***	319.7154			L	357.2496	179.1285	340.2231	170.6152	3
8	***766.5185***	383.7629	749.4920	375.2496	K	***244.1656***	122.5864	227.1390	114.0731	2
9					P	116.0706	58.5389			1





NCBI **BLAST** search of VGLALALKP
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.4	880.5746	-0.0004	VGIALALKP

AT3G01280.1

14.4	880.5746	-0.0004	VGLALALKP

Mascot: http://www.matrixscience.com/

AT3G01390.1

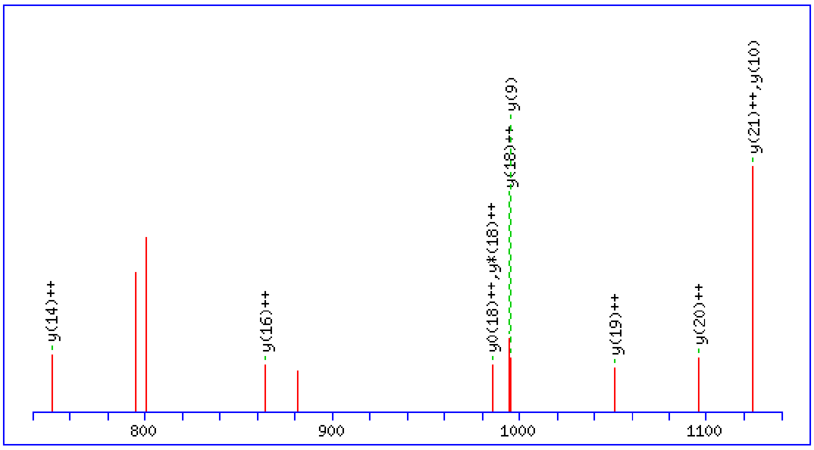
Mascot Search Results

Peptide View

MS/MS Fragmentation of GQGSIQQLLAAEVEAQHIVNAAR
Found in AT3G01390.1 in TAIR_Arabidopsis, Symbols: AVMA10, VMA10 | VMA10 (VACUOLAR MEMBRANE ATPASE 10) | chr3:150272-150929 REVERSE

Match to Query 10212: 2435.172123 from(812.731317,3+) index(9756)
Title: Elution from: 90.251 to 90.251 scan no 13612 cid35.00 polarity:+
Data file 0-1_3.mgf

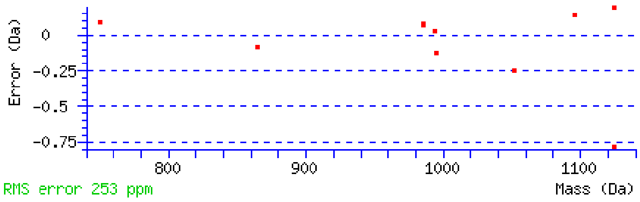
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 740 to 1140 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

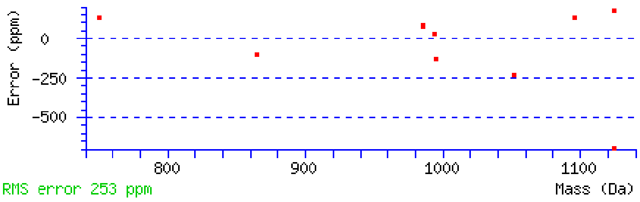


Monoisotopic mass of neutral peptide Mr(calc): 2435.1687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00078
Matches : 10/238 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	59.0258	30.0165					**G**							**23**
2	189.0784	95.0428	171.0548	86.0311			**Q**	2378.1576	1189.5824	2360.1340	1180.5706	2360.1470	1180.5771	**22**
3	247.0969	124.0521	229.0733	115.0403			**G**	2248.1049	1124.5561	2230.0813	1115.5443	2230.0943	1115.5508	**21**
4	335.1260	168.0666	317.1024	159.0548	317.1154	159.0613	**S**	2190.0864	1095.5468	2172.0628	1086.5350	2172.0758	1086.5416	**20**
5	449.2071	225.1072	431.1835	216.0954	431.1965	216.1019	**I**	2102.0573	1051.5323	2084.0338	1042.5205	2084.0468	1042.5270	**19**
6	579.2597	290.1335	561.2361	281.1217	561.2492	281.1282	**Q**	1987.9762	994.4918	1969.9527	985.4800	1969.9657	985.4865	**18**
7	709.3124	355.1598	691.2888	346.1480	691.3018	346.1545	**Q**	1857.9236	929.4654	1839.9000	920.4536	1839.9130	920.4602	**17**
8	823.3935	412.2004	805.3699	403.1886	805.3829	403.1951	**L**	1727.8709	864.4391	1709.8474	855.4273	1709.8604	855.4338	**16**
9	937.4746	469.2409	919.4510	460.2291	919.4640	460.2356	**L**	1613.7898	807.3986	1595.7663	798.3868	1595.7793	798.3933	**15**
10	1009.5087	505.2580	991.4851	496.2462	991.4982	496.2527	**A**	1499.7088	750.3580	1481.6852	741.3462	1481.6982	741.3527	**14**
11	1081.5429	541.2751	1063.5193	532.2633	1063.5323	532.2698	**A**	1427.6746	714.3409	1409.6510	705.3291	1409.6640	705.3357	**13**
12	1211.5825	606.2949	1193.5589	597.2831	1193.5719	597.2896	**E**	1355.6405	678.3239	1337.6169	669.3121	1337.6299	669.3186	**12**
13	1311.6479	656.3276	1293.6244	647.3158	1293.6374	647.3223	**V**	1225.6008	613.3041	1207.5772	604.2923	1207.5903	604.2988	**11**
14	1441.6876	721.3474	1423.6640	712.3356	1423.6770	712.3421	**E**	**1125.5354**	563.2713	1107.5118	554.2595	1107.5248	554.2660	**10**
15	1513.7217	757.3645	1495.6981	748.3527	1495.7112	748.3592	**A**	**995.4957**	498.2515	977.4722	489.2397			**9**
16	1643.7744	822.3908	1625.7508	813.3790	1625.7638	813.3855	**Q**	923.4616	462.2344	905.4380	453.2226			**8**
17	1783.8244	892.4158	1765.8008	883.4040	1765.8138	883.4106	**H**	793.4090	397.2081	775.3854	388.1963			**7**
18	1897.9055	949.4564	1879.8819	940.4446	1879.8949	940.4511	**I**	653.3589	327.1831	635.3354	318.1713			**6**
19	1997.9709	999.4891	1979.9474	990.4773	1979.9604	990.4838	**V**	539.2778	270.1426	521.2543	261.1308			**5**
20	2114.0079	1057.5076	2095.9844	1048.4958	2095.9974	1048.5023	**N**	439.2124	220.1098	421.1888	211.0980			**4**
21	2186.0421	1093.5247	2168.0185	1084.5129	2168.0315	1084.5194	**A**	323.1754	162.0913	305.1518	153.0795			**3**
22	2258.0762	1129.5418	2240.0526	1120.5300	2240.0657	1120.5365	**A**	251.1412	126.0743	233.1177	117.0625			**2**
23							**R**	179.1071	90.0572	161.0835	81.0454			**1**

AT3G01390.1





NCBI **BLAST** search of GQGSIQQLLAAEVEAQHIVNAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.4	2435.1687	0.0034	GQGSIQQLLAAEVEAQHIVNAAR
1.5	2435.1732	-0.0011	HLLYNVVNQESANVQHLLWK
1.2	2435.1754	-0.0033	WGIQVLTVFAFSTDNWIRPR

Mascot: http://www.matrixscience.com/

AT3G01480.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESELTPSNSNILDGR**
Found in **AT3G01480.1** in **TAIR_Arabidopsis**, Symbols: CYP38 | CYP38 (CYCLOPHILIN 38); peptidyl-prolyl cis-trans isomerase | chr3:188576-190681 FORWARD

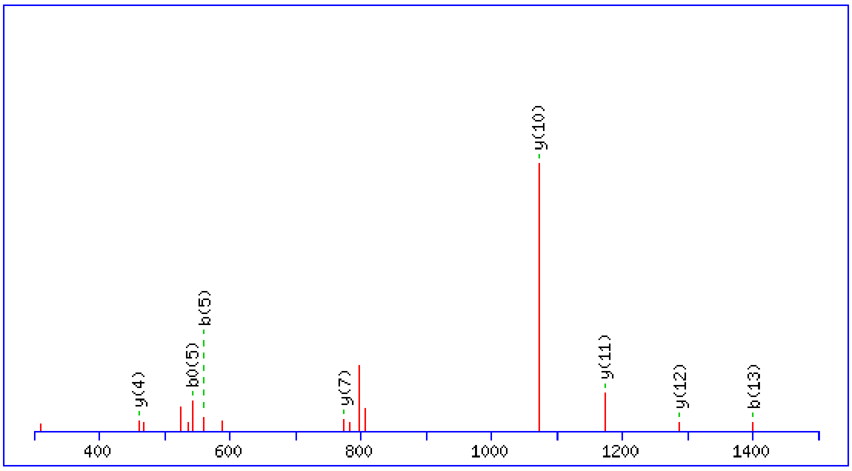
Match to Query 7420: 1630.780434 from(816.397493,2+) index(4478)
Title: Elution from: 41.538 to 41.538 scan no 5670 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

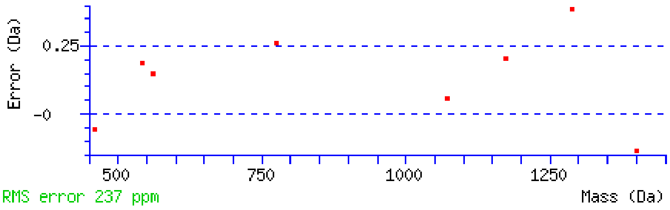
Label all possible matches ○ Label matches used for scoring ●

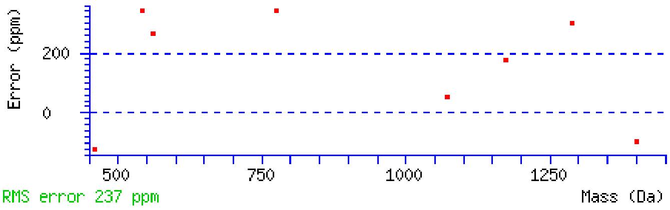
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1630.7798
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00082
Matches : 8/150 fragment ions using 13 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	217.0819	109.0446			199.0713	100.0393	S	1502.7445	751.8759	1485.7180	743.3626	1484.7340	742.8706	14
3	346.1245	173.5659			328.1139	164.5606	E	1415.7125	708.3599	1398.6859	699.8466	1397.7019	699.3546	13
4	459.2086	230.1079			441.1980	221.1026	L	***1286.6699***	643.8386	1269.6434	635.3253	1268.6593	634.8333	12
5	**560.2562**	280.6318			542.2457	271.6265	T	***1173.5858***	587.2966	1156.5593	578.7833	1155.5753	578.2913	11
6	657.3090	329.1581			639.2984	320.1529	P	***1072.5382***	536.7727	1055.5116	528.2594	1054.5276	527.7674	10
7	744.3410	372.6742			726.3305	363.6689	S	975.4854	488.2463	958.4588	479.7331	957.4748	479.2411	9
8	858.3840	429.6956	841.3574	421.1823	840.3734	420.6903	N	888.4534	444.7303	871.4268	436.2170	870.4428	435.7250	8
9	945.4160	473.2116	928.3894	464.6984	927.4054	464.2063	S	***774.4104***	387.7089	757.3839	379.1956	756.3999	378.7036	7
10	1059.4589	530.2331	1042.4324	521.7198	1041.4483	521.2278	N	687.3784	344.1928	670.3519	335.6796	669.3678	335.1876	6
11	1172.5430	586.7751	1155.5164	578.2618	1154.5324	577.7698	I	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
12	1285.6270	643.3172	1268.6005	634.8039	1267.6165	634.3119	L	***460.2514***	230.6293	443.2249	222.1161	442.2409	221.6241	4
13	**1400.6540**	700.8306	1383.6274	692.3174	1382.6434	691.8253	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
14	1457.6754	729.3414	1440.6489	720.8281	1439.6649	720.3361	G	232.1404	116.5738	215.1139	108.0606			2
15							R	175.1190	88.0631	158.0924	79.5498			1





AT3G01480.1

NCBI **BLAST** search of ESELTPSNSNILDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.4	1630.7798	0.0006	ESELTPSNSNILDGR
3.1	1630.7773	0.0031	KEATIANEEWGMPR

AT3G01500.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEQITAALQTGTSSDKK**
Found in **AT3G01500.1** in **TAIR_Arabidopsis**, Symbols: CA1 | CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding | chr3:194860-196723 REVERSE

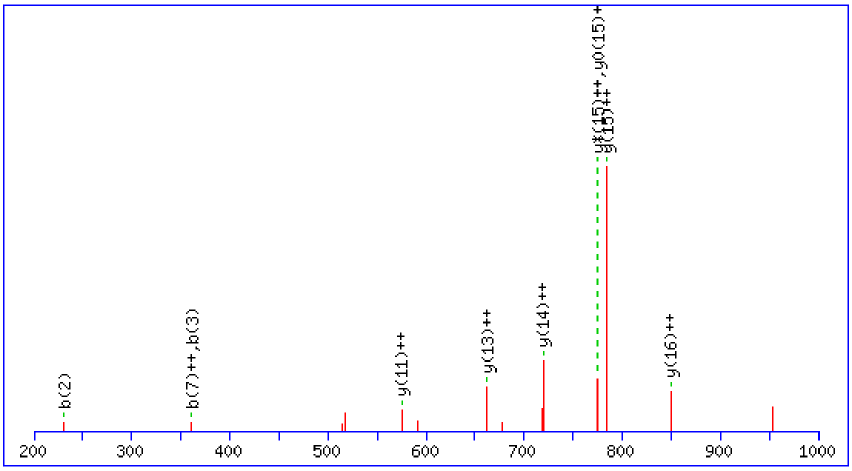
Match to Query 8410: 1796.863431 from(599.961753,3+) index(2936)
Title: Elution from: 29.935 to 29.935 scan no 3676 cid35.00 polarity:+
Data file D6h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

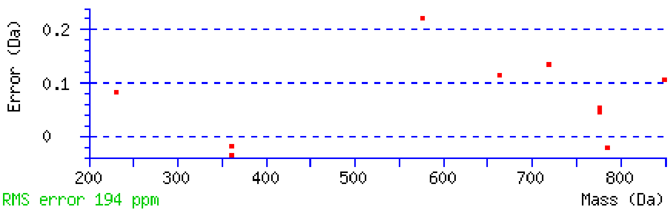
Show Y-axis ☐

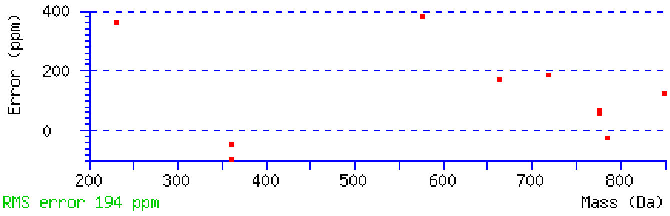


Monoisotopic mass of neutral peptide Mr(calc): 1796.8642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.012
Matches : 10/182 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							17
2	**231.1124**	116.0598			213.1018	107.0545	E	1697.8061	849.4067	1679.7825	840.3949	1679.7955	840.4014	16
3	**361.1650**	181.0861	343.1414	172.0743	343.1544	172.0809	Q	1567.7664	784.3869	1549.7429	775.3751	1549.7559	775.3816	15
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	I	1437.7138	719.3605	1419.6902	710.3487	1419.7032	710.3553	14
5	577.2908	289.1490	559.2672	280.1373	559.2802	280.1438	T	1323.6327	662.3200	1305.6091	653.3082	1305.6221	653.3147	13
6	649.3250	325.1661	631.3014	316.1543	631.3144	316.1608	A	1221.5880	611.2976	1203.5644	602.2858	1203.5774	602.2923	12
7	721.3591	361.1832	703.3355	352.1714	703.3485	352.1779	A	1149.5538	575.2806	1131.5302	566.2688	1131.5433	566.2753	11
8	835.4402	418.2237	817.4166	409.2120	817.4296	409.2185	L	1077.5197	539.2635	1059.4961	530.2517	1059.5091	530.2582	10
9	965.4929	483.2501	947.4693	474.2383	947.4823	474.2448	Q	963.4386	482.2229	945.4150	473.2111	945.4280	473.2176	9
10	1067.5376	534.2724	1049.5140	525.2606	1049.5270	525.2671	T	833.3859	417.1966	815.3624	408.1848	815.3754	408.1913	8
11	1125.5561	563.2817	1107.5325	554.2699	1107.5455	554.2764	G	731.3412	366.1742	713.3176	357.1625	713.3307	357.1690	7
12	1227.6008	614.3040	1209.5772	605.2922	1209.5902	605.2987	T	673.3227	337.1650	655.2991	328.1532	655.3122	328.1597	6
13	1315.6298	658.3186	1297.6063	649.3068	1297.6193	649.3133	S	571.2780	286.1426	553.2544	277.1309	553.2674	277.1374	5
14	1403.6589	702.3331	1385.6353	693.3213	1385.6483	693.3278	S	483.2489	242.1281	465.2254	233.1163	465.2384	233.1228	4
15	1519.6829	760.3451	1501.6593	751.3333	1501.6723	751.3398	D	395.2199	198.1136	377.1963	189.1018	377.2093	189.1083	3
16	1649.7719	825.3896	1631.7483	816.3778	1631.7614	816.3843	K	279.1959	140.1016	261.1723	131.0898			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT3G01500.1





NCBI **BLAST** search of VEQITAALQTGTSSDKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.2	1796.8642	-0.0008	VEQITAALQTGTSSDKK
19.7	1796.8644	-0.0010	KVAGHDMEILYLGRR
15.6	1796.8665	-0.0030	DLKTANILLDEGYNAK
15.3	1796.8624	0.0010	DLKEMIMKDLESALK
9.0	1796.8665	-0.0030	DIKSSNVLIFDNDVAK
7.5	1796.8624	0.0010	DLKEMIMKDLESALK
6.0	1796.8617	0.0017	DLLQWVREMTTIQK
3.9	1796.8617	0.0017	NLVRLLGFCLEGEEK
3.4	1796.8651	-0.0017	VQRVNTMMTILDDLK
2.2	1796.8651	-0.0017	EKVIAAMVSNVEAMIR

AT3G01500.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCPSHVLDFQPGDAFVVR**
Found in **AT3G01500.2** in **TAIR_Arabidopsis**, Symbols: CA1 | CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding | chr3:194860-197880 REVERSE

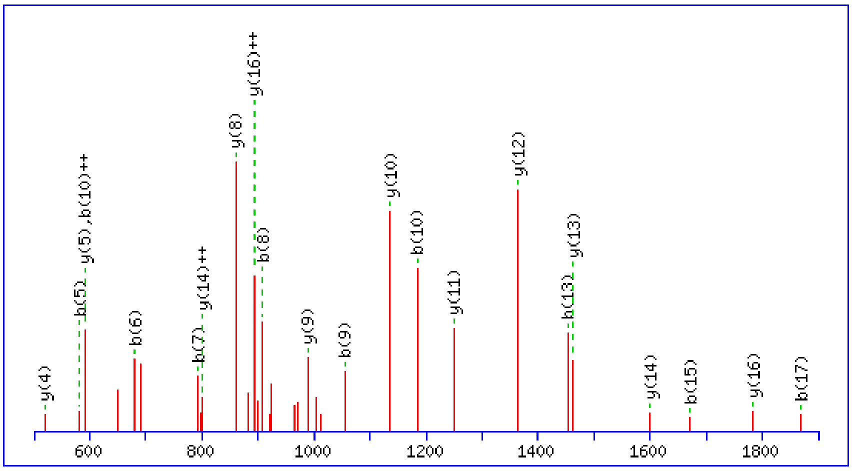
Match to Query 9550: 2042.004638 from(1022.009595,2+) index(8276)
Title: Elution from: 72.920 to 72.920 scan no 10825 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

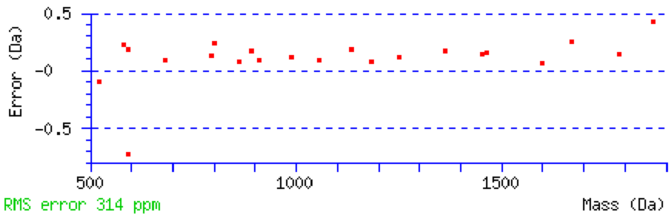
Show Y-axis ☐

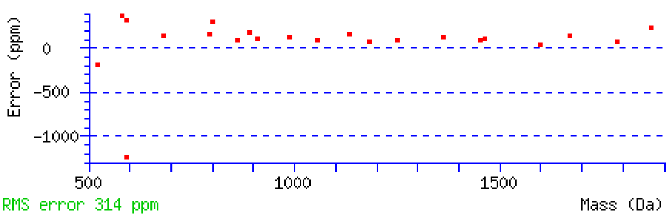


Monoisotopic mass of neutral peptide Mr(calc): 2042.0044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 95 **Expect:** 1.5e-009
Matches : 22/170 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							18
2	260.1063	130.5568					C	1943.9432	972.4753	1926.9167	963.9620	1925.9327	963.4700	17
3	357.1591	179.0832					P	***1783.9126***	892.4599	1766.8860	883.9467	1765.9020	883.4547	16
4	444.1911	222.5992			426.1806	213.5939	S	1686.8598	843.9336	1669.8333	835.4203	1668.8493	834.9283	15
5	***581.2500***	291.1287			563.2395	282.1234	H	***1599.8278***	800.4175	1582.8013	791.9043	1581.8172	791.4123	14
6	***680.3185***	340.6629			662.3079	331.6576	V	***1462.7689***	731.8881	1445.7423	723.3748	1444.7583	722.8828	13
7	***793.4025***	397.2049			775.3920	388.1996	L	***1363.7005***	682.3539	1346.6739	673.8406	1345.6899	673.3486	12
8	***908.4295***	454.7184			890.4189	445.7131	D	***1250.6164***	625.8118	1233.5899	617.2986	1232.6058	616.8066	11
9	***1055.4979***	528.2526			1037.4873	519.2473	F	***1135.5895***	568.2984	1118.5629	559.7851	1117.5789	559.2931	10
10	***1183.5565***	592.2819	1166.5299	583.7686	1165.5459	583.2766	Q	***988.5211***	494.7642	971.4945	486.2509	970.5105	485.7589	9
11	1280.6092	640.8082	1263.5827	632.2950	1262.5987	631.8030	P	***860.4625***	430.7349	843.4359	422.2216	842.4519	421.7296	8
12	1337.6307	669.3190	1320.6041	660.8057	1319.6201	660.3137	G	763.4097	382.2085	746.3832	373.6952	745.3992	373.2032	7
13	***1452.6576***	726.8325	1435.6311	718.3192	1434.6471	717.8272	D	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
14	1523.6947	762.3510	1506.6682	753.8377	1505.6842	753.3457	A	***591.3613***	296.1843	574.3348	287.6710			5
15	***1670.7632***	835.8852	1653.7366	827.3719	1652.7526	826.8799	F	***520.3242***	260.6657	503.2976	252.1525			4
16	1769.8316	885.4194	1752.8050	876.9061	1751.8210	876.4141	V	373.2558	187.1315	356.2292	178.6183			3
17	***1868.9000***	934.9536	1851.8734	926.4404	1850.8894	925.9483	V	274.1874	137.5973	257.1608	129.0840			2
18							R	175.1190	88.0631	158.0924	79.5498			1

AT3G01500.2





NCBI **BLAST** search of VCPSHVLDFQPGDAFVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.0	2042.0044	0.0002	VCPSHVLDFQPGDAFVVR
3.6	2042.0005	0.0041	EMQMIKHFLDYFPSLK
3.6	2042.0005	0.0041	EMQMIKHFLDYFPSLK

Mascot: http://www.matrixscience.com/

AT3G02080.1

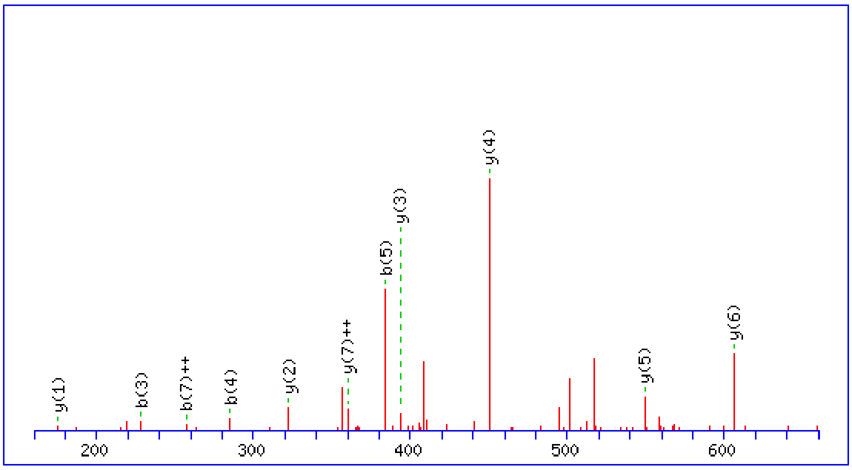
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGLGVGAFR**
Found in **AT3G02080.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S19 (RPS19A) | chr3:364145-365168 REVERSE

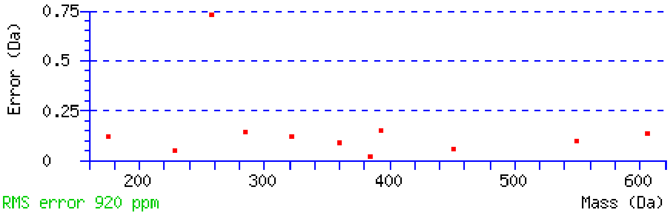
Match to Query 1213: 832.454726 from(417.234639,2+) index(3666)
Title: Elution from: 33.849 to 33.849 scan no 4529 cid35.00 polarity:+
Data file C7-2_3.mgf

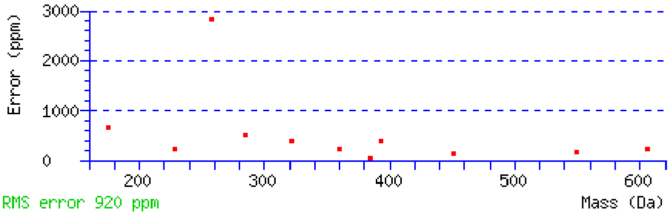
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 832.4556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00036
Matches : 11/48 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.5180	G					9
2	115.0502	58.0287	G	776.4413	388.7243	759.4148	380.2110	8
3	**228.1343**	114.5708	L	719.4199	360.2136	702.3933	351.7003	7
4	**285.1557**	143.0815	G	***606.3358***	303.6715	589.3093	295.1583	6
5	**384.2241**	192.6157	V	***549.3144***	275.1608	532.2878	266.6475	5
6	441.2456	221.1264	G	***450.2459***	225.6266	433.2194	217.1133	4
7	512.2827	256.6450	A	***393.2245***	197.1159	376.1979	188.6026	3
8	659.3511	330.1792	F	***322.1874***	161.5973	305.1608	153.0840	2
9			R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of GGLGVGAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.0	832.4556	-0.0008	GGLGVGAFR

AT3G02080.1

7.3	832.4555	-0.0008	AAQLQFR

Mascot: http://www.matrixscience.com/

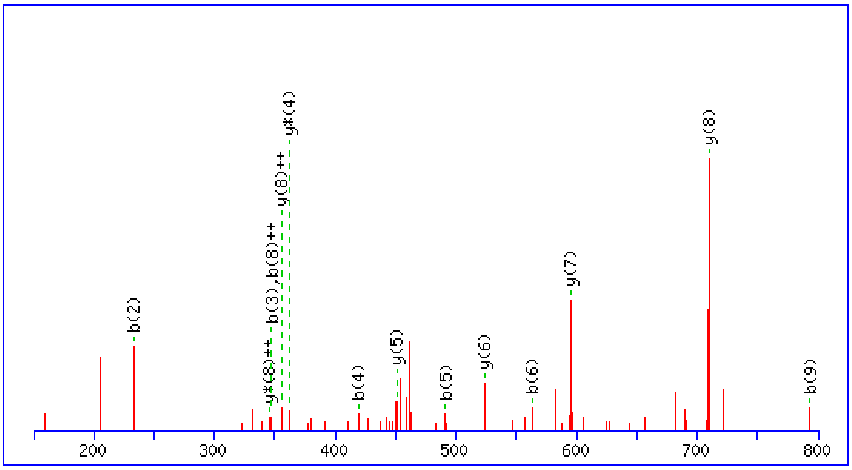
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVIAAAGAVK**
Found in **AT3G02090.1** in **TAIR_Arabidopsis**, Symbols: MPPBETA | MPPBETA; metalloendopeptidase | chr3:365631-368533 FORWARD

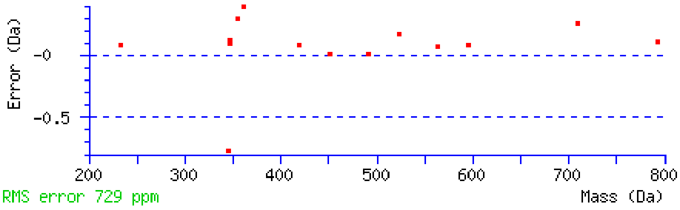
Match to Query 1972: 940.504298 from(471.259425,2+) index(2721)
Title: Elution from: 27.916 to 27.916 scan no 3390 cid35.00 polarity:+
Data file C7-1_1.mgf

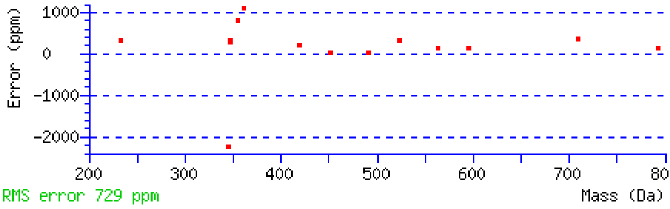
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 940.5042
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0008
Matches : 14/54 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	133.0448	67.0260	M					10
2	***233.1102***	117.0588	V	809.4740	405.2406	791.4504	396.2288	9
3	***347.1913***	174.0993	I	**709.4085**	355.2079	691.3849	346.1961	8
4	***419.2255***	210.1164	A	**595.3274**	298.1673	577.3038	289.1556	7
5	***491.2596***	246.1335	A	**523.2933**	262.1503	505.2697	253.1385	6
6	***563.2938***	282.1505	A	**451.2591**	226.1332	433.2355	217.1214	5
7	621.3123	311.1598	G	379.2250	190.1161	361.2014	181.1043	4
8	693.3464	347.1769	A	321.2065	161.1069	303.1829	152.0951	3
9	***793.4119***	397.2096	V	249.1723	125.0898	231.1487	116.0780	2
10			K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MVIAAAGAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G02090.1

35.9	940.5042	0.0001	MVIAAAGAVK
2.9	940.5042	0.0001	MVAGVTPKK
2.9	940.5042	0.0001	MVNIPKTK
0.0	940.5042	0.0001	MAQPLVKK

AT3G02200.1

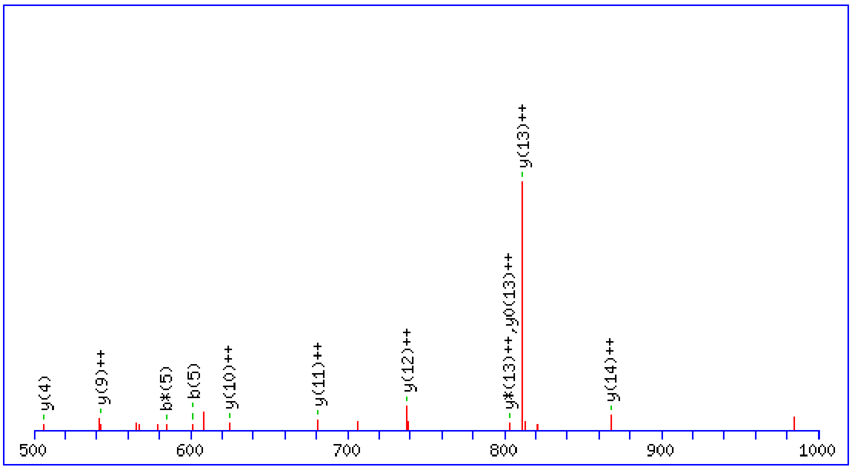
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILFNLYNLVDHPYAR**
Found in **AT3G02200.1** in **TAIR_Arabidopsis**, Symbols: | proteasome family protein | chr3:406699-408682 FORWARD

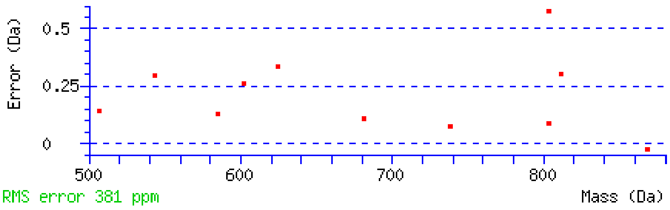
Match to Query 8447: 1846.975863 from(616.665897,3+) index(9420)
Title: Elution from: 87.238 to 87.238 scan no 13159 cid35.00 polarity:+
Data file D6h-2_3.mgf

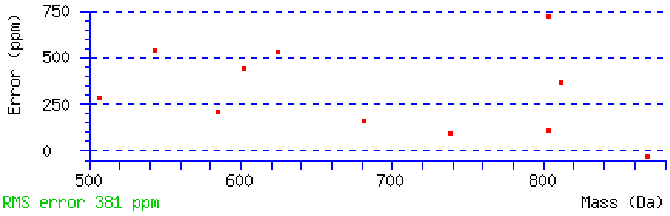
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1846.9730
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.011
Matches : 11/134 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							15
2	227.1754	114.0913					L	1734.8962	867.9517	1717.8697	859.4385	1716.8857	858.9465	14
3	374.2438	187.6255					F	1621.8122	811.4097	1604.7856	802.8964	1603.8016	802.4044	13
4	488.2867	244.6470	471.2602	236.1337			N	1474.7437	737.8755	1457.7172	729.3622	1456.7332	728.8702	12
5	601.3708	301.1890	584.3443	292.6758			L	1360.7008	680.8540	1343.6743	672.3408	1342.6902	671.8488	11
6	764.4341	382.7207	747.4076	374.2074			Y	1247.6167	624.3120	1230.5902	615.7987	1229.6062	615.3067	10
7	878.4771	439.7422	861.4505	431.2289			N	1084.5534	542.7803	1067.5269	534.2671	1066.5429	533.7751	9
8	991.5611	496.2842	974.5346	487.7709			L	970.5105	485.7589	953.4839	477.2456	952.4999	476.7536	8
9	1090.6295	545.8184	1073.6030	537.3051			V	857.4264	429.2169	840.3999	420.7036	839.4159	420.2116	7
10	1205.6565	603.3319	1188.6299	594.8186	1187.6459	594.3266	D	758.3580	379.6826	741.3315	371.1694	740.3474	370.6774	6
11	1342.7154	671.8613	1325.6888	663.3481	1324.7048	662.8561	H	643.3311	322.1692	626.3045	313.6559			5
12	1439.7682	720.3877	1422.7416	711.8744	1421.7576	711.3824	P	506.2722	253.6397	489.2456	245.1264			4
13	1602.8315	801.9194	1585.8049	793.4061	1584.8209	792.9141	Y	409.2194	205.1133	392.1928	196.6001			3
14	1673.8686	837.4379	1656.8421	828.9247	1655.8580	828.4327	A	246.1561	123.5817	229.1295	115.0684			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ILFNLYNLVDHPYAR

AT3G02200.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	1846.9730	0.0029	ILFNLYNLVDHPYAR
7.9	1846.9789	-0.0030	LIETGDSEQIFQKAIR
7.3	1846.9723	0.0036	LFLLLRAADNESAMQR
4.3	1846.9788	-0.0030	QLISQIEANSEFVNKK
4.2	1846.9763	-0.0005	INKFSGMIEGLIWSPR
3.7	1846.9757	0.0002	GVAQQSMLNIVMQLRK
0.8	1846.9723	0.0036	RYNMNGVAEVLLALER

AT3G02230.1

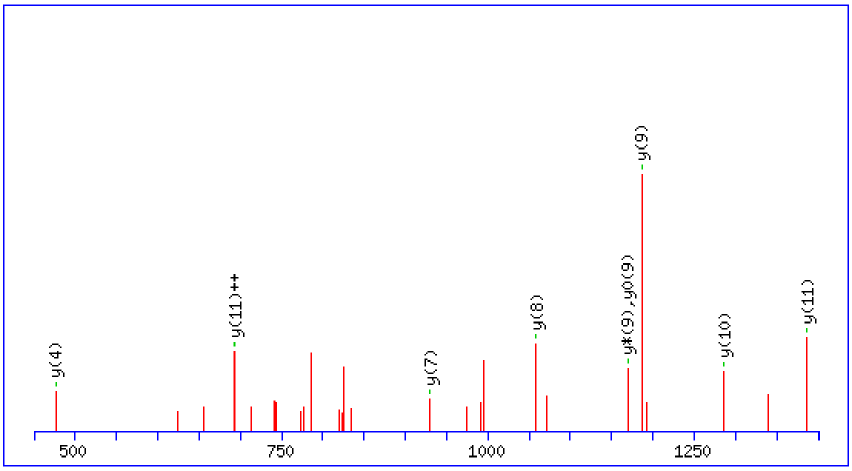
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAVTVQQCYMELSK**
Found in **AT3G02230.1** in **TAIR_Arabidopsis**, Symbols: ATRGP1, ATRGP, RGP1 | RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1) | chr3:415470-417311 FORWARD

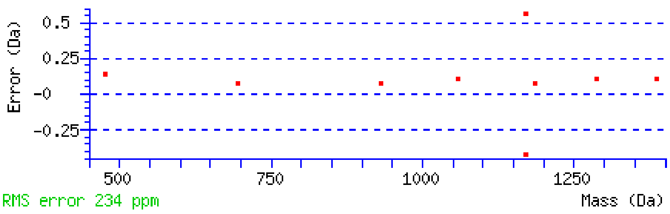
Match to Query 7535: 1684.779822 from(843.397187,2+) index(5301)
Title: Elution from: 50.630 to 50.630 scan no 6857 cid35.00 polarity:+
Data file D1d-2_2.mgf

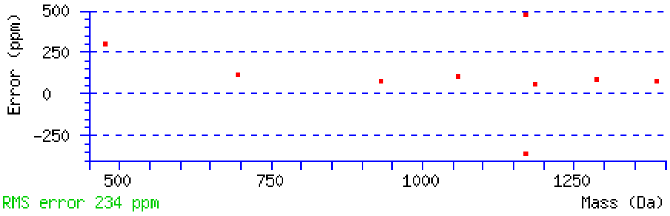
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1684.7800
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00019
Matches : 9/144 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**14**
2	201.0870	101.0471			183.0764	92.0418	**A**	1556.7447	778.8760	1539.7182	770.3627	1538.7342	769.8707	**13**
3	300.1554	150.5813			282.1448	141.5761	**V**	1485.7076	743.3574	1468.6811	734.8442	1467.6971	734.3522	**12**
4	401.2031	201.1052			383.1925	192.0999	**T**	***1386.6392***	693.8232	1369.6127	685.3100	1368.6286	684.8180	**11**
5	500.2715	250.6394			482.2609	241.6341	**V**	***1285.5915***	643.2994	1268.5650	634.7861	1267.5810	634.2941	**10**
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	**Q**	***1186.5231***	593.7652	1169.4966	585.2519	1168.5125	584.7599	**9**
7	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	**Q**	***1058.4645***	529.7359	1041.4380	521.2226	1040.4540	520.7306	**8**
8	916.4193	458.7133	899.3927	450.2000	898.4087	449.7080	**C**	***930.4060***	465.7066	913.3794	457.1933	912.3954	456.7013	**7**
9	1079.4826	540.2450	1062.4561	531.7317	1061.4721	531.2397	**Y**	770.3753	385.6913	753.3488	377.1780	752.3647	376.6860	**6**
10	1210.5231	605.7652	1193.4966	597.2519	1192.5125	596.7599	**M**	607.3120	304.1596	590.2854	295.6464	589.3014	295.1543	**5**
11	1339.5657	670.2865	1322.5392	661.7732	1321.5551	661.2812	**E**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
12	1452.6498	726.8285	1435.6232	718.3152	1434.6392	717.8232	**L**	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	**3**
13	1539.6818	770.3445	1522.6552	761.8313	1521.6712	761.3393	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EAVTVQQCYMELSK

AT3G02230.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.5	1684.7800	-0.0002	EAVTVQQCYMELSK

AT3G02260.1

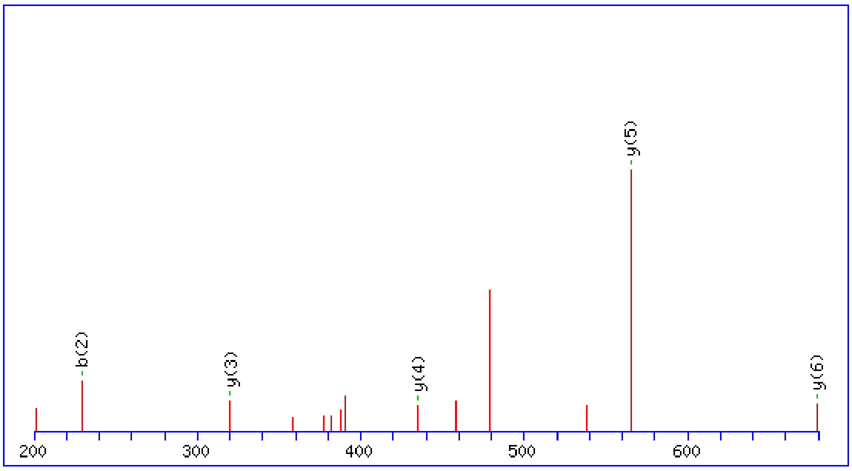
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLELLGK**
Found in **AT3G02260.1** in **TAIR_Arabidopsis**, Symbols: DOC1, TIR3, UMB1, LPR1, ASA1, CRM1, BIG | BIG (DARK OVER-EXPRESSION OF CAB 1); binding / ubiquitin-protein ligase/ zinc ion binding | chr3:431159-448496 REVERSE

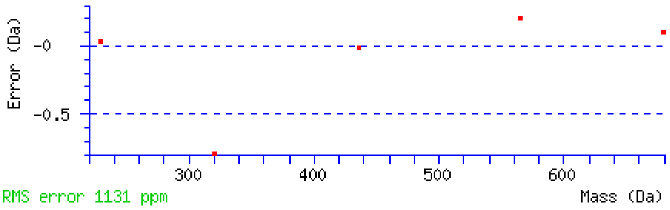
Match to Query 975: 792.482428 from(397.248490,2+) index(5473)
Title: Elution from: 49.142 to 49.142 scan no 6861 cid35.00 polarity:+
Data file D12h-3_1.mgf

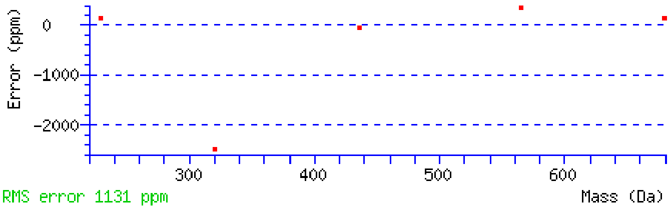
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 680 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 792.4821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.015
Matches : 5/48 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							7
2	229.1695	115.0884			L	***679.4083***	340.2078	661.3847	331.1960	661.3977	331.2025	6
3	359.2091	180.1082	341.1985	171.1029	E	***565.3272***	283.1672	547.3036	274.1554	547.3166	274.1620	5
4	473.2902	237.1487	455.2796	228.1435	L	***435.2876***	218.1474	417.2640	209.1356			4
5	587.3713	294.1893	569.3607	285.1840	L	***321.2065***	161.1069	303.1829	152.0951			3
6	645.3898	323.1985	627.3792	314.1933	G	207.1254	104.0663	189.1018	95.0545			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LLELLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	792.4821	0.0003	LLEILGK
23.1	792.4821	0.0003	LLELGLK

AT3G02260.1

23.1	792.4821	0.0003	LLELLGK
23.1	792.4821	0.0003	LLELVAK
22.9	792.4821	0.0003	ILEGLLK
13.0	792.4821	0.0003	LLEAVLK
10.6	792.4821	0.0003	LIGELLK
10.6	792.4821	0.0003	LLADILK
10.6	792.4821	0.0003	LLGELIK
10.6	792.4821	0.0003	LLVELAK

AT3G02360.1

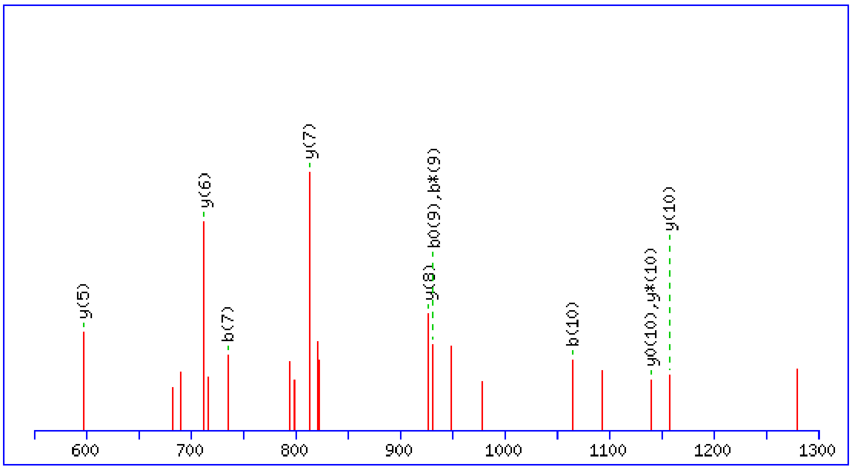
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NAELANLLVDPEFAK**
Found in **AT3G02360.1** in **TAIR_Arabidopsis**, Symbols: | 6-phosphogluconate dehydrogenase family protein | chr3:482505-483965 FORWARD

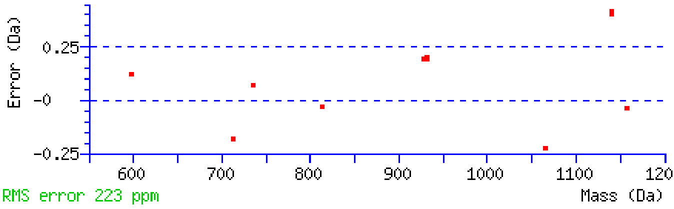
Match to Query 7568: 1660.807614 from(831.411083,2+) index(9070)
Title: Elution from: 81.966 to 81.966 scan no 12395 cid35.00 polarity:+
Data file D12h-1_3.mgf

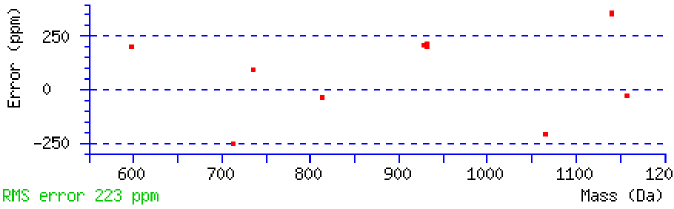
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1660.8033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0021
Matches : 11/158 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							15
2	189.0784	95.0428	171.0548	86.0311			A	1545.7735	773.3904	1527.7500	764.3786	1527.7630	764.3851	14
3	319.1180	160.0627	301.0945	151.0509	301.1075	151.0574	E	1473.7394	737.3733	1455.7158	728.3615	1455.7288	728.3681	13
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	L	1343.6998	672.3535	1325.6762	663.3417	1325.6892	663.3482	12
5	505.2333	253.1203	487.2097	244.1085	487.2227	244.1150	A	1229.6187	615.3130	1211.5951	606.3012	1211.6081	606.3077	11
6	621.2703	311.1388	603.2467	302.1270	603.2597	302.1335	N	***1157.5845***	579.2959	1139.5609	570.2841	1139.5740	570.2906	10
7	**735.3514**	368.1793	717.3278	359.1675	717.3408	359.1741	L	1041.5475	521.2774	1023.5239	512.2656	1023.5370	512.2721	9
8	849.4325	425.2199	831.4089	416.2081	831.4219	416.2146	L	***927.4664***	464.2369	909.4428	455.2251	909.4559	455.2316	8
9	949.4979	475.2526	931.4744	466.2408	931.4874	466.2473	V	***813.3853***	407.1963	795.3617	398.1845	795.3748	398.1910	7
10	**1065.5219**	533.2646	1047.4983	524.2528	1047.5114	524.2593	D	***713.3199***	357.1636	695.2963	348.1518	695.3093	348.1583	6
11	1163.5717	582.2895	1145.5481	573.2777	1145.5612	573.2842	P	***597.2959***	299.1516	579.2723	290.1398	579.2853	290.1463	5
12	1293.6113	647.3093	1275.5878	638.2975	1275.6008	638.3040	E	499.2461	250.1267	481.2225	241.1149	481.2355	241.1214	4
13	1441.6768	721.3420	1423.6532	712.3302	1423.6662	712.3368	F	369.2065	185.1069	351.1829	176.0951			3
14	1513.7109	757.3591	1495.6874	748.3473	1495.7004	748.3538	A	221.1410	111.0741	203.1174	102.0624			2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NAELANLLVDPEFAK

AT3G02360.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.0	1660.8033	0.0043	NAELANLLVDPEFAK
11.3	1660.8120	-0.0044	SRCSVIVLHPSVQR
3.7	1660.8123	-0.0047	CLESSPLMPLLEKK
1.4	1660.8115	-0.0039	ETAKAFKYMGQIVR
0.8	1660.8059	0.0017	VPLGQHASQVSDKFK
0.0	1660.8046	0.0030	KMGGIVQALNMVHNK

AT3G02520.1

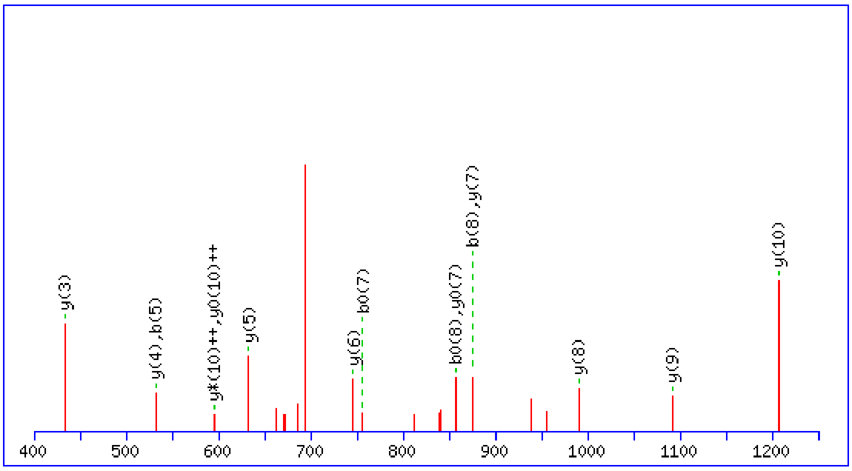
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVDTDELTVEER**
Found in **AT3G02520.1** in **TAIR_Arabidopsis**, Symbols: GF14 NU, GRF7 | GRF7 (GENERAL REGULATORY FACTOR 7); protein phosphorylated amino acid binding | chr3:526807-527922 REVERSE

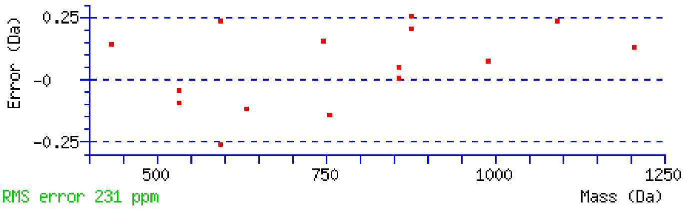
Match to Query 5358: 1405.657450 from(703.836001,2+) index(3141)
Title: Elution from: 31.327 to 31.327 scan no 3913 cid35.00 polarity:+
Data file D6h-1_3.mgf

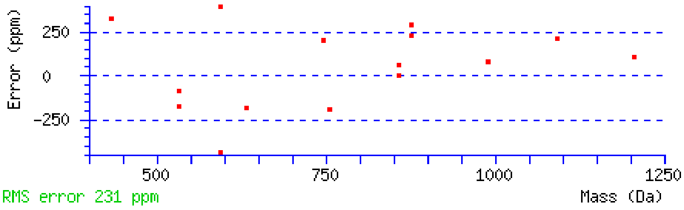
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1405.6573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 1.3e-008
Matches : 15/108 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							12
2	201.1234	101.0653	183.1128	92.0600	V	1305.6169	653.3121	1288.5903	644.7988	1287.6063	644.3068	11
3	316.1503	158.5788	298.1397	149.5735	D	***1206.5485***	603.7779	1189.5219	595.2646	1188.5379	594.7726	10
4	417.1980	209.1026	399.1874	200.0974	T	***1091.5215***	546.2644	1074.4950	537.7511	1073.5109	537.2591	9
5	**532.2249**	266.6161	514.2144	257.6108	D	***990.4738***	495.7406	973.4473	487.2273	972.4633	486.7353	8
6	661.2675	331.1374	643.2570	322.1321	E	***875.4469***	438.2271	858.4203	429.7138	857.4363	429.2218	7
7	774.3516	387.6794	756.3410	378.6742	L	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
8	**875.3993**	438.2033	857.3887	429.1980	T	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
9	974.4677	487.7375	956.4571	478.7322	V	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
10	1103.5103	552.2588	1085.4997	543.2535	E	***433.2041***	217.1057	416.1776	208.5924	415.1936	208.1004	3
11	1232.5529	616.7801	1214.5423	607.7748	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TVDTDELTVEER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G02520.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.1	1405.6573	0.0002	TVDTDELTVEER
13.5	1405.6573	0.0002	SIDESDGLQSDLK

AT3G02560.1

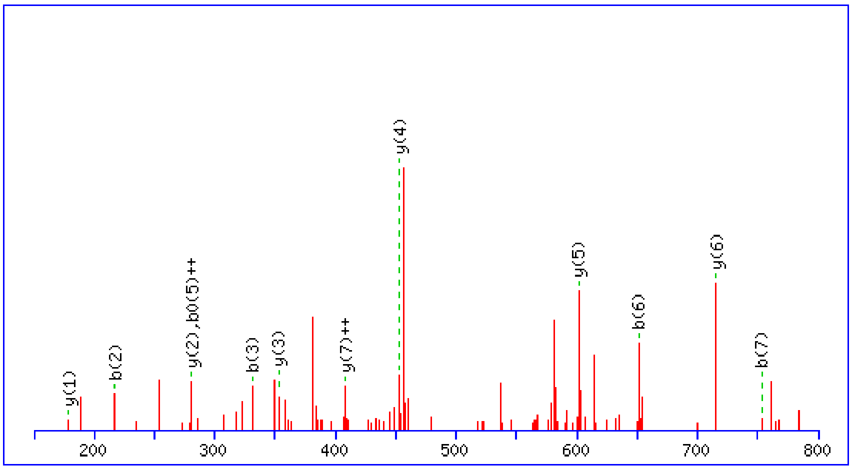
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVIFVATR**
Found in **AT3G02560.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S7 (RPS7B) | chr3:542348-543175 FORWARD

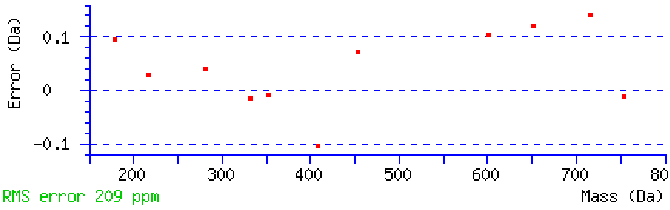
Match to Query 1588: 930.480484 from(466.247518,2+) index(4067)
Title: Elution from: 41.013 to 41.013 scan no 5236 cid35.00 polarity:+
Data file D1d-2_2.mgf

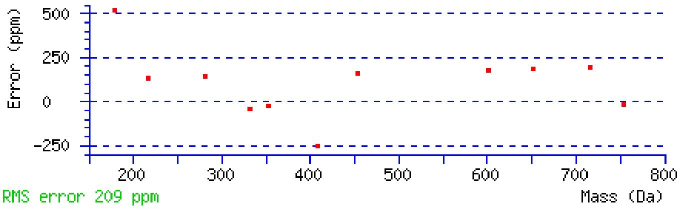
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 930.4801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0074
Matches : 12/68 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							8
2	**217.0967**	109.0520	199.0861	100.0467	V	815.4634	408.2353	797.4398	399.2235	797.4528	399.2301	7
3	**331.1778**	166.0925	313.1672	157.0873	I	***715.3980***	358.2026	697.3744	349.1908	697.3874	349.1973	6
4	479.2433	240.1253	461.2327	231.1200	F	***601.3169***	301.1621	583.2933	292.1503	583.3063	292.1568	5
5	579.3087	290.1580	561.2981	281.1527	V	***453.2514***	227.1293	435.2278	218.1175	435.2408	218.1241	4
6	**651.3428**	326.1751	633.3323	317.1698	A	***353.1860***	177.0966	335.1624	168.0848	335.1754	168.0913	3
7	**753.3876**	377.1974	735.3770	368.1921	T	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	2
8					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DVIFVATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.4	930.4801	0.0004	DVIFVATR
11.6	930.4801	0.0004	YIAGLQQK

AT3G02560.1

8.5	930.4801	0.0004	FAVLDVTR
8.3	930.4828	-0.0023	VNLHGIHK
8.2	930.4805	-0.0000	NSRVLATR
7.9	930.4801	0.0004	FKAVAEQK
6.6	930.4801	0.0004	FLLADSVR
3.8	930.4801	0.0004	FQEQLKK
3.4	930.4801	0.0004	EFVIASVR
3.0	930.4801	0.0004	FSLGDILR

AT3G02730.1

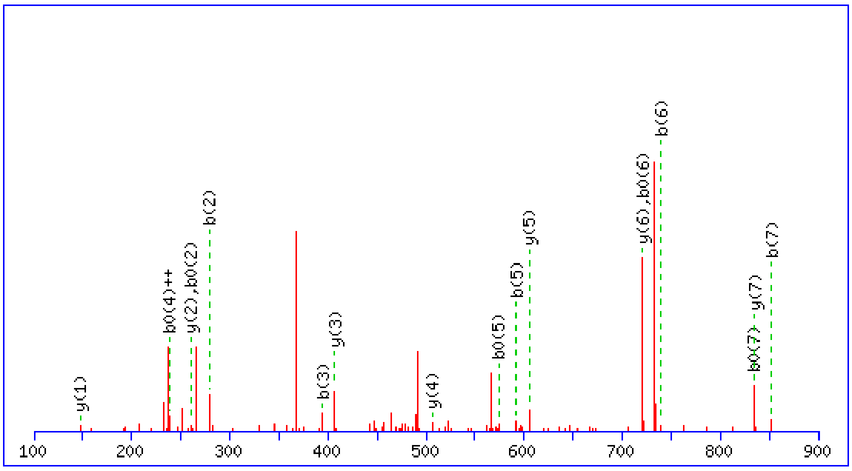
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDDVVFLK**
Found in **AT3G02730.1** in **TAIR_Arabidopsis**, Symbols: TRXF1, ATF1 | ATF1/TRXF1 (THIOREDOXIN F-TYPE 1); thiol-disulfide exchange intermediate | chr3:588577-589598 REVERSE

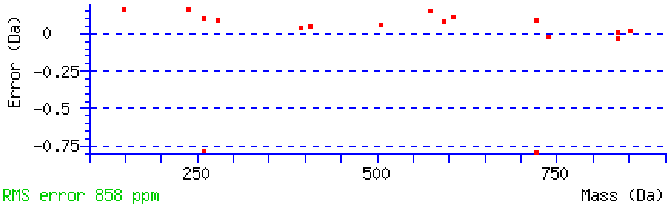
Match to Query 2634: 997.514316 from(499.764434,2+) index(5699)
Title: Elution from: 49.644 to 49.644 scan no 7190 cid35.00 polarity:+
Data file D1d-3_2.mgf

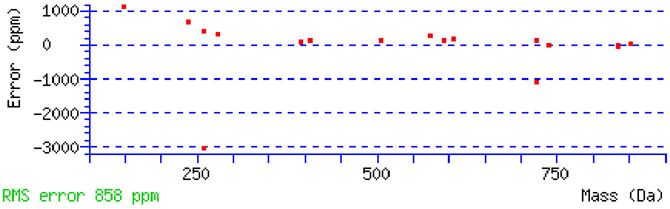
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 997.5121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.00074
Matches : 17/58 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							8
2	**279.0975**	140.0524	261.0870	131.0471	D	***835.4560***	418.2316	818.4294	409.7184	817.4454	409.2264	7
3	**394.1245**	197.5659	376.1139	188.5606	D	***720.4291***	360.7182	703.4025	352.2049	702.4185	351.7129	6
4	493.1929	247.1001	475.1823	238.0948	V	***605.4021***	303.2047	588.3756	294.6914			5
5	**592.2613**	296.6343	574.2508	287.6290	V	***506.3337***	253.6705	489.3071	245.1572			4
6	**739.3297**	370.1685	721.3192	361.1632	F	***407.2653***	204.1363	390.2387	195.6230			3
7	**852.4138**	426.7105	834.4032	417.7053	L	***260.1969***	130.6021	243.1703	122.0888			2
8					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YDDVVFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.6	997.5121	0.0023	YDDVVFLK

AT3G02730.1

5.3	997.5122	0.0021	MMMKKTTK

Mascot: http://www.matrixscience.com/

AT3G02750.1

Mascot Search Results

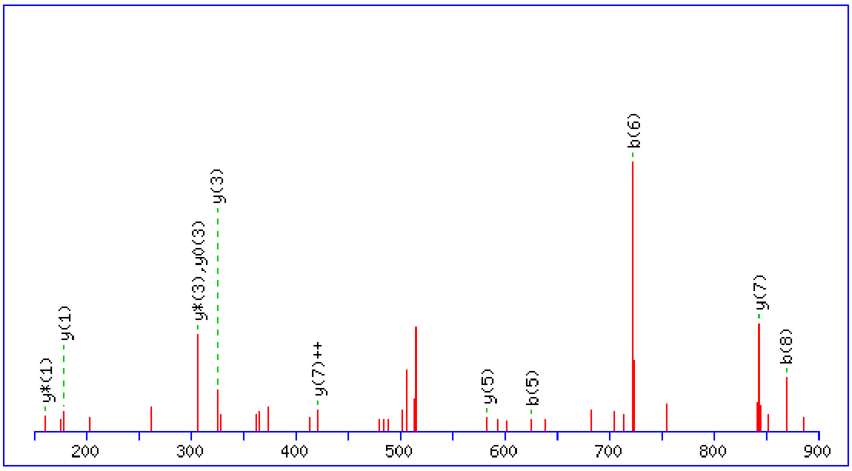
Peptide View

MS/MS Fragmentation of **NSKKRPGSR**
Found in **AT3G02750.1** in **TAIR_Arabidopsis**, Symbols: | protein phosphatase 2C family protein / PP2C family protein | chr3:593608-595464 REVERSE

Match to Query 3071: 1046.529706 from(524.272129,2+) index(1429)
Title: Elution from: 19.574 to 19.574 scan no 1941 cid35.00 polarity:+
Data file D6h-1_1.mgf

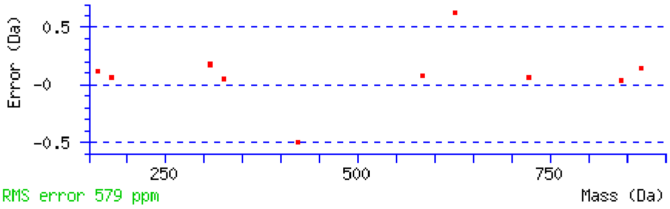
Click mouse within plot area to zoom in by factor of two about that point

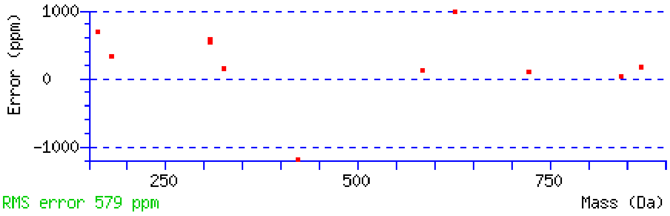
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1046.5306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.043
Matches : 11/92 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	205.0733	103.0403	187.0498	94.0285	187.0628	94.0350	S	931.5008	466.2541	913.4772	457.2423	913.4903	457.2488	8
3	335.1624	168.0848	317.1388	159.0730	317.1518	159.0795	K	***843.4718***	422.2395	825.4482	413.2277	825.4612	413.2342	7
4	465.2514	233.1293	447.2278	224.1175	447.2408	224.1241	K	713.3827	357.1950	695.3592	348.1832	695.3722	348.1897	6
5	***625.3407***	313.1740	607.3171	304.1622	607.3301	304.1687	R	***583.2937***	292.1505	565.2701	283.1387	565.2831	283.1452	5
6	***723.3905***	362.1989	705.3669	353.1871	705.3799	353.1936	P	423.2045	212.1059	405.1809	203.0941	405.1939	203.1006	4
7	781.4090	391.2081	763.3854	382.1963	763.3984	382.2028	G	***325.1547***	163.0810	307.1311	154.0692	307.1441	154.0757	3
8	***869.4380***	435.2226	851.4144	426.2109	851.4274	426.2174	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NSKKRPGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G02750.1

24.6	1046.5306	-0.0009	NSKKRPGSR
7.7	1046.5305	-0.0008	NSRRVIER
6.6	1046.5279	0.0018	SSKDKPSKR
6.4	1046.5305	-0.0008	RVNERSLR
6.1	1046.5305	-0.0008	RTELAQRR
4.5	1046.5278	0.0019	TGIVGRTGSGK
3.9	1046.5279	0.0018	ADSSQKKIR
3.7	1046.5279	0.0018	EARSLLTSR
3.1	1046.5306	-0.0009	SLSRRAPSR
0.3	1046.5305	-0.0008	RDNITRVR

AT3G02780.1

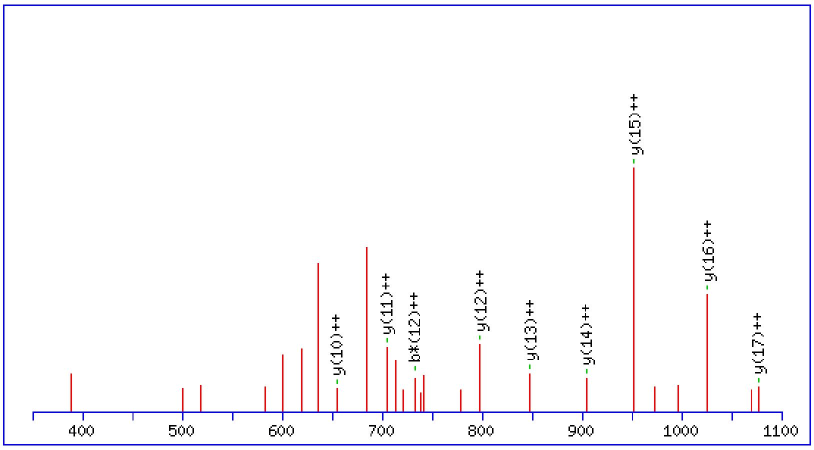
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTFPLVWTNTCCSHPLYR**
Found in **AT3G02780.1** in **TAIR_Arabidopsis**, Symbols: IPP2, IPIAT1, IDI2 | IDI2/IPIAT1/IPP2 (ISOPENTENYL DIPHOSPHATE ISOMERASE 2, ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2); isopentenyl-diphosphate delta-isomerase | chr3:602585-604655 REVERSE

Match to Query 10382: 2250.073227 from(751.031685,3+) index(8949)
Title: Elution from: 78.598 to 78.598 scan no 11776 cid35.00 polarity:+
Data file D12h-1_1.mgf

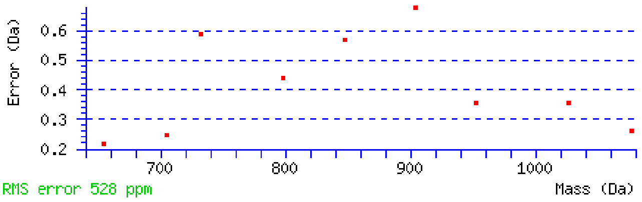
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

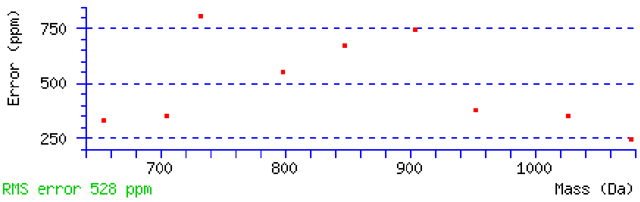


Monoisotopic mass of neutral peptide Mr(calc): 2250.0714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0019
Matches : 9/176 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							18
2	201.1234	101.0653			183.1128	92.0600	T	2152.0103	1076.5088	2134.9837	1067.9955	2133.9997	1067.5035	17
3	348.1918	174.5995			330.1812	165.5942	F	2050.9626	1025.9849	2033.9361	1017.4717	2032.9520	1016.9797	16
4	445.2445	223.1259			427.2340	214.1206	P	1903.8942	952.4507	1886.8676	943.9375	1885.8836	943.4454	15
5	558.3286	279.6679			540.3180	270.6627	L	1806.8414	903.9243	1789.8149	895.4111	1788.8309	894.9191	14
6	657.3970	329.2022			639.3865	320.1969	V	1693.7574	847.3823	1676.7308	838.8690	1675.7468	838.3770	13
7	843.4763	422.2418			825.4658	413.2365	W	1594.6889	797.8481	1577.6624	789.3348	1576.6784	788.8428	12
8	944.5240	472.7656			926.5135	463.7604	T	1408.6096	704.8085	1391.5831	696.2952	1390.5991	695.8032	11
9	1058.5669	529.7871	1041.5404	521.2738	1040.5564	520.7818	N	1307.5620	654.2846	1290.5354	645.7713	1289.5514	645.2793	10
10	1159.6146	580.3109	1142.5881	571.7977	1141.6041	571.3057	T	1193.5190	597.2632	1176.4925	588.7499	1175.5085	588.2579	9
11	1319.6453	660.3263	1302.6187	651.8130	1301.6347	651.3210	C	1092.4713	546.7393	1075.4448	538.2260	1074.4608	537.7340	8
12	1479.6759	740.3416	1462.6494	731.8283	1461.6654	731.3363	C	932.4407	466.7240	915.4141	458.2107	914.4301	457.7187	7
13	1566.7079	783.8576	1549.6814	775.3443	1548.6974	774.8523	S	772.4100	386.7087	755.3835	378.1954	754.3995	377.7034	6
14	1703.7669	852.3871	1686.7403	843.8738	1685.7563	843.3818	H	685.3780	343.1926	668.3515	334.6794			5
15	1800.8196	900.9135	1783.7931	892.4002	1782.8091	891.9082	P	548.3191	274.6632	531.2926	266.1499			4
16	1913.9037	957.4555	1896.8771	948.9422	1895.8931	948.4502	L	451.2663	226.1368	434.2398	217.6235			3
17	2076.9670	1038.9871	2059.9405	1030.4739	2058.9565	1029.9819	Y	338.1823	169.5948	321.1557	161.0815			2
18							R	175.1190	88.0631	158.0924	79.5498			1

AT3G02780.1





NCBI **BLAST** search of VTFPLVWTNTCCSHPLYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.0	2250.0714	0.0018	VTFPLVWTNTCCSHPLYR
2.1	2250.0692	0.0040	EIPEDLTPGLYGFTEADLDR
1.5	2250.0685	0.0047	IEELEKVCTLNSGEGEASASK
1.1	2250.0733	-0.0001	IETGVCQGQKVVSCDVQSTR
1.0	2250.0726	0.0006	VKTLEGMLGEWITDGEVDDK

Mascot: http://www.matrixscience.com/

AT3G03250.1

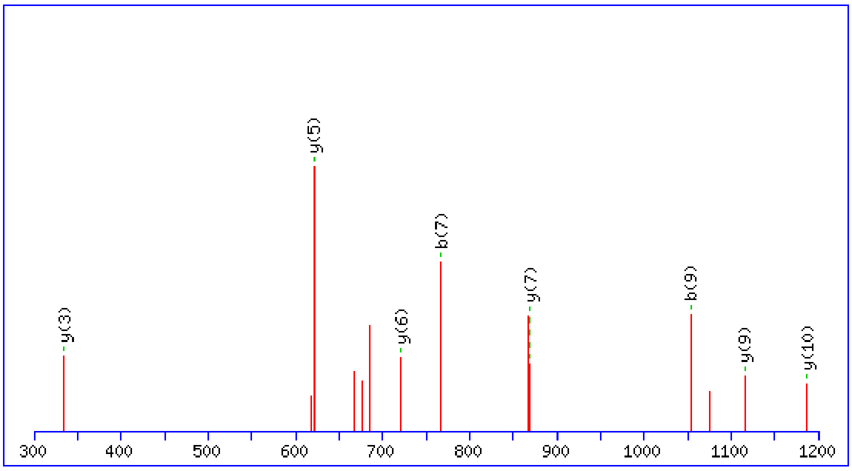
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVADEFVPWPSK**
Found in **AT3G03250.1** in **TAIR_Arabidopsis**, Symbols: UGP | UGP (UDP-glucose pyrophosphorylase); UTP:glucose-1-phosphate uridylyltransferase | chr3:749768-754021 REVERSE

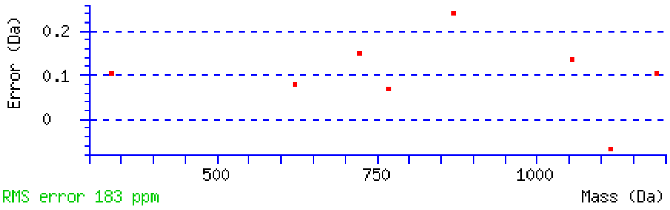
Match to Query 5394: 1386.660692 from(694.337622,2+) index(7881)
Title: Elution from: 69.630 to 69.630 scan no 10338 cid35.00 polarity:+
Data file D6h-3_1.mgf

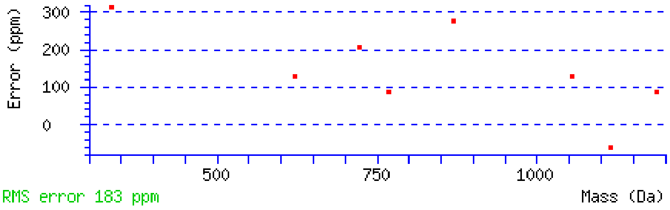
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1386.6612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00013
Matches : 8/102 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400			**V**							**12**
2	201.1382	101.0727			**V**	1287.6030	644.3051	1269.5794	635.2934	1269.5925	635.2999	**11**
3	273.1723	137.0898			**A**	***1187.5376***	594.2724	1169.5140	585.2606	1169.5270	585.2671	**10**
4	389.1963	195.1018	371.1857	186.0965	**D**	***1115.5034***	558.2553	1097.4798	549.2436	1097.4929	549.2501	**9**
5	519.2359	260.1216	501.2254	251.1163	**E**	999.4794	500.2434	981.4559	491.2316	981.4689	491.2381	**8**
6	667.3014	334.1543	649.2908	325.1490	**F**	***869.4398***	435.2235	851.4162	426.2118	851.4293	426.2183	**7**
7	**767.3668**	384.1871	749.3563	375.1818	**V**	***721.3744***	361.1908	703.3508	352.1790	703.3638	352.1855	**6**
8	865.4166	433.2120	847.4061	424.2067	**P**	***621.3089***	311.1581	603.2853	302.1463	603.2984	302.1528	**5**
9	**1053.4900**	527.2486	1035.4794	518.2434	**W**	523.2591	262.1332	505.2355	253.1214	505.2486	253.1279	**4**
10	1151.5398	576.2735	1133.5292	567.2683	**P**	***335.1857***	168.0965	317.1622	159.0847	317.1752	159.0912	**3**
11	1239.5689	620.2881	1221.5583	611.2828	**S**	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	**2**
12					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of VVADEFVPWPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G03250.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.6	1386.6612	-0.0005	VVADEFVPWPSK
12.2	1386.6594	0.0013	LREVNIDEAPGR
11.5	1386.6616	-0.0009	DAGVSAIVFHPTR
4.4	1386.6616	-0.0009	RNQLVSFSGFSK
4.3	1386.6567	0.0040	GQEGAGIVTVSPEK
1.8	1386.6616	-0.0009	FALPVDSEHRAK
0.3	1386.6567	0.0040	AQIAEAGAPTDISK

AT3G03780.1

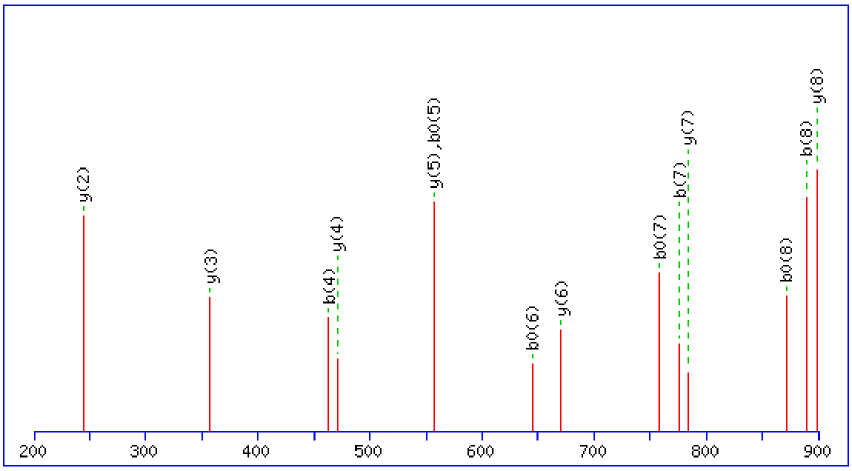
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFDLLSLLPK**
Found in **AT3G03780.1** in **TAIR_Arabidopsis**, Symbols: AtMS2 | AtMS2 (Arabidopsis thaliana methionine synthase 2); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase | chr3:957609-960747 FORWARD

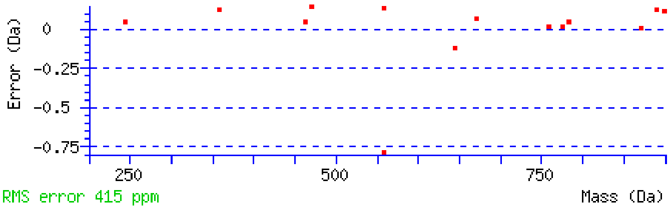
Match to Query 3610: 1131.654666 from(566.834609,2+) index(10884)
Title: Elution from: 108.612 to 108.612 scan no 15886 cid35.00 polarity:+
Data file C7-1_2.mgf

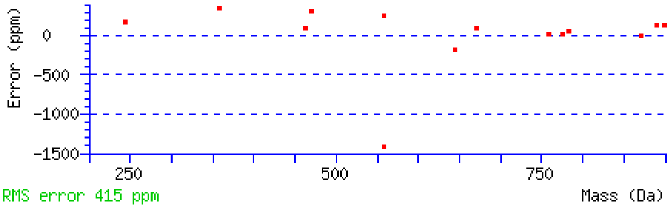
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1131.6539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 2.4e-008
Matches : 14/82 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							10
2	235.1077	118.0575	217.0972	109.0522	F	1045.6292	523.3182	1028.6027	514.8050	1027.6186	514.3130	9
3	350.1347	175.5710	332.1241	166.5657	D	***898.5608***	449.7840	881.5342	441.2708	880.5502	440.7788	8
4	**463.2187**	232.1130	445.2082	223.1077	L	***783.5339***	392.2706	766.5073	383.7573	765.5233	383.2653	7
5	576.3028	288.6550	558.2922	279.6498	L	***670.4498***	335.7285	653.4232	327.2153	652.4392	326.7232	6
6	663.3348	332.1710	645.3243	323.1658	S	***557.3657***	279.1865	540.3392	270.6732	539.3552	270.1812	5
7	**776.4189**	388.7131	758.4083	379.7078	L	***470.3337***	235.6705	453.3071	227.1572			4
8	**889.5029**	445.2551	871.4924	436.2498	L	***357.2496***	179.1285	340.2231	170.6152			3
9	986.5557	493.7815	968.5451	484.7762	P	***244.1656***	122.5864	227.1390	114.0731			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SFDLLSLLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G03780.1

Score	Mr(calc)	Delta	Sequence
77.7	1131.6539	0.0007	SFDLLSLLPK

AT3G03920.1

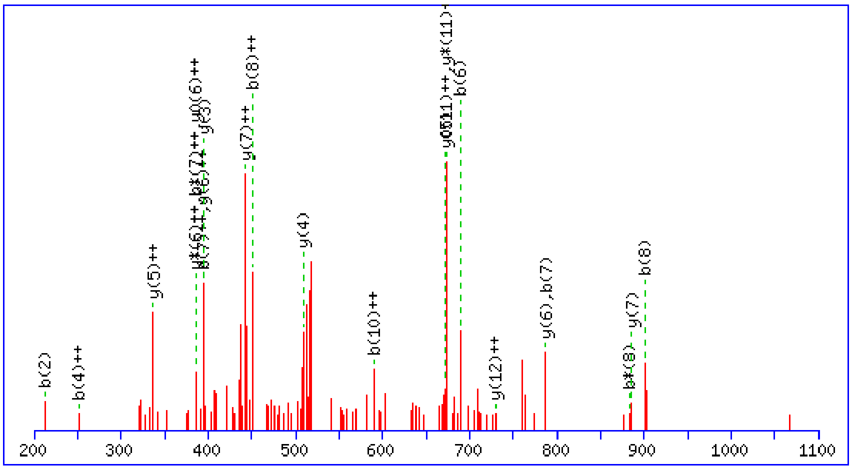
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPHFNAPIYLENK**
Found in **AT3G03920.1** in **TAIR_Arabidopsis**, Symbols: | Gar1 RNA-binding region family protein | chr3:1009130-1010386 REVERSE

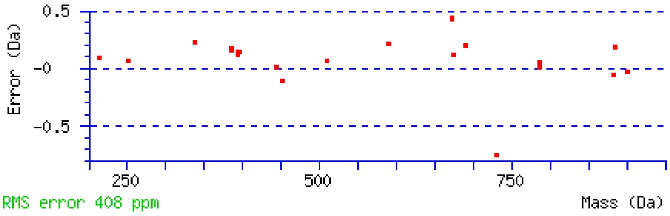
Match to Query 6946: 1572.764838 from(525.262222,3+) index(6068)
Title: Elution from: 54.164 to 54.164 scan no 7801 cid35.00 polarity:+
Data file 0-2_2.mgf

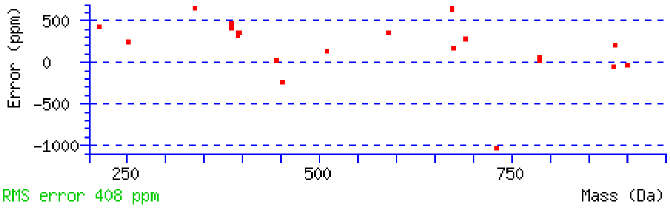
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1572.7661
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.03
Matches : 23/112 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							13
2	***213.1382***	107.0727					P	1459.6923	730.3498	1441.6687	721.3380	1441.6817	721.3445	12
3	353.1882	177.0977					H	1361.6425	681.3249	1343.6189	672.3131	1343.6319	672.3196	11
4	501.2536	***251.1305***					F	1221.5925	611.2999	1203.5689	602.2881	1203.5819	602.2946	10
5	617.2906	309.1490	599.2671	300.1372			N	1073.5270	537.2671	1055.5034	528.2553	1055.5164	528.2619	9
6	***689.3248***	345.1660	671.3012	336.1542			A	957.4900	479.2486	939.4664	470.2369	939.4794	470.2434	8
7	***787.3746***	***394.1909***	769.3510	385.1791			P	***885.4559***	443.2316	867.4323	434.2198	867.4453	434.2263	7
8	***901.4557***	***451.2315***	883.4321	442.2197			I	***787.4061***	394.2067	769.3825	385.1949	769.3955	385.2014	6
9	1065.5160	533.2617	1047.4925	524.2499			Y	***673.3250***	337.1661	655.3014	328.1543	655.3144	328.1608	5
10	1179.5971	***590.3022***	1161.5736	581.2904			L	***509.2646***	255.1359	491.2410	246.1241	491.2540	246.1307	4
11	1309.6368	655.3220	1291.6132	646.3102	1291.6262	646.3167	E	***395.1835***	198.0954	377.1599	189.0836	377.1729	189.0901	3
12	1425.6738	713.3405	1407.6502	704.3287	1407.6632	704.3352	N	265.1439	133.0756	247.1203	124.0638			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IPHFNAPIYLENK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G03920.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	1572.7661	-0.0013	IPHFNAPIYLENK
1.2	1572.7695	-0.0046	LLHAKNVEFEPMK
0.7	1572.7612	0.0037	SLTYALEDDFKKK
0.3	1572.7616	0.0032	DLEPPSQRPKTSAK

AT3G03960.1

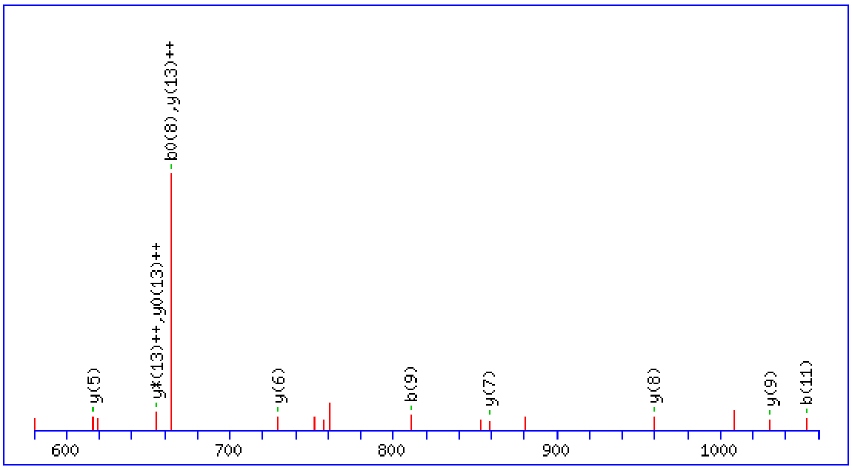
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVPGAAATEIELAQR**
Found in **AT3G03960.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr3:1024439-1027611 FORWARD

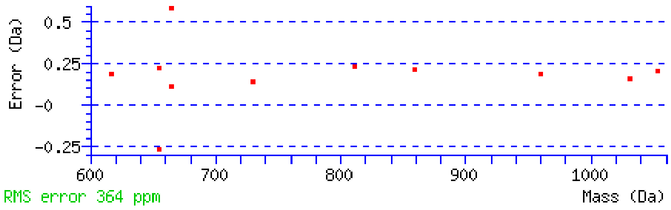
Match to Query 6842: 1537.845362 from(769.929957,2+) index(5866)
Title: Elution from: 52.370 to 52.370 scan no 7407 cid35.00 polarity:+
Data file D12h-3_1.mgf

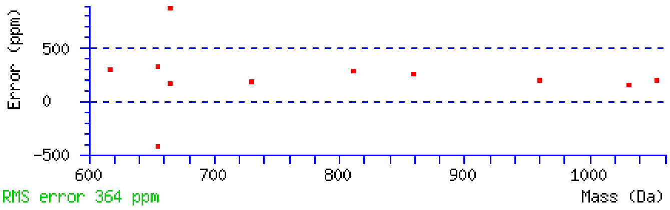
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 580 to 1060 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1537.8464
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00038
Matches : 11/120 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							15
2	213.1598	107.0835					V	1425.7696	713.3884	1408.7431	704.8752	1407.7591	704.3832	14
3	310.2125	155.6099					P	1326.7012	663.8542	1309.6747	655.3410	1308.6906	654.8490	13
4	367.2340	184.1206					G	1229.6484	615.3279	1212.6219	606.8146	1211.6379	606.3226	12
5	438.2711	219.6392					A	1172.6270	586.8171	1155.6004	578.3039	1154.6164	577.8118	11
6	509.3082	255.1577					A	1101.5899	551.2986	1084.5633	542.7853	1083.5793	542.2933	10
7	580.3453	290.6763					A	***1030.5528***	515.7800	1013.5262	507.2667	1012.5422	506.7747	9
8	681.3930	341.2001			663.3824	332.1949	T	***959.5156***	480.2615	942.4891	471.7482	941.5051	471.2562	8
9	**810.4356**	405.7214			792.4250	396.7162	E	***858.4680***	429.7376	841.4414	421.2243	840.4574	420.7323	7
10	923.5197	462.2635			905.5091	453.2582	I	***729.4254***	365.2163	712.3988	356.7030	711.4148	356.2110	6
11	**1052.5623**	526.7848			1034.5517	517.7795	E	***616.3413***	308.6743	599.3148	300.1610	598.3307	299.6690	5
12	1165.6463	583.3268			1147.6358	574.3215	L	487.2987	244.1530	470.2722	235.6397			4
13	1236.6834	618.8454			1218.6729	609.8401	A	374.2146	187.6110	357.1881	179.0977			3
14	1364.7420	682.8746	1347.7155	674.3614	1346.7314	673.8694	Q	303.1775	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IVPGAAATEIELAQR

AT3G03960.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.5	1537.8464	-0.0010	IVPGAAATEIELAQR

AT3G04120.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AASFNIIPSSTGAAK**
Found in **AT3G04120.1** in **TAIR_Arabidopsis**, Symbols: GAPC-1, GAPC | GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase | chr3:1081084-1083138 FORWARD

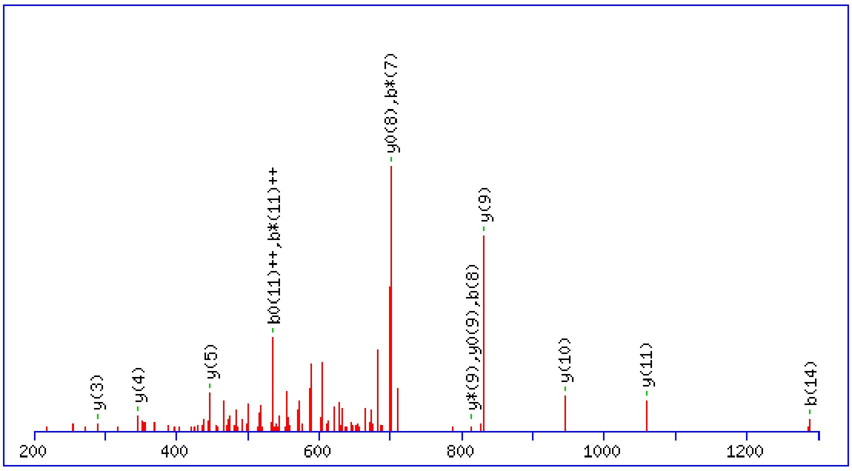
Match to Query 5711: 1433.749810 from(717.882181,2+) index(5345)
Title: Elution from: 47.725 to 47.725 scan no 6739 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

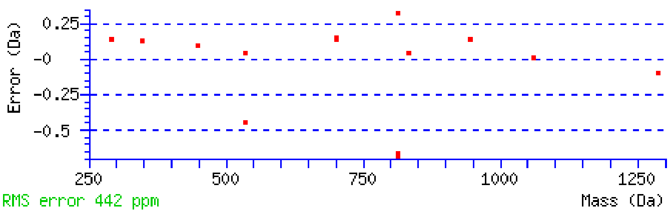
Label all possible matches ○ Label matches used for scoring ●

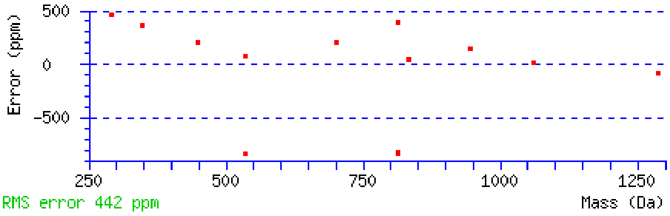
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1433.7514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 1.3e-005
Matches : 14/148 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**15**
2	143.0815	72.0444					**A**	1363.7216	682.3644	1346.6951	673.8512	1345.7110	673.3592	**14**
3	230.1135	115.5604			212.1030	106.5551	**S**	1292.6845	646.8459	1275.6579	638.3326	1274.6739	637.8406	**13**
4	377.1819	189.0946			359.1714	180.0893	**F**	1205.6525	603.3299	1188.6259	594.8166	1187.6419	594.3246	**12**
5	491.2249	246.1161	474.1983	237.6028	473.2143	237.1108	**N**	***1058.5840***	529.7957	1041.5575	521.2824	1040.5735	520.7904	**11**
6	604.3089	302.6581	587.2824	294.1448	586.2984	293.6528	**I**	***944.5411***	472.7742	927.5146	464.2609	926.5306	463.7689	**10**
7	717.3930	359.2001	700.3665	350.6869	699.3824	350.1949	**I**	***831.4571***	416.2322	814.4305	407.7189	813.4465	407.2269	**9**
8	**814.4458**	407.7265	797.4192	399.2132	796.4352	398.7212	**P**	718.3730	359.6901	701.3464	351.1769	700.3624	350.6849	**8**
9	901.4778	451.2425	884.4512	442.7293	883.4672	442.2373	**S**	621.3202	311.1638	604.2937	302.6505	603.3097	302.1585	**7**
10	988.5098	494.7585	971.4833	486.2453	970.4993	485.7533	**S**	534.2882	267.6477	517.2617	259.1345	516.2776	258.6425	**6**
11	1089.5575	545.2824	1072.5310	536.7691	1071.5469	536.2771	**T**	***447.2562***	224.1317	430.2296	215.6185	429.2456	215.1264	**5**
12	1146.5790	573.7931	1129.5524	565.2798	1128.5684	564.7878	**G**	***346.2085***	173.6079	329.1819	165.0946			**4**
13	1217.6161	609.3117	1200.5895	600.7984	1199.6055	600.3064	**A**	***289.1870***	145.0972	272.1605	136.5839			**3**
14	**1288.6532**	644.8302	1271.6266	636.3170	1270.6426	635.8250	**A**	218.1499	109.5786	201.1234	101.0653			**2**
15							**K**	147.1128	74.0600	130.0863	65.5468			**1**





AT3G04120.1

NCBI **BLAST** search of AASFNIIPSSTGAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.6	1433.7514	-0.0016	AASFNIIPSSTGAAK

AT3G04550.1

MATRIX SCIENCE

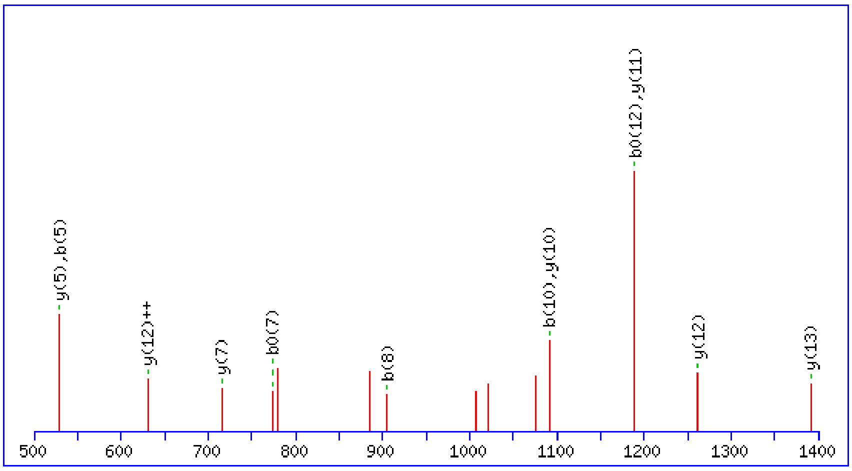
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILEAPMEIIAGGDFK**
Found in **AT3G04550.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1) | chr3:1225967-1227316 FORWARD

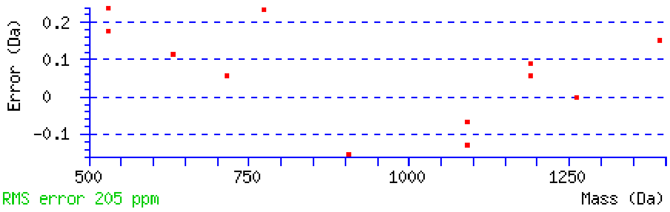
Match to Query 7411: 1618.788634 from(810.401593,2+) index(9669)
Title: Elution from: 86.741 to 86.741 scan no 13214 cid35.00 polarity:+
Data file D1d-3_2.mgf

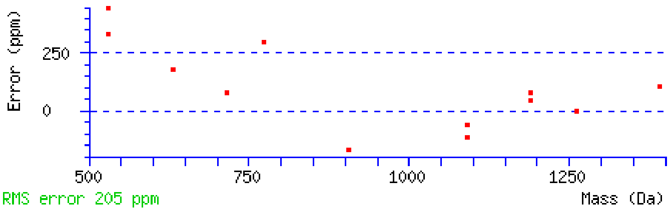
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1618.7853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.001
Matches : 12/132 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			I							15
2	229.1695	115.0884			L	1505.7115	753.3594	1487.6879	744.3476	1487.7009	744.3541	14
3	359.2091	180.1082	341.1985	171.1029	E	***1391.6304***	696.3188	1373.6068	687.3070	1373.6198	687.3135	13
4	431.2433	216.1253	413.2327	207.1200	A	***1261.5907***	631.2990	1243.5672	622.2872	1243.5802	622.2937	12
5	**529.2930**	265.1502	511.2825	256.1449	P	***1189.5566***	595.2819	1171.5330	586.2701	1171.5460	586.2767	11
6	661.3306	331.1689	643.3200	322.1636	M	***1091.5068***	546.2570	1073.4832	537.2452	1073.4962	537.2518	10
7	791.3702	396.1887	773.3596	387.1835	E	959.4693	480.2383	941.4457	471.2265	941.4587	471.2330	9
8	**905.4513**	453.2293	887.4407	444.2240	I	829.4296	415.2185	811.4061	406.2067	811.4191	406.2132	8
9	1019.5324	510.2698	1001.5218	501.2646	I	***715.3485***	358.1779	697.3250	349.1661	697.3380	349.1726	7
10	**1091.5665**	546.2869	1073.5560	537.2816	A	601.2674	301.1374	583.2439	292.1256	583.2569	292.1321	6
11	1149.5850	575.2962	1131.5745	566.2909	G	***529.2333***	265.1203	511.2097	256.1085	511.2227	256.1150	5
12	1207.6035	604.3054	1189.5930	595.3001	G	471.2148	236.1110	453.1912	227.0992	453.2042	227.1058	4
13	1323.6275	662.3174	1305.6170	653.3121	D	413.1963	207.1018	395.1727	198.0900	395.1857	198.0965	3
14	1471.6930	736.3501	1453.6824	727.3448	F	297.1723	149.0898	279.1487	140.0780			2
15					K	149.1069	75.0571	131.0833	66.0453			1





AT3G04550.1

NCBI **BLAST** search of ILEAPMEIIAGGDFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.6	1618.7853	0.0034	ILEAPMEIIAGGDFK

AT3G04790.1

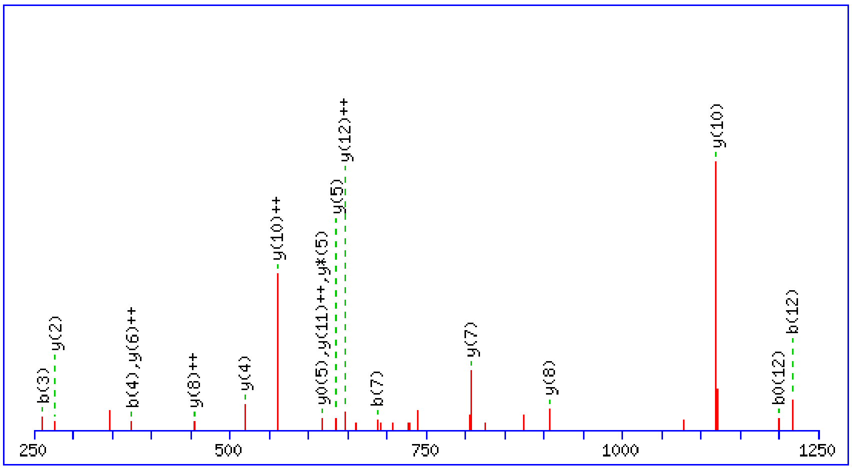
Mascot Search Results

Peptide View

MS/MS Fragmentation of SLGIPLVGLDTHPR
Found in AT3G04790.1 in TAIR_Arabidopsis, Symbols: | ribose 5-phosphate isomerase-related | chr3:1313371-1314201 FORWARD

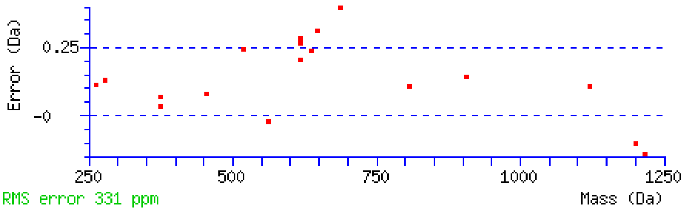
Match to Query 6142: 1492.771424 from(747.392988,2+) index(7137)
Title: Elution from: 63.109 to 63.109 scan no 9294 cid35.00 polarity:+
Data file 0-3_2.mgf

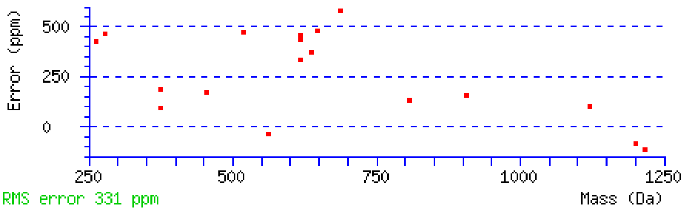
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1492.7740
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 8.9e-006
Matches : 18/124 fragment ions using 24 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218	71.0258	36.0165	S							14
2	203.1174	102.0624	185.1069	93.0571	L	1405.7522	703.3798	1387.7287	694.3680	1387.7417	694.3745	13
3	**261.1359**	131.0716	243.1254	122.0663	G	1291.6711	646.3392	1273.6476	637.3274	1273.6606	637.3339	12
4	**375.2170**	188.1122	357.2065	179.1069	I	1233.6526	617.3300	1215.6291	608.3182	1215.6421	608.3247	11
5	473.2668	237.1371	455.2563	228.1318	P	***1119.5715***	560.2894	1101.5480	551.2776	1101.5610	551.2841	10
6	587.3479	294.1776	569.3374	285.1723	L	1021.5217	511.2645	1003.4982	502.2527	1003.5112	502.2592	9
7	**687.4134**	344.2103	669.4028	335.2050	V	***907.4406***	454.2240	889.4171	445.2122	889.4301	445.2187	8
8	745.4319	373.2196	727.4213	364.2143	G	***807.3752***	404.1912	789.3516	395.1794	789.3646	395.1860	7
9	859.5130	430.2601	841.5024	421.2548	L	749.3567	375.1820	731.3331	366.1702	731.3461	366.1767	6
10	975.5370	488.2721	957.5264	479.2668	D	***635.2756***	318.1414	617.2520	309.1296	617.2650	309.1362	5
11	1077.5817	539.2945	1059.5711	530.2892	T	***519.2516***	260.1294	501.2280	251.1177	501.2411	251.1242	4
12	**1217.6317**	609.3195	1199.6211	600.3142	H	417.2069	209.1071	399.1833	200.0953			3
13	1315.6815	658.3444	1297.6709	649.3391	P	***277.1569***	139.0821	259.1333	130.0703			2
14					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SLGIPLVGLDTHPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G04790.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.9	1492.7740	-0.0026	SLGIPLVGLDTHPR
4.4	1492.7713	0.0001	TLVGVISQEKFEK
1.9	1492.7722	-0.0008	VPMDILVFKLMR

AT3G04840.1

Mascot Search Results

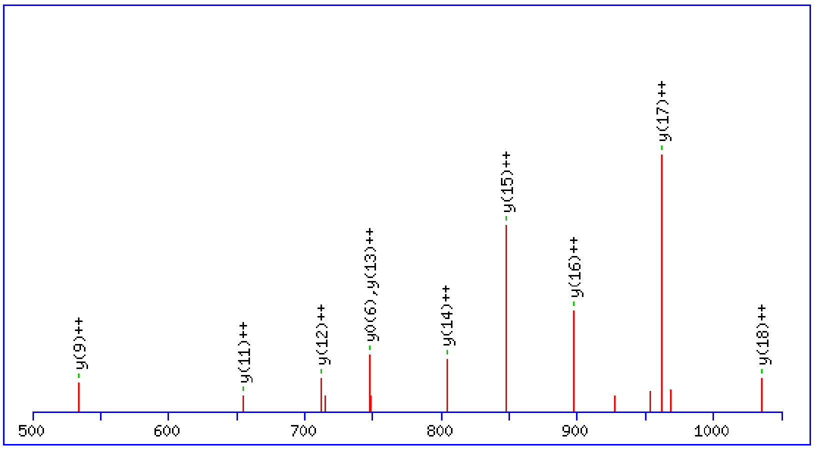
Peptide View

MS/MS Fragmentation of **VFEVSLADLQGDEDNAYRK**
Found in **AT3G04840.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S3A (RPS3aA) | chr3:1329757-1331424 FORWARD

Match to Query 9735: 2168.034960 from(723.685596,3+) index(7716)
Title: Elution from: 66.912 to 66.912 scan no 10046 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

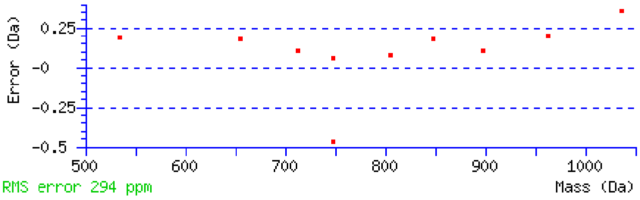
Or, Plot from 500 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

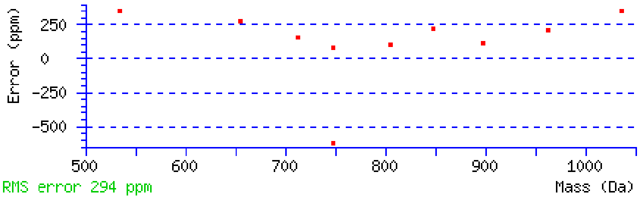


Monoisotopic mass of neutral peptide Mr(calc): 2168.0386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 1.1e-008
Matches : 10/184 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							19
2	247.1441	124.0757					F	2069.9774	1035.4924	2052.9509	1026.9791	2051.9669	1026.4871	18
3	376.1867	188.5970			358.1761	179.5917	E	1922.9090	961.9582	1905.8825	953.4449	1904.8985	952.9529	17
4	475.2551	238.1312			457.2445	229.1259	V	1793.8664	897.4369	1776.8399	888.9236	1775.8559	888.4316	16
5	562.2871	281.6472			544.2766	272.6419	S	1694.7980	847.9026	1677.7715	839.3894	1676.7875	838.8974	15
6	675.3712	338.1892			657.3606	329.1840	L	1607.7660	804.3866	1590.7394	795.8734	1589.7554	795.3814	14
7	746.4083	373.7078			728.3978	364.7025	A	1494.6819	747.8446	1477.6554	739.3313	1476.6714	738.8393	13
8	861.4353	431.2213			843.4247	422.2160	D	1423.6448	712.3260	1406.6183	703.8128	1405.6342	703.3208	12
9	974.5193	487.7633			956.5088	478.7580	L	1308.6179	654.8126	1291.5913	646.2993	1290.6073	645.8073	11
10	1102.5779	551.7926	1085.5514	543.2793	1084.5673	542.7873	Q	1195.5338	598.2705	1178.5073	589.7573	1177.5232	589.2653	10
11	1159.5994	580.3033	1142.5728	571.7900	1141.5888	571.2980	G	1067.4752	534.2413	1050.4487	525.7280	1049.4647	525.2360	9
12	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	D	1010.4538	505.7305	993.4272	497.2172	992.4432	496.7252	8
13	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	E	895.4268	448.2170	878.4003	439.7038	877.4163	439.2118	7
14	1518.6958	759.8516	1501.6693	751.3383	1500.6853	750.8463	D	766.3842	383.6958	749.3577	375.1825	748.3737	374.6905	6
15	1632.7388	816.8730	1615.7122	808.3597	1614.7282	807.8677	N	651.3573	326.1823	634.3307	317.6690			5
16	1703.7759	852.3916	1686.7493	843.8783	1685.7653	843.3863	A	537.3144	269.1608	520.2878	260.6475			4
17	1866.8392	933.9232	1849.8127	925.4100	1848.8287	924.9180	Y	466.2772	233.6423	449.2507	225.1290			3
18	2022.9403	1011.9738	2005.9138	1003.4605	2004.9298	1002.9685	R	303.2139	152.1106	286.1874	143.5973			2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT3G04840.1





NCBI **BLAST** search of VFEVSLADLQGDEDNAYRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.4	2168.0386	-0.0036	VFEVSLADLQGDEDNAYRK
4.6	2168.0289	0.0061	SCNLAMCLIKQGRFEEGR
2.4	2168.0368	-0.0018	RLGAFEQHTTGFGSRMMAR
2.0	2168.0287	0.0063	FLSQLSKDYHAWASGDTSR
1.5	2168.0307	0.0043	TAQEAMTPIESTFSLDVNSK

Mascot: http://www.matrixscience.com/

AT3G04870.1

Mascot Search Results

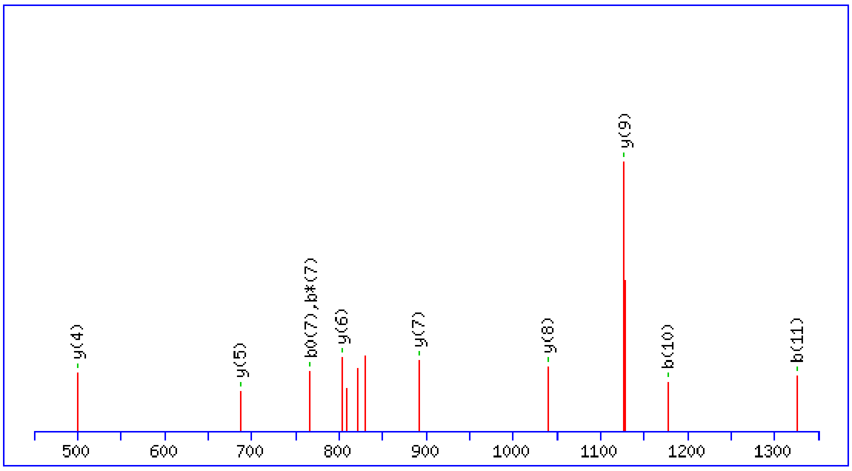
Peptide View

MS/MS Fragmentation of **NLDSISFSDWFLSK**
Found in **AT3G04870.1** in **TAIR_Arabidopsis**, Symbols: PDE181, ZDS | ZDS (ZETA-CAROTENE DESATURASE); carotene 7,8-desaturase | chr3:1342848-1346195 FORWARD

Match to Query 7908: 1674.748558 from(838.381555,2+) index(10717)
Title: Elution from: 103.207 to 103.207 scan no 15434 cid35.00 polarity:+
Data file C7-1_2.mgf

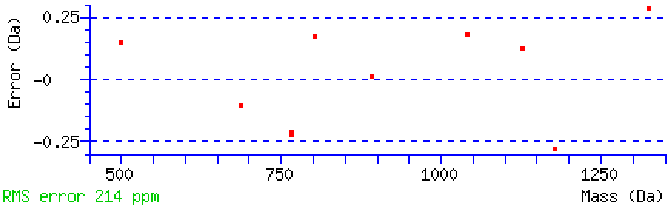
Click mouse within plot area to zoom in by factor of two about that point

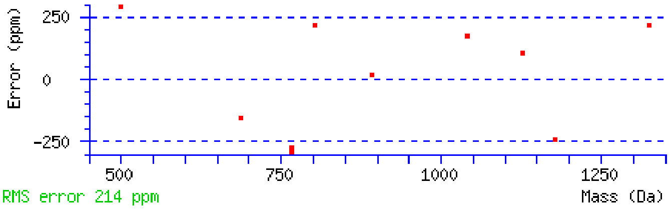
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1674.7484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 4.3e-005
Matches : 10/150 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							14
2	231.1254	116.0663	213.1018	107.0545			L	1559.7187	780.3630	1541.6951	771.3512	1541.7081	771.3577	13
3	347.1493	174.0783	329.1258	165.0665	329.1388	165.0730	D	1445.6376	723.3224	1427.6140	714.3106	1427.6270	714.3171	12
4	435.1784	218.0928	417.1548	209.0811	417.1678	209.0876	S	1329.6136	665.3104	1311.5900	656.2986	1311.6030	656.3051	11
5	549.2595	275.1334	531.2359	266.1216	531.2489	266.1281	I	1241.5845	621.2959	1223.5609	612.2841	1223.5740	612.2906	10
6	637.2886	319.1479	619.2650	310.1361	619.2780	310.1426	S	***1127.5034***	564.2553	1109.4798	555.2436	1109.4929	555.2501	9
7	785.3540	393.1807	767.3304	384.1689	767.3435	384.1754	F	***1039.4744***	520.2408	1021.4508	511.2290	1021.4638	511.2355	8
8	873.3831	437.1952	855.3595	428.1834	855.3725	428.1899	S	***891.4089***	446.2081	873.3853	437.1963	873.3983	437.2028	7
9	989.4071	495.2072	971.3835	486.1954	971.3965	486.2019	D	***803.3798***	402.1936	785.3563	393.1818	785.3693	393.1883	6
10	**1177.4804**	589.2439	1159.4569	580.2321	1159.4699	580.2386	W	***687.3559***	344.1816	669.3323	335.1698	669.3453	335.1763	5
11	**1325.5459**	663.2766	1307.5223	654.2648	1307.5353	654.2713	F	***499.2825***	250.1449	481.2589	241.1331	481.2719	241.1396	4
12	1439.6270	720.3171	1421.6034	711.3053	1421.6164	711.3119	L	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
13	1527.6561	764.3317	1509.6325	755.3199	1509.6455	755.3264	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NLDSISFSDWFLSK

AT3G04870.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.7	1674.7484	0.0002	NLDSISFSDWFLSK
3.3	1674.7466	0.0020	TSSVPRFDSSTNLSR

AT3G04920.1

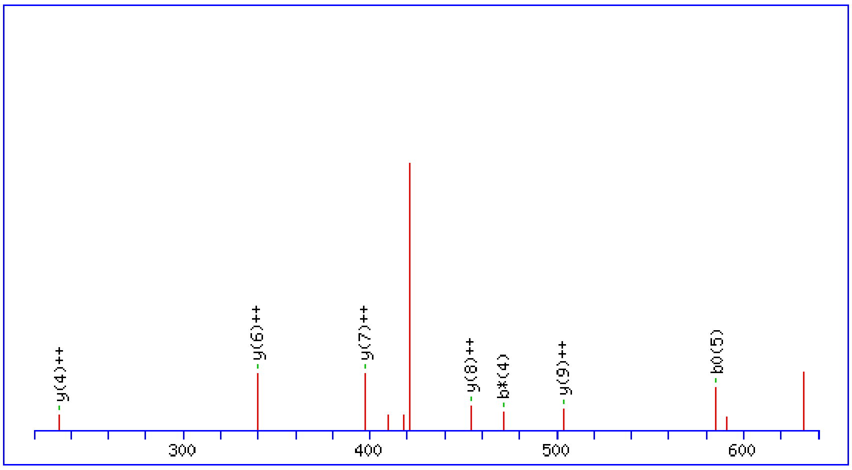
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFVIDVLHPGR**
Found in **AT3G04920.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S24 (RPS24A) | chr3:1360995-1362071 FORWARD

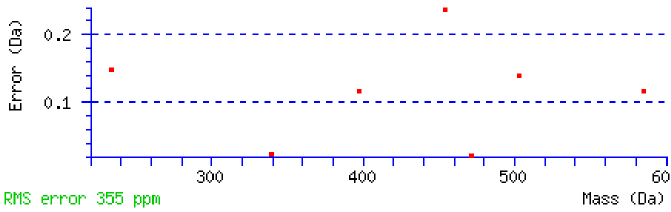
Match to Query 4628: 1279.702974 from(427.574934,3+) index(6655)
Title: Elution from: 58.670 to 58.670 scan no 8595 cid35.00 polarity:+
Data file D6h-3_2.mgf

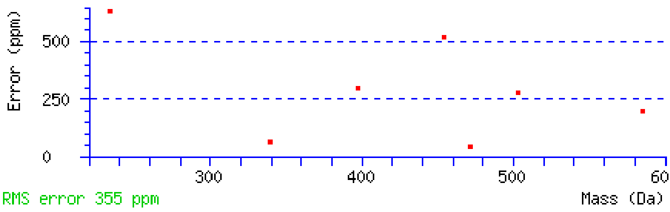
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 640 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1279.7037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0037
Matches : 7/100 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	276.1343	138.5708	259.1077	130.0575			F	1152.6524	576.8298	1135.6259	568.3166	1134.6418	567.8246	10
3	375.2027	188.1050	358.1761	179.5917			V	1005.5840	503.2956	988.5574	494.7824	987.5734	494.2904	9
4	488.2867	244.6470	471.2602	236.1337			I	906.5156	453.7614	889.4890	445.2482	888.5050	444.7561	8
5	603.3137	302.1605	586.2871	293.6472	585.3031	293.1552	D	793.4315	397.2194	776.4050	388.7061	775.4209	388.2141	7
6	702.3821	351.6947	685.3556	343.1814	684.3715	342.6894	V	678.4046	339.7059	661.3780	331.1926			6
7	815.4662	408.2367	798.4396	399.7234	797.4556	399.2314	L	579.3362	290.1717	562.3096	281.6584			5
8	952.5251	476.7662	935.4985	468.2529	934.5145	467.7609	H	466.2521	233.6297	449.2255	225.1164			4
9	1049.5778	525.2926	1032.5513	516.7793	1031.5673	516.2873	P	329.1932	165.1002	312.1666	156.5870			3
10	1106.5993	553.8033	1089.5728	545.2900	1088.5887	544.7980	G	232.1404	116.5738	215.1139	108.0606			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QFVIDVLHPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G04920.1

Score	Mr(calc)	Delta	Sequence
28.3	1279.7037	-0.0007	QFVIDVLHPGR
4.5	1279.6997	0.0033	SKSHHTNTKLK
1.0	1279.7037	-0.0007	AFSVFNQLRAK
1.0	1279.6999	0.0031	FLANVTFLMPK
1.0	1279.6997	0.0033	GRKHSPETLQK

Mascot: http://www.matrixscience.com/

AT3G05060.1

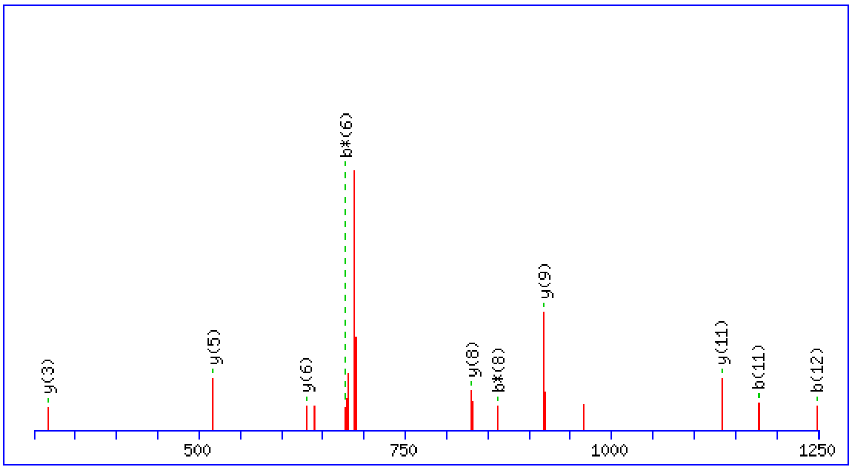
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDNTSEALEAVAK**
Found in **AT3G05060.1** in **TAIR_Arabidopsis**, Symbols: | SAR DNA-binding protein, putative | chr3:1413180-1415570 REVERSE

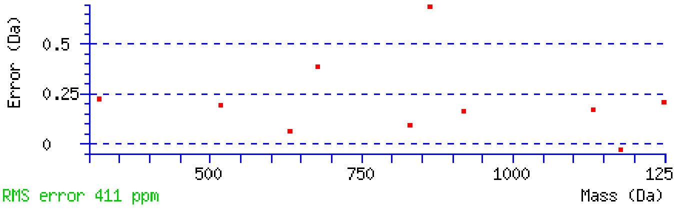
Match to Query 5227: 1393.672842 from(697.843697,2+) index(4899)
Title: Elution from: 47.397 to 47.397 scan no 6308 cid35.00 polarity:+
Data file D12h-2_1.mgf

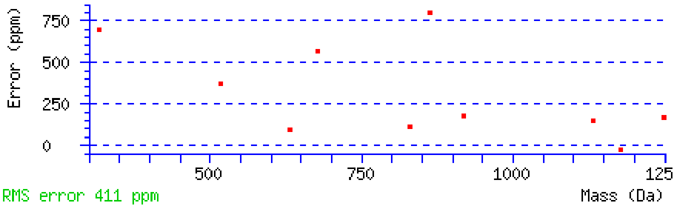
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1393.6725
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 9.5e-005
Matches : 10/130 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	148.0757	74.5415					F							13
2	263.1026	132.0550			245.0921	123.0497	D	1247.6114	624.3093	1230.5848	615.7961	1229.6008	615.3040	12
3	377.1456	189.0764	360.1190	180.5631	359.1350	180.0711	N	***1132.5844***	566.7959	1115.5579	558.2826	1114.5739	557.7906	11
4	478.1932	239.6003	461.1667	231.0870	460.1827	230.5950	T	1018.5415	509.7744	1001.5150	501.2611	1000.5310	500.7691	10
5	565.2253	283.1163	548.1987	274.6030	547.2147	274.1110	S	***917.4938***	459.2506	900.4673	450.7373	899.4833	450.2453	9
6	694.2679	347.6376	677.2413	339.1243	676.2573	338.6323	E	***830.4618***	415.7345	813.4353	407.2213	812.4512	406.7293	8
7	765.3050	383.1561	748.2784	374.6429	747.2944	374.1508	A	701.4192	351.2132	684.3927	342.7000	683.4087	342.2080	7
8	878.3890	439.6982	861.3625	431.1849	860.3785	430.6929	L	***630.3821***	315.6947	613.3556	307.1814	612.3715	306.6894	6
9	1007.4316	504.2195	990.4051	495.7062	989.4211	495.2142	E	***517.2980***	259.1527	500.2715	250.6394	499.2875	250.1474	5
10	1078.4687	539.7380	1061.4422	531.2247	1060.4582	530.7327	A	388.2554	194.6314	371.2289	186.1181			4
11	**1177.5372**	589.2722	1160.5106	580.7589	1159.5266	580.2669	V	***317.2183***	159.1128	300.1918	150.5995			3
12	**1248.5743**	624.7908	1231.5477	616.2775	1230.5637	615.7855	A	218.1499	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FDNTSEALEAVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G05060.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.9	1393.6725	0.0003	FDNTSEALEAVAK
12.0	1393.6732	-0.0004	CRTGRQSTVSDK
6.4	1393.6693	0.0035	DLMNRMTLQEK
4.7	1393.6725	0.0004	NFNEITSIEEAK
4.2	1393.6725	0.0003	LESFTEAVADANK
3.9	1393.6707	0.0022	VMAEQWRMRR
2.9	1393.6759	-0.0030	IKMTGIDEQTDK
2.8	1393.6738	-0.0010	YRALEETGNWR
2.5	1393.6767	-0.0039	EMVKLCENLMK
2.5	1393.6734	-0.0005	KMEEDMGWLKK

AT3G05090.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSAPRILR**
Found in **AT3G05090.1** in **TAIR_Arabidopsis**, Symbols: | transducin family protein / WD-40 repeat family protein | chr3:1418579-1422729 REVERSE

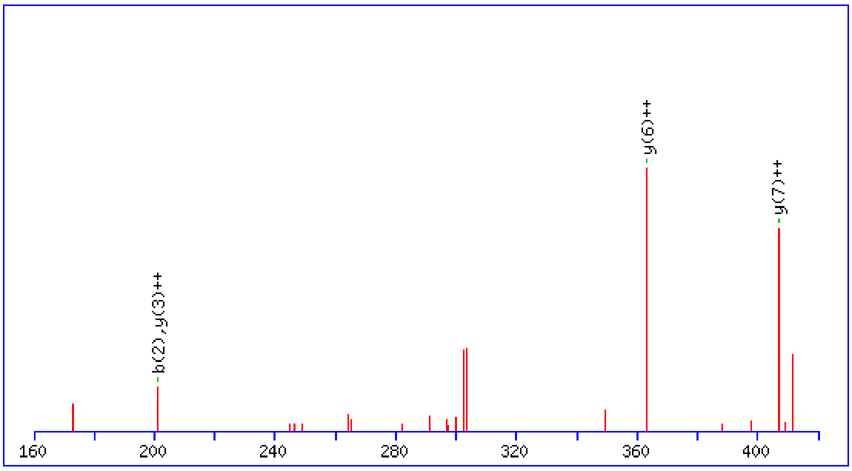
Match to Query 1718: 924.587643 from(309.203157,3+) index(1417)
Title: Elution from: 18.948 to 18.948 scan no 1905 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 160 to 420 Da Full range

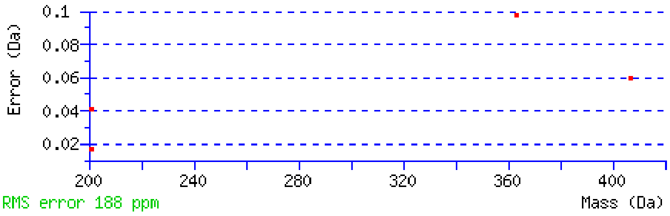
Label all possible matches ○ Label matches used for scoring ●

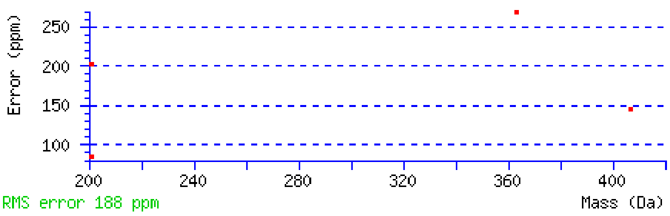
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 924.5869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0021
Matches : 4/62 fragment ions using 3 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							8
2	201.1234	101.0653			183.1128	92.0600	S	812.5101	406.7587	795.4835	398.2454	794.4995	397.7534	7
3	272.1605	136.5839			254.1499	127.5786	A	725.4781	363.2427	708.4515	354.7294			6
4	369.2132	185.1103			351.2027	176.1050	P	654.4410	327.7241	637.4144	319.2108			5
5	525.3144	263.1608	508.2878	254.6475	507.3038	254.1555	R	557.3882	279.1977	540.3616	270.6845			4
6	638.3984	319.7028	621.3719	311.1896	620.3879	310.6976	I	401.2871	201.1472	384.2605	192.6339			3
7	751.4825	376.2449	734.4559	367.7316	733.4719	367.2396	L	288.2030	144.6051	271.1765	136.0919			2
8							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LSAPRILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	924.5869	0.0008	LSAPRILR

AT3G05090.1

16.1	924.5869	0.0008	LSVVPVRR
1.1	924.5869	0.0008	NIPGLKRK

AT3G05170.1

Mascot Search Results

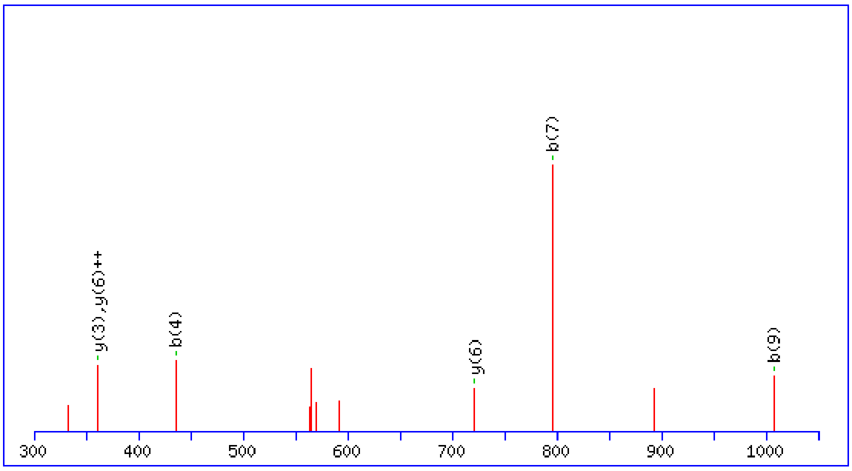
Peptide View

MS/MS Fragmentation of **MSPDNKLLPK**
Found in **AT3G05170.1** in **TAIR_Arabidopsis**, Symbols: | phosphoglycerate/bisphosphoglycerate mutase family protein | chr3:1466744-1468225 FORWARD

Match to Query 3885: 1154.578588 from(578.296570,2+) index(9318)
Title: Elution from: 83.679 to 83.679 scan no 12610 cid35.00 polarity:+
Data file D6h-3_1.mgf

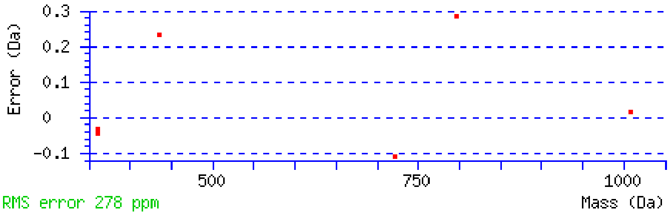
Click mouse within plot area to zoom in by factor of two about that point

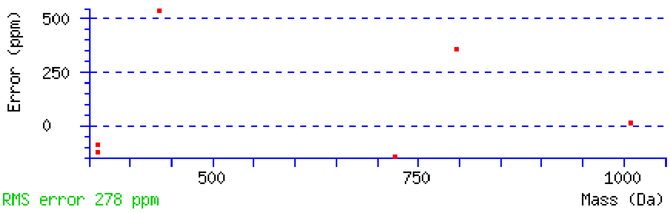
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.5780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.024
Matches : 6/86 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					**M**							**10**
2	221.0739	111.0406			203.0633	102.0353	**S**	1023.5477	512.2775	1005.5242	503.2657	1005.5372	503.2722	**9**
3	319.1237	160.0655			301.1131	151.0602	**P**	935.5187	468.2630	917.4951	459.2512	917.5081	459.2577	**8**
4	***435.1476***	218.0775			417.1371	209.0722	**D**	837.4689	419.2381	819.4453	410.2263	819.4583	410.2328	**7**
5	551.1846	276.0960	533.1610	267.0842	533.1741	267.0907	**N**	**721.4449**	361.2261	703.4213	352.2143			**6**
6	681.2737	341.1405	663.2501	332.1287	663.2631	332.1352	**K**	605.4079	303.2076	587.3843	294.1958			**5**
7	***795.3548***	398.1810	777.3312	389.1692	777.3442	389.1757	**L**	475.3189	238.1631	457.2953	229.1513			**4**
8	909.4359	455.2216	891.4123	446.2098	891.4253	446.2163	**L**	**361.2378**	181.1225	343.2142	172.1107			**3**
9	***1007.4857***	504.2465	989.4621	495.2347	989.4751	495.2412	**P**	247.1567	124.0820	229.1331	115.0702			**2**
10							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MSPDNKLLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G05170.1

Score	Mr(calc)	Delta	Sequence
20.2	1154.5780	0.0006	MSPDNKLLPK
5.4	1154.5773	0.0013	FHALPLASQR
3.6	1154.5807	-0.0021	TVRAMALHPK

AT3G05560.1

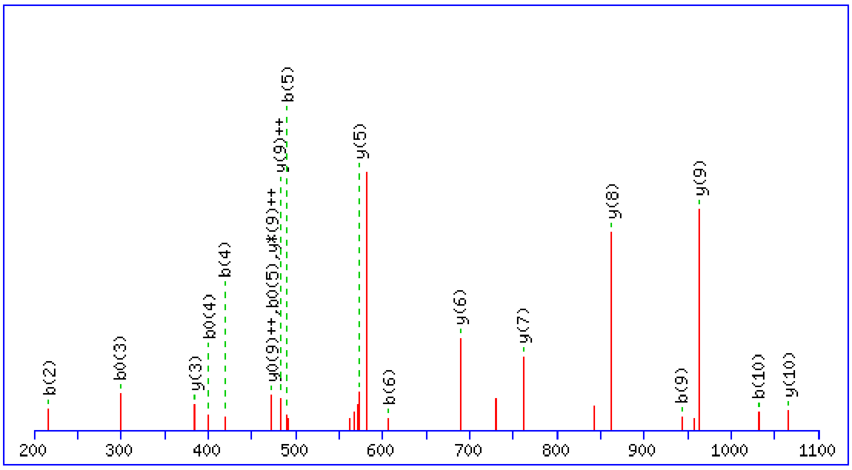
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITVTADGQFSK**
Found in **AT3G05560.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L22-2 (RPL22B) | chr3:1614647-1615210 FORWARD

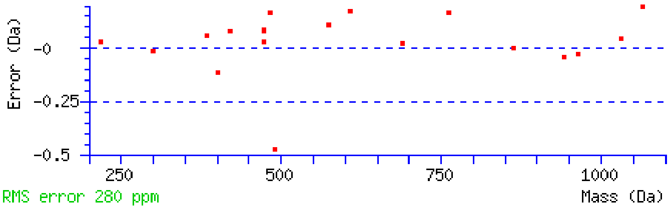
Match to Query 3906: 1178.557812 from(590.286182,2+) index(3104)
Title: Elution from: 32.210 to 32.210 scan no 3892 cid35.00 polarity:+
Data file D6h-2_2.mgf

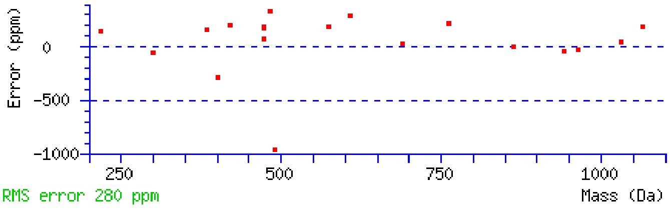
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1178.5593
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 3.1e-006
Matches : 19/102 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					**I**							**11**
2	***217.1331***	109.0702			199.1225	100.0649	**T**	***1065.4855***	533.2464	1047.4619	524.2346	1047.4750	524.2411	**10**
3	317.1985	159.1029			299.1880	150.0976	**V**	***963.4408***	482.2240	945.4172	473.2123	945.4303	473.2188	**9**
4	***419.2432***	210.1253			401.2327	201.1200	**T**	***863.3754***	432.1913	845.3518	423.1795	845.3648	423.1860	**8**
5	***491.2774***	246.1423			473.2668	237.1371	**A**	***761.3307***	381.1690	743.3071	372.1572	743.3201	372.1637	**7**
6	***607.3014***	304.1543			589.2908	295.1490	**D**	***689.2965***	345.1519	671.2729	336.1401	671.2859	336.1466	**6**
7	665.3199	333.1636			647.3093	324.1583	**G**	***573.2725***	287.1399	555.2489	278.1281	555.2620	278.1346	**5**
8	795.3725	398.1899	777.3489	389.1781	777.3620	389.1846	**Q**	515.2540	258.1307	497.2304	249.1189	497.2435	249.1254	**4**
9	***943.4380***	472.2226	925.4144	463.2108	925.4274	463.2173	**F**	***385.2014***	193.1043	367.1778	184.0925	367.1908	184.0990	**3**
10	***1031.4670***	516.2372	1013.4435	507.2254	1013.4565	507.2319	**S**	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	**2**
11							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of ITVTADGQFSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G05560.1

Score	Mr(calc)	Delta	Sequence
64.9	1178.5593	-0.0015	ITVTADGQFSK
9.5	1178.5594	-0.0015	SKPTEKFDSK
8.8	1178.5546	0.0032	ITACDGLLFR
6.9	1178.5550	0.0028	VDNLRRCTK
2.0	1178.5594	-0.0015	LLSEHLDDPK
1.8	1178.5593	-0.0015	SFTGNTLLGEK
0.9	1178.5580	-0.0002	LEMLKQTMR
0.8	1178.5602	-0.0024	MLGIFGMGGVGK
0.8	1178.5594	-0.0016	SSAESLFNLAK
0.6	1178.5602	-0.0024	MQKLGFPAMK

Mascot: http://www.matrixscience.com/

AT3G05590.1

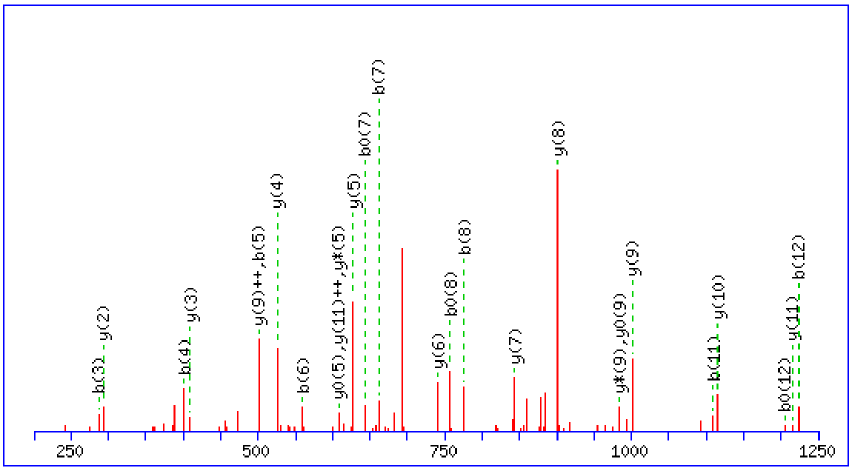
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAVLVGTITDDLR**
Found in **AT3G05590.1** in **TAIR_Arabidopsis**, Symbols: RPL18 | RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome | chr3:1621517-1622781 FORWARD

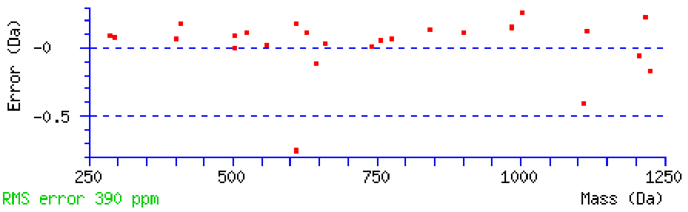
Match to Query 5435: 1400.744918 from(701.379735,2+) index(8506)
Title: Elution from: 75.339 to 75.339 scan no 11298 cid35.00 polarity:+
Data file C7-1_2.mgf

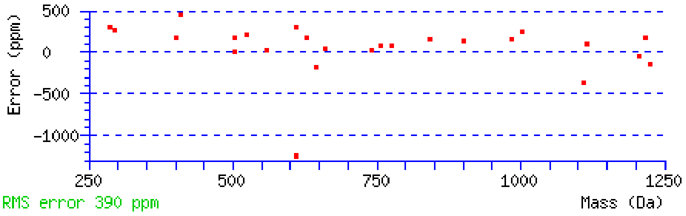
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1400.7451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 101 **Expect:** 2.9e-010
Matches : 27/104 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			I							13
2	187.1225	94.0649			A	1287.6713	644.3393	1269.6477	635.3275	1269.6608	635.3340	12
3	**287.1880**	144.0976			V	***1215.6372***	608.3222	1197.6136	599.3104	1197.6266	599.3169	11
4	**401.2691**	201.1382			L	***1115.5717***	558.2895	1097.5481	549.2777	1097.5612	549.2842	10
5	**501.3345**	251.1709			V	***1001.4906***	501.2489	983.4670	492.2372	983.4801	492.2437	9
6	**559.3530**	280.1801			G	***901.4252***	451.2162	883.4016	442.2044	883.4146	442.2109	8
7	**661.3977**	331.2025	643.3872	322.1972	T	***843.4067***	422.2070	825.3831	413.1952	825.3961	413.2017	7
8	**775.4788**	388.2431	757.4683	379.2378	I	***741.3620***	371.1846	723.3384	362.1728	723.3514	362.1793	6
9	877.5235	439.2654	859.5130	430.2601	T	***627.2809***	314.1441	609.2573	305.1323	609.2703	305.1388	5
10	993.5475	497.2774	975.5370	488.2721	D	***525.2361***	263.1217	507.2126	254.1099	507.2256	254.1164	4
11	**1109.5715**	555.2894	1091.5609	546.2841	D	***409.2122***	205.1097	391.1886	196.0979	391.2016	196.1044	3
12	**1223.6526**	612.3299	1205.6420	603.3247	L	***293.1882***	147.0977	275.1646	138.0859			2
13					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IAVLVGTITDDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G05590.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.2	1400.7451	-0.0002	IAVLVGTITDDLR
14.2	1400.7451	-0.0002	SVPLVETAKNSLK
3.6	1400.7478	-0.0029	SVVLGGKSGVPNIR
3.2	1400.7451	-0.0002	AILSSEIAVVDLR
1.5	1400.7451	-0.0002	ITVLELSDINIR

AT3G05750.1

Mascot Search Results

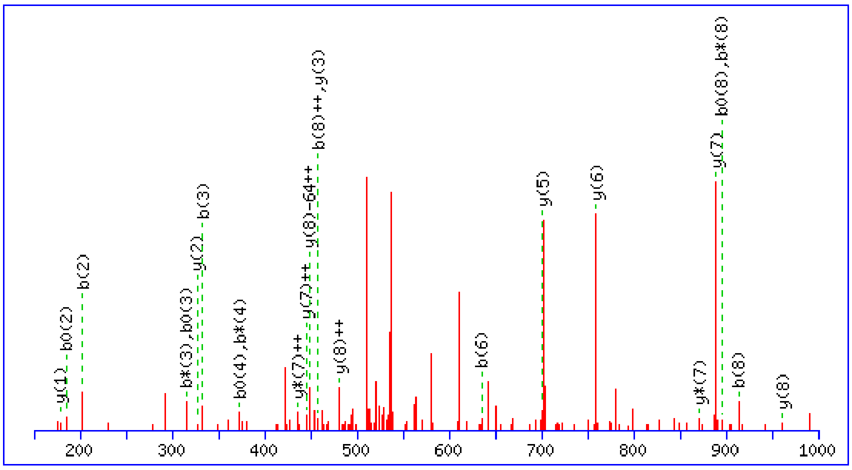
Peptide View

MS/MS Fragmentation of **EAQGLKKMR**
Found in **AT3G05750.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G26910.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO17458.1); contains InterPro domain Homeodomain-like (InterPro:IPR009057) | chr3:1704683-1707552 FORWARD

Match to Query 3121: 1090.533884 from(546.274218,2+) index(4411)
Title: Elution from: 40.030 to 40.030 scan no 5529 cid35.00 polarity:+
Data file 0-3_3.mgf

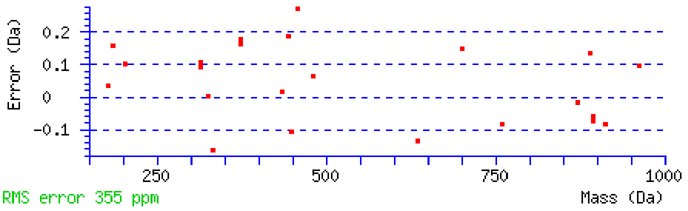
Click mouse within plot area to zoom in by factor of two about that point

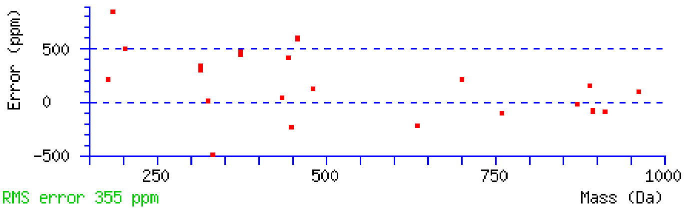
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1090.5363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.035
Matches : 24/110 fragment ions using 62 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	131.0469	66.0271			113.0363	57.0218	E					9
2	**203.0811**	102.0442			185.0705	93.0389	A	***961.5040***	481.2556	943.4804	472.2438	8
3	**333.1337**	167.0705	315.1101	158.0587	315.1231	158.0652	Q	***889.4698***	445.2386	871.4463	436.2268	7
4	391.1522	196.0797	373.1286	187.0679	373.1416	187.0745	G	***759.4172***	380.2122	741.3936	371.2004	6
5	505.2333	253.1203	487.2097	244.1085	487.2227	244.1150	L	***701.3987***	351.2030	683.3751	342.1912	5
6	**635.3223**	318.1648	617.2987	309.1530	617.3118	309.1595	K	587.3176	294.1624	569.2940	285.1506	4
7	765.4114	383.2093	747.3878	374.1975	747.4008	374.2040	K	***457.2286***	229.1179	439.2050	220.1061	3
8	**913.4438**	457.2255	895.4202	448.2137	895.4332	448.2203	M	***327.1395***	164.0734	309.1159	155.0616	2
9							R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of EAQGLKKMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G05750.1

Score	Mr(calc)	Delta	Sequence
26.1	1090.5363	-0.0024	EAQGLKKMR
25.6	1090.5363	-0.0025	KAGAMNSLIR
13.2	1090.5329	0.0009	LSWAGKGTTR
7.2	1090.5307	0.0032	SIEARGLSSR
7.2	1090.5363	-0.0025	SLKMEAKNR
7.1	1090.5363	-0.0024	KKAQMLDAR
5.9	1090.5363	-0.0024	NKTCTAILR
5.8	1090.5330	0.0009	QANIFRAEK
5.1	1090.5337	0.0002	SSNKLIMSSL
4.5	1090.5334	0.0005	LGRNRSDVR

Mascot: http://www.matrixscience.com/

AT3G05970.1

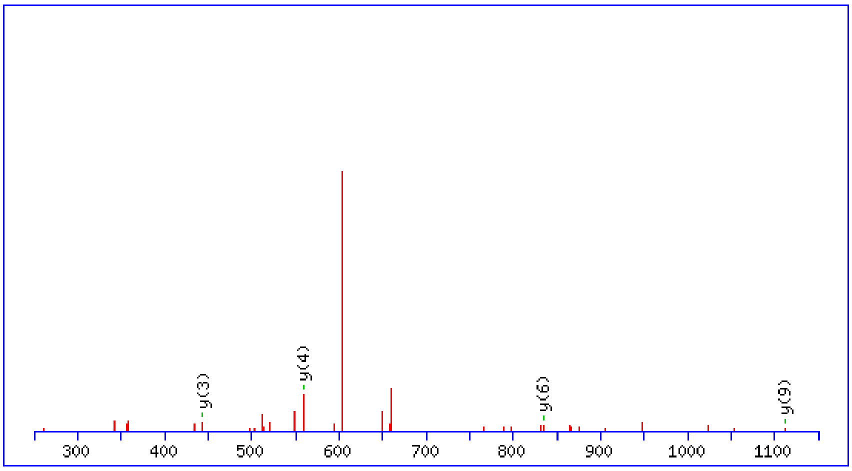
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNTGSWNVYR**
Found in **AT3G05970.1** in **TAIR_Arabidopsis**, Symbols: LACS6 | LACS6 (LONG-CHAIN ACYL-COA SYNTHETASE 6) | chr3:1786516-1791752 REVERSE

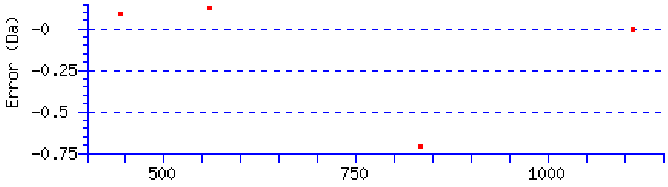
Match to Query 4078: 1224.548406 from(613.281479,2+) index(6152)
Title: Elution from: 54.804 to 54.804 scan no 7935 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

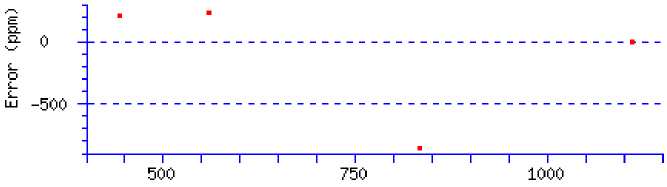


Monoisotopic mass of neutral peptide Mr(calc): 1224.5464
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.023
Matches : 4/92 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**10**
2	231.1254	116.0663	213.1018	107.0545			**N**	***1111.4726***	556.2399	1093.4490	547.2281	1093.4620	547.2346	**9**
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	**T**	995.4356	498.2214	977.4120	489.2096	977.4250	489.2161	**8**
4	391.1886	196.0979	373.1650	187.0861	373.1780	187.0926	**G**	893.3908	447.1991	875.3673	438.1873	875.3803	438.1938	**7**
5	479.2176	240.1125	461.1941	231.1007	461.2071	231.1072	**S**	***835.3723***	418.1898	817.3488	409.1780	817.3618	409.1845	**6**
6	667.2910	334.1492	649.2674	325.1374	649.2805	325.1439	**W**	747.3433	374.1753	729.3197	365.1635			**5**
7	783.3280	392.1677	765.3044	383.1559	765.3175	383.1624	**N**	***559.2699***	280.1386	541.2463	271.1268			**4**
8	883.3935	442.2004	865.3699	433.1886	865.3829	433.1951	**V**	***443.2329***	222.1201	425.2093	213.1083			**3**
9	1047.4538	524.2306	1029.4303	515.2188	1029.4433	515.2253	**Y**	343.1675	172.0874	325.1439	163.0756			**2**
10							**R**	179.1071	90.0572	161.0835	81.0454			**1**



RMS error 453 ppm



RMS error 453 ppm

NCBI **BLAST** search of LNTGSWNVYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G05970.1

Score	Mr(calc)	Delta	Sequence
25.5	1224.5464	0.0020	LNTGSWNVYR
3.8	1224.5448	0.0036	SLDASTMTTLR
3.7	1224.5513	-0.0029	IMKISMAMCK
3.7	1224.5471	0.0013	MAPSSSSGLTFK
3.1	1224.5475	0.0009	LLRNDSMTSR
2.4	1224.5448	0.0036	SIGDMSSKDKK
2.0	1224.5497	-0.0013	NAEMAQRVFK
2.0	1224.5486	-0.0002	FQHFTDLFR
1.5	1224.5497	-0.0013	LQDKLGGYCR
1.4	1224.5471	0.0013	EVQMASVSAFK

AT3G06050.1

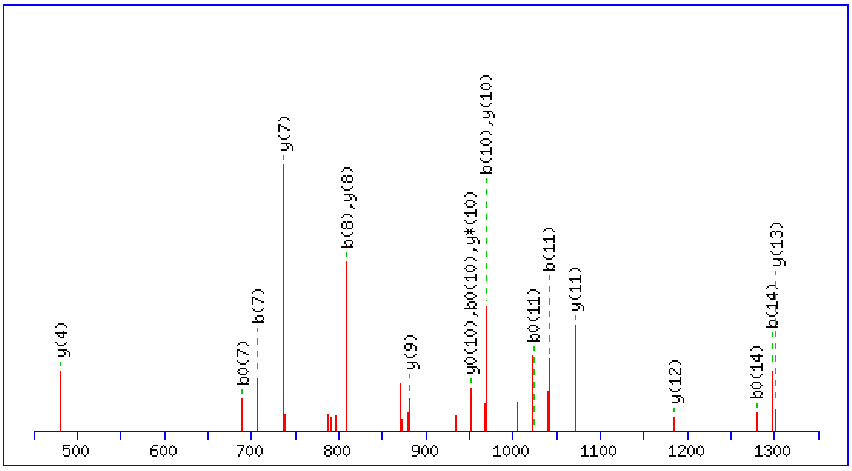
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAEGTDITSAAPGVSLQK**
Found in **AT3G06050.1** in **TAIR_Arabidopsis**, Symbols: PRXIIF, ATPRXIIF | ATPRXIIF/PRXIIF (PEROXIREDOXIN IIF); antioxidant/ peroxidase | chr3:1826317-1827815 REVERSE

Match to Query 8794: 1776.859740 from(889.437146,2+) index(5347)
Title: Elution from: 47.944 to 47.944 scan no 6694 cid35.00 polarity:+
Data file C7-2_1.mgf

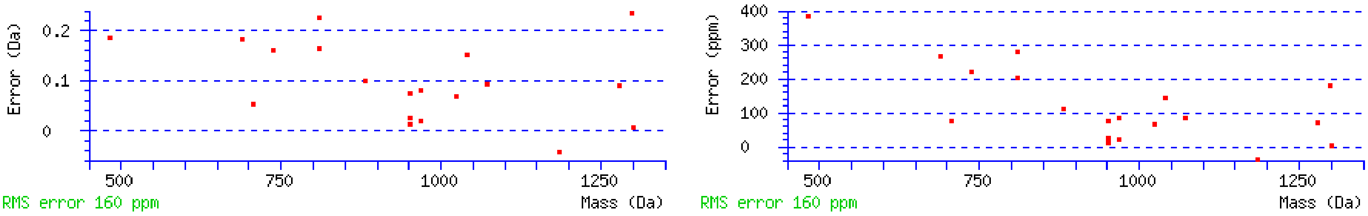
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1776.8614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 6.3e-008
Matches : 19/162 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					**L**							**18**
2	187.1225	94.0649					**A**	1663.7876	832.3974	1645.7640	823.3856	1645.7770	823.3921	**17**
3	317.1622	159.0847			299.1516	150.0794	**E**	1591.7534	796.3803	1573.7298	787.3686	1573.7429	787.3751	**16**
4	375.1807	188.0940			357.1701	179.0887	**G**	1461.7138	731.3605	1443.6902	722.3487	1443.7032	722.3553	**15**
5	477.2254	239.1163			459.2148	230.1110	**T**	1403.6953	702.3513	1385.6717	693.3395	1385.6847	693.3460	**14**
6	593.2493	297.1283			575.2388	288.1230	**D**	***1301.6506***	651.3289	1283.6270	642.3171	1283.6400	642.3236	**13**
7	**707.3304**	354.1689			689.3199	345.1636	**I**	***1185.6266***	593.3169	1167.6030	584.3051	1167.6160	584.3117	**12**
8	**809.3752**	405.1912			791.3646	396.1859	**T**	***1071.5455***	536.2764	1053.5219	527.2646	1053.5349	527.2711	**11**
9	897.4042	449.2057			879.3937	440.2005	**S**	***969.5008***	485.2540	951.4772	476.2422	951.4902	476.2488	**10**
10	**969.4384**	485.2228			951.4278	476.2175	**A**	***881.4717***	441.2395	863.4481	432.2277	863.4612	432.2342	**9**
11	**1041.4725**	521.2399			1023.4619	512.2346	**A**	***809.4376***	405.2224	791.4140	396.2106	791.4270	396.2171	**8**
12	1139.5223	570.2648			1121.5117	561.2595	**P**	***737.4034***	369.2054	719.3798	360.1936	719.3929	360.2001	**7**
13	1197.5408	599.2740			1179.5302	590.2688	**G**	639.3536	320.1805	621.3300	311.1687	621.3431	311.1752	**6**
14	**1297.6063**	649.3068			1279.5957	640.3015	**V**	581.3351	291.1712	563.3115	282.1594	563.3246	282.1659	**5**
15	1385.6353	693.3213			1367.6248	684.3160	**S**	***481.2697***	241.1385	463.2461	232.1267	463.2591	232.1332	**4**
16	1499.7164	750.3618			1481.7059	741.3566	**L**	393.2406	197.1239	375.2170	188.1122			**3**
17	1629.7691	815.3882	1611.7455	806.3764	1611.7585	806.3829	**Q**	279.1595	140.0834	261.1359	131.0716			**2**
18							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT3G06050.1



NCBI **BLAST** search of LAEGTDITSAAPGVSLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
80.2	1776.8614	-0.0016	LAEGTDITSAAPGVSLQK
6.8	1776.8555	0.0042	LQSYFRYLPDLSAGK
4.5	1776.8577	0.0020	RLGFDVEYVWTVFK
1.6	1776.8640	-0.0043	TDTRLANNGLPVEVQK

Mascot: http://www.matrixscience.com/

AT3G06470.1

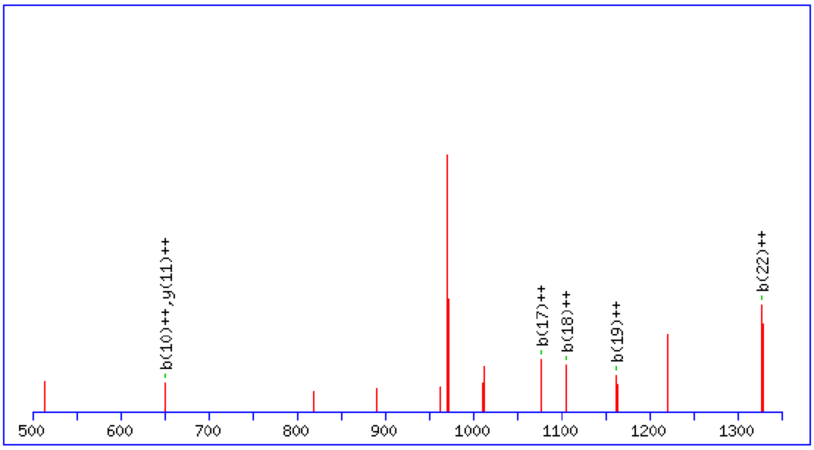
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WKRLVTDCQIVQFVFSFGLSGWMLR**
Found in **AT3G06470.1** in **TAIR_Arabidopsis**, Symbols: | GNS1/SUR4 membrane family protein | chr3:1984212-1985048 FORWARD

Match to Query 10800: 3072.592101 from(1025.204643,3+) index(10207)
Title: Elution from: 94.500 to 94.500 scan no 14295 cid35.00 polarity:+
Data file D1d-3_2.mgf

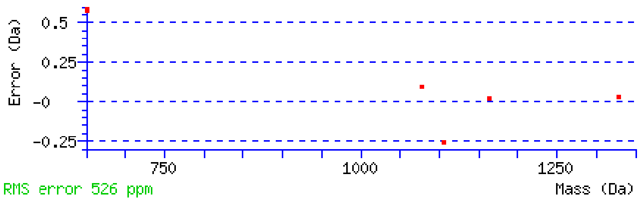
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

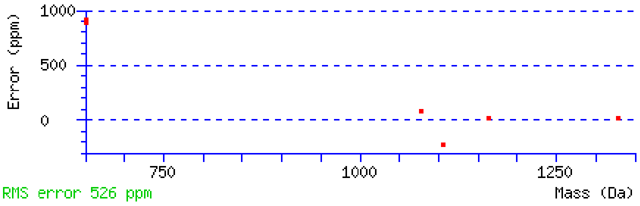


Monoisotopic mass of neutral peptide Mr(calc): 3072.5830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.027
Matches : 6/266 fragment ions using 13 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							25
2	315.1816	158.0944	298.1550	149.5811			K	2887.5110	1444.2591	2870.4844	1435.7459	2869.5004	1435.2538	24
3	471.2827	236.1450	454.2561	227.6317			R	2759.4160	1380.2116	2742.3895	1371.6984	2741.4054	1371.2064	23
4	584.3667	292.6870	567.3402	284.1737			L	2603.3149	1302.1611	2586.2884	1293.6478	2585.3043	1293.1558	22
5	683.4351	342.2212	666.4086	333.7079			V	2490.2308	1245.6191	2473.2043	1237.1058	2472.2203	1236.6138	21
6	784.4828	392.7450	767.4563	384.2318	766.4723	383.7398	T	2391.1624	1196.0848	2374.1359	1187.5716	2373.1519	1187.0796	20
7	899.5098	450.2585	882.4832	441.7452	881.4992	441.2532	D	2290.1147	1145.5610	2273.0882	1137.0477	2272.1042	1136.5557	19
8	1059.5404	530.2738	1042.5139	521.7606	1041.5298	521.2686	C	2175.0878	1088.0475	2158.0613	1079.5343	2157.0772	1079.0423	18
9	1187.5990	594.3031	1170.5724	585.7899	1169.5884	585.2979	Q	2015.0572	1008.0322	1998.0306	999.5189	1997.0466	999.0269	17
10	1300.6831	***650.8452***	1283.6565	642.3319	1282.6725	641.8399	I	1886.9986	944.0029	1869.9720	935.4897	1868.9880	934.9976	16
11	1399.7515	700.3794	1382.7249	691.8661	1381.7409	691.3741	V	1773.9145	887.4609	1756.8880	878.9476	1755.9039	878.4556	15
12	1527.8100	764.4087	1510.7835	755.8954	1509.7995	755.4034	Q	1674.8461	837.9267	1657.8195	829.4134	1656.8355	828.9214	14
13	1674.8785	837.9429	1657.8519	829.4296	1656.8679	828.9376	F	1546.7875	773.8974	1529.7610	765.3841	1528.7770	764.8921	13
14	1773.9469	887.4771	1756.9203	878.9638	1755.9363	878.4718	V	1399.7191	700.3632	1382.6926	691.8499	1381.7085	691.3579	12
15	1921.0153	961.0113	1903.9887	952.4980	1903.0047	952.0060	F	1300.6507	650.8290	1283.6241	642.3157	1282.6401	641.8237	11
16	2008.0473	1004.5273	1991.0208	996.0140	1990.0368	995.5220	S	1153.5823	577.2948	1136.5557	568.7815	1135.5717	568.2895	10
17	2155.1157	***1078.0615***	2138.0892	1069.5482	2137.1052	1069.0562	F	1066.5502	533.7788	1049.5237	525.2655	1048.5397	524.7735	9
18	2212.1372	***1106.5722***	2195.1106	1098.0590	2194.1266	1097.5670	G	919.4818	460.2446	902.4553	451.7313	901.4713	451.2393	8
19	2325.2213	***1163.1143***	2308.1947	1154.6010	2307.2107	1154.1090	L	862.4604	431.7338	845.4338	423.2205	844.4498	422.7285	7
20	2412.2533	1206.6303	2395.2267	1198.1170	2394.2427	1197.6250	S	749.3763	375.1918	732.3498	366.6785	731.3657	366.1865	6
21	2469.2748	1235.1410	2452.2482	1226.6277	2451.2642	1226.1357	G	662.3443	331.6758	645.3177	323.1625			5
22	2655.3541	***1328.1807***	2638.3275	1319.6674	2637.3435	1319.1754	W	605.3228	303.1650	588.2963	294.6518			4
23	2786.3945	1393.7009	2769.3680	1385.1876	2768.3840	1384.6956	M	419.2435	210.1254	402.2170	201.6121			3
24	2899.4786	1450.2429	2882.4521	1441.7297	2881.4680	1441.2377	L	288.2030	144.6051	271.1765	136.0919			2
25							R	175.1190	88.0631	158.0924	79.5498			1

AT3G06470.1





NCBI **BLAST** search of WKRLVTDCQIVQFVFSFGLSGWMLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.5	3072.5830	0.0091	WKRLVTDCQIVQFVFSFGLSGWMLR
3.3	3072.5949	-0.0028	LGILDMTTDVYIFGMILLELLMGSKDR
2.6	3072.5949	-0.0028	LGILDMTTDVYIFGMILLELLMGSKDR
1.7	3072.5848	0.0073	NMLSLGILLQGHRCLEGKFSSLEADLR

Mascot: http://www.matrixscience.com/

AT3G06490.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WNSLSRCAGLQR**
Found in **AT3G06490.1** in **TAIR_Arabidopsis**, Symbols: AtMYB108, BOS1, MYB108 | MYB108 (MYB DOMAIN PROTEIN 108); DNA binding / transcription factor | chr3:2004304-2006364 FORWARD

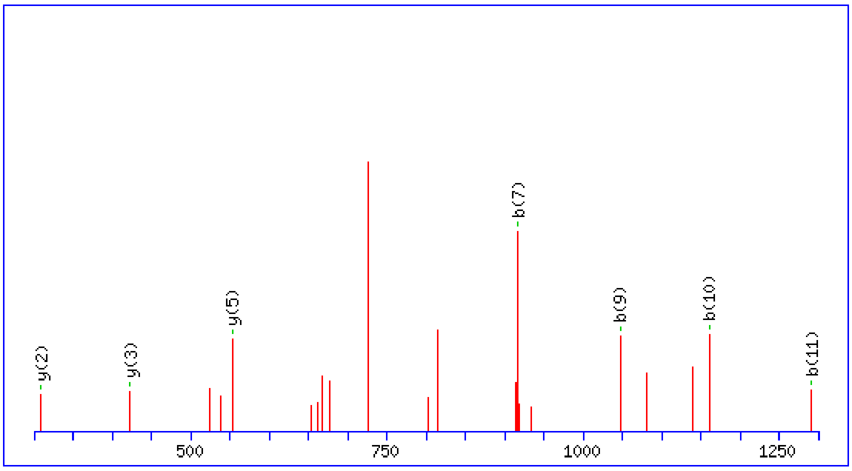
Match to Query 5689: 1468.646558 from(735.330555,2+) index(7253)
Title: Elution from: 64.606 to 64.606 scan no 9550 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1300 Da Full range

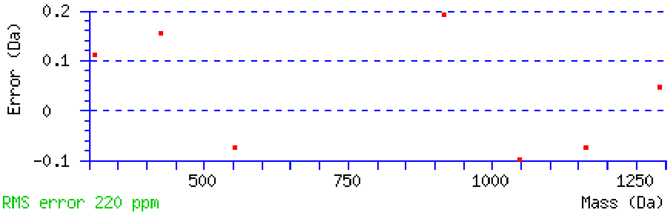
Label all possible matches ○ Label matches used for scoring ●

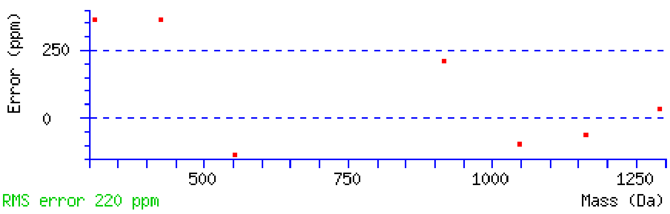
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.6498
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.014
Matches : 7/112 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440					**W**							**12**
2	305.1177	153.0625	287.0941	144.0507			**N**	1281.5837	641.2955	1263.5601	632.2837	1263.5731	632.2902	**11**
3	393.1467	197.0770	375.1231	188.0652	375.1362	188.0717	**S**	1165.5467	583.2770	1147.5231	574.2652	1147.5361	574.2717	**10**
4	507.2278	254.1175	489.2042	245.1058	489.2173	245.1123	**L**	1077.5176	539.2624	1059.4940	530.2507	1059.5071	530.2572	**9**
5	595.2569	298.1321	577.2333	289.1203	577.2463	289.1268	**S**	963.4365	482.2219	945.4129	473.2101	945.4260	473.2166	**8**
6	755.3461	378.1767	737.3225	369.1649	737.3356	369.1714	**R**	875.4075	438.2074	857.3839	429.1956			**7**
7	***917.3709***	459.1891	899.3473	450.1773	899.3603	450.1838	**C**	715.3182	358.1627	697.2946	349.1509			**6**
8	989.4050	495.2061	971.3814	486.1943	971.3944	486.2009	**A**	**553.2935**	277.1504	535.2699	268.1386			**5**
9	***1047.4235***	524.2154	1029.3999	515.2036	1029.4129	515.2101	**G**	481.2593	241.1333	463.2358	232.1215			**4**
10	***1161.5046***	581.2559	1143.4810	572.2441	1143.4940	572.2507	**L**	**423.2408**	212.1241	405.2173	203.1123			**3**
11	***1291.5572***	646.2823	1273.5337	637.2705	1273.5467	637.2770	**Q**	**309.1597**	155.0835	291.1362	146.0717			**2**
12							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of WNSLSRCAGLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G06490.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.5	1468.6498	-0.0032	WNSLSRCAGLQR
15.3	1468.6505	-0.0039	LPSMSTMDRIQR
15.3	1468.6505	-0.0039	LPSMSTMDRIQR
15.3	1468.6422	0.0044	SSDMKDLKDIER
12.8	1468.6471	-0.0006	SMLSDYSNIHKR
6.8	1468.6449	0.0017	RKASTAMGIDEDR
4.3	1468.6449	0.0017	CETQVNNTSIRK
4.1	1468.6496	-0.0030	RSSVDSGAGSLTGEK
3.4	1468.6478	-0.0013	DVMRMEAESLLK
2.0	1468.6442	0.0024	DLQRFNQNQQR

Mascot: http://www.matrixscience.com/

AT3G06530.1

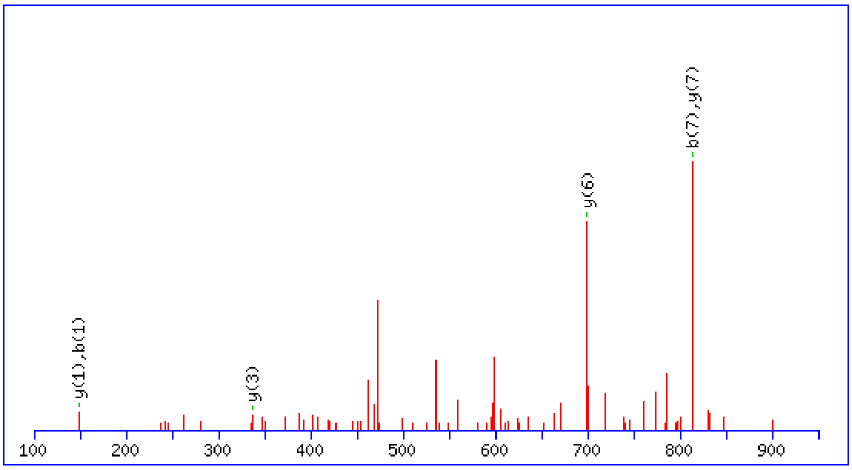
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLSLRSVK**
Found in **AT3G06530.1** in **TAIR_Arabidopsis**, Symbols: | BAP28-related | chr3:2022602-2033643 FORWARD

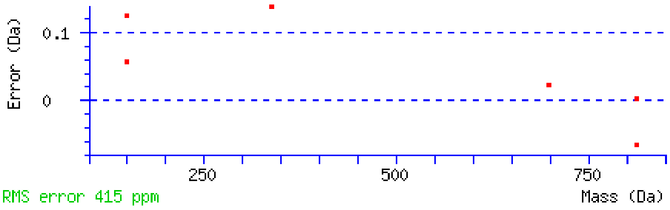
Match to Query 2326: 960.507378 from(481.260965,2+) index(3551)
Title: Elution from: 34.219 to 34.219 scan no 4371 cid35.00 polarity:+
Data file D12h-1_1.mgf

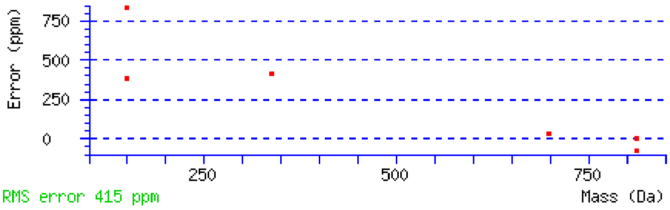
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 960.5071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.008
Matches : 6/98 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**149.0397**	75.0235					M							8
2	263.1208	132.0640					L	***813.4819***	407.2446	795.4583	398.2328	795.4713	398.2393	7
3	351.1499	176.0786			333.1393	167.0733	S	***699.4008***	350.2040	681.3772	341.1922	681.3902	341.1988	6
4	465.2310	233.1191			447.2204	224.1138	L	611.3717	306.1895	593.3482	297.1777	593.3612	297.1842	5
5	625.3202	313.1637	607.2966	304.1520	607.3097	304.1585	R	497.2906	249.1490	479.2671	240.1372	479.2801	240.1437	4
6	713.3493	357.1783	695.3257	348.1665	695.3387	348.1730	S	***337.2014***	169.1043	319.1778	160.0925	319.1908	160.0990	3
7	**813.4147**	407.2110	795.3912	398.1992	795.4042	398.2057	V	249.1723	125.0898	231.1487	116.0780			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MLSLRSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.0	960.5071	0.0003	MLSLRSVK

AT3G06530.1

10.3	960.5071	0.0003	KLSQKSMK
8.0	960.5097	-0.0023	CLRRTLK
4.3	960.5071	0.0003	NTALKKMK
3.4	960.5071	0.0003	MSIVSKLR
2.8	960.5097	-0.0023	MRRGLVAK
2.8	960.5071	0.0003	MSRVLISK
2.2	960.5071	0.0003	AMKKQSLK
0.7	960.5071	0.0003	AMKASIKGK
0.7	960.5097	-0.0023	MRVRASVK

AT3G06540.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKSLTLLEK**
Found in **AT3G06540.1** in **TAIR_Arabidopsis**, Symbols: | GDP dissociation inhibitor family protein / Rab GTPase activator family protein | chr3:2035207-2037668 REVERSE

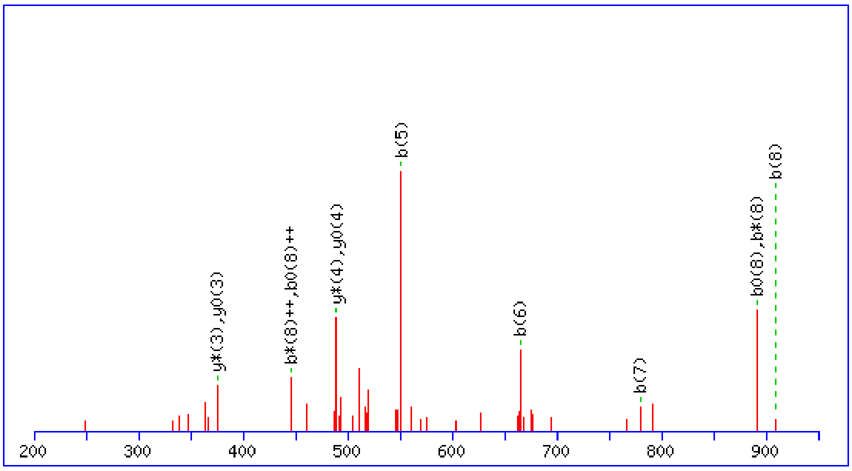
Match to Query 3181: 1056.567730 from(529.291141,2+) index(8546)
Title: Elution from: 74.884 to 74.884 scan no 11339 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

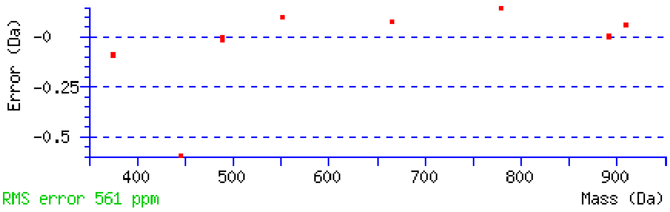
Label all possible matches ○ Label matches used for scoring ●

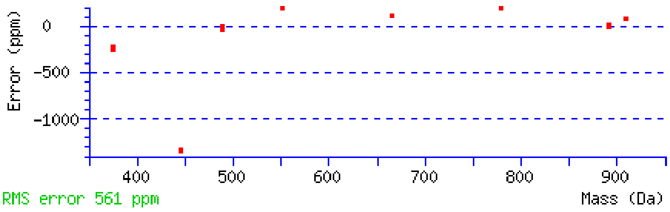
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.5693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.027
Matches : 12/92 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							9
2	247.1203	124.0638	229.0967	115.0520	229.1097	115.0585	K	941.5526	471.2799	923.5290	462.2682	923.5420	462.2747	8
3	335.1493	168.0783	317.1258	159.0665	317.1388	159.0730	S	811.4636	406.2354	793.4400	397.2236	793.4530	397.2301	7
4	449.2304	225.1189	431.2069	216.1071	431.2199	216.1136	L	723.4345	362.2209	705.4109	353.2091	705.4239	353.2156	6
5	***551.2752***	276.1412	533.2516	267.1294	533.2646	267.1359	T	609.3534	305.1803	591.3298	296.1686	591.3428	296.1751	5
6	***665.3563***	333.1818	647.3327	324.1700	647.3457	324.1765	L	507.3087	254.1580	489.2851	245.1462	489.2981	245.1527	4
7	***779.4374***	390.2223	761.4138	381.2105	761.4268	381.2170	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
8	***909.4770***	455.2421	891.4534	446.2303	891.4664	446.2368	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DKSLTLLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G06540.1

20.0	1056.5693	-0.0016	DKSLTLLEK
14.0	1056.5693	-0.0016	SISAISLEVK
13.6	1056.5646	0.0032	IKNMGIEIK
9.4	1056.5693	-0.0016	ISLGLSTIDK
9.3	1056.5646	0.0032	KGIALMDIGK
8.6	1056.5646	0.0032	AVQMVKLEK
8.6	1056.5646	0.0032	MISQPTLKK
8.6	1056.5693	-0.0016	DTILSLKEK
5.3	1056.5693	-0.0016	LDTEISKLK
4.0	1056.5646	0.0032	VQMKLIDAK

AT3G06580.1

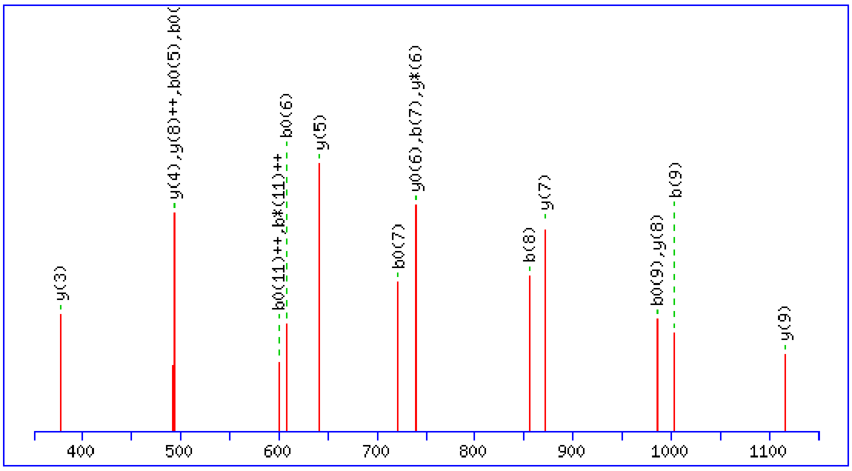
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGFAELIDFNPVR**
Found in **AT3G06580.1** in **TAIR_Arabidopsis**, Symbols: GALK, GAL1 | GAL1 (GALACTOSE KINASE 1); ATP binding / galactokinase | chr3:2049147-2051873 REVERSE

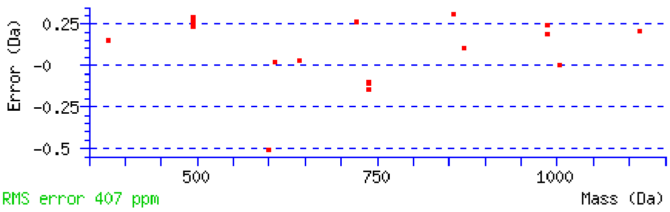
Match to Query 6251: 1494.703568 from(748.359060,2+) index(9721)
Title: Elution from: 90.161 to 90.161 scan no 13553 cid35.00 polarity:+
Data file 0-2_2.mgf

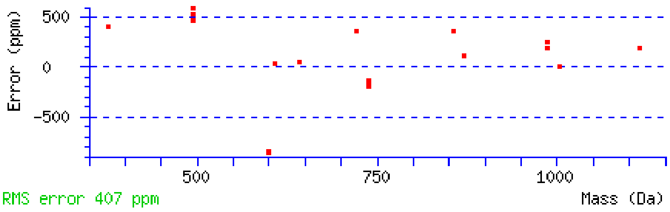
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1494.7061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 1e-005
Matches : 19/116 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							13
2	161.0705	81.0389			143.0599	72.0336	G	1393.6687	697.3380	1375.6451	688.3262	1375.6581	688.3327	12
3	309.1359	155.0716			291.1254	146.0663	F	1335.6502	668.3287	1317.6266	659.3169	1317.6396	659.3234	11
4	381.1701	191.0887			363.1595	182.0834	A	1187.5847	594.2960	1169.5612	585.2842	1169.5742	585.2907	10
5	511.2097	256.1085			493.1991	247.1032	E	***1115.5506***	558.2789	1097.5270	549.2671	1097.5400	549.2737	9
6	625.2908	313.1490			607.2802	304.1438	L	***985.5110***	493.2591	967.4874	484.2473	967.5004	484.2538	8
7	**739.3719**	370.1896			721.3613	361.1843	I	***871.4299***	436.2186	853.4063	427.2068	853.4193	427.2133	7
8	**855.3959**	428.2016			837.3853	419.1963	D	757.3488	379.1780	739.3252	370.1662	739.3382	370.1727	6
9	**1003.4613**	502.2343			985.4508	493.2290	F	***641.3248***	321.1660	623.3012	312.1542			5
10	1119.4983	560.2528	1101.4748	551.2410	1101.4878	551.2475	N	***493.2593***	247.1333	475.2358	238.1215			4
11	1217.5481	609.2777	1199.5246	600.2659	1199.5376	600.2724	P	***377.2223***	189.1148	359.1988	180.1030			3
12	1317.6136	659.3104	1299.5900	650.2986	1299.6030	650.3051	V	279.1725	140.0899	261.1490	131.0781			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TGFAELIDFNPVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G06580.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.6	1494.7061	-0.0025	TGFAELIDFNPVR
13.6	1494.7073	-0.0037	KENDIKANGTLMK
8.9	1494.7025	0.0011	VGVGEQICLARMK
7.0	1494.7043	-0.0007	NASNVSLGETVRAR
5.8	1494.7018	0.0017	RLESILHHMGHK
5.8	1494.7016	0.0019	TLDRLISTGESER
5.4	1494.7068	-0.0032	EYTMEDILVQLK
4.7	1494.7061	-0.0025	TEEFLIGKNWNK
3.2	1494.7025	0.0011	QLVMMARDVLER
3.2	1494.7061	-0.0025	LYDPGYLNTAPVR

AT3G06650.1

Mascot Search Results

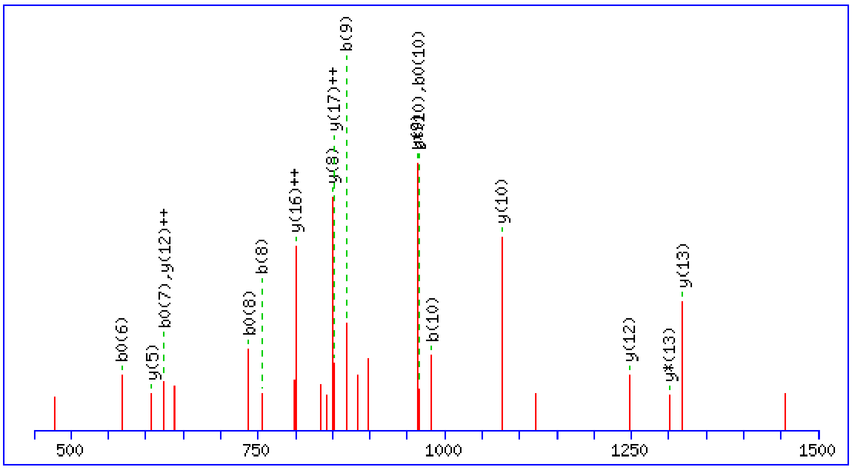
Peptide View

MS/MS Fragmentation of **ETPSVAGIINPGSEGFQK**
Found in **AT3G06650.1** in **TAIR_Arabidopsis**, Symbols: ACLB-1 | ACLB-1 (ATP-citrate lyase B-1) | chr3:2079253-2082639 REVERSE

Match to Query 8355: 1829.919366 from(915.966959,2+) index(6581)
Title: Elution from: 58.206 to 58.206 scan no 8616 cid35.00 polarity:+
Data file D12h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

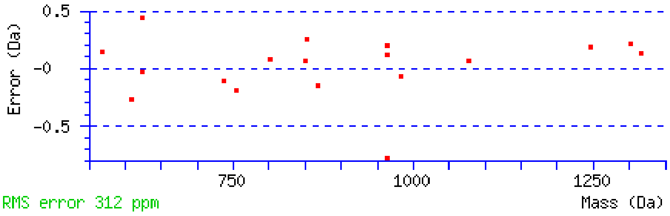
Or, Plot from 450 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

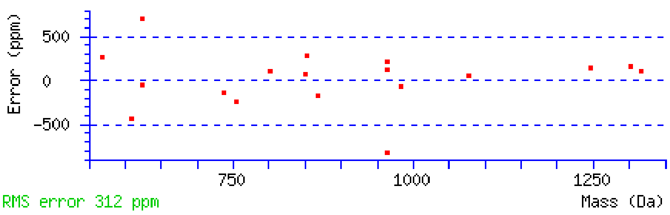


Monoisotopic mass of neutral peptide Mr(calc): 1829.9159
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00034
Matches : 18/178 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							18
2	231.0975	116.0524			213.0870	107.0471	T	1701.8806	851.4440	1684.8541	842.9307	1683.8701	842.4387	17
3	328.1503	164.5788			310.1397	155.5735	P	1600.8329	800.9201	1583.8064	792.4068	1582.8224	791.9148	16
4	415.1823	208.0948			397.1718	199.0895	S	1503.7802	752.3937	1486.7536	743.8805	1485.7696	743.3884	15
5	514.2508	257.6290			496.2402	248.6237	V	1416.7482	708.8777	1399.7216	700.3644	1398.7376	699.8724	14
6	585.2879	293.1476			567.2773	284.1423	A	***1317.6797***	659.3435	1300.6532	650.8302	1299.6692	650.3382	13
7	642.3093	321.6583			624.2988	312.6530	G	***1246.6426***	623.8250	1229.6161	615.3117	1228.6321	614.8197	12
8	**755.3934**	378.2003			737.3828	369.1951	I	1189.6212	595.3142	1172.5946	586.8009	1171.6106	586.3089	11
9	**868.4775**	434.7424			850.4669	425.7371	I	***1076.5371***	538.7722	1059.5106	530.2589	1058.5265	529.7669	10
10	**982.5204**	491.7638	965.4938	483.2506	964.5098	482.7585	N	***963.4530***	482.2302	946.4265	473.7169	945.4425	473.2249	9
11	1079.5732	540.2902	1062.5466	531.7769	1061.5626	531.2849	P	***849.4101***	425.2087	832.3836	416.6954	831.3995	416.2034	8
12	1136.5946	568.8009	1119.5681	560.2877	1118.5840	559.7957	G	752.3573	376.6823	735.3308	368.1690	734.3468	367.6770	7
13	1223.6266	612.3170	1206.6001	603.8037	1205.6161	603.3117	S	695.3359	348.1716	678.3093	339.6583	677.3253	339.1663	6
14	1352.6692	676.8383	1335.6427	668.3250	1334.6587	667.8330	E	***608.3039***	304.6556	591.2773	296.1423	590.2933	295.6503	5
15	1409.6907	705.3490	1392.6642	696.8357	1391.6801	696.3437	G	479.2613	240.1343	462.2347	231.6210			4
16	1556.7591	778.8832	1539.7326	770.3699	1538.7485	769.8779	F	422.2398	211.6235	405.2132	203.1103			3
17	1684.8177	842.9125	1667.7911	834.3992	1666.8071	833.9072	Q	275.1714	138.0893	258.1448	129.5761			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT3G06650.1





NCBI **BLAST** search of ETPSVAGIINPGSEGFQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.5	1829.9159	0.0034	ETPSVAGIINPGSEGFQK

Mascot: http://www.matrixscience.com/

AT3G06720.1

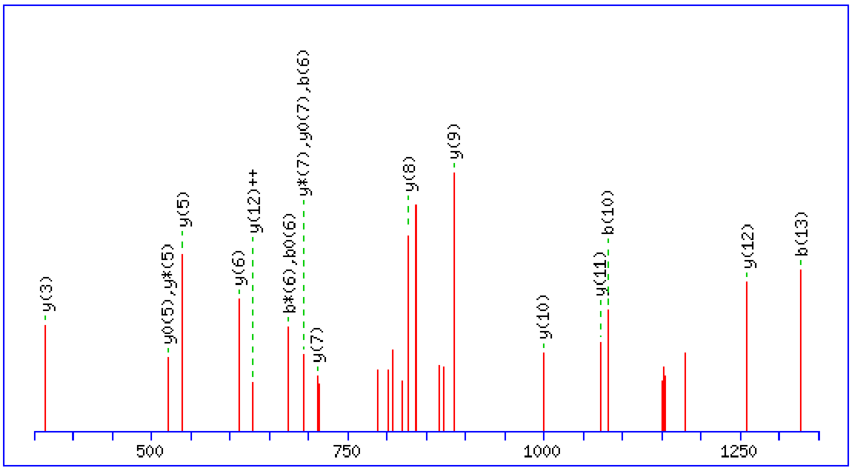
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQAVWALGNVAGDSPR**
Found in **AT3G06720.1** in **TAIR_Arabidopsis**, Symbols: ATKAP ALPHA, AT-IMP | AT-IMP (Arabidopsis thaliana importin alpha); protein transporter | chr3:2120565-2123561 FORWARD

Match to Query 8026: 1690.757586 from(846.386069,2+) index(6852)
Title: Elution from: 61.280 to 61.280 scan no 8903 cid35.00 polarity:+
Data file 0-1_2.mgf

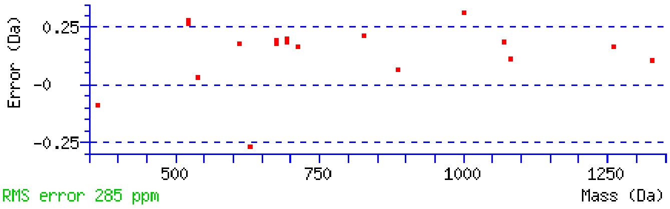
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

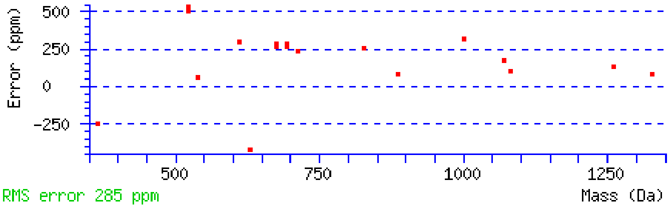


Monoisotopic mass of neutral peptide Mr(calc): 1690.7567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.8e-007
Matches : 19/174 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	**E**							**16**
2	261.0996	131.0534	243.0760	122.0416	243.0890	122.0481	**Q**	1561.7244	781.3658	1543.7008	772.3540	1543.7138	772.3606	**15**
3	333.1337	167.0705	315.1101	158.0587	315.1231	158.0652	**A**	1431.6718	716.3395	1413.6482	707.3277	1413.6612	707.3342	**14**
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	**V**	1359.6376	680.3224	1341.6140	671.3106	1341.6270	671.3172	**13**
5	621.2725	311.1399	603.2489	302.1281	603.2620	302.1346	**W**	***1259.5722***	630.2897	1241.5486	621.2779	1241.5616	621.2844	**12**
6	**693.3067**	347.1570	675.2831	338.1452	675.2961	338.1517	**A**	***1071.4988***	536.2530	1053.4752	527.2412	1053.4882	527.2477	**11**
7	807.3878	404.1975	789.3642	395.1857	789.3772	395.1922	**L**	***999.4646***	500.2360	981.4410	491.2242	981.4541	491.2307	**10**
8	865.4063	433.2068	847.3827	424.1950	847.3957	424.2015	**G**	***885.3835***	443.1954	867.3599	434.1836	867.3730	434.1901	**9**
9	981.4433	491.2253	963.4197	482.2135	963.4327	482.2200	**N**	***827.3650***	414.1862	809.3414	405.1744	809.3545	405.1809	**8**
10	**1081.5087**	541.2580	1063.4851	532.2462	1063.4982	532.2527	**V**	***711.3280***	356.1677	693.3044	347.1559	693.3175	347.1624	**7**
11	1153.5429	577.2751	1135.5193	568.2633	1135.5323	568.2698	**A**	***611.2626***	306.1349	593.2390	297.1231	593.2520	297.1296	**6**
12	1211.5614	606.2843	1193.5378	597.2725	1193.5508	597.2790	**G**	***539.2284***	270.1179	521.2048	261.1061	521.2179	261.1126	**5**
13	**1327.5854**	664.2963	1309.5618	655.2845	1309.5748	655.2910	**D**	481.2099	241.1086	463.1863	232.0968	463.1994	232.1033	**4**
14	1415.6144	708.3108	1397.5908	699.2991	1397.6038	699.3056	**S**	***365.1860***	183.0966	347.1624	174.0848	347.1754	174.0913	**3**
15	1513.6642	757.3357	1495.6406	748.3240	1495.6536	748.3305	**P**	277.1569	139.0821	259.1333	130.0703			**2**
16							**R**	179.1071	90.0572	161.0835	81.0454			**1**

AT3G06720.1





NCBI **BLAST** search of EQAVWALGNVAGDSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.7	1690.7567	0.0009	EQAVWALGNVAGDSPR
10.1	1690.7527	0.0049	VPMDPQLCKAAEQGK
8.5	1690.7601	-0.0026	LMSNATAFSINNSKR
0.6	1690.7597	-0.0021	VVYDYLGGMEDIRK
0.1	1690.7576	-0.0000	MLNRPYAFNCVLR

Mascot: http://www.matrixscience.com/

AT3G06730.1

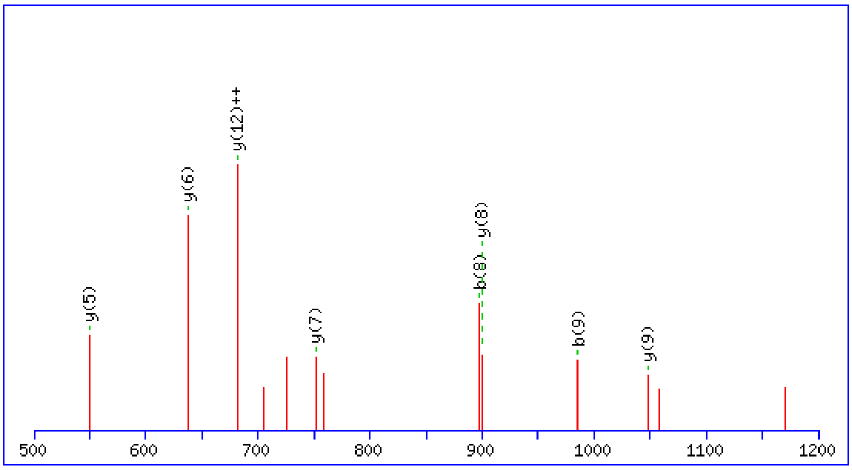
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLPTLFFISPDPSK**
Found in **AT3G06730.1** in **TAIR_Arabidopsis**, Symbols: | thioredoxin family protein | chr3:2124282-2125851 FORWARD

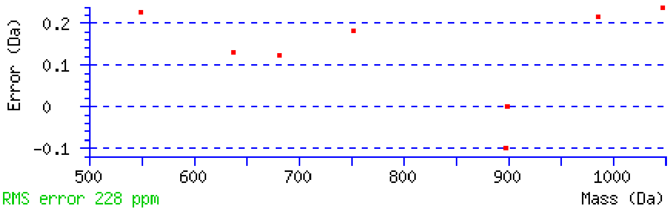
Match to Query 7017: 1532.767456 from(767.391004,2+) index(10497)
Title: Elution from: 96.573 to 96.573 scan no 14534 cid35.00 polarity:+
Data file D12h-1_1.mgf

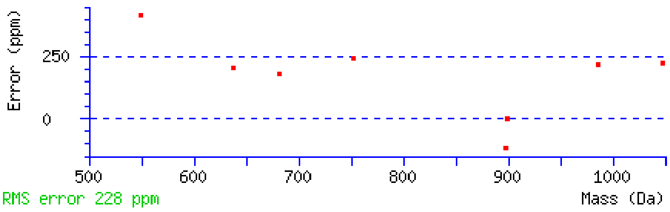
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1532.7685
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0031
Matches : 8/122 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			**G**							**14**
2	173.1069	87.0571			**L**	1475.7573	738.3823	1457.7337	729.3705	1457.7467	729.3770	**13**
3	271.1567	136.0820			**P**	1361.6762	681.3417	1343.6526	672.3299	1343.6656	672.3364	**12**
4	373.2014	187.1043	355.1908	178.0990	**T**	1263.6264	632.3168	1245.6028	623.3050	1245.6158	623.3115	**11**
5	487.2825	244.1449	469.2719	235.1396	**L**	1161.5817	581.2945	1143.5581	572.2827	1143.5711	572.2892	**10**
6	635.3479	318.1776	617.3374	309.1723	**F**	***1047.5006***	524.2539	1029.4770	515.2421	1029.4900	515.2486	**9**
7	783.4134	392.2103	765.4028	383.2050	**F**	***899.4351***	450.2212	881.4115	441.2094	881.4246	441.2159	**8**
8	**897.4945**	449.2509	879.4839	440.2456	**I**	***751.3697***	376.1885	733.3461	367.1767	733.3591	367.1832	**7**
9	**985.5235**	493.2654	967.5130	484.2601	**S**	***637.2886***	319.1479	619.2650	310.1361	619.2780	310.1426	**6**
10	1083.5733	542.2903	1065.5628	533.2850	**P**	***549.2595***	275.1334	531.2359	266.1216	531.2489	266.1281	**5**
11	1199.5973	600.3023	1181.5868	591.2970	**D**	451.2097	226.1085	433.1861	217.0967	433.1991	217.1032	**4**
12	1297.6471	649.3272	1279.6366	640.3219	**P**	335.1857	168.0965	317.1622	159.0847	317.1752	159.0912	**3**
13	1385.6762	693.3417	1367.6656	684.3364	**S**	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	**2**
14					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of GLPTLFFISPDPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G06730.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.9	1532.7685	-0.0011	GLPTLFFISPDPSK
2.0	1532.7667	0.0008	GNEVNDIKALSVVR
2.0	1532.7667	0.0008	REDVELNIKELR
1.7	1532.7663	0.0012	VEEAFKPSAELAVK
1.6	1532.7667	0.0007	KNNLSAGDKITPQK
0.4	1532.7716	-0.0042	EKPGYSRPGKKHK
0.4	1532.7640	0.0034	EKELKTAVVENEK

AT3G07000.1

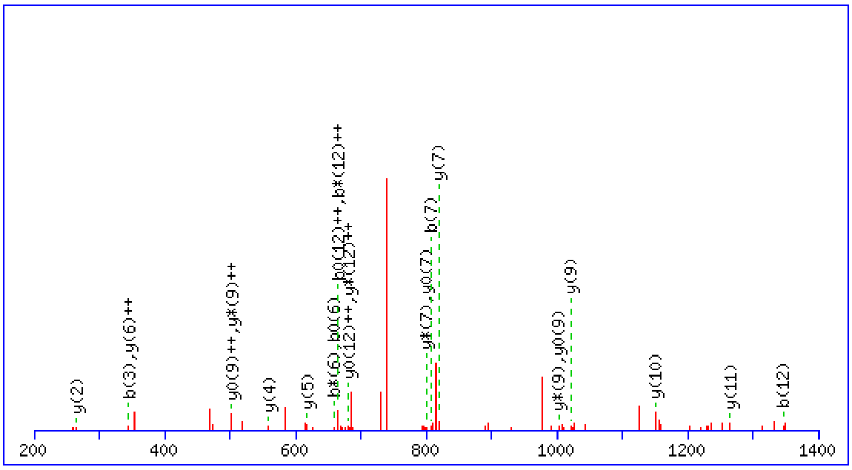
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDLQVTKAGEYNK**
Found in **AT3G07000.1** in **TAIR_Arabidopsis**, Symbols: | DC1 domain-containing protein | chr3:2209509-2211233 FORWARD

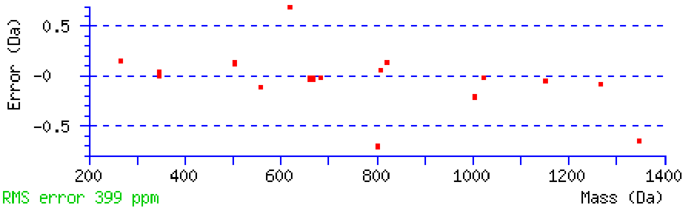
Match to Query 6161: 1494.725742 from(748.370147,2+) index(6268)
Title: Elution from: 55.515 to 55.515 scan no 8044 cid35.00 polarity:+
Data file 0-3_2.mgf

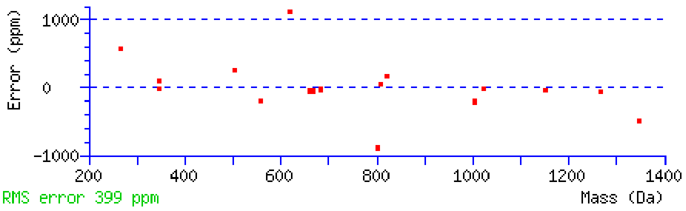
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1494.7272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.037
Matches : 23/130 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							13
2	231.1124	116.0598			213.1018	107.0545	D	1381.6534	691.3304	1363.6298	682.3186	1363.6429	682.3251	12
3	**345.1935**	173.1004			327.1829	164.0951	L	***1265.6295***	633.3184	1247.6059	624.3066	1247.6189	624.3131	11
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	Q	***1151.5484***	576.2778	1133.5248	567.2660	1133.5378	567.2725	10
5	575.3115	288.1594	557.2880	279.1476	557.3010	279.1541	V	***1021.4957***	511.2515	1003.4721	502.2397	1003.4851	502.2462	9
6	677.3563	339.1818	659.3327	330.1700	659.3457	330.1765	T	921.4303	461.2188	903.4067	452.2070	903.4197	452.2135	8
7	**807.4453**	404.2263	789.4217	395.2145	789.4347	395.2210	K	***819.3855***	410.1964	801.3620	401.1846	801.3750	401.1911	7
8	879.4794	440.2434	861.4559	431.2316	861.4689	431.2381	A	689.2965	345.1519	671.2729	336.1401	671.2859	336.1466	6
9	937.4979	469.2526	919.4744	460.2408	919.4874	460.2473	G	***617.2624***	309.1348	599.2388	300.1230	599.2518	300.1295	5
10	1067.5376	534.2724	1049.5140	525.2606	1049.5270	525.2671	E	***559.2439***	280.1256	541.2203	271.1138	541.2333	271.1203	4
11	1231.5979	616.3026	1213.5744	607.2908	1213.5874	607.2973	Y	429.2042	215.1058	411.1807	206.0940			3
12	**1347.6349**	674.3211	1329.6113	665.3093	1329.6244	665.3158	N	***265.1439***	133.0756	247.1203	124.0638			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LDLQVTKAGEYNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G07000.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	1494.7272	-0.0015	LDLQVTKAGEYNK
2.4	1494.7225	0.0033	VEDAVMLAFAQKR
2.3	1494.7299	-0.0042	INLNHISVVDSHK
1.3	1494.7299	-0.0042	RRLEEIEVEFR
1.0	1494.7247	0.0010	AACYLKLHDFIK
0.9	1494.7295	-0.0037	KYSSSKFGYIATK
0.6	1494.7272	-0.0015	DLEEKIRVYEGK
0.6	1494.7272	-0.0015	IEREEGSTLFAVK
0.3	1494.7246	0.0012	VIELSTYIDSDVK
0.2	1494.7295	-0.0037	NSQYDISILIWK

AT3G07090.1

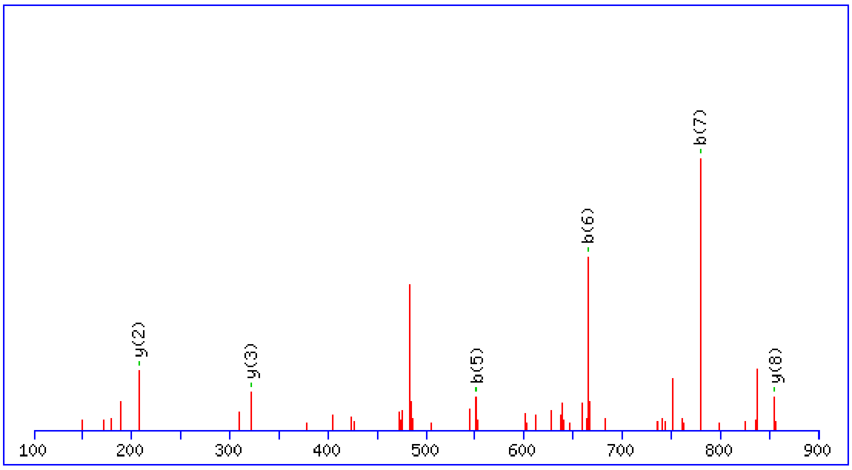
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLSQSLLGK**
Found in **AT3G07090.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46108.1); contains InterPro domain Protein of unknown function DUF862, eukaryotic (InterPro:IPR008580) | ch

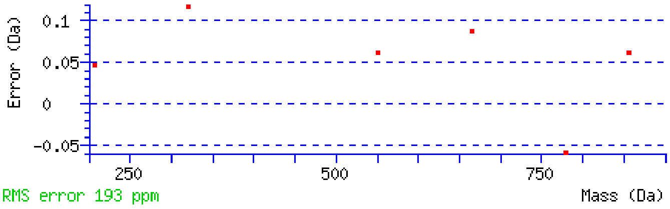
Match to Query 2446: 984.523032 from(493.268792,2+) index(1939)
Title: Elution from: 22.812 to 22.812 scan no 2503 cid35.00 polarity:+
Data file C7-2_2.mgf

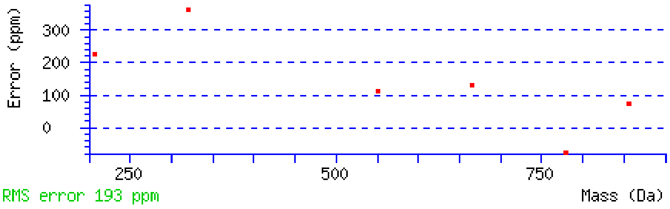
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.5248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.011
Matches : 6/84 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							9
2	245.1410	123.0741	227.1174	114.0624			L	***855.4794***	428.2434	837.4559	419.2316	837.4689	419.2381	8
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	S	741.3983	371.2028	723.3748	362.1910	723.3878	362.1975	7
4	463.2227	232.1150	445.1991	223.1032	445.2122	223.1097	Q	653.3693	327.1883	635.3457	318.1765	635.3587	318.1830	6
5	***551.2518***	276.1295	533.2282	267.1177	533.2412	267.1243	S	523.3166	262.1620	505.2930	253.1502	505.3061	253.1567	5
6	***665.3329***	333.1701	647.3093	324.1583	647.3223	324.1648	L	435.2876	218.1474	417.2640	209.1356			4
7	***779.4140***	390.2106	761.3904	381.1988	761.4034	381.2054	L	***321.2065***	161.1069	303.1829	152.0951			3
8	837.4325	419.2199	819.4089	410.2081	819.4219	410.2146	G	***207.1254***	104.0663	189.1018	95.0545			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QLSQSLLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G07090.1

Score	Mr(calc)	Delta	Sequence
28.6	984.5248	-0.0018	QLSQSLLGK
19.9	984.5248	-0.0018	REIEKLSV
9.6	984.5248	-0.0018	LEEVSLKR
7.9	984.5248	-0.0018	NIKSLDVGK
6.6	984.5248	-0.0018	ELSTVGVIR
5.8	984.5248	-0.0018	SINQITGLK
5.5	984.5248	-0.0018	KESLVAAQK
5.5	984.5248	-0.0018	QSKVIAEAK
4.5	984.5248	-0.0018	KIEVGGDKK
3.1	984.5248	-0.0018	KLKQEEAK

AT3G07110.1

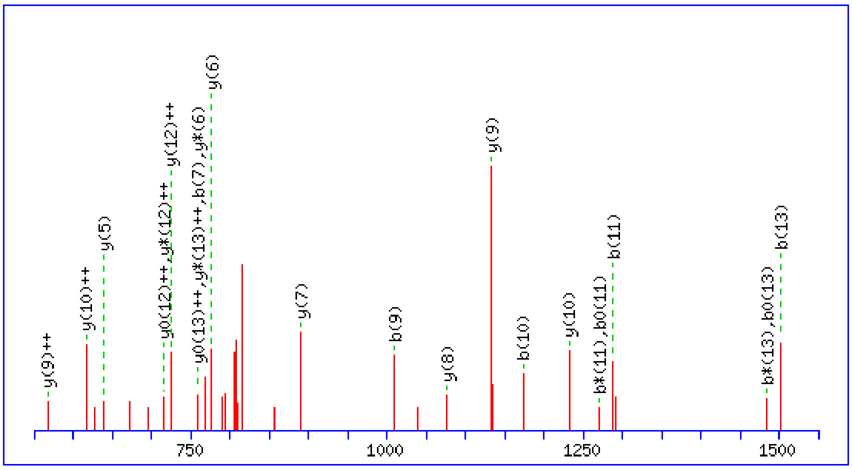
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSEVGWNHYDTIK**
Found in **AT3G07110.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L13A (RPL13aA) | chr3:2252098-2253338 FORWARD

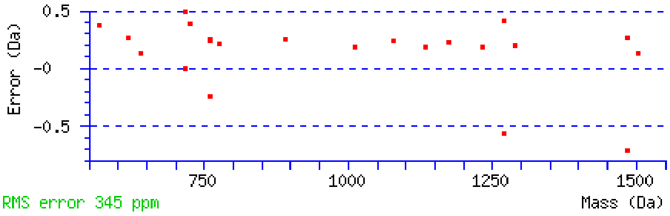
Match to Query 7472: 1647.787214 from(824.900883,2+) index(4184)
Title: Elution from: 42.199 to 42.199 scan no 5392 cid35.00 polarity:+
Data file D1d-1_1.mgf

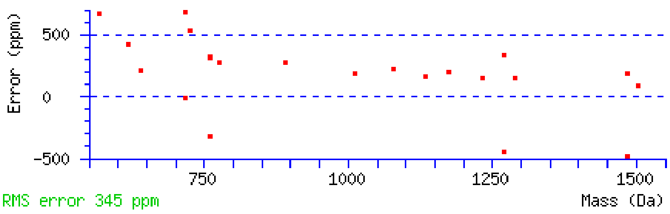
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1550 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1647.7893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 3.3e-006
Matches : 23/136 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	201.1234	101.0653			183.1128	92.0600	S	1535.7125	768.3599	1518.6859	759.8466	1517.7019	759.3546	13
3	288.1554	144.5813			270.1448	135.5761	S	1448.6805	724.8439	1431.6539	716.3306	1430.6699	715.8386	12
4	417.1980	209.1026			399.1874	200.0973	E	1361.6484	681.3279	1344.6219	672.8146	1343.6379	672.3226	11
5	516.2664	258.6368			498.2558	249.6316	V	***1232.6058***	616.8066	1215.5793	608.2933	1214.5953	607.8013	10
6	573.2879	287.1476			555.2773	278.1423	G	***1133.5374***	567.2724	1116.5109	558.7591	1115.5269	558.2671	9
7	***759.3672***	380.1872			741.3566	371.1819	W	***1076.5160***	538.7616	1059.4894	530.2483	1058.5054	529.7563	8
8	873.4101	437.2087	856.3836	428.6954	855.3995	428.2034	N	***890.4367***	445.7220	873.4101	437.2087	872.4261	436.7167	7
9	***1010.4690***	505.7381	993.4425	497.2249	992.4585	496.7329	H	***776.3937***	388.7005	759.3672	380.1872	758.3832	379.6952	6
10	***1173.5323***	587.2698	1156.5058	578.7565	1155.5218	578.2645	Y	***639.3348***	320.1710	622.3083	311.6578	621.3243	311.1658	5
11	***1288.5593***	644.7833	1271.5327	636.2700	1270.5487	635.7780	D	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
12	1389.6070	695.3071	1372.5804	686.7938	1371.5964	686.3018	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
13	***1502.6910***	751.8492	1485.6645	743.3359	1484.6805	742.8439	I	260.1969	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LSSEVGWNHYDTIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G07110.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.8	1647.7893	-0.0021	LSSEVGWNHYDTIK
7.7	1647.7886	-0.0014	DVETASLRMDNLER
0.3	1647.7886	-0.0014	QALTNVGNIAGECSSK
0.3	1647.7895	-0.0023	DKRCGVCGPVLMEK

AT3G07350.1

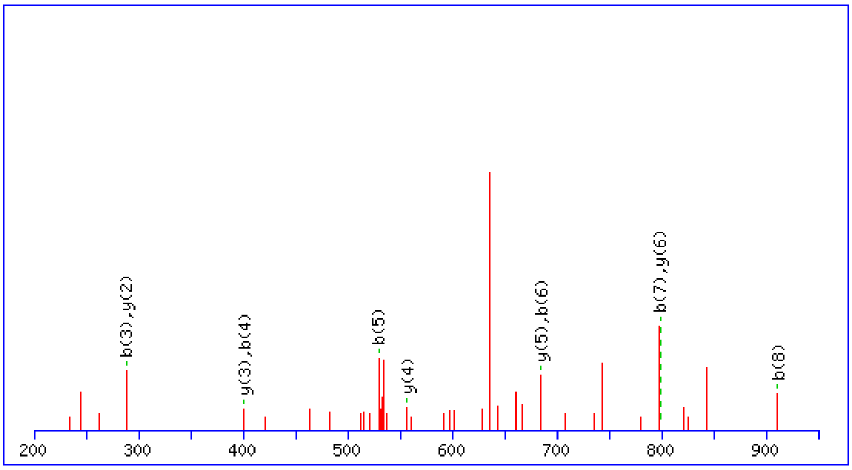
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDDLKRILR**
Found in **AT3G07350.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G25240.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO38687.1); contains InterPro domain Protein of unknown function DUF506, plant (InterPro:IPR006502) | chr3:23

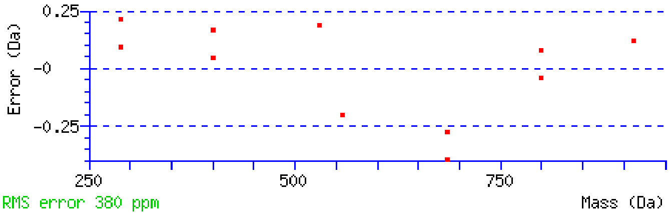
Match to Query 3426: 1084.633508 from(543.324030,2+) index(8660)
Title: Elution from: 76.578 to 76.578 scan no 11414 cid35.00 polarity:+
Data file C7-3_1.mgf

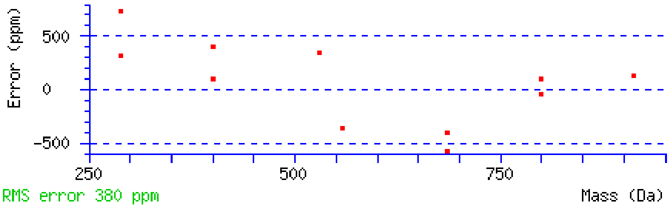
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1084.6353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00045
Matches : 11/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							9
2	173.0557	87.0315			155.0451	78.0262	D	1028.6211	514.8142	1011.5946	506.3009	1010.6105	505.8089	8
3	***288.0826***	144.5450			270.0721	135.5397	D	913.5942	457.3007	896.5676	448.7874	895.5836	448.2954	7
4	***401.1667***	201.0870			383.1561	192.0817	L	**798.5672**	399.7872	781.5407	391.2740			6
5	***529.2617***	265.1345	512.2351	256.6212	511.2511	256.1292	K	**685.4832**	343.2452	668.4566	334.7319			5
6	***685.3628***	343.1850	668.3362	334.6717	667.3522	334.1797	R	**557.3882**	279.1977	540.3616	270.6845			4
7	***798.4468***	399.7271	781.4203	391.2138	780.4363	390.7218	I	**401.2871**	201.1472	384.2605	192.6339			3
8	***911.5309***	456.2691	894.5043	447.7558	893.5203	447.2638	L	**288.2030**	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GDDLKRILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G07350.1

Score	Mr(calc)	Delta	Sequence
39.7	1084.6353	-0.0018	GDDLKRILR
9.5	1084.6353	-0.0018	GQRTLELIR
3.5	1084.6353	-0.0018	GARLLEGTIR
2.7	1084.6353	-0.0018	IRTGKQSAPK
1.3	1084.6353	-0.0017	LRTEAINLR

AT3G07390.1

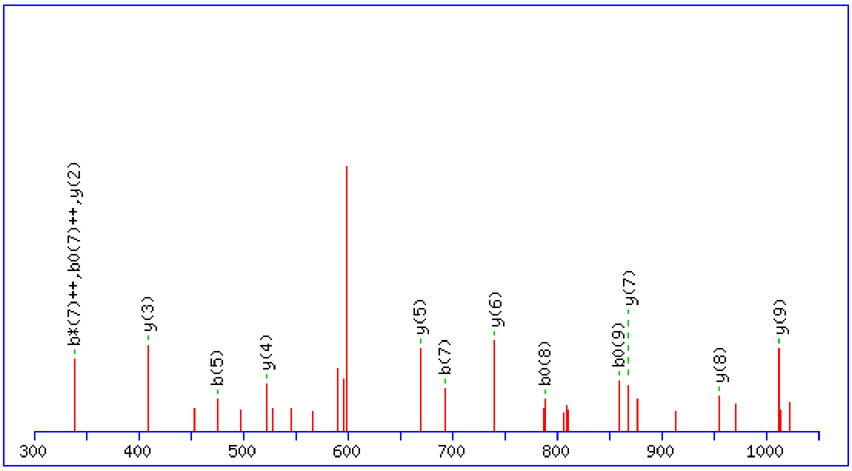
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAGSQAFLAYR**
Found in **AT3G07390.1** in **TAIR_Arabidopsis**, Symbols: AIR12 | AIR12 (Auxin-Induced in Root cultures 12); extracellular matrix structural constituent | chr3:2365458-2366279 FORWARD

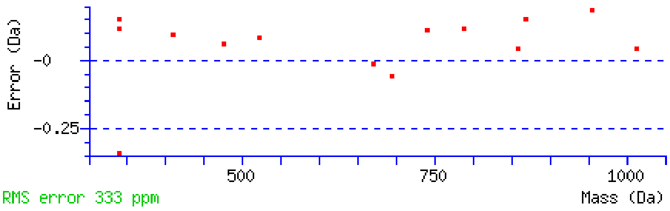
Match to Query 3689: 1213.589984 from(607.802268,2+) index(4606)
Title: Elution from: 43.302 to 43.302 scan no 5884 cid35.00 polarity:+
Data file D12h-2_3.mgf

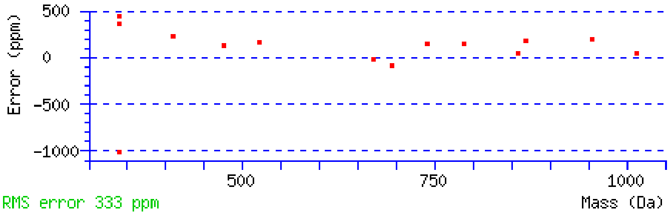
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1213.5914
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90 **Expect:** 1.7e-009
Matches : 14/92 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							11
2	203.0849	102.0461					A	1083.5582	542.2827	1066.5316	533.7694	1065.5476	533.2774	10
3	260.1063	130.5568					G	***1012.5211***	506.7642	995.4945	498.2509	994.5105	497.7589	9
4	347.1384	174.0728			329.1278	165.0675	S	***955.4996***	478.2534	938.4730	469.7402	937.4890	469.2482	8
5	**475.1969**	238.1021	458.1704	229.5888	457.1864	229.0968	Q	***868.4676***	434.7374	851.4410	426.2241			7
6	546.2341	273.6207	529.2075	265.1074	528.2235	264.6154	A	***740.4090***	370.7081	723.3824	362.1949			6
7	**693.3025**	347.1549	676.2759	338.6416	675.2919	338.1496	F	***669.3719***	335.1896	652.3453	326.6763			5
8	806.3865	403.6969	789.3600	395.1836	788.3760	394.6916	L	***522.3035***	261.6554	505.2769	253.1421			4
9	877.4237	439.2155	860.3971	430.7022	859.4131	430.2102	A	***409.2194***	205.1133	392.1928	196.6001			3
10	1040.4870	520.7471	1023.4604	512.2339	1022.4764	511.7418	Y	***338.1823***	169.5948	321.1557	161.0815			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MAGSQAFLAYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G07390.1

Score	Mr(calc)	Delta	Sequence
90.3	1213.5914	-0.0014	MAGSQAFLAYR
0.1	1213.5900	-0.0000	MVEYDITSLK

Mascot: http://www.matrixscience.com/

AT3G07590.1

Mascot Search Results

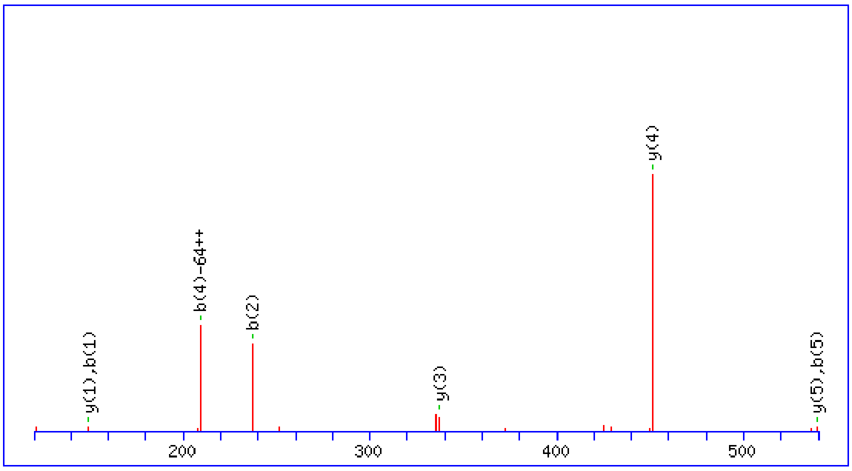
Peptide View

MS/MS Fragmentation of **MSLKGK**
Found in **AT3G07590.1** in **TAIR_Arabidopsis**, Symbols: | small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative | chr3:2423152-2423964 FORWARD

Match to Query 639: 686.348588 from(344.181570,2+) index(5138)
Title: Elution from: 46.470 to 46.470 scan no 6452 cid35.00 polarity:+
Data file 0-2_1.mgf

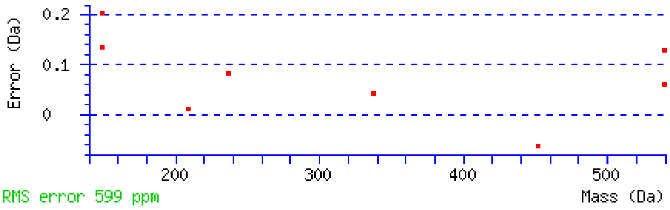
Click mouse within plot area to zoom in by factor of two about that point

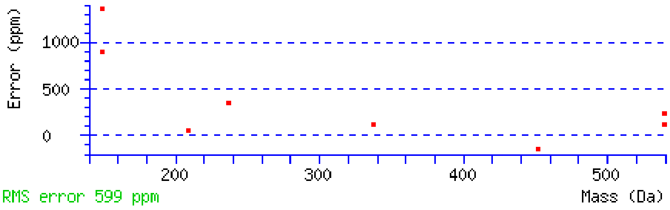
Or, Plot from 120 to 540 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 686.3497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 **Expect:** 0.0079
Matches : 8/66 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**149.0397**	75.0235					M							6
2	**237.0688**	119.0380			219.0582	110.0327	S	***539.3246***	270.1659	521.3010	261.1541	521.3140	261.1606	5
3	351.1499	176.0786			333.1393	167.0733	L	***451.2955***	226.1514	433.2719	217.1396			4
4	481.2389	241.1231	463.2153	232.1113	463.2283	232.1178	K	***337.2144***	169.1108	319.1908	160.0990			3
5	**539.2574**	270.1323	521.2338	261.1205	521.2468	261.1271	G	207.1254	104.0663	189.1018	95.0545			2
6							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MSLKGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.4	686.3497	-0.0011	MSLKGK
29.7	686.3486	0.0000	FSLWK

AT3G07590.1

29.7	686.3497	-0.0011	MAKVSK
25.6	686.3497	-0.0011	MLSKGK
19.7	686.3497	-0.0011	AKMVSK
19.7	686.3497	-0.0011	KGMLSK
19.7	686.3486	0.0000	SFLWK
19.7	686.3486	0.0000	WFISK
19.6	686.3486	0.0000	YAWIK
18.7	686.3497	-0.0011	MGLKSK

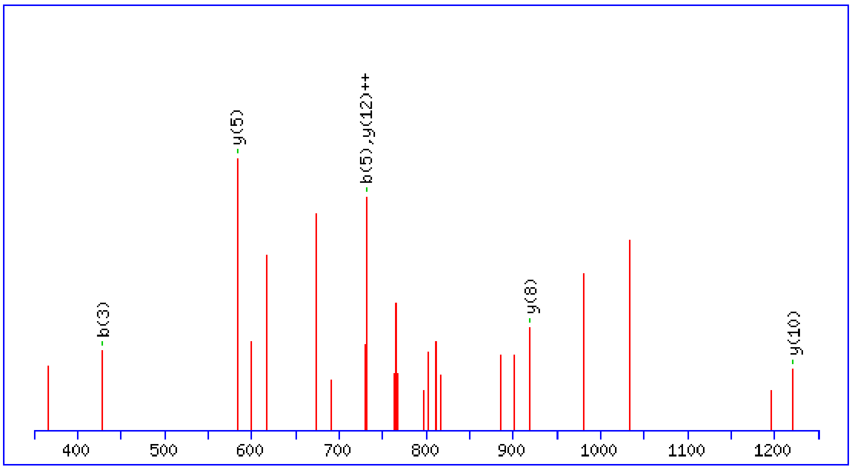
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WVHCHCDGISDDK**
Found in **AT3G08020.1** in **TAIR_Arabidopsis**, Symbols: | protein binding / zinc ion binding | chr3:2557759-2561540 REVERSE

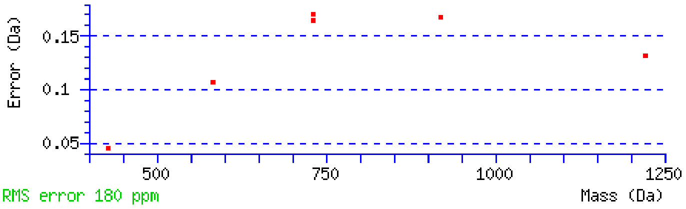
Match to Query 7595: 1648.590638 from(825.302595,2+) index(2837)
Title: Elution from: 29.365 to 29.365 scan no 3588 cid35.00 polarity:+
Data file 0-2_2.mgf

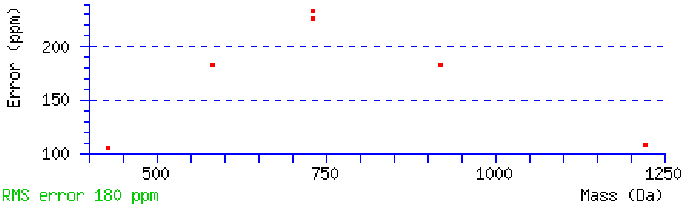
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1648.5885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 0.032
Matches : 6/106 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440			**W**							**13**
2	289.1461	145.0767			**V**	1461.5224	731.2648	1443.4988	722.2530	1443.5118	722.2595	**12**
3	**429.1961**	215.1017			**H**	1361.4569	681.2321	1343.4334	672.2203	1343.4464	672.2268	**11**
4	591.2208	296.1141			**C**	***1221.4069***	611.2071	1203.3833	602.1953	1203.3964	602.2018	**10**
5	**731.2709**	366.1391			**H**	1059.3822	530.1947	1041.3586	521.1829	1041.3716	521.1895	**9**
6	893.2956	447.1514			**C**	***919.3322***	460.1697	901.3086	451.1579	901.3216	451.1644	**8**
7	1009.3196	505.1634	991.3090	496.1581	**D**	757.3075	379.1574	739.2839	370.1456	739.2969	370.1521	**7**
8	1067.3381	534.1727	1049.3275	525.1674	**G**	641.2835	321.1454	623.2599	312.1336	623.2729	312.1401	**6**
9	1181.4192	591.2132	1163.4086	582.2079	**I**	***583.2650***	292.1361	565.2414	283.1243	565.2544	283.1309	**5**
10	1269.4482	635.2277	1251.4377	626.2225	**S**	469.1839	235.0956	451.1603	226.0838	451.1733	226.0903	**4**
11	1385.4722	693.2397	1367.4616	684.2345	**D**	381.1548	191.0811	363.1312	182.0693	363.1443	182.0758	**3**
12	1501.4962	751.2517	1483.4856	742.2464	**D**	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	**2**
13					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of WVHCHCDGISDDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G08020.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.9	1648.5885	0.0022	WVHCHCDGISDDK

Mascot: http://www.matrixscience.com/

AT3G08030.1

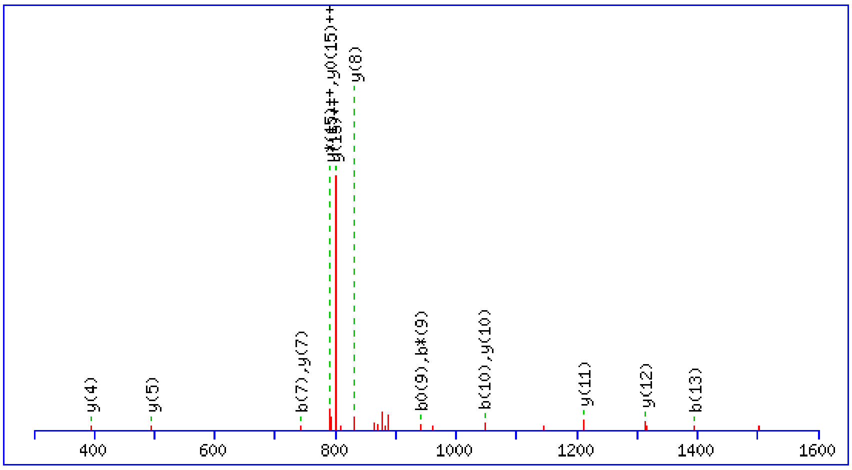
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSPGQTYTLSFVVGDAK**
Found in **AT3G08030.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G41800.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40802.1); contains InterPro domain Protein of unknown function DUF642 (InterPro:IPR006946) | chr3:2564197-2

Match to Query 7994: 1788.823760 from(895.419156,2+) index(6940)
Title: Elution from: 62.717 to 62.717 scan no 9152 cid35.00 polarity:+
Data file D1d-2_3.mgf

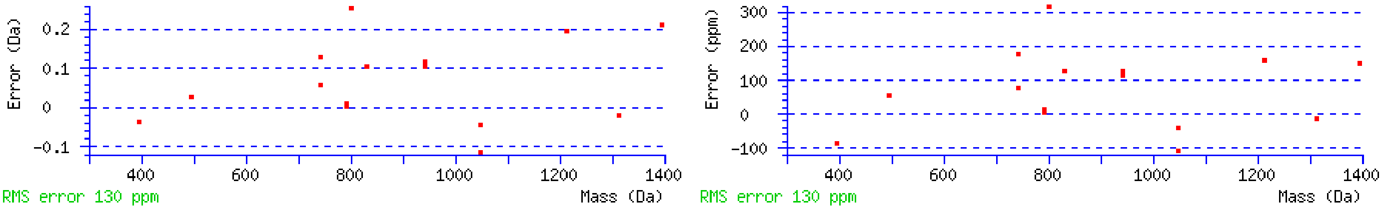
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1788.8272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00012
Matches : 15/180 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							17
2	191.0811	96.0442			173.0705	87.0389	S	1687.7898	844.3985	1669.7662	835.3867	1669.7792	835.3933	16
3	289.1309	145.0691			271.1203	136.0638	P	1599.7607	800.3840	1581.7372	791.3722	1581.7502	791.3787	15
4	347.1494	174.0783			329.1388	165.0730	G	1501.7109	751.3591	1483.6874	742.3473	1483.7004	742.3538	14
5	477.2020	239.1046	459.1784	230.0928	459.1914	230.0994	Q	1443.6924	722.3499	1425.6689	713.3381	1425.6819	713.3446	13
6	579.2467	290.1270	561.2231	281.1152	561.2361	281.1217	T	***1313.6398***	657.3235	1295.6162	648.3117	1295.6292	648.3183	12
7	**743.3071**	372.1572	725.2835	363.1454	725.2965	363.1519	Y	***1211.5951***	606.3012	1193.5715	597.2894	1193.5845	597.2959	11
8	845.3518	423.1795	827.3282	414.1677	827.3412	414.1742	T	***1047.5347***	524.2710	1029.5111	515.2592	1029.5242	515.2657	10
9	959.4329	480.2201	941.4093	471.2083	941.4223	471.2148	L	945.4900	473.2486	927.4664	464.2369	927.4794	464.2434	9
10	**1047.4619**	524.2346	1029.4384	515.2228	1029.4514	515.2293	S	***831.4089***	416.2081	813.3853	407.1963	813.3983	407.2028	8
11	1195.5274	598.2673	1177.5038	589.2555	1177.5168	589.2621	F	***743.3798***	372.1936	725.3563	363.1818	725.3693	363.1883	7
12	1295.5928	648.3001	1277.5693	639.2883	1277.5823	639.2948	V	595.3144	298.1608	577.2908	289.1490	577.3038	289.1556	6
13	**1395.6583**	698.3328	1377.6347	689.3210	1377.6477	689.3275	V	***495.2489***	248.1281	477.2254	239.1163	477.2384	239.1228	5
14	1453.6768	727.3420	1435.6532	718.3302	1435.6662	718.3368	G	***395.1835***	198.0954	377.1599	189.0836	377.1729	189.0901	4
15	1569.7008	785.3540	1551.6772	776.3422	1551.6902	776.3487	D	337.1650	169.0861	319.1414	160.0743	319.1544	160.0809	3
16	1641.7349	821.3711	1623.7113	812.3593	1623.7244	812.3658	A	221.1410	111.0741	203.1174	102.0624			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT3G08030.1



NCBI **BLAST** search of TSPGQTYTLSFVVGDAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.3	1788.8272	-0.0034	TSPGQTYTLSFVVGDAK
3.0	1788.8237	0.0001	MKSNIELMVSTNGGKK
2.0	1788.8203	0.0035	MGITNTVVSNYNINTK
1.9	1788.8218	0.0020	GKNQYSWKGFGEIPR

Mascot: http://www.matrixscience.com/

AT3G08530.1

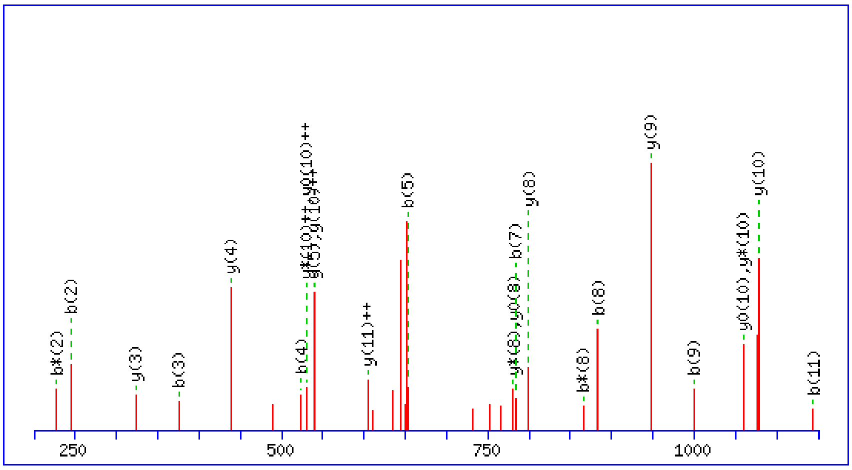
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQQFQGAVDAAR**
Found in **AT3G08530.1** in **TAIR_Arabidopsis**, Symbols: | clathrin heavy chain, putative | chr3:2587177-2595417 REVERSE

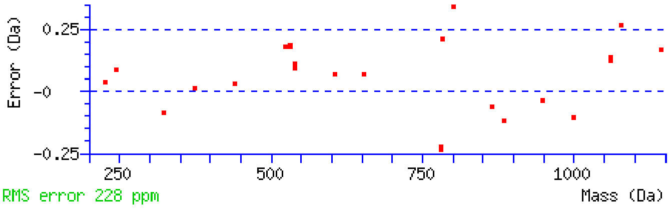
Match to Query 4817: 1320.613116 from(661.313834,2+) index(2952)
Title: Elution from: 28.653 to 28.653 scan no 3640 cid35.00 polarity:+
Data file C7-2_3.mgf

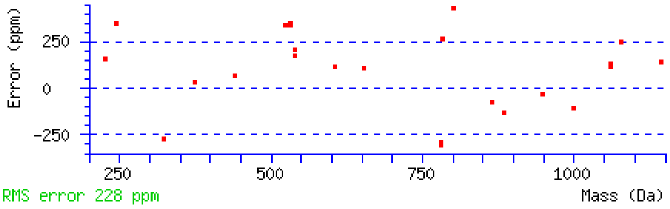
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.6146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 4.1e-008
Matches : 24/108 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							12
2	***245.1410***	123.0741	227.1174	114.0624			Q	1207.5409	604.2741	1189.5173	595.2623	1189.5303	595.2688	11
3	***375.1937***	188.1005	357.1701	179.0887			Q	**1077.4882**	539.2477	1059.4646	530.2360	1059.4776	530.2425	10
4	***523.2591***	262.1332	505.2355	253.1214			F	**947.4356**	474.2214	929.4120	465.2096	929.4250	465.2161	9
5	***653.3118***	327.1595	635.2882	318.1477			Q	**799.3701**	400.1887	781.3465	391.1769	781.3595	391.1834	8
6	711.3303	356.1688	693.3067	347.1570			G	669.3175	335.1624	651.2939	326.1506	651.3069	326.1571	7
7	***783.3644***	392.1858	765.3408	383.1741			A	611.2990	306.1531	593.2754	297.1413	593.2884	297.1478	6
8	***883.4299***	442.2186	865.4063	433.2068			V	**539.2648**	270.1360	521.2412	261.1243	521.2543	261.1308	5
9	***999.4538***	500.2306	981.4303	491.2188	981.4433	491.2253	D	**439.1994**	220.1033	421.1758	211.0915	421.1888	211.0980	4
10	1071.4880	536.2476	1053.4644	527.2358	1053.4774	527.2423	A	**323.1754**	162.0913	305.1518	153.0795			3
11	***1143.5221***	572.2647	1125.4986	563.2529	1125.5116	563.2594	A	251.1412	126.0743	233.1177	117.0625			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LQQFQGAVDAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G08530.1

Score	Mr(calc)	Delta	Sequence
83.9	1320.6146	-0.0015	LQQFQGAVDAAR
16.5	1320.6154	-0.0023	ELEAMLDKSVR
16.5	1320.6154	-0.0023	ELKDMEKEIR
14.2	1320.6169	-0.0038	QIEVNFYVHR
11.9	1320.6147	-0.0016	RNYPAANVVDGK
10.8	1320.6154	-0.0023	LEERKLEDMK
6.9	1320.6133	-0.0002	LPQICMNVRR
4.9	1320.6133	-0.0002	MKAAIERACPR
4.9	1320.6124	0.0007	IENDTKEAARR
2.3	1320.6154	-0.0023	ELNISGCSSLVK

Mascot: http://www.matrixscience.com/

AT3G08580.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEGFGSLWR**
Found in **AT3G08580.1** in **TAIR_Arabidopsis**, Symbols: AAC1 | AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding | chr3:2605712-2607036 REVERSE

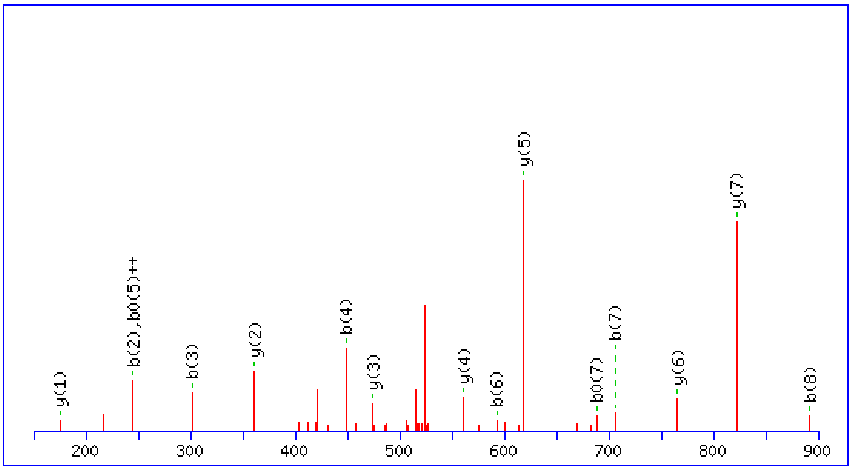
Match to Query 3151: 1065.487938 from(533.751245,2+) index(7301)
Title: Elution from: 63.505 to 63.505 scan no 9551 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

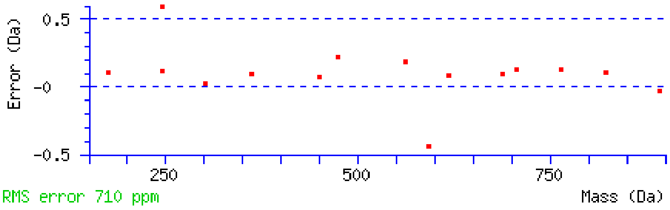
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

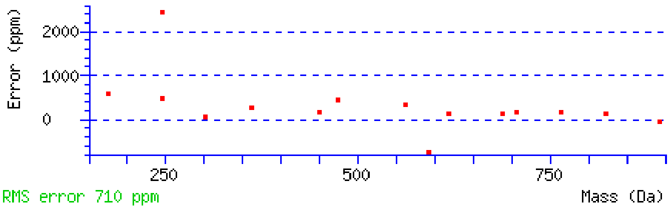


Monoisotopic mass of neutral peptide Mr(calc): 1065.4880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 2e-007
Matches : 15/74 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	**245.0768**	123.0420	227.0662	114.0368	E	951.4683	476.2378	934.4417	467.7245	933.4577	467.2325	8
3	**302.0983**	151.5528	284.0877	142.5475	G	***822.4257***	411.7165	805.3992	403.2032	804.4151	402.7112	7
4	**449.1667**	225.0870	431.1561	216.0817	F	***765.4042***	383.2058	748.3777	374.6925	747.3937	374.2005	6
5	506.1882	253.5977	488.1776	244.5924	G	***618.3358***	309.6715	601.3093	301.1583	600.3253	300.6663	5
6	**593.2202**	297.1137	575.2096	288.1084	S	***561.3144***	281.1608	544.2878	272.6475	543.3038	272.1555	4
7	**706.3042**	353.6558	688.2937	344.6505	L	***474.2823***	237.6448	457.2558	229.1315			3
8	**892.3836**	446.6954	874.3730	437.6901	W	***361.1983***	181.1028	344.1717	172.5895			2
9					R	***175.1190***	88.0631	158.0924	79.5498			1



RMS error 710 ppm



RMS error 710 ppm

NCBI **BLAST** search of DEGFGSLWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G08580.1

69.9	1065.4880	-0.0000	DEGFGSLWR
7.1	1065.4873	0.0006	AQMSGSDKSR
5.1	1065.4880	-0.0000	SDNPFSFPR
3.5	1065.4880	-0.0000	DWNTVFER
2.9	1065.4873	0.0006	AVSSTSMNNR
2.3	1065.4879	-0.0000	FEDGWEKR
2.0	1065.4873	0.0006	ECSKVSNSR

AT3G08590.1

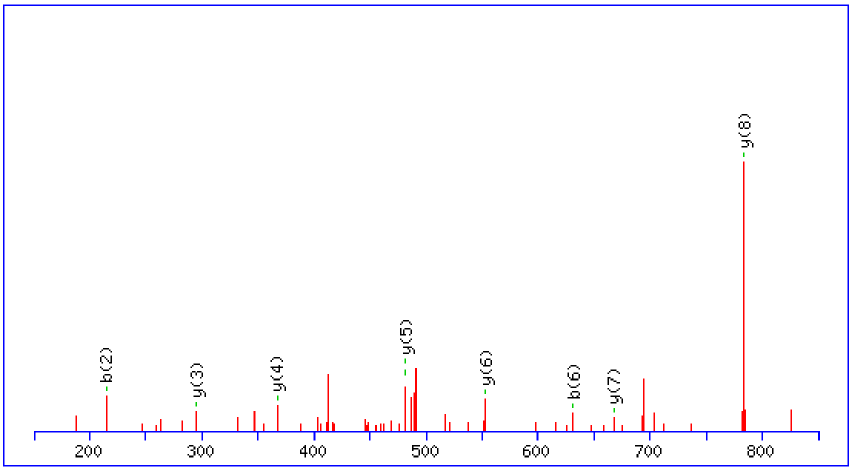
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVDLALASGK**
Found in **AT3G08590.1** in **TAIR_Arabidopsis**, Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative | chr3:2608689-2611243 REVERSE

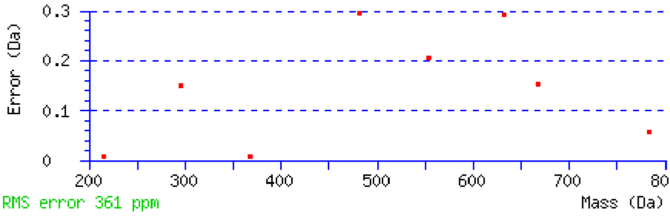
Match to Query 2580: 996.548316 from(499.281434,2+) index(4672)
Title: Elution from: 42.619 to 42.619 scan no 5823 cid35.00 polarity:+
Data file C7-3_1.mgf

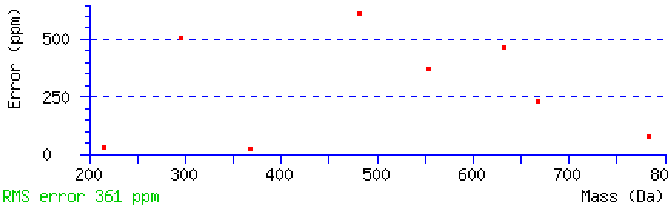
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 996.5482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00095
Matches : 8/82 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			**L**							**10**
2	**215.1538**	108.0805			**V**	883.4744	442.2408	865.4508	433.2290	865.4638	433.2355	**9**
3	331.1778	166.0925	313.1672	157.0873	**D**	***783.4089***	392.2081	765.3853	383.1963	765.3983	383.2028	**8**
4	445.2589	223.1331	427.2483	214.1278	**L**	***667.3849***	334.1961	649.3613	325.1843	649.3744	325.1908	**7**
5	517.2930	259.1502	499.2825	250.1449	**A**	***553.3038***	277.1556	535.2802	268.1438	535.2933	268.1503	**6**
6	**631.3741**	316.1907	613.3636	307.1854	**L**	***481.2697***	241.1385	463.2461	232.1267	463.2591	232.1332	**5**
7	703.4083	352.2078	685.3977	343.2025	**A**	***367.1886***	184.0979	349.1650	175.0861	349.1780	175.0926	**4**
8	791.4374	396.2223	773.4268	387.2170	**S**	***295.1544***	148.0809	277.1309	139.0691	277.1439	139.0756	**3**
9	849.4559	425.2316	831.4453	416.2263	**G**	207.1254	104.0663	189.1018	95.0545			**2**
10					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of LVDLALASGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G08590.1

Score	Mr(calc)	Delta	Sequence
37.6	996.5482	0.0001	LVDLALASGK

Mascot: http://www.matrixscience.com/

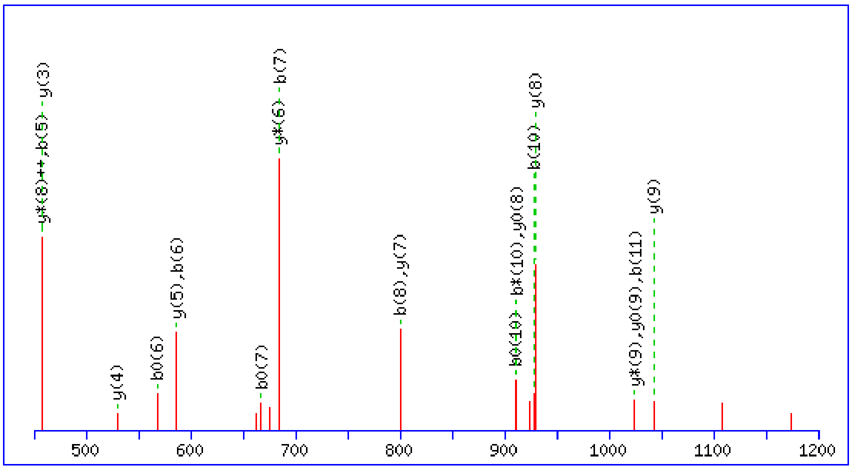
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGTNIEVDGAPWR**
Found in **AT3G08740.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor P (EF-P) family protein | chr3:2654794-2656160 REVERSE

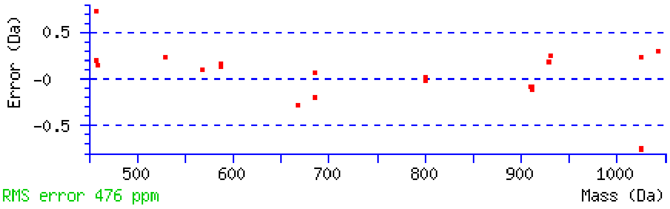
Match to Query 5426: 1384.674026 from(693.344289,2+) index(5332)
Title: Elution from: 47.142 to 47.142 scan no 6652 cid35.00 polarity:+
Data file C7-2_2.mgf

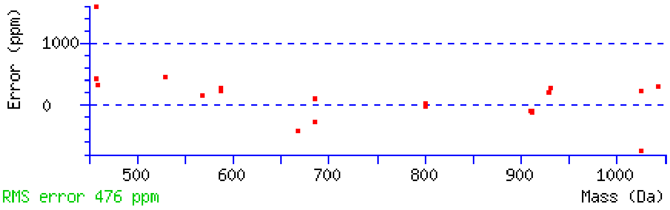
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1384.6735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.3e-006
Matches : 21/124 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	72.0444	36.5258					A							13
2	129.0659	65.0366					G	1314.6437	657.8255	1297.6171	649.3122	1296.6331	648.8202	12
3	230.1135	115.5604			212.1030	106.5551	T	1257.6222	629.3148	1240.5957	620.8015	1239.6117	620.3095	11
4	344.1565	172.5819	327.1299	164.0686	326.1459	163.5766	N	1156.5745	578.7909	1139.5480	570.2776	1138.5640	569.7856	10
5	***457.2405***	229.1239	440.2140	220.6106	439.2300	220.1186	I	***1042.5316***	521.7694	1025.5051	513.2562	1024.5211	512.7642	9
6	***586.2831***	293.6452	569.2566	285.1319	568.2726	284.6399	E	***929.4476***	465.2274	912.4210	456.7141	911.4370	456.2221	8
7	***685.3515***	343.1794	668.3250	334.6661	667.3410	334.1741	V	***800.4050***	400.7061	783.3784	392.1928	782.3944	391.7008	7
8	***800.3785***	400.6929	783.3519	392.1796	782.3679	391.6876	D	701.3365	351.1719	684.3100	342.6586	683.3260	342.1666	6
9	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	G	***586.3096***	293.6584	569.2831	285.1452			5
10	***928.4371***	464.7222	911.4105	456.2089	910.4265	455.7169	A	***529.2881***	265.1477	512.2616	256.6344			4
11	***1025.4898***	513.2485	1008.4633	504.7353	1007.4793	504.2433	P	***458.2510***	229.6292	441.2245	221.1159			3
12	1211.5691	606.2882	1194.5426	597.7749	1193.5586	597.2829	W	361.1983	181.1028	344.1717	172.5895			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AGTNIEVDGAPWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G08740.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.5	1384.6735	0.0005	AGTNIEVDGAPWR
0.4	1384.6769	-0.0029	ALQESMNVGSPPR
0.2	1384.6744	-0.0004	KLGVMGFCFGGGR

{MATRIX SCIENCE} Mascot Search Results

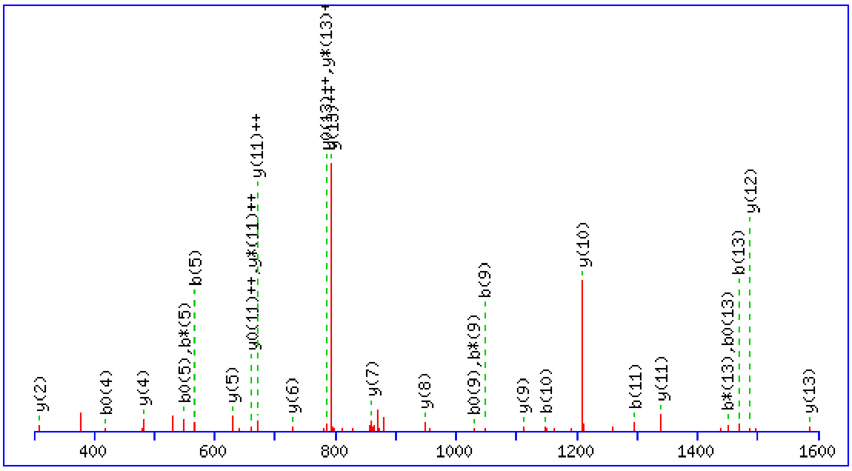
Peptide View

MS/MS Fragmentation of **STPFQPYSEVFGLQR**
Found in **AT3G08940.1** in **TAIR_Arabidopsis**, Symbols: LHCB4.2 | LHCB4.2 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding | chr3:2717722-2718405 FORWARD

Match to Query 8451: 1774.803370 from(888.408961,2+) index(8466)
Title: Elution from: 74.890 to 74.890 scan no 11207 cid35.00 polarity:+
Data file D12h-1_2.mgf

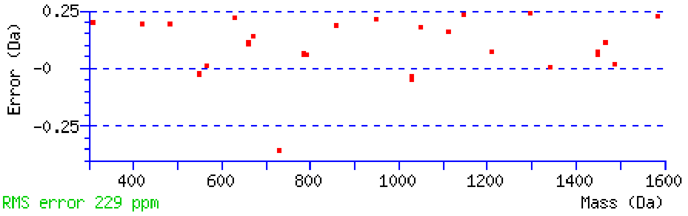
Click mouse within plot area to zoom in by factor of two about that point

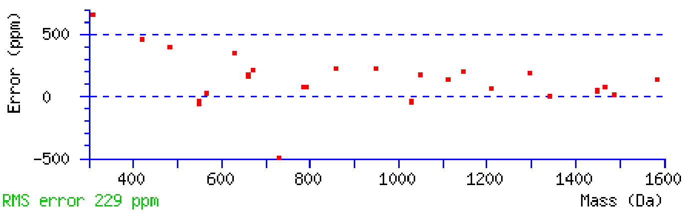
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1774.8035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 93 **Expect:** 4.9e-009
Matches : 29/148 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							15
2	191.0811	96.0442			173.0705	87.0389	T	1687.7817	844.3945	1669.7581	835.3827	1669.7711	835.3892	14
3	289.1309	145.0691			271.1203	136.0638	P	***1585.7370***	793.3721	1567.7134	784.3603	1567.7264	784.3668	13
4	437.1963	219.1018			419.1857	210.0965	F	***1487.6872***	744.3472	1469.6636	735.3354	1469.6766	735.3419	12
5	**567.2489**	284.1281	549.2254	275.1163	549.2384	275.1228	Q	***1339.6217***	670.3145	1321.5982	661.3027	1321.6112	661.3092	11
6	665.2987	333.1530	647.2752	324.1412	647.2882	324.1477	P	***1209.5691***	605.2882	1191.5455	596.2764	1191.5585	596.2829	10
7	829.3591	415.1832	811.3355	406.1714	811.3485	406.1779	Y	***1111.5193***	556.2633	1093.4957	547.2515	1093.5087	547.2580	9
8	917.3882	459.1977	899.3646	450.1859	899.3776	450.1924	S	***947.4589***	474.2331	929.4353	465.2213	929.4484	465.2278	8
9	**1047.4278**	524.2175	1029.4042	515.2057	1029.4172	515.2123	E	***859.4299***	430.2186	841.4063	421.2068	841.4193	421.2133	7
10	**1147.4933**	574.2503	1129.4697	565.2385	1129.4827	565.2450	V	***729.3902***	365.1988	711.3667	356.1870			6
11	**1295.5587**	648.2830	1277.5351	639.2712	1277.5481	639.2777	F	***629.3248***	315.1660	611.3012	306.1542			5
12	1353.5772	677.2922	1335.5536	668.2804	1335.5666	668.2870	G	***481.2593***	241.1333	463.2358	232.1215			4
13	**1467.6583**	734.3328	1449.6347	725.3210	1449.6477	725.3275	L	423.2408	212.1241	405.2173	203.1123			3
14	1597.7109	799.3591	1579.6874	790.3473	1579.7004	790.3538	Q	***309.1597***	155.0835	291.1362	146.0717			2
15							R	179.1071	90.0572	161.0835	81.0454			1





AT3G08940.1

NCBI **BLAST** search of STPFQPYSEVFGLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
92.7	1774.8035	-0.0001	STPFQPYSEVFGIQR
92.7	1774.8035	-0.0001	STPFQPYSEVFGLQR
3.0	1774.8046	-0.0013	MKENAASVLADLFSSR
2.7	1774.7992	0.0042	MGWDNKSGGFNRILR
1.0	1774.8013	0.0021	AVQSPNWSLLPEEER
0.7	1774.8055	-0.0021	GMQRLLVYELMCNK
0.5	1774.8008	0.0026	EEIDDPKFFYSIQK

AT3G08940.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFDPLGLASDPVKK**
Found in **AT3G08940.2** in **TAIR_Arabidopsis**, Symbols: LHCB4.2 | LHCB4.2 (LIGHT HARVESTING COMPLEX PSII) | chr3:2717722-2718670 FORWARD

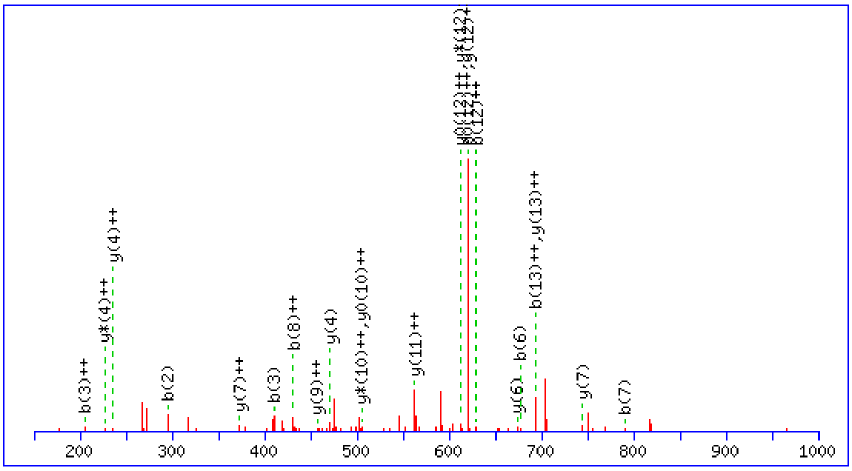
Match to Query 6518: 1532.824308 from(511.948712,3+) index(8023)
Title: Elution from: 70.257 to 70.257 scan no 10497 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

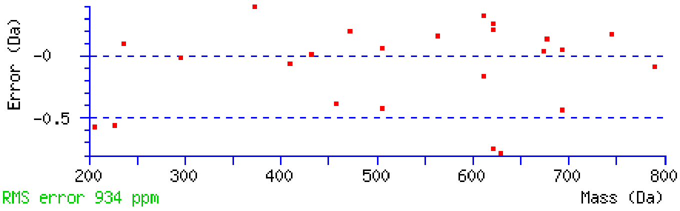
Label all possible matches ○ Label matches used for scoring ●

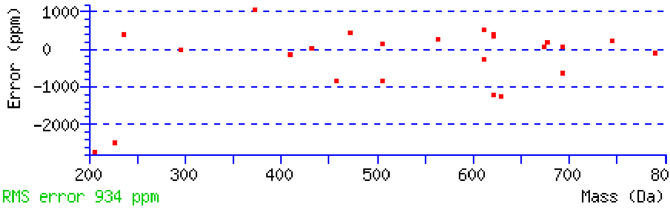
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1532.8239
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.022
Matches : 24/120 fragment ions using 56 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							14
2	***295.1441***	148.0757					F	1386.7627	693.8850	1369.7362	685.3717	1368.7522	684.8797	13
3	***410.1710***	***205.5892***			392.1605	196.5839	D	1239.6943	620.3508	1222.6678	611.8375	1221.6838	611.3455	12
4	507.2238	254.1155			489.2132	245.1103	P	1124.6674	562.8373	1107.6408	554.3241	1106.6568	553.8320	11
5	***620.3079***	310.6576			602.2973	301.6523	L	1027.6146	514.3109	1010.5881	505.7977	1009.6041	505.3057	10
6	***677.3293***	339.1683			659.3188	330.1630	G	914.5306	457.7689	897.5040	449.2556	896.5200	448.7636	9
7	***790.4134***	395.7103			772.4028	386.7051	L	857.5091	429.2582	840.4825	420.7449	839.4985	420.2529	8
8	861.4505	***431.2289***			843.4400	422.2236	A	**744.4250**	372.7162	727.3985	364.2029	726.4145	363.7109	7
9	948.4825	474.7449			930.4720	465.7396	S	**673.3879**	337.1976	656.3614	328.6843	655.3774	328.1923	6
10	1063.5095	532.2584			1045.4989	523.2531	D	586.3559	293.6816	569.3293	285.1683	568.3453	284.6763	5
11	1160.5623	580.7848			1142.5517	571.7795	P	**471.3289**	236.1681	454.3024	227.6548			4
12	1259.6307	***630.3190***			1241.6201	621.3137	V	374.2762	187.6417	357.2496	179.1285			3
13	1387.7256	***694.3665***	1370.6991	685.8532	1369.7151	685.3612	K	275.2078	138.1075	258.1812	129.5942			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FFDPLGLASDPVKK

AT3G08940.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.9	1532.8239	0.0004	FFDPLGLASDPVKK
4.0	1532.8232	0.0011	LLERTALAEKDMK
3.1	1532.8272	-0.0029	EENLVFLPGKIMK
3.0	1532.8272	-0.0029	LVIDAMGNFSPILK
1.7	1532.8232	0.0011	QVAELATISGAKSMK
1.0	1532.8232	0.0011	ELMLIKVAADTSAR

AT3G09070.1

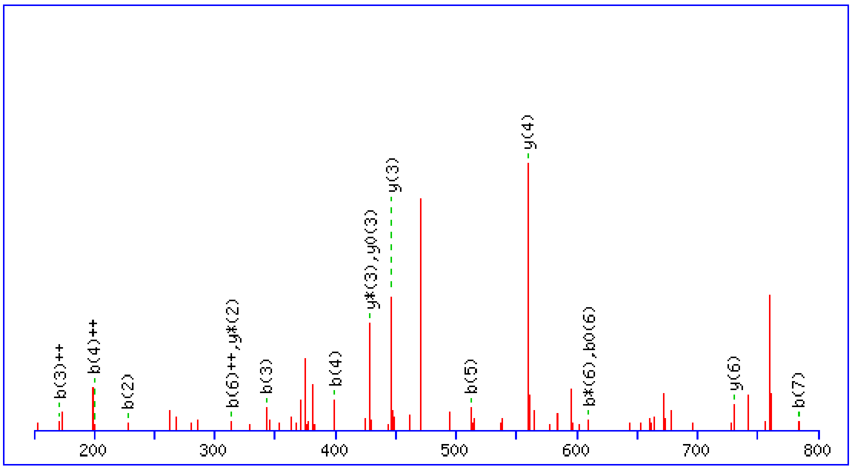
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVNGLDRR**
Found in **AT3G09070.1** in **TAIR_Arabidopsis**, Symbols: | glycine-rich protein | chr3:2768885-2770942 REVERSE

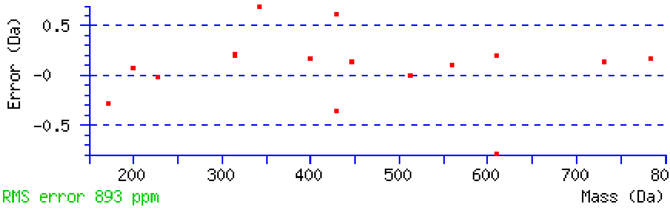
Match to Query 1845: 956.550876 from(479.282714,2+) index(4971)
Title: Elution from: 47.085 to 47.085 scan no 6335 cid35.00 polarity:+
Data file D1d-2_1.mgf

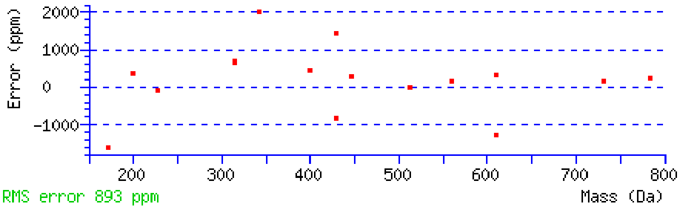
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 956.5515
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.045
Matches : 16/70 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							8
2	***228.1707***	114.5890	211.1441	106.0757			V	829.4639	415.2356	812.4373	406.7223	811.4533	406.2303	7
3	***342.2136***	**171.6104**	325.1870	163.0972			N	**730.3955**	365.7014	713.3689	357.1881	712.3849	356.6961	6
4	***399.2350***	**200.1212**	382.2085	191.6079			G	616.3525	308.6799	599.3260	300.1666	598.3420	299.6746	5
5	***512.3191***	256.6632	495.2926	248.1499			L	**559.3311**	280.1692	542.3045	271.6559	541.3205	271.1639	4
6	627.3461	**314.1767**	610.3195	305.6634	609.3355	305.1714	D	**446.2470**	223.6271	429.2205	215.1139	428.2364	214.6219	3
7	***783.4472***	392.2272	766.4206	383.7139	765.4366	383.2219	R	331.2201	166.1137	314.1935	157.6004			2
8							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KVNGLDRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.5	956.5515	-0.0007	KVNGLDRR
4.7	956.5515	-0.0007	IGGSRPSKR

AT3G09070.1

2.1	956.5515	-0.0007	ERLRVER
1.3	956.5515	-0.0007	VQSQIRAR
0.2	956.5515	-0.0007	RNKSLPSR

AT3G09200.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IHSENTGNTAILNLLPLLQGNVGLIFTK**
Found in **AT3G09200.1** in **TAIR_Arabidopsis**, Symbols: | 60S acidic ribosomal protein P0 (RPP0B) | chr3:2823370-2825026 REVERSE

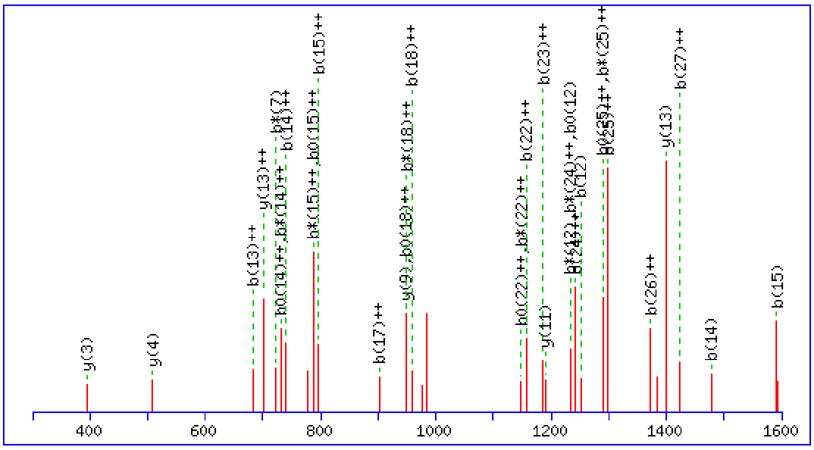
Match to Query 10859: 2989.654140 from(997.558656,3+) index(11086)
Title: Elution from: 124.013 to 124.013 scan no 16823 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

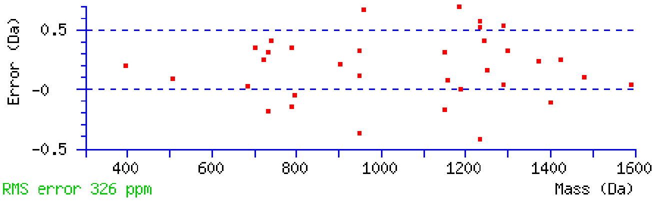
Show Y-axis ☐

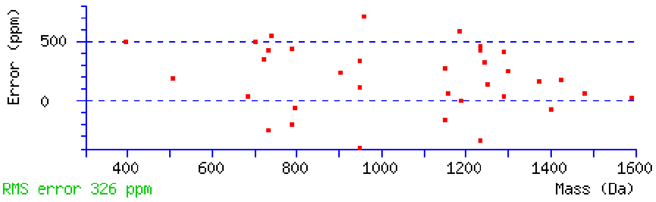


Monoisotopic mass of neutral peptide Mr(calc): 2989.6600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 5.3e-009
Matches : 34/310 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							28
2	251.1503	126.0788					H	2877.5833	1439.2953	2860.5567	1430.7820	2859.5727	1430.2900	27
3	338.1823	169.5948			320.1717	160.5895	S	2740.5244	1370.7658	2723.4978	1362.2525	2722.5138	1361.7605	26
4	467.2249	234.1161			449.2143	225.1108	E	2653.4923	1327.2498	2636.4658	1318.7365	2635.4818	1318.2445	25
5	581.2678	291.1375	564.2413	282.6243	563.2572	282.1323	N	2524.4497	1262.7285	2507.4232	1254.2152	2506.4392	1253.7232	24
6	682.3155	341.6614	665.2889	333.1481	664.3049	332.6561	T	2410.4068	1205.7070	2393.3803	1197.1938	2392.3962	1196.7018	23
7	739.3369	370.1721	722.3104	361.6588	721.3264	361.1668	G	2309.3591	1155.1832	2292.3326	1146.6699	2291.3486	1146.1779	22
8	853.3799	427.1936	836.3533	418.6803	835.3693	418.1883	N	2252.3377	1126.6725	2235.3111	1118.1592	2234.3271	1117.6672	21
9	954.4275	477.7174	937.4010	469.2041	936.4170	468.7121	T	2138.2947	1069.6510	2121.2682	1061.1377	2120.2842	1060.6457	20
10	1025.4647	513.2360	1008.4381	504.7227	1007.4541	504.2307	A	2037.2471	1019.1272	2020.2205	1010.6139	2019.2365	1010.1219	19
11	1138.5487	569.7780	1121.5222	561.2647	1120.5382	560.7727	I	1966.2099	983.6086	1949.1834	975.0953	1948.1994	974.6033	18
12	**1251.6328**	626.3200	1234.6062	617.8068	1233.6222	617.3148	L	1853.1259	927.0666	1836.0993	918.5533	1835.1153	918.0613	17
13	1365.6757	***683.3415***	1348.6492	674.8282	1347.6652	674.3362	N	1740.0418	870.5245	1723.0153	862.0113	1722.0313	861.5193	16
14	**1478.7598**	***739.8835***	1461.7332	731.3703	1460.7492	730.8782	L	1625.9989	813.5031	1608.9723	804.9898	1607.9883	804.4978	15
15	**1591.8438**	***796.4256***	1574.8173	787.9123	1573.8333	787.4203	L	1512.9148	756.9611	1495.8883	748.4478	1494.9043	747.9558	14
16	1688.8966	844.9519	1671.8701	836.4387	1670.8860	835.9467	P	**1399.8308**	700.4190	1382.8042	691.9057	1381.8202	691.4137	13
17	1801.9807	***901.4940***	1784.9541	892.9807	1783.9701	892.4887	L	1302.7780	651.8926	1285.7515	643.3794	1284.7674	642.8874	12
18	1915.0647	***958.0360***	1898.0382	949.5227	1897.0542	949.0307	L	**1189.6939**	595.3506	1172.6674	586.8373	1171.6834	586.3453	11
19	2043.1233	1022.0653	2026.0968	1013.5520	2025.1128	1013.0600	Q	1076.6099	538.8086	1059.5833	530.2953	1058.5993	529.8033	10
20	2100.1448	1050.5760	2083.1182	1042.0628	2082.1342	1041.5707	G	**948.5513**	474.7793	931.5247	466.2660	930.5407	465.7740	9
21	2214.1877	1107.5975	2197.1612	1099.0842	2196.1771	1098.5922	N	891.5298	446.2686	874.5033	437.7553	873.5193	437.2633	8
22	2313.2561	***1157.1317***	2296.2296	1148.6184	2295.2456	1148.1264	V	777.4869	389.2471	760.4604	380.7338	759.4763	380.2418	7
23	2370.2776	***1185.6424***	2353.2510	1177.1292	2352.2670	1176.6371	G	678.4185	339.7129	661.3919	331.1996	660.4079	330.7076	6
24	2483.3616	***1242.1845***	2466.3351	1233.6712	2465.3511	1233.1792	L	621.3970	311.2022	604.3705	302.6889	603.3865	302.1969	5
25	2596.4457	***1298.7265***	2579.4192	1290.2132	2578.4351	1289.7212	I	**508.3130**	254.6601	491.2864	246.1468	490.3024	245.6548	4

26	2743.5141	***1372.2607***	2726.4876	1363.7474	2725.5036	1363.2554	**F**	**395.2289**	198.1181	378.2023	189.6048	377.2183	189.1128	**3**
27	2844.5618	***1422.7845***	2827.5353	1414.2713	2826.5512	1413.7793	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
28							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of IHSENTGNTAILNLLPLLQGNVGLIFTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.5	2989.6600	-0.0059	IHSENTGNTAILNLLPLLQGNVGLIFTK
4.4	2989.6463	0.0078	LVTKQFVPMLGTYIFNGIDHKSQLLK
0.8	2989.6562	-0.0021	LRFDYLLITALAISTVSVVMAQVPPEK

Mascot: http://www.matrixscience.com/

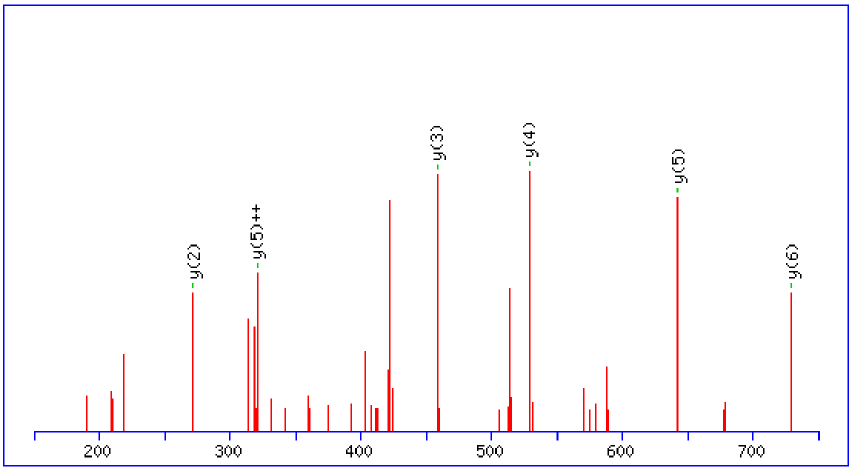
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSIAWPR**
Found in **AT3G09260.1** in **TAIR_Arabidopsis**, Symbols: PSR3.1, PYK10 | PYK10 (phosphate starvation-response 3.1); hydrolase, hydrolyzing O-glycosyl compounds | chr3:2840663-2843736 REVERSE

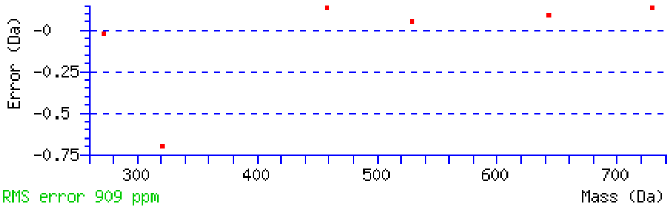
Match to Query 1263: 859.437322 from(430.725937,2+) index(5176)
Title: Elution from: 45.802 to 45.802 scan no 6508 cid35.00 polarity:+
Data file 0-3_3.mgf

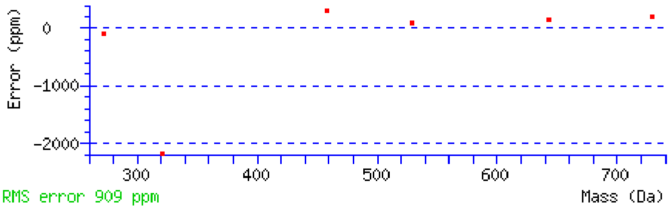
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 859.4374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 2.3e-005
Matches : 6/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.0478	66.5275			M							7
2	219.0798	110.0435	201.0692	101.0382	S	***729.4042***	365.2058	712.3777	356.6925	711.3937	356.2005	6
3	332.1639	166.5856	314.1533	157.5803	I	***642.3722***	321.6897	625.3457	313.1765			5
4	403.2010	202.1041	385.1904	193.0988	A	***529.2881***	265.1477	512.2616	256.6344			4
5	589.2803	295.1438	571.2697	286.1385	W	***458.2510***	229.6292	441.2245	221.1159			3
6	686.3330	343.6702	668.3225	334.6649	P	***272.1717***	136.5895	255.1452	128.0762			2
7					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MSIAWPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.4	859.4374	-0.0001	MSIAWPR

AT3G09260.1

Mascot: http://www.matrixscience.com/

AT3G09440.1

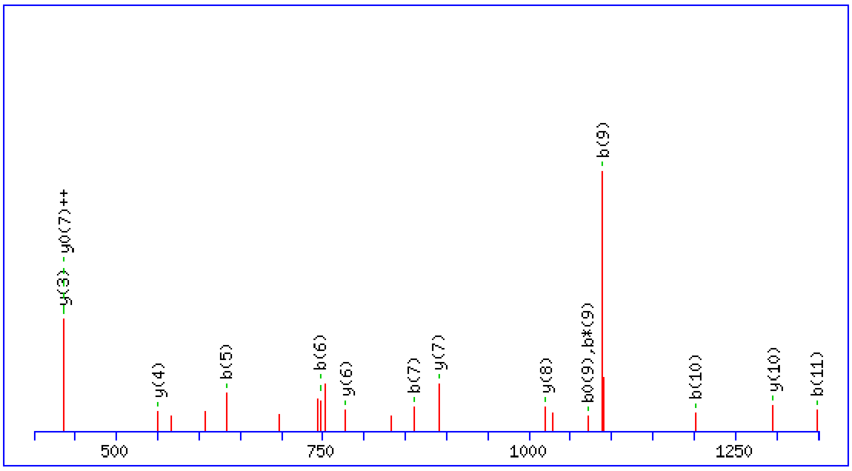
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ARFEELNIDLFR**
Found in **AT3G09440.1** in **TAIR_Arabidopsis**, Symbols: | heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) | chr3:2903440-2905638 REVERSE

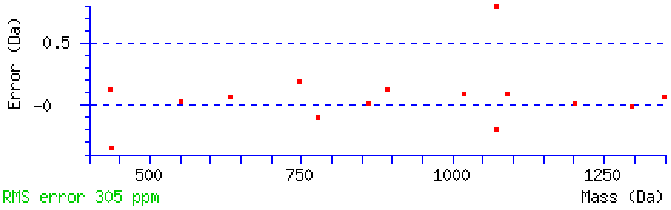
Match to Query 6586: 1521.794208 from(761.904380,2+) index(8552)
Title: Elution from: 75.312 to 75.312 scan no 11350 cid35.00 polarity:+
Data file C7-3_2.mgf

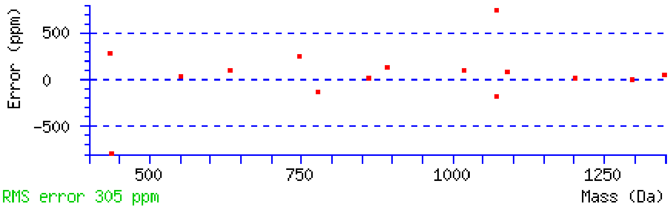
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1521.7939
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 6.9e-006
Matches : 15/118 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	228.1455	114.5764	211.1190	106.0631			R	1451.7641	726.3857	1434.7376	717.8724	1433.7536	717.3804	11
3	375.2139	188.1106	358.1874	179.5973			F	***1295.6630***	648.3352	1278.6365	639.8219	1277.6525	639.3299	10
4	504.2565	252.6319	487.2300	244.1186	486.2459	243.6266	E	1148.5946	574.8009	1131.5681	566.2877	1130.5840	565.7957	9
5	***633.2991***	317.1532	616.2726	308.6399	615.2885	308.1479	E	***1019.5520***	510.2796	1002.5255	501.7664	1001.5415	501.2744	8
6	***746.3832***	373.6952	729.3566	365.1819	728.3726	364.6899	L	***890.5094***	445.7584	873.4829	437.2451	872.4989	436.7531	7
7	***860.4261***	430.7167	843.3995	422.2034	842.4155	421.7114	N	***777.4254***	389.2163	760.3988	380.7030	759.4148	380.2110	6
8	973.5102	487.2587	956.4836	478.7454	955.4996	478.2534	I	663.3824	332.1949	646.3559	323.6816	645.3719	323.1896	5
9	***1088.5371***	544.7722	1071.5106	536.2589	1070.5265	535.7669	D	***550.2984***	275.6528	533.2718	267.1396	532.2878	266.6475	4
10	***1201.6212***	601.3142	1184.5946	592.8009	1183.6106	592.3089	L	***435.2714***	218.1394	418.2449	209.6261			3
11	***1348.6896***	674.8484	1331.6630	666.3352	1330.6790	665.8431	F	322.1874	161.5973	305.1608	153.0840			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ARFEELNIDLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G09440.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.1	1521.7939	0.0003	ARFEELNIDLFR
1.9	1521.7899	0.0043	RSIGENFKSSELR
0.2	1521.7980	-0.0038	YLGLWIDDPRFK

AT3G09560.1

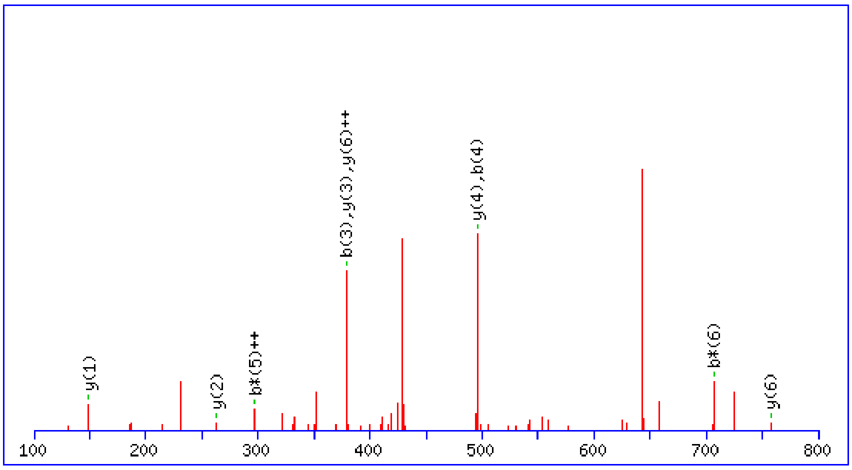
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFLNNLK**
Found in **AT3G09560.1** in **TAIR_Arabidopsis**, Symbols: | lipin family protein | chr3:2934958-2938678 REVERSE

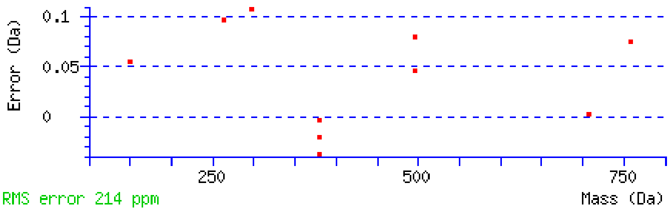
Match to Query 1375: 872.440046 from(437.227299,2+) index(4216)
Title: Elution from: 38.845 to 38.845 scan no 5278 cid35.00 polarity:+
Data file D12h-1_3.mgf

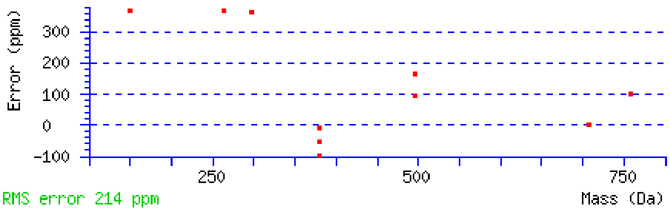
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 872.4382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.043
Matches : 10/48 fragment ions using 19 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	#
1	117.0443	59.0258	99.0207	50.0140	N					7
2	265.1097	133.0585	247.0861	124.0467	F	***757.4085***	379.2079	739.3849	370.1961	6
3	**379.1908**	190.0990	361.1672	181.0873	L	609.3431	305.1752	591.3195	296.1634	5
4	**495.2278**	248.1175	477.2042	239.1058	N	***495.2620***	248.1346	477.2384	239.1228	4
5	611.2648	306.1360	593.2412	297.1243	N	***379.2250***	190.1161	361.2014	181.1043	3
6	725.3459	363.1766	707.3223	354.1648	L	***263.1880***	132.0976	245.1644	123.0858	2
7					K	***149.1069***	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of NFLNNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.7	872.4382	0.0018	NFLNNLK
17.1	872.4416	-0.0016	RSMLDIK
16.6	872.4416	-0.0016	DMRISLK

AT3G09560.1

15.6	872.4416	-0.0016	NKMGTALK
13.3	872.4416	-0.0016	VMKNLNK
12.9	872.4416	-0.0016	MERIGLK
12.2	872.4382	0.0018	NNIQVFK
12.1	872.4416	-0.0015	EVTMVRK
11.2	872.4416	-0.0016	DALLRMK
10.7	872.4416	-0.0016	DLLMRAK

AT3G09630.1

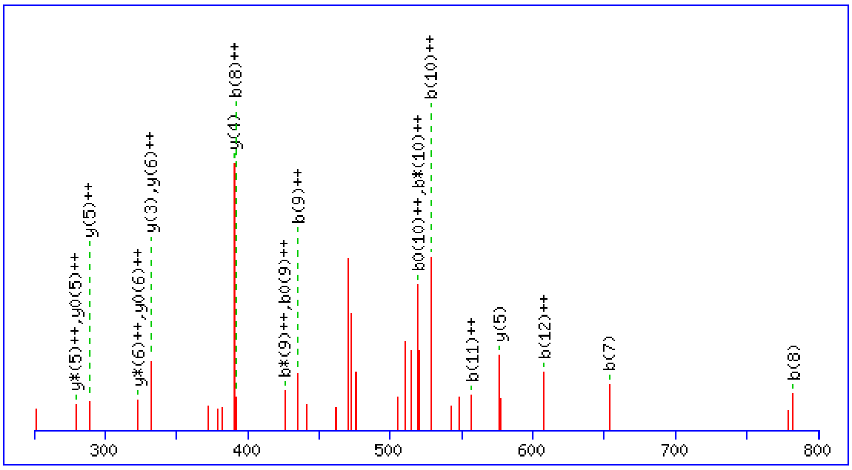
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGHQTSAESWGTGR**
Found in **AT3G09630.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L4/L1 (RPL4A) | chr3:2953818-2955449 FORWARD

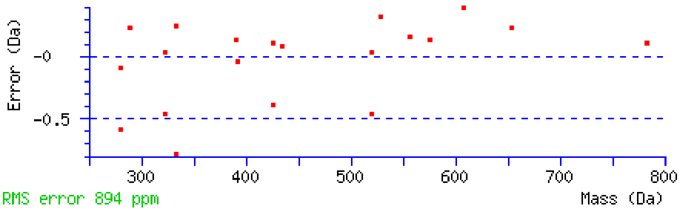
Match to Query 5521: 1443.649155 from(482.223661,3+) index(530)
Title: Elution from: 10.570 to 10.570 scan no 791 cid35.00 polarity:+
Data file D6h-2_3.mgf

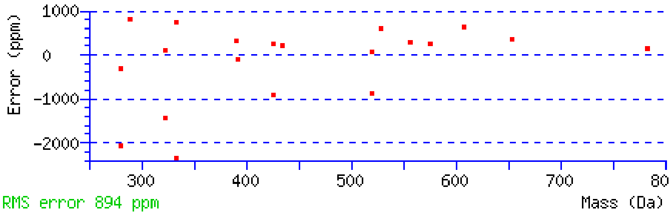
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1443.6491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.00058
Matches : 20/138 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							14
2	129.0659	65.0366					G	1373.6193	687.3133	1356.5927	678.8000	1355.6087	678.3080	13
3	266.1248	133.5660					H	1316.5978	658.8025	1299.5713	650.2893	1298.5872	649.7973	12
4	394.1833	197.5953	377.1568	189.0820			Q	1179.5389	590.2731	1162.5123	581.7598	1161.5283	581.2678	11
5	495.2310	248.1191	478.2045	239.6059	477.2205	239.1139	T	1051.4803	526.2438	1034.4538	517.7305	1033.4697	517.2385	10
6	582.2631	291.6352	565.2365	283.1219	564.2525	282.6299	S	950.4326	475.7200	933.4061	467.2067	932.4221	466.7147	9
7	**653.3002**	327.1537	636.2736	318.6404	635.2896	318.1484	A	863.4006	432.2039	846.3741	423.6907	845.3900	423.1987	8
8	**782.3428**	***391.6750***	765.3162	383.1617	764.3322	382.6697	E	792.3635	396.6854	775.3369	388.1721	774.3529	387.6801	7
9	869.3748	***435.1910***	852.3482	426.6778	851.3642	426.1857	S	663.3209	332.1641	646.2944	323.6508	645.3103	323.1588	6
10	1055.4541	***528.2307***	1038.4276	519.7174	1037.4435	519.2254	W	**576.2889**	288.6481	559.2623	280.1348	558.2783	279.6428	5
11	1112.4756	***556.7414***	1095.4490	548.2281	1094.4650	547.7361	G	**390.2096**	195.6084	373.1830	187.0951	372.1990	186.6031	4
12	1213.5232	***607.2653***	1196.4967	598.7520	1195.5127	598.2600	T	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	3
13	1270.5447	635.7760	1253.5182	627.2627	1252.5341	626.7707	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AGHQTSAESWGTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G09630.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.0	1443.6491	0.0000	AGHQTSAESWGTGR
2.2	1443.6486	0.0006	MEAKYREMENK
1.1	1443.6493	-0.0001	EGILGFYGDCWK

AT3G09650.1

Mascot Search Results

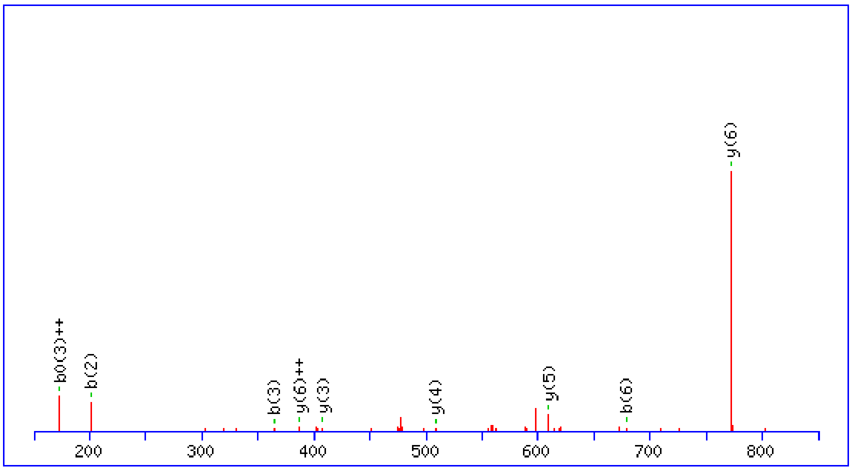
Peptide View

MS/MS Fragmentation of **ISYTTLMK**
Found in **AT3G09650.1** in **TAIR_Arabidopsis**, Symbols: CRM3, HCF152 | HCF152 (HIGH CHLOROPHYLL FLUORESCENCE 152) | chr3:2958709-2961045 FORWARD

Match to Query 2211: 971.497556 from(486.756054,2+) index(5539)
Title: Elution from: 49.760 to 49.760 scan no 7060 cid35.00 polarity:+
Data file 0-2_2.mgf

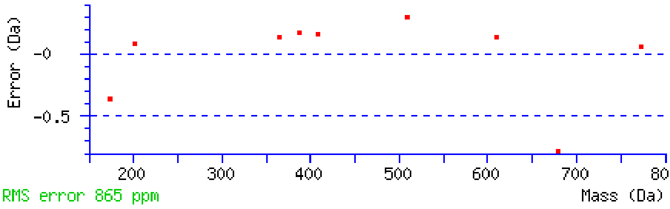
Click mouse within plot area to zoom in by factor of two about that point

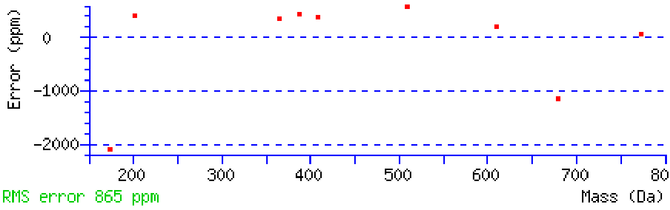
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 971.4998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 14 **Expect:** 0.044
Matches : 9/98 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							8
2	***201.1234***	101.0653	183.1128	92.0600	S	859.4230	430.2151	842.3964	421.7019	841.4124	421.2098	7
3	***364.1867***	182.5970	346.1761	173.5917	Y	***772.3910***	386.6991	755.3644	378.1858	754.3804	377.6938	6
4	465.2344	233.1208	447.2238	224.1155	T	***609.3276***	305.1675	592.3011	296.6542	591.3171	296.1622	5
5	566.2821	283.6447	548.2715	274.6394	T	***508.2799***	254.6436	491.2534	246.1303	490.2694	245.6383	4
6	***679.3661***	340.1867	661.3556	331.1814	L	***407.2323***	204.1198	390.2057	195.6065			3
7	826.4015	413.7044	808.3910	404.6991	M	294.1482	147.5777	277.1217	139.0645			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ISYTTLMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G09650.1

13.8	971.4998	-0.0022	ISYTTLMK
6.2	971.4964	0.0012	SIYDFTVK
6.2	971.4964	0.0012	SLYDFTVK
3.0	971.4998	-0.0022	VTTTLYMK

AT3G09820.1

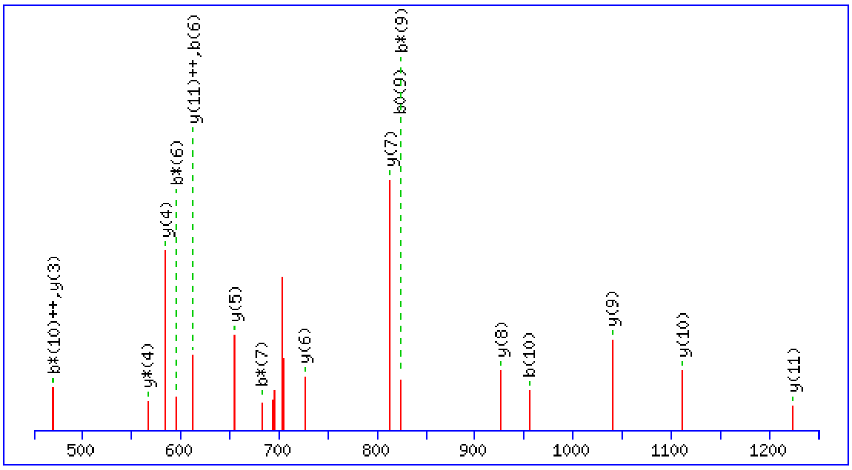
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLIANLSAANCYK**
Found in **AT3G09820.1** in **TAIR_Arabidopsis**, Symbols: ADK1 | ADK1 (ADENOSINE KINASE 1) | chr3:3012127-3014629 FORWARD

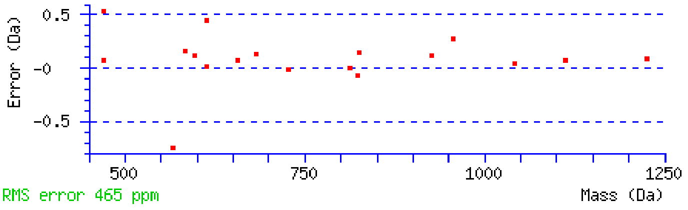
Match to Query 5526: 1423.709982 from(712.862267,2+) index(5789)
Title: Elution from: 52.497 to 52.497 scan no 7338 cid35.00 polarity:+
Data file D6h-2_2.mgf

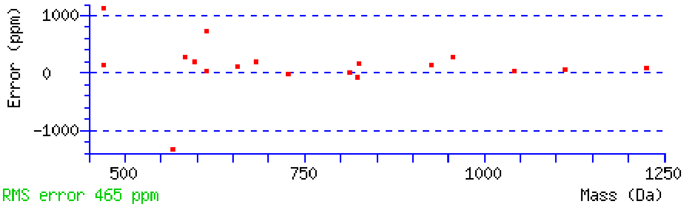
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1423.7129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 102 **Expect:** 3.3e-010
Matches : 18/124 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	201.1234	101.0653			183.1128	92.0600	L	1337.6882	669.3477	1320.6616	660.8345	1319.6776	660.3425	12
3	314.2074	157.6074			296.1969	148.6021	I	***1224.6041***	612.8057	1207.5776	604.2924	1206.5936	603.8004	11
4	385.2445	193.1259			367.2340	184.1206	A	***1111.5201***	556.2637	1094.4935	547.7504	1093.5095	547.2584	10
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	N	***1040.4830***	520.7451	1023.4564	512.2318	1022.4724	511.7398	9
6	**612.3715**	306.6894	595.3450	298.1761	594.3610	297.6841	L	***926.4400***	463.7237	909.4135	455.2104	908.4295	454.7184	8
7	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	S	***813.3560***	407.1816	796.3294	398.6683	795.3454	398.1763	7
8	770.4407	385.7240	753.4141	377.2107	752.4301	376.7187	A	***726.3239***	363.6656	709.2974	355.1523			6
9	841.4778	421.2425	824.4512	412.7293	823.4672	412.2373	A	***655.2868***	328.1470	638.2603	319.6338			5
10	**955.5207**	478.2640	938.4942	469.7507	937.5102	469.2587	N	***584.2497***	292.6285	567.2232	284.1152			4
11	1115.5514	558.2793	1098.5248	549.7660	1097.5408	549.2740	C	***470.2068***	235.6070	453.1802	227.0938			3
12	1278.6147	639.8110	1261.5881	631.2977	1260.6041	630.8057	Y	310.1761	155.5917	293.1496	147.0784			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SLIANLSAANCYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G09820.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.7	1423.7129	-0.0029	SLIANLSAANCYK
1.9	1423.7129	-0.0029	ASNILLDADMHPK
0.5	1423.7129	-0.0029	ADALNATCKYIGK

AT3G09820.2

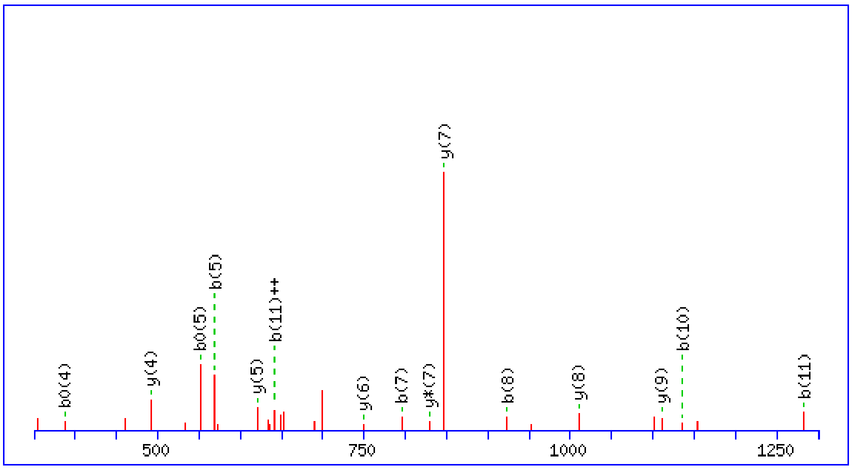
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGCTYPEKPDFN**
Found in **AT3G09820.2** in **TAIR_Arabidopsis**, Symbols: ADK1 | ADK1 (ADENOSINE KINASE 1) | chr3:3012650-3014629 FORWARD

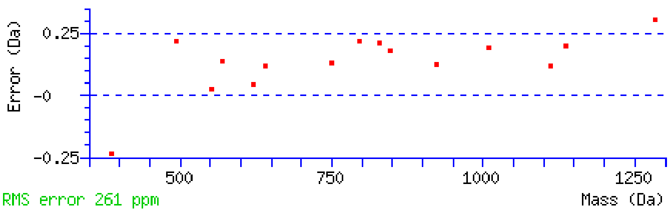
Match to Query 5697: 1413.585926 from(707.800239,2+) index(2691)
Title: Elution from: 28.665 to 28.665 scan no 3378 cid35.00 polarity:+
Data file D12h-3_1.mgf

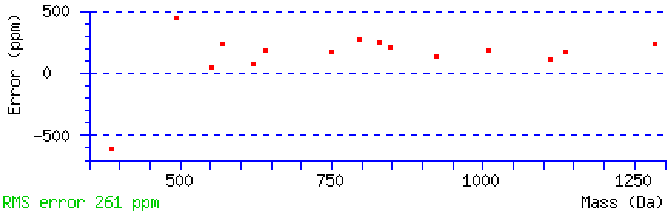
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1413.5871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 2.9e-005
Matches : 15/114 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	145.0608	73.0340			127.0502	64.0287	G	1327.5623	664.2848	1310.5358	655.7715	1309.5518	655.2795	11
3	305.0914	153.0493			287.0809	144.0441	C	1270.5409	635.7741	1253.5143	627.2608	1252.5303	626.7688	10
4	406.1391	203.5732			388.1285	194.5679	T	***1110.5102***	555.7587	1093.4837	547.2455	1092.4997	546.7535	9
5	***569.2024***	285.1049			551.1919	276.0996	Y	***1009.4625***	505.2349	992.4360	496.7216	991.4520	496.2296	8
6	666.2552	333.6312			648.2446	324.6260	P	***846.3992***	423.7032	829.3727	415.1900	828.3886	414.6980	7
7	***795.2978***	398.1525			777.2872	389.1472	E	***749.3464***	375.1769	732.3199	366.6636	731.3359	366.1716	6
8	***923.3927***	462.2000	906.3662	453.6867	905.3822	453.1947	K	***620.3039***	310.6556	603.2773	302.1423	602.2933	301.6503	5
9	1020.4455	510.7264	1003.4190	502.2131	1002.4349	501.7211	P	***492.2089***	246.6081	475.1823	238.0948	474.1983	237.6028	4
10	***1135.4725***	568.2399	1118.4459	559.7266	1117.4619	559.2346	D	395.1561	198.0817	378.1296	189.5684	377.1456	189.0764	3
11	***1282.5409***	641.7741	1265.5143	633.2608	1264.5303	632.7688	F	280.1292	140.5682	263.1026	132.0550			2
12							N	133.0608	67.0340	116.0342	58.5207			1





NCBI **BLAST** search of SGCTYPEKPDFN
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G09820.2

Score	Mr(calc)	Delta	Sequence
45.4	1413.5871	-0.0012	SGCTYPEKPDFN
1.8	1413.5830	0.0029	KESFQCSDEER

AT3G09840.1

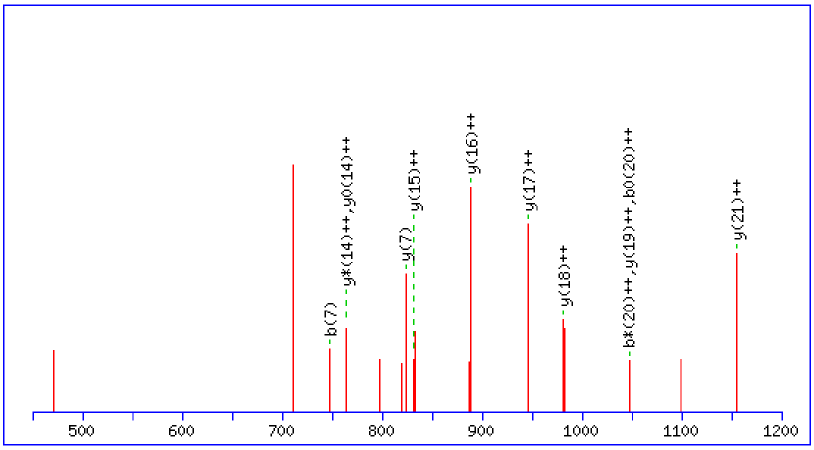
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVVDEAINDDNSVVSLHPATMEK**
Found in **AT3G09840.1** in **TAIR_Arabidopsis**, Symbols: ATCDC48, CDC48A, CDC48 | CDC48 (CELL DIVISION CYCLE 48); ATPase | chr3:3019499-3022837 FORWARD

Match to Query 10993: 2523.144024 from(842.055284,3+) index(7515)
Title: Elution from: 65.013 to 65.013 scan no 9675 cid35.00 polarity:+
Data file C7-1_1.mgf

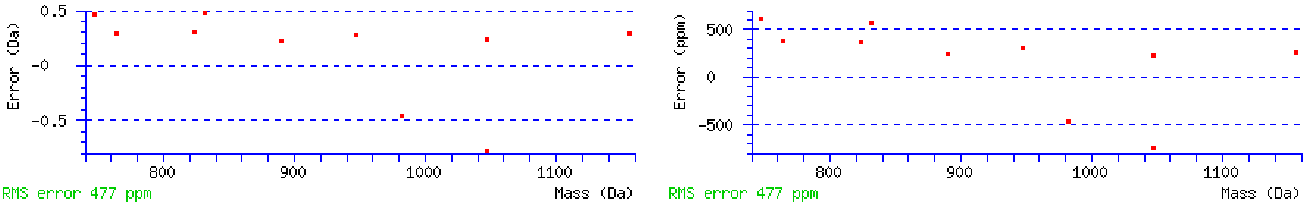
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2523.1383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.016
Matches : 12/242 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							23
2	215.1538	108.0805					V	2410.0645	1205.5359	2392.0409	1196.5241	2392.0540	1196.5306	22
3	315.2193	158.1133					V	2309.9991	1155.5032	2291.9755	1146.4914	2291.9885	1146.4979	21
4	431.2433	216.1253			413.2327	207.1200	D	2209.9336	1105.4705	2191.9100	1096.4587	2191.9231	1096.4652	20
5	561.2829	281.1451			543.2723	272.1398	E	2093.9096	1047.4585	2075.8861	1038.4467	2075.8991	1038.4532	19
6	633.3170	317.1622			615.3065	308.1569	A	1963.8700	982.4386	1945.8464	973.4269	1945.8595	973.4334	18
7	747.3981	374.2027			729.3876	365.1974	I	1891.8359	946.4216	1873.8123	937.4098	1873.8253	937.4163	17
8	863.4351	432.2212	845.4115	423.2094	845.4246	423.2159	N	1777.7548	889.3810	1759.7312	880.3692	1759.7442	880.3757	16
9	979.4591	490.2332	961.4355	481.2214	961.4485	481.2279	D	1661.7178	831.3625	1643.6942	822.3507	1643.7072	822.3572	15
10	1095.4831	548.2452	1077.4595	539.2334	1077.4725	539.2399	D	1545.6938	773.3505	1527.6702	764.3387	1527.6832	764.3453	14
11	1211.5201	606.2637	1193.4965	597.2519	1193.5095	597.2584	N	1429.6698	715.3385	1411.6462	706.3268	1411.6593	706.3333	13
12	1299.5491	650.2782	1281.5256	641.2664	1281.5386	641.2729	S	1313.6328	657.3200	1295.6092	648.3083	1295.6223	648.3148	12
13	1399.6146	700.3109	1381.5910	691.2991	1381.6040	691.3056	V	1225.6038	613.3055	1207.5802	604.2937	1207.5932	604.3002	11
14	1499.6800	750.3437	1481.6565	741.3319	1481.6695	741.3384	V	1125.5383	563.2728	1107.5147	554.2610	1107.5277	554.2675	10
15	1587.7091	794.3582	1569.6855	785.3464	1569.6985	785.3529	S	1025.4729	513.2401	1007.4493	504.2283	1007.4623	504.2348	9
16	1701.7902	851.3987	1683.7666	842.3869	1683.7796	842.3935	L	937.4438	469.2255	919.4202	460.2137	919.4332	460.2203	8
17	1841.8402	921.4237	1823.8166	912.4120	1823.8297	912.4185	H	823.3627	412.1850	805.3391	403.1732	805.3521	403.1797	7
18	1939.8900	970.4486	1921.8664	961.4369	1921.8795	961.4434	P	683.3127	342.1600	665.2891	333.1482	665.3021	333.1547	6
19	2011.9242	1006.4657	1993.9006	997.4539	1993.9136	997.4604	A	585.2629	293.1351	567.2393	284.1233	567.2523	284.1298	5
20	2113.9689	1057.4881	2095.9453	1048.4763	2095.9583	1048.4828	T	513.2287	257.1180	495.2052	248.1062	495.2182	248.1127	4
21	2246.0064	1123.5068	2227.9828	1114.4950	2227.9958	1114.5016	M	411.1840	206.0956	393.1604	197.0839	393.1735	197.0904	3
22	2376.0460	1188.5267	2358.0224	1179.5149	2358.0355	1179.5214	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
23							K	149.1069	75.0571	131.0833	66.0453			1

AT3G09840.1



NCBI **BLAST** search of LVVDEAINDDNSVVSLHPATMEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.8	2523.1383	0.0057	LVVDEAINDDNSVVSLHPATMEK
4.9	2523.1381	0.0059	NPLFIVWNEDNSAMYCLGILK
4.5	2523.1436	0.0004	AVVHGKDVADTVTQLNGSYMRGR
1.2	2523.1467	-0.0026	NENLKKIFNESMTNHTSIVMK
1.2	2523.1460	-0.0019	AGPGSSRWSMYSIPAKEELRPR
0.6	2523.1387	0.0053	LVDQTQQDVSKASCSNVKLDTR
0.6	2523.1444	-0.0004	RPTMSQVTNELKQCLTLENSK
0.4	2523.1432	0.0008	DKFTWTAMVVGLANNGQGQEAIK
0.3	2523.1388	0.0052	MLTASSSSSTTANIVYKRSQSTR

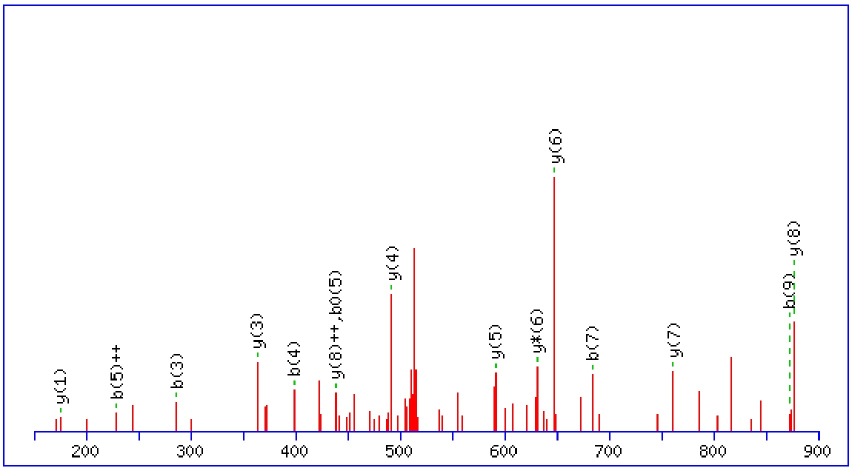
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLDLGVEGMR**
Found in **AT3G10060.1** in **TAIR_Arabidopsis**, Symbols: | immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative | chr3:3102296-3103806 FORWARD

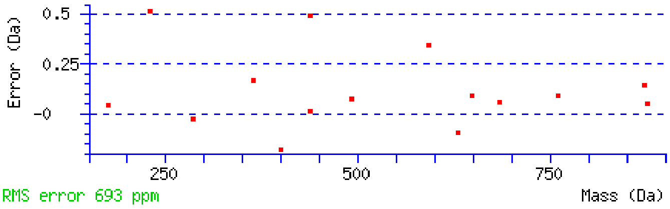
Match to Query 2864: 1045.523706 from(523.769129,2+) index(5243)
Title: Elution from: 47.273 to 47.273 scan no 6638 cid35.00 polarity:+
Data file 0-2_2.mgf

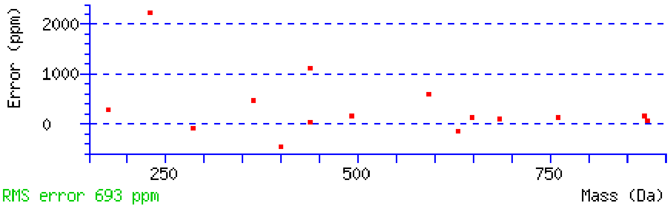
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1045.5226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 5.8e-005
Matches : 15/80 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180			**G**							**10**
2	171.1128	86.0600			**L**	989.5084	495.2579	972.4819	486.7446	971.4979	486.2526	**9**
3	**286.1397**	143.5735	268.1292	134.5682	**D**	***876.4244***	438.7158	859.3978	430.2026	858.4138	429.7105	**8**
4	**399.2238**	200.1155	381.2132	191.1103	**L**	***761.3974***	381.2024	744.3709	372.6891	743.3869	372.1971	**7**
5	456.2453	228.6263	438.2347	219.6210	**G**	***648.3134***	324.6603	631.2868	316.1470	630.3028	315.6550	**6**
6	555.3137	278.1605	537.3031	269.1552	**V**	***591.2919***	296.1496	574.2654	287.6363	573.2813	287.1443	**5**
7	**684.3563**	342.6818	666.3457	333.6765	**E**	***492.2235***	246.6154	475.1969	238.1021	474.2129	237.6101	**4**
8	741.3777	371.1925	723.3672	362.1872	**G**	***363.1809***	182.0941	346.1544	173.5808			**3**
9	**872.4182**	436.7128	854.4077	427.7075	**M**	306.1594	153.5834	289.1329	145.0701			**2**
10					**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GLDLGVEGMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G10060.1

Score	Mr(calc)	Delta	Sequence
48.8	1045.5226	0.0011	GLDLGVEGMR
0.7	1045.5264	-0.0027	ERSIDRDR
0.6	1045.5226	0.0011	GLESPALMGR

AT3G10090.1

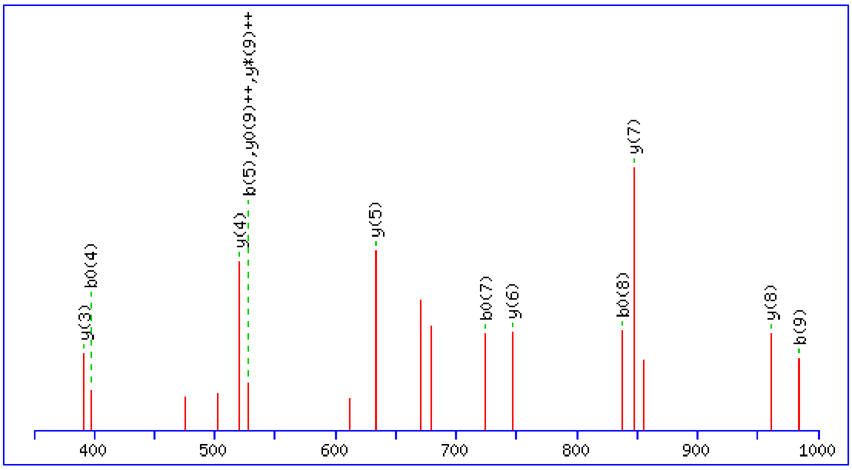
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDILTLLESER**
Found in **AT3G10090.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S28 (RPS28A) | chr3:3108965-3109159 REVERSE

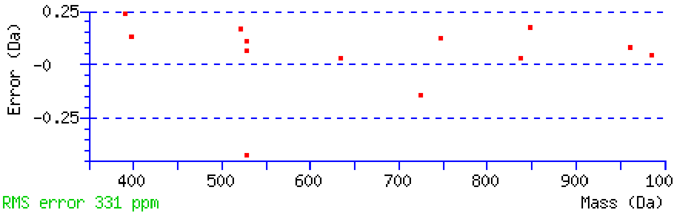
Match to Query 5215: 1373.703474 from(687.859013,2+) index(9647)
Title: Elution from: 88.865 to 88.865 scan no 13320 cid35.00 polarity:+
Data file 0-1_2.mgf

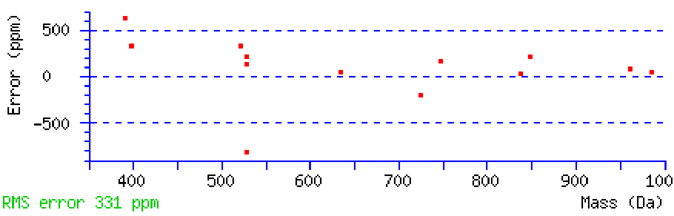
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1373.7038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.8e-006
Matches : 13/108 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							12
2	187.0713	94.0393	169.0608	85.0340	G	1245.6685	623.3379	1228.6420	614.8246	1227.6579	614.3326	11
3	302.0983	151.5528	284.0877	142.5475	D	1188.6470	594.8272	1171.6205	586.3139	1170.6365	585.8219	10
4	415.1823	208.0948	397.1718	199.0895	I	1073.6201	537.3137	1056.5936	528.8004	1055.6095	528.3084	9
5	**528.2664**	264.6368	510.2558	255.6316	L	***960.5360***	480.7717	943.5095	472.2584	942.5255	471.7664	8
6	629.3141	315.1607	611.3035	306.1554	T	***847.4520***	424.2296	830.4254	415.7164	829.4414	415.2243	7
7	742.3981	371.7027	724.3876	362.6974	L	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
8	855.4822	428.2447	837.4716	419.2395	L	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
9	**984.5248**	492.7660	966.5142	483.7608	E	***520.2362***	260.6217	503.2096	252.1084	502.2256	251.6164	4
10	1071.5568	536.2821	1053.5463	527.2768	S	***391.1936***	196.1004	374.1670	187.5871	373.1830	187.0951	3
11	1200.5994	600.8034	1182.5889	591.7981	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EGDILTLLESER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G10090.1

Score	Mr(calc)	Delta	Sequence
60.9	1373.7038	-0.0003	EGDILTLLESER

Mascot: http://www.matrixscience.com/

AT3G10540.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLIDRLLDTDPSR**
Found in **AT3G10540.1** in **TAIR_Arabidopsis**, Symbols: | 3-phosphoinositide-dependent protein kinase, putative | chr3:3289921-3292434 FORWARD

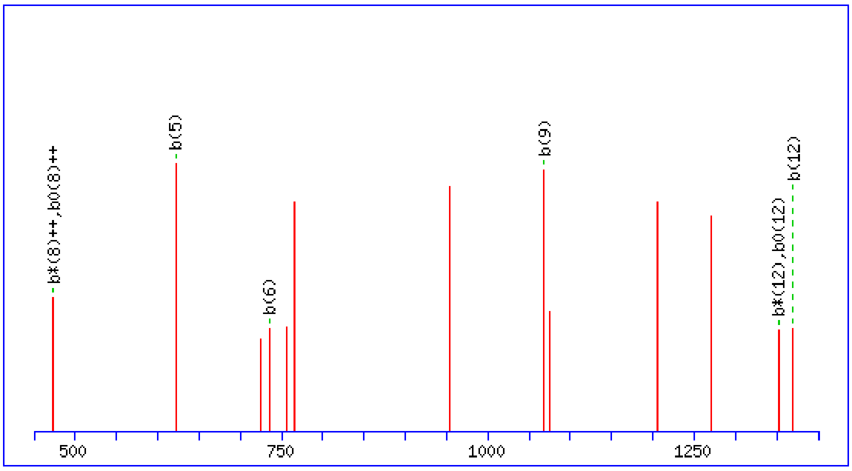
Match to Query 6452: 1546.733002 from(774.373777,2+) index(10094)
Title: Elution from: 95.353 to 95.353 scan no 14484 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1400 Da Full range

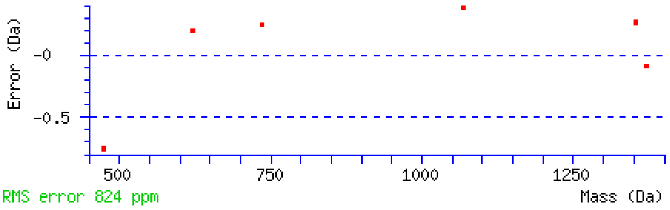
Label all possible matches ○ Label matches used for scoring ●

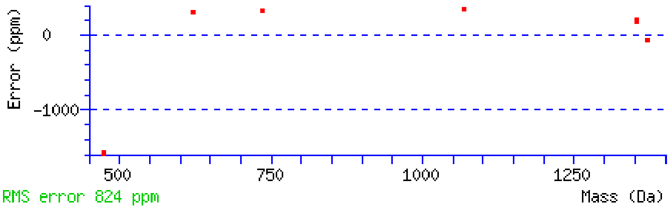
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1546.7329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.031
Matches : 8/134 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							13
2	231.1124	116.0598			213.1018	107.0545	L	1431.7162	716.3618	1413.6927	707.3500	1413.7057	707.3565	12
3	345.1935	173.1004			327.1829	164.0951	I	1317.6351	659.3212	1299.6116	650.3094	1299.6246	650.3159	11
4	461.2174	231.1124			443.2069	222.1071	D	1203.5540	602.2807	1185.5305	593.2689	1185.5435	593.2754	10
5	***621.3067***	311.1570	603.2831	302.1452	603.2961	302.1517	R	1087.5301	544.2687	1069.5065	535.2569	1069.5195	535.2634	9
6	***735.3878***	368.1975	717.3642	359.1857	717.3772	359.1922	L	927.4408	464.2240	909.4172	455.2123	909.4303	455.2188	8
7	849.4689	425.2381	831.4453	416.2263	831.4583	416.2328	L	813.3597	407.1835	795.3361	398.1717	795.3492	398.1782	7
8	965.4929	483.2501	947.4693	474.2383	947.4823	474.2448	D	699.2786	350.1429	681.2550	341.1312	681.2681	341.1377	6
9	***1067.5376***	534.2724	1049.5140	525.2606	1049.5270	525.2671	T	583.2546	292.1310	565.2311	283.1192	565.2441	283.1257	5
10	1183.5615	592.2844	1165.5380	583.2726	1165.5510	583.2791	D	481.2099	241.1086	463.1863	232.0968	463.1994	232.1033	4
11	1281.6113	641.3093	1263.5878	632.2975	1263.6008	632.3040	P	365.1860	183.0966	347.1624	174.0848	347.1754	174.0913	3
12	***1369.6404***	685.3238	1351.6168	676.3121	1351.6298	676.3186	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DLIDRLLDTDPSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G10540.1
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1546.7329	0.0001	DLIDRLLDTDPSR
2.4	1546.7303	0.0027	SSEATVTQPLLEEK
2.0	1546.7352	-0.0022	EWTLEGGALVLADR
1.7	1546.7303	0.0027	IQELEEQVSSLEK
1.6	1546.7352	-0.0022	FSPEEKIHSQTVK
1.5	1546.7352	-0.0022	LEPEVEASSRWVK
1.3	1546.7300	0.0030	IYEAFGMYGQILK
0.4	1546.7303	0.0027	EVESKDLAAAEIEK

AT3G10920.1

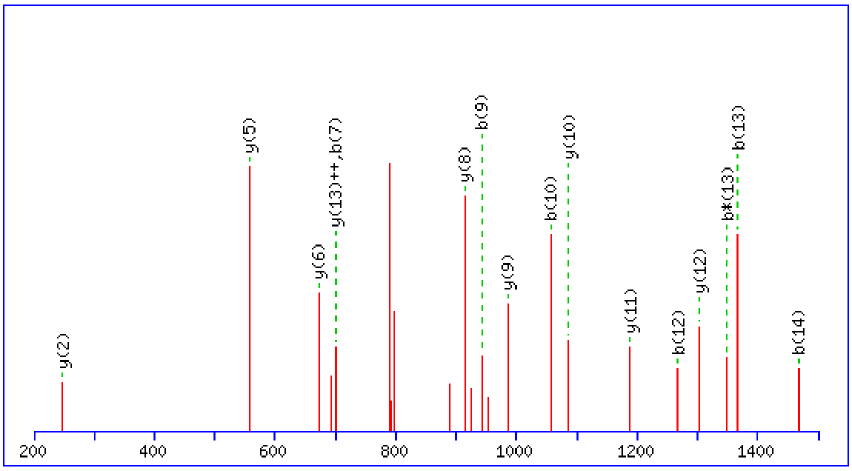
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVVDTTANQDPLVTK**
Found in **AT3G10920.1** in **TAIR_Arabidopsis**, Symbols: MEE33, MSD1 | MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); manganese superoxide dismutase | chr3:3418020-3419586 FORWARD

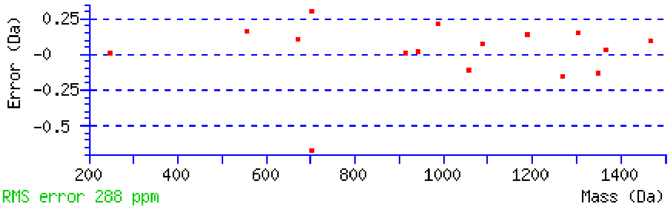
Match to Query 7254: 1612.864566 from(807.439559,2+) index(4784)
Title: Elution from: 45.645 to 45.645 scan no 6093 cid35.00 polarity:+
Data file D1d-2_1.mgf

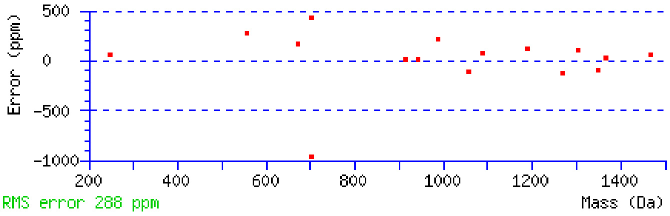
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1612.8672
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 1.2e-008
Matches : 16/146 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							15
2	213.1598	107.0835					V	1500.7904	750.8988	1483.7639	742.3856	1482.7799	741.8936	14
3	312.2282	156.6177					V	1401.7220	701.3646	1384.6955	692.8514	1383.7114	692.3594	13
4	427.2551	214.1312			409.2445	205.1259	D	***1302.6536***	651.8304	1285.6270	643.3172	1284.6430	642.8251	12
5	528.3028	264.6550			510.2922	255.6498	T	***1187.6266***	594.3170	1170.6001	585.8037	1169.6161	585.3117	11
6	629.3505	315.1789			611.3399	306.1736	T	***1086.5790***	543.7931	1069.5524	535.2798	1068.5684	534.7878	10
7	***700.3876***	350.6974			682.3770	341.6921	A	***985.5313***	493.2693	968.5047	484.7560	967.5207	484.2640	9
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	N	***914.4942***	457.7507	897.4676	449.2375	896.4836	448.7454	8
9	***942.4891***	471.7482	925.4625	463.2349	924.4785	462.7429	Q	800.4512	400.7293	783.4247	392.2160	782.4407	391.7240	7
10	***1057.5160***	529.2617	1040.4895	520.7484	1039.5055	520.2564	D	***672.3927***	336.7000	655.3661	328.1867	654.3821	327.6947	6
11	1154.5688	577.7880	1137.5422	569.2748	1136.5582	568.7828	P	***557.3657***	279.1865	540.3392	270.6732	539.3552	270.1812	5
12	***1267.6529***	634.3301	1250.6263	625.8168	1249.6423	625.3248	L	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
13	***1366.7213***	683.8643	1349.6947	675.3510	1348.7107	674.8590	V	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
14	***1467.7690***	734.3881	1450.7424	725.8748	1449.7584	725.3828	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
15							K	147.1128	74.0600	130.0863	65.5468			1





AT3G10920.1

NCBI **BLAST** search of LVVDTTANQDPLVTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.3	1612.8672	-0.0027	LVVDTTANQDPLVTK
4.1	1612.8647	-0.0001	HNELVPTLMAIFTK
1.4	1612.8685	-0.0040	GEDVRKGFLSHIQK
0.4	1612.8672	-0.0026	KEDAIAQAGIVIEEK

AT3G11130.1

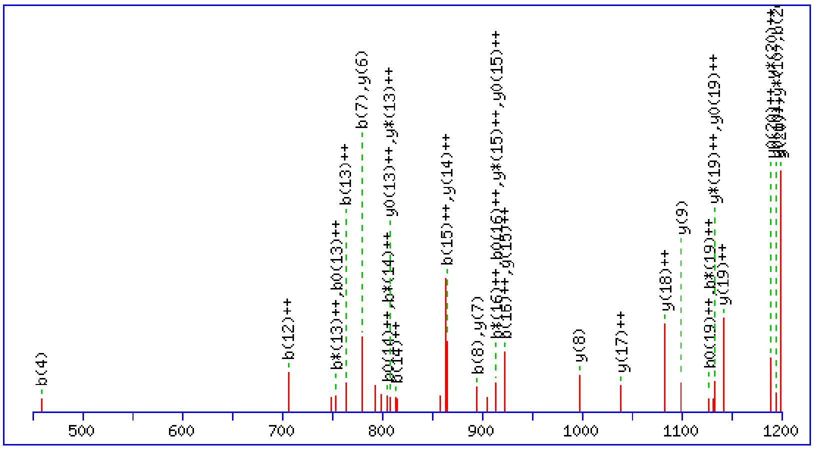
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIIDSNNNPEHFLTTNPYYDSK**
Found in **AT3G11130.1** in **TAIR_Arabidopsis**, Symbols: | clathrin heavy chain, putative | chr3:3482581-3491673 REVERSE

Match to Query 10853: 2623.142958 from(875.388262,3+) index(8258)
Title: Elution from: 73.854 to 73.854 scan no 10891 cid35.00 polarity:+
Data file 0-3_1.mgf

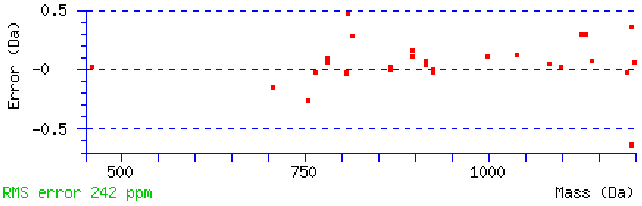
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

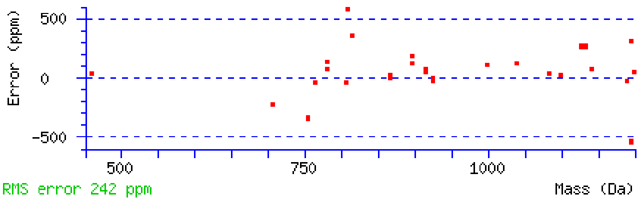


Monoisotopic mass of neutral peptide Mr(calc): 2623.1429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.5e-005
Matches : 37/234 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							22
2	229.1695	115.0884					I	2510.0691	1255.5382	2492.0455	1246.5264	2492.0585	1246.5329	21
3	343.2506	172.1289					I	2395.9880	1198.4976	2377.9644	1189.4858	2377.9774	1189.4923	20
4	**459.2746**	230.1409			441.2640	221.1356	D	2281.9069	1141.4571	2263.8833	1132.4453	2263.8963	1132.4518	19
5	547.3036	274.1554			529.2930	265.1502	S	2165.8829	1083.4451	2147.8593	1074.4333	2147.8723	1074.4398	18
6	663.3406	332.1739	645.3170	323.1622	645.3300	323.1687	N	2077.8538	1039.4306	2059.8303	1030.4188	2059.8433	1030.4253	17
7	**779.3776**	390.1924	761.3540	381.1807	761.3670	381.1872	N	1961.8169	981.4121	1943.7933	972.4003	1943.8063	972.4068	16
8	**895.4146**	448.2109	877.3910	439.1991	877.4040	439.2057	N	1845.7799	923.3936	1827.7563	914.3818	1827.7693	914.3883	15
9	993.4644	497.2358	975.4408	488.2240	975.4538	488.2306	P	1729.7429	865.3751	1711.7193	856.3633	1711.7323	856.3698	14
10	1123.5040	562.2557	1105.4804	553.2439	1105.4935	553.2504	E	1631.6931	816.3502	1613.6695	807.3384	1613.6825	807.3449	13
11	1263.5540	632.2807	1245.5305	623.2689	1245.5435	623.2754	H	1501.6534	751.3304	1483.6298	742.3186	1483.6429	742.3251	12
12	1411.6195	***706.3134***	1393.5959	697.3016	1393.6089	697.3081	F	1361.6034	681.3053	1343.5798	672.2936	1343.5928	672.3001	11
13	1525.7006	***763.3539***	1507.6770	754.3421	1507.6900	754.3487	L	1213.5380	607.2726	1195.5144	598.2608	1195.5274	598.2673	10
14	1627.7453	***814.3763***	1609.7217	805.3645	1609.7347	805.3710	T	**1099.4569**	550.2321	1081.4333	541.2203	1081.4463	541.2268	9
15	1729.7900	***865.3986***	1711.7664	856.3869	1711.7795	856.3934	T	**997.4122**	499.2097	979.3886	490.1979	979.4016	490.2044	8
16	1845.8270	***923.4171***	1827.8034	914.4054	1827.8165	914.4119	N	**895.3674**	448.1874	877.3439	439.1756	877.3569	439.1821	7
17	1943.8768	972.4420	1925.8532	963.4303	1925.8663	963.4368	P	**779.3304**	390.1689	761.3069	381.1571	761.3199	381.1636	6
18	2107.9372	1054.4722	2089.9136	1045.4604	2089.9266	1045.4669	Y	681.2806	341.1440	663.2571	332.1322	663.2701	332.1387	5
19	2271.9975	1136.5024	2253.9740	1127.4906	2253.9870	1127.4971	Y	517.2203	259.1138	499.1967	250.1020	499.2097	250.1085	4
20	2388.0215	***1194.5144***	2369.9979	1185.5026	2370.0110	1185.5091	D	353.1599	177.0836	335.1363	168.0718	335.1494	168.0783	3
21	2476.0506	1238.5289	2458.0270	1229.5171	2458.0400	1229.5236	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
22							K	149.1069	75.0571	131.0833	66.0453			1

AT3G11130.1





NCBI **BLAST** search of IIIDSNNNPEHFLTTNPYYDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.6	2623.1429	0.0000	IIIDSNNNPEHFLTTNPYYDSK
4.4	2623.1420	0.0010	ENRHMVIVIAEGAGQDYVAQSMR
0.6	2623.1449	-0.0020	VFDRMPERSLVSSTAMITCYAK
0.2	2623.1488	-0.0058	TLSIDLDEDSNLPIVTFSDNSGSR

Mascot: http://www.matrixscience.com/

AT3G11240.1

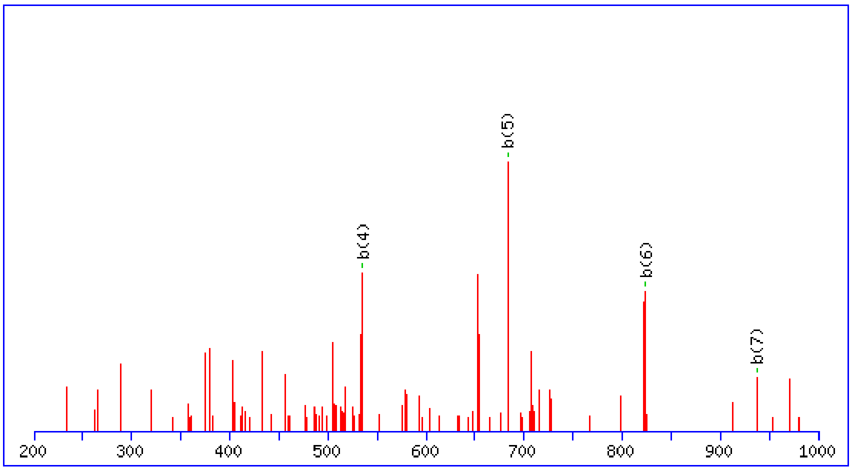
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RKLEMHLK**
Found in **AT3G11240.1** in **TAIR_Arabidopsis**, Symbols: | arginine-tRNA-protein transferase, putative / arginyltransferase, putative / arginyl-tRNA-protein transferase, putative | chr3:3518671-3521098 REVERSE

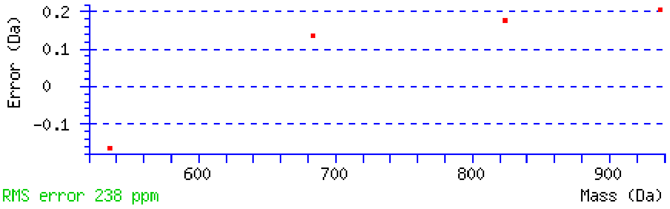
Match to Query 3486: 1084.563118 from(543.288835,2+) index(8515)
Title: Elution from: 74.459 to 74.459 scan no 11104 cid35.00 polarity:+
Data file D12h-1_1.mgf

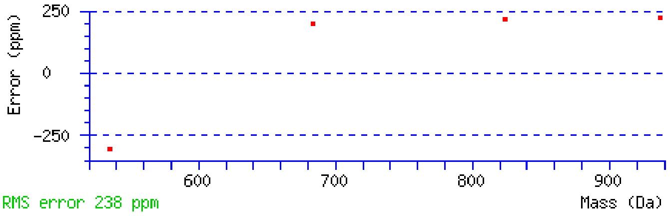
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1084.5622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.018
Matches : 4/110 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							8
2	291.1856	146.0964	273.1620	137.0846			K	925.4802	463.2437	907.4566	454.2319	907.4696	454.2384	7
3	405.2667	203.1370	387.2431	194.1252			L	795.3912	398.1992	777.3676	389.1874	777.3806	389.1939	6
4	***535.3063***	268.1568	517.2827	259.1450	517.2957	259.1515	E	681.3101	341.1587	663.2865	332.1469	663.2995	332.1534	5
5	***683.3387***	342.1730	665.3151	333.1612	665.3282	333.1677	M	551.2704	276.1389	533.2468	267.1271			4
6	***823.3887***	412.1980	805.3652	403.1862	805.3782	403.1927	H	403.2380	202.1226	385.2144	193.1108			3
7	***937.4698***	469.2386	919.4463	460.2268	919.4593	460.2333	L	263.1880	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RKLEMHLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G11240.1

20.6	1084.5622	0.0010	RKLEMHLK
11.2	1084.5622	0.0010	MLHRSGLLK
9.9	1084.5621	0.0010	GKVLMITHR
9.2	1084.5642	-0.0011	EEIKSDLIK
2.3	1084.5651	-0.0020	LMMIVDKPK
0.1	1084.5642	-0.0011	LGLSLDDLTK

AT3G11400.1

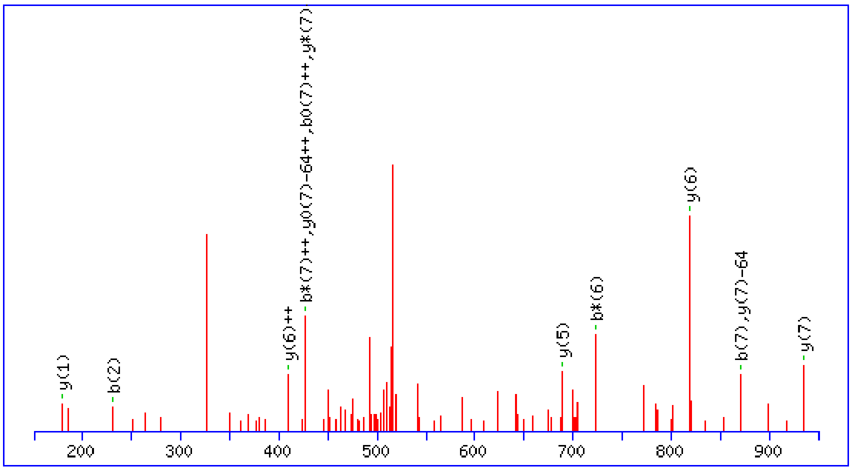
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNKRAMER**
Found in **AT3G11400.1** in **TAIR_Arabidopsis**, Symbols: ATEIF3G1, EIF3G1 | EIF3G1 (eukaryotic translation initiation factor 3G1); RNA binding / translation initiation factor | chr3:3578542-3580372 FORWARD

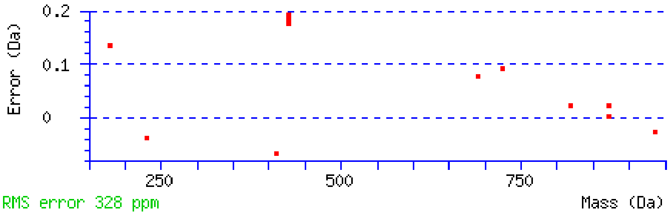
Match to Query 2818: 1048.503094 from(525.258823,2+) index(4815)
Title: Elution from: 44.852 to 44.852 scan no 6050 cid35.00 polarity:+
Data file D6h-2_2.mgf

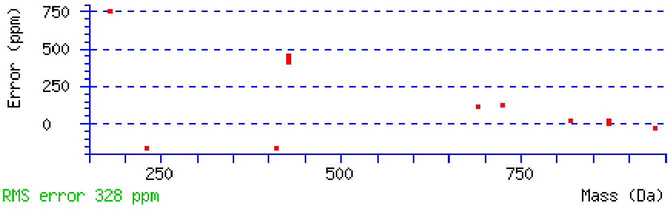
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1048.5024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.045
Matches : 13/108 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							8
2	**231.1254**	116.0663	213.1018	107.0545			N	***935.4286***	468.2179	917.4050	459.2061	917.4180	459.2126	7
3	361.2144	181.1108	343.1908	172.0990			K	***819.3916***	410.1994	801.3680	401.1876	801.3810	401.1941	6
4	521.3037	261.1555	503.2801	252.1437			R	***689.3026***	345.1549	671.2790	336.1431	671.2920	336.1496	5
5	593.3378	297.1725	575.3142	288.1607			A	529.2133	265.1103	511.1897	256.0985	511.2027	256.1050	4
6	741.3702	371.1888	723.3467	362.1770			M	457.1792	229.0932	439.1556	220.0814	439.1686	220.0879	3
7	**871.4099**	436.2086	853.3863	427.1968	853.3993	427.2033	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LNKRAMER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G11400.1

22.2	1048.5024	0.0007	LNKRAMER
12.9	1048.5053	-0.0022	LKEMITMR
12.9	1048.5020	0.0011	LTPEKMFR
12.5	1048.5046	-0.0015	MPFSRIGAR
12.3	1048.5020	0.0011	MLDINLFR
10.4	1048.5053	-0.0022	KMGKGIMEK
9.9	1048.5053	-0.0022	RTIMLMEK
9.5	1048.5020	0.0011	LFNIDMIR
9.1	1048.5024	0.0007	EVKRCVSR
8.7	1048.5024	0.0007	KQNNKMVR

AT3G11630.1

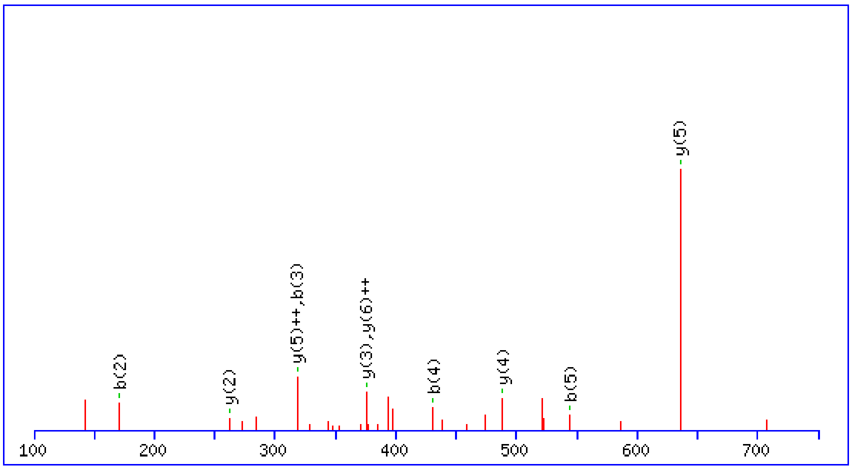
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLFIIDK**
Found in **AT3G11630.1** in **TAIR_Arabidopsis**, Symbols: | 2-cys peroxiredoxin, chloroplast (BAS1) | chr3:3672195-3673943 FORWARD

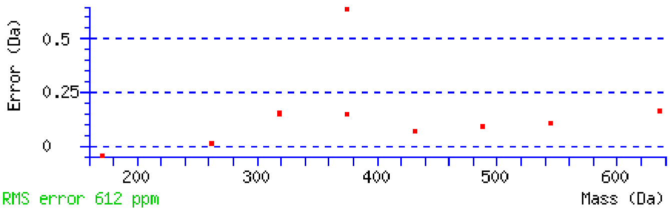
Match to Query 993: 804.474568 from(403.244560,2+) index(5939)
Title: Elution from: 53.248 to 53.248 scan no 7595 cid35.00 polarity:+
Data file D6h-1_2.mgf

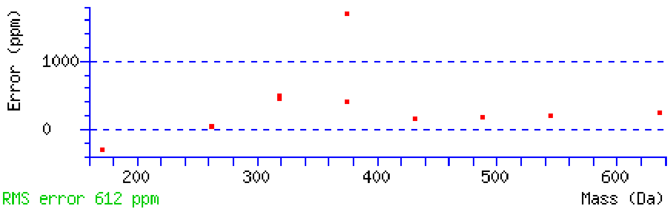
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [750] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 804.4745
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0053
Matches : 10/48 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							7
2	***171.1128***	86.0600			L	748.4604	374.7338	731.4338	366.2205	730.4498	365.7285	6
3	***318.1812***	159.5942			F	***635.3763***	318.1918	618.3497	309.6785	617.3657	309.1865	5
4	***431.2653***	216.1363			I	***488.3079***	244.6576	471.2813	236.1443	470.2973	235.6523	4
5	***544.3493***	272.6783			I	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
6	659.3763	330.1918	641.3657	321.1865	D	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
7					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GLFIIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.8	804.4745	0.0000	GLFIIDK
25.3	804.4745	0.0000	LGILFDK
16.8	804.4745	0.0000	AVFLVEK

AT3G11630.1

13.1	804.4745	0.0000	GLLVFEK
13.0	804.4745	0.0000	VALLDFK
5.0	804.4745	0.0000	AVIEFVK
4.5	804.4745	0.0000	IAVFDLK
1.7	804.4745	0.0000	AVDIFLK

Mascot: http://www.matrixscience.com/

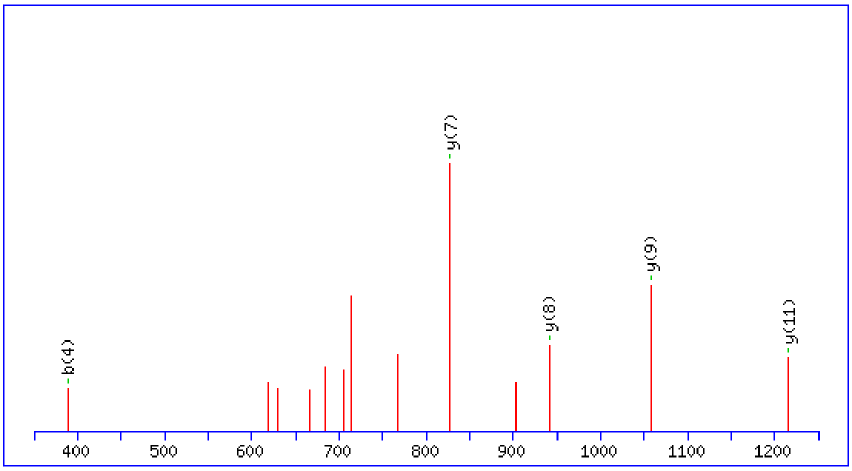
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQGVDITPYPIAR**
Found in **AT3G11780.1** in **TAIR_Arabidopsis**, Symbols: | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein | chr3:3724332-3725482 REVERSE

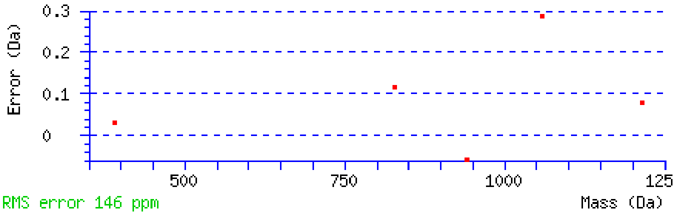
Match to Query 6049: 1444.724682 from(723.369617,2+) index(6277)
Title: Elution from: 55.280 to 55.280 scan no 7929 cid35.00 polarity:+
Data file C7-2_1.mgf

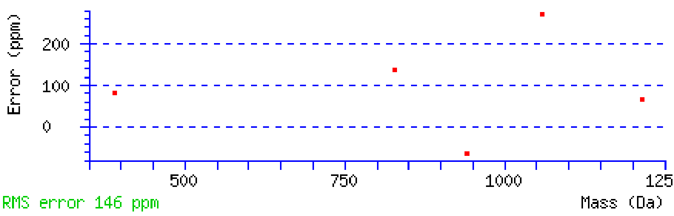
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1444.7268
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0097
Matches : 5/122 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							13
2	231.1254	116.0663	213.1018	107.0545			Q	1345.6687	673.3380	1327.6451	664.3262	1327.6581	664.3327	12
3	289.1439	145.0756	271.1203	136.0638			G	***1215.6160***	608.3117	1197.5925	599.2999	1197.6055	599.3064	11
4	389.2093	195.1083	371.1857	186.0965			V	1157.5975	579.3024	1139.5740	570.2906	1139.5870	570.2971	10
5	505.2333	253.1203	487.2097	244.1085	487.2227	244.1150	D	***1057.5321***	529.2697	1039.5085	520.2579	1039.5215	520.2644	9
6	619.3144	310.1608	601.2908	301.1490	601.3038	301.1556	I	***941.5081***	471.2577	923.4845	462.2459	923.4975	462.2524	8
7	721.3591	361.1832	703.3355	352.1714	703.3485	352.1779	T	***827.4270***	414.2171	809.4034	405.2054	809.4165	405.2119	7
8	819.4089	410.2081	801.3853	401.1963	801.3983	401.2028	P	725.3823	363.1948	707.3587	354.1830			6
9	983.4693	492.2383	965.4457	483.2265	965.4587	483.2330	Y	627.3325	314.1699	609.3089	305.1581			5
10	1081.5191	541.2632	1063.4955	532.2514	1063.5085	532.2579	P	463.2721	232.1397	445.2486	223.1279			4
11	1195.6002	598.3037	1177.5766	589.2919	1177.5896	589.2984	I	365.2223	183.1148	347.1988	174.1030			3
12	1267.6343	634.3208	1249.6107	625.3090	1249.6238	625.3155	A	251.1412	126.0743	233.1177	117.0625			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VQGVDITPYPIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G11780.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.6	1444.7268	-0.0022	VQGVDITPYPIAR
12.5	1444.7246	0.0001	IAEDALLNAIQTR
2.3	1444.7225	0.0021	ACHAIGLIGVTRR
1.3	1444.7273	-0.0026	LLPSDSRLRPDR

AT3G11930.1

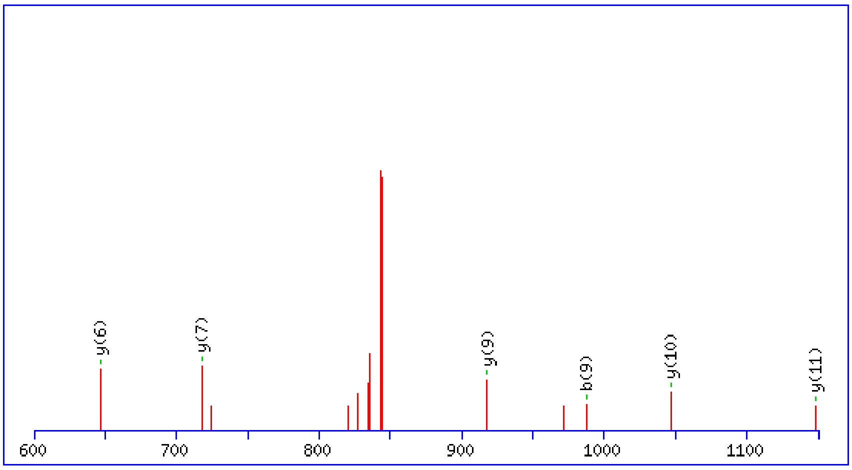
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPETTTEAEAPSLTTK**
Found in **AT3G11930.1** in **TAIR_Arabidopsis**, Symbols: | universal stress protein (USP) family protein | chr3:3776377-3777399 FORWARD

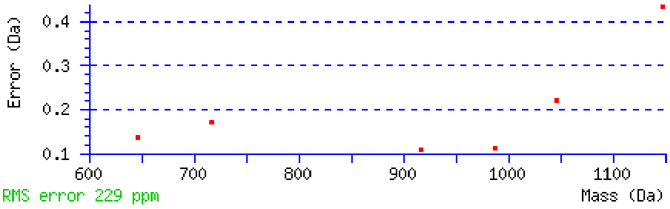
Match to Query 8625: 1702.821852 from(852.418202,2+) index(2493)
Title: Elution from: 27.400 to 27.400 scan no 3158 cid35.00 polarity:+
Data file 0-1_1.mgf

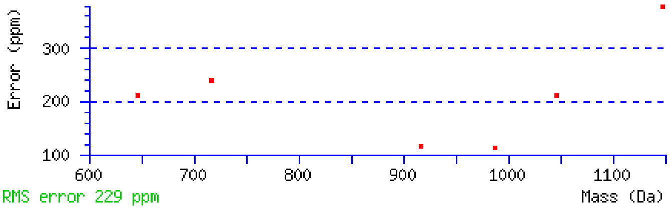
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [600] to [1150] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1702.8261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00078
Matches : 6/174 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							16
2	226.1186	113.5629	209.0921	105.0497			P	1575.7748	788.3911	1558.7483	779.8778	1557.7643	779.3858	15
3	355.1612	178.0842	338.1347	169.5710	337.1506	169.0790	E	1478.7221	739.8647	1461.6955	731.3514	1460.7115	730.8594	14
4	456.2089	228.6081	439.1823	220.0948	438.1983	219.6028	T	1349.6795	675.3434	1332.6529	666.8301	1331.6689	666.3381	13
5	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	T	1248.6318	624.8195	1231.6052	616.3063	1230.6212	615.8143	12
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	T	***1147.5841***	574.2957	1130.5576	565.7824	1129.5735	565.2904	11
7	787.3468	394.1771	770.3203	385.6638	769.3363	385.1718	E	***1046.5364***	523.7719	1029.5099	515.2586	1028.5259	514.7666	10
8	858.3840	429.6956	841.3574	421.1823	840.3734	420.6903	A	***917.4938***	459.2506	900.4673	450.7373	899.4833	450.2453	9
9	987.4265	494.2169	970.4000	485.7036	969.4160	485.2116	E	846.4567	423.7320	829.4302	415.2187	828.4462	414.7267	8
10	1058.4637	529.7355	1041.4371	521.2222	1040.4531	520.7302	A	***717.4141***	359.2107	700.3876	350.6974	699.4036	350.2054	7
11	1155.5164	578.2619	1138.4899	569.7486	1137.5059	569.2566	P	***646.3770***	323.6921	629.3505	315.1789	628.3665	314.6869	6
12	1242.5485	621.7779	1225.5219	613.2646	1224.5379	612.7726	S	549.3243	275.1658	532.2977	266.6525	531.3137	266.1605	5
13	1355.6325	678.3199	1338.6060	669.8066	1337.6220	669.3146	L	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
14	1456.6802	728.8437	1439.6536	720.3305	1438.6696	719.8385	T	349.2082	175.1077	332.1816	166.5944	331.1976	166.1024	3
15	1557.7279	779.3676	1540.7013	770.8543	1539.7173	770.3623	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
16							K	147.1128	74.0600	130.0863	65.5468			1





AT3G11930.1

NCBI **BLAST** search of QPETTTEAEAPSLTTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.4	1702.8261	-0.0043	QPETTTEAEAPSLTTK
5.0	1702.8195	0.0023	QLEELLMNANDELR
5.0	1702.8195	0.0023	QLEEMIKDANDELR
4.0	1702.8261	-0.0043	QDDGLSDLSDILGDLK
3.6	1702.8196	0.0023	TIMEEKQNNSPVGEK

Mascot: http://www.matrixscience.com/

AT3G12290.1

Mascot Search Results

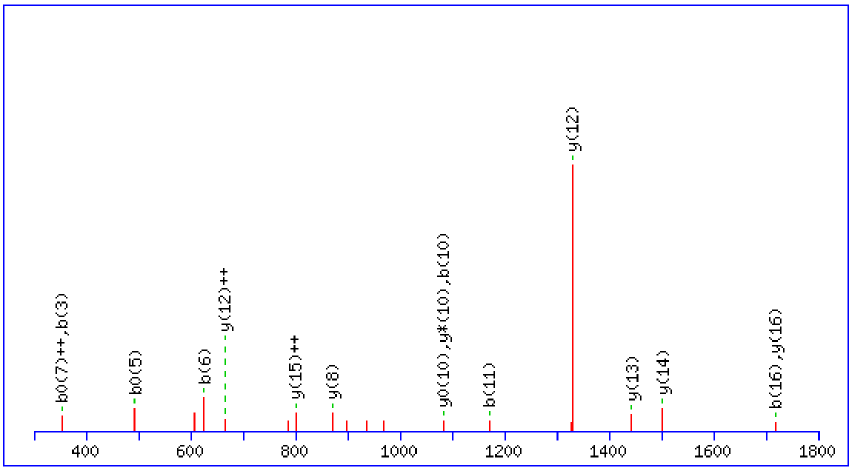
Peptide View

MS/MS Fragmentation of **SFDVGLPEEVSEADLISK**
Found in **AT3G12290.1** in **TAIR_Arabidopsis**, Symbols: | tetrahydrofolate dehydrogenase/cyclohydrolase, putative | chr3:3919598-3921333 FORWARD

Match to Query 9152: 1952.900406 from(977.457479,2+) index(9169)
Title: Elution from: 81.710 to 81.710 scan no 12358 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

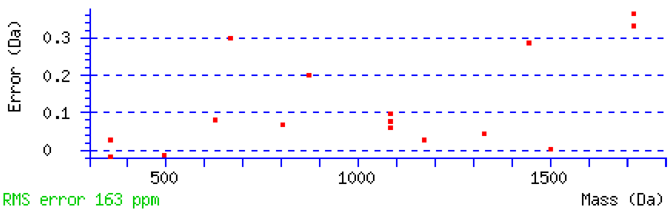
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

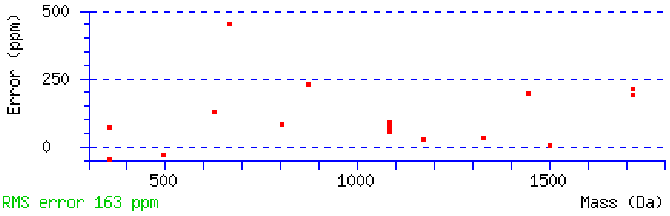


Monoisotopic mass of neutral peptide Mr(calc): 1952.8957
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.6e-005
Matches : 16/168 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	**S**							**18**
2	237.1018	119.0545	219.0912	110.0492	**F**	1865.8739	933.4406	1847.8503	924.4288	1847.8634	924.4353	**17**
3	***353.1258***	177.0665	335.1152	168.0612	**D**	***1717.8085***	859.4079	1699.7849	850.3961	1699.7979	850.4026	**16**
4	453.1912	227.0992	435.1807	218.0940	**V**	1601.7845	801.3959	1583.7609	792.3841	1583.7739	792.3906	**15**
5	511.2097	256.1085	493.1991	247.1032	**G**	***1501.7191***	751.3632	1483.6955	742.3514	1483.7085	742.3579	**14**
6	***625.2908***	313.1490	607.2802	304.1438	**L**	***1443.7006***	722.3539	1425.6770	713.3421	1425.6900	713.3486	**13**
7	723.3406	362.1739	705.3300	353.1687	**P**	***1329.6195***	665.3134	1311.5959	656.3016	1311.6089	656.3081	**12**
8	853.3802	427.1938	835.3697	418.1885	**E**	1231.5697	616.2885	1213.5461	607.2767	1213.5591	607.2832	**11**
9	983.4199	492.2136	965.4093	483.2083	**E**	1101.5300	551.2687	1083.5064	542.2569	1083.5195	542.2634	**10**
10	***1083.4853***	542.2463	1065.4748	533.2410	**V**	971.4904	486.2488	953.4668	477.2370	953.4798	477.2436	**9**
11	***1171.5144***	586.2608	1153.5038	577.2555	**S**	***871.4250***	436.2161	853.4014	427.2043	853.4144	427.2108	**8**
12	1301.5540	651.2806	1283.5434	642.2754	**E**	783.3959	392.2016	765.3723	383.1898	765.3853	383.1963	**7**
13	1373.5882	687.2977	1355.5776	678.2924	**A**	653.3563	327.1818	635.3327	318.1700	635.3457	318.1765	**6**
14	1489.6121	745.3097	1471.6016	736.3044	**D**	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	**5**
15	1603.6932	802.3503	1585.6827	793.3450	**L**	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	**4**
16	***1717.7743***	859.3908	1699.7638	850.3855	**I**	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	**3**
17	1805.8034	903.4053	1787.7928	894.4001	**S**	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	**2**
18					**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT3G12290.1





NCBI **BLAST** search of SFDVGLPEEVSEADLISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.0	1952.8957	0.0047	SFDVGLPEEVSEADLISK
8.6	1952.9040	-0.0036	GSMDDITVVIIDLNHYK
3.8	1952.8957	0.0047	EDEVFPTINILDTSVDK
1.7	1952.8959	0.0045	AVSGHIDMLYDLLHYGK

Mascot: http://www.matrixscience.com/

AT3G12390.1

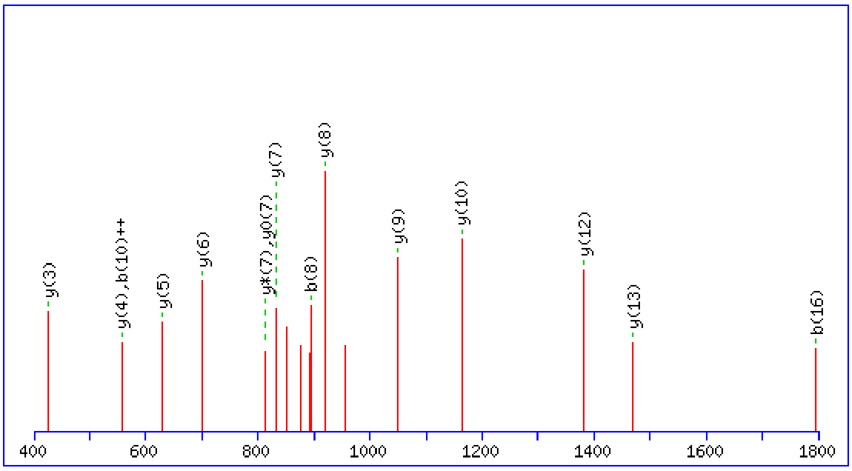
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEDLSSQIQSQAAEQFK**
Found in **AT3G12390.1** in **TAIR_Arabidopsis**, Symbols: | nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative | chr3:3942351-3943602 FORWARD

Match to Query 9301: 1942.881732 from(972.448142,2+) index(7341)
Title: Elution from: 66.010 to 66.010 scan no 9567 cid35.00 polarity:+
Data file D6h-2_1.mgf

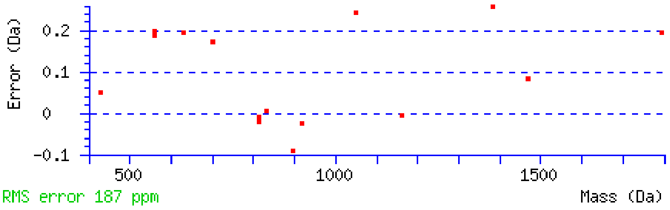
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

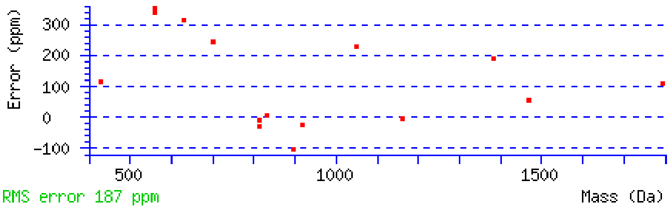


Monoisotopic mass of neutral peptide Mr(calc): 1942.8776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 99 **Expect:** 1.3e-009
Matches : 15/172 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					**I**							**17**
2	245.1280	123.0676			227.1174	114.0624	**E**	1829.8038	915.4056	1811.7802	906.3938	1811.7933	906.4003	**16**
3	361.1520	181.0796			343.1414	172.0743	**D**	1699.7642	850.3857	1681.7406	841.3739	1681.7536	841.3805	**15**
4	475.2331	238.1202			457.2225	229.1149	**L**	1583.7402	792.3738	1565.7166	783.3620	1565.7297	783.3685	**14**
5	563.2621	282.1347			545.2516	273.1294	**S**	***1469.6591***	735.3332	1451.6355	726.3214	1451.6486	726.3279	**13**
6	651.2912	326.1492			633.2806	317.1440	**S**	***1381.6301***	691.3187	1363.6065	682.3069	1363.6195	682.3134	**12**
7	781.3439	391.1756	763.3203	382.1638	763.3333	382.1703	**Q**	1293.6010	647.3041	1275.5774	638.2923	1275.5904	638.2989	**11**
8	**895.4250**	448.2161	877.4014	439.2043	877.4144	439.2108	**I**	***1163.5484***	582.2778	1145.5248	573.2660	1145.5378	573.2725	**10**
9	1025.4776	513.2424	1007.4540	504.2306	1007.4670	504.2372	**Q**	***1049.4673***	525.2373	1031.4437	516.2255	1031.4567	516.2320	**9**
10	1113.5067	557.2570	1095.4831	548.2452	1095.4961	548.2517	**S**	***919.4146***	460.2109	901.3910	451.1991	901.4040	451.2057	**8**
11	1243.5593	622.2833	1225.5357	613.2715	1225.5487	613.2780	**Q**	***831.3855***	416.1964	813.3620	407.1846	813.3750	407.1911	**7**
12	1315.5935	658.3004	1297.5699	649.2886	1297.5829	649.2951	**A**	***701.3329***	351.1701	683.3093	342.1583	683.3223	342.1648	**6**
13	1387.6276	694.3174	1369.6040	685.3056	1369.6170	685.3122	**A**	***629.2987***	315.1530	611.2752	306.1412	611.2882	306.1477	**5**
14	1517.6672	759.3373	1499.6437	750.3255	1499.6567	750.3320	**E**	***557.2646***	279.1359	539.2410	270.1241	539.2540	270.1307	**4**
15	1647.7199	824.3636	1629.6963	815.3518	1629.7093	815.3583	**Q**	***427.2250***	214.1161	409.2014	205.1043			**3**
16	**1795.7853**	898.3963	1777.7617	889.3845	1777.7748	889.3910	**F**	297.1723	149.0898	279.1487	140.0780			**2**
17							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT3G12390.1





NCBI **BLAST** search of IEDLSSQIQSQAAEQFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
98.7	1942.8776	0.0041	IEDLSSQIQSQAAEQFK
98.7	1942.8776	0.0041	IEDLSSQLQSQAAEQFK
3.1	1942.8778	0.0039	ARWARDALQLWEEMK
0.6	1942.8774	0.0044	RIYECYTWKIYAEK

Mascot: http://www.matrixscience.com/

AT3G12490.1

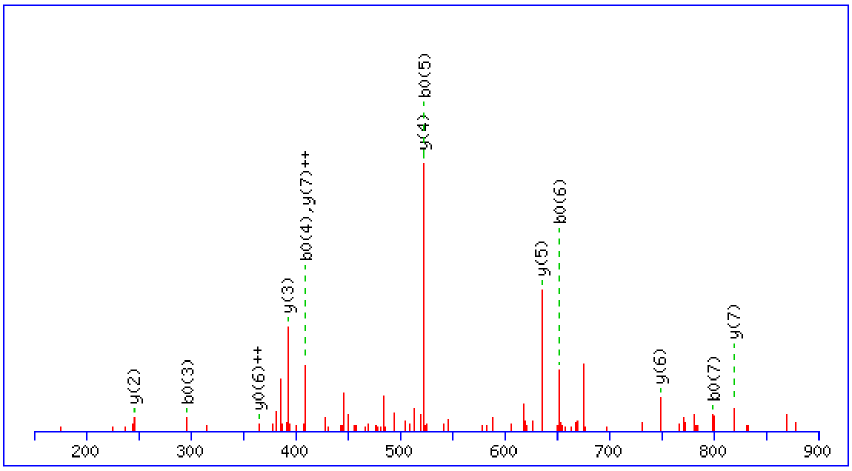
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENALLEFAR**
Found in **AT3G12490.1** in **TAIR_Arabidopsis**, Symbols: | cysteine protease inhibitor, putative / cystatin, putative | chr3:3960530-3961784 REVERSE

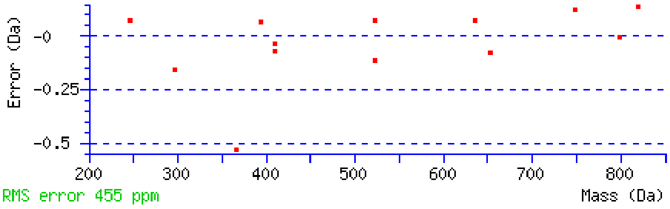
Match to Query 3117: 1061.549960 from(531.782256,2+) index(6293)
Title: Elution from: 54.475 to 54.475 scan no 8062 cid35.00 polarity:+
Data file D1d-3_3.mgf

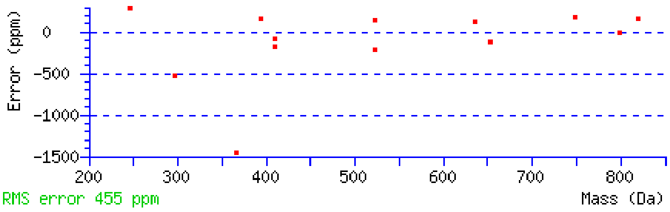
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1061.5505
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00032
Matches : 13/88 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	N	933.5152	467.2613	916.4887	458.7480	915.5047	458.2560	8
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	A	***819.4723***	410.2398	802.4458	401.7265	801.4617	401.2345	7
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	L	***748.4352***	374.7212	731.4087	366.2080	730.4246	365.7160	6
5	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	L	***635.3511***	318.1792	618.3246	309.6659	617.3406	309.1739	5
6	670.3406	335.6740	653.3141	327.1607	652.3301	326.6687	E	***522.2671***	261.6372	505.2405	253.1239	504.2565	252.6319	4
7	817.4090	409.2082	800.3825	400.6949	799.3985	400.2029	F	***393.2245***	197.1159	376.1979	188.6026			3
8	888.4462	444.7267	871.4196	436.2134	870.4356	435.7214	A	***246.1561***	123.5817	229.1295	115.0684			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ENALLEFAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G12490.1

40.5	1061.5505	-0.0006	ENALLEFAR
1.6	1061.5506	-0.0006	FPEISTNVR
1.3	1061.5505	-0.0006	KDAHTSIYK
0.9	1061.5505	-0.0006	LFDAAVEAAR

AT3G12780.1

Mascot Search Results

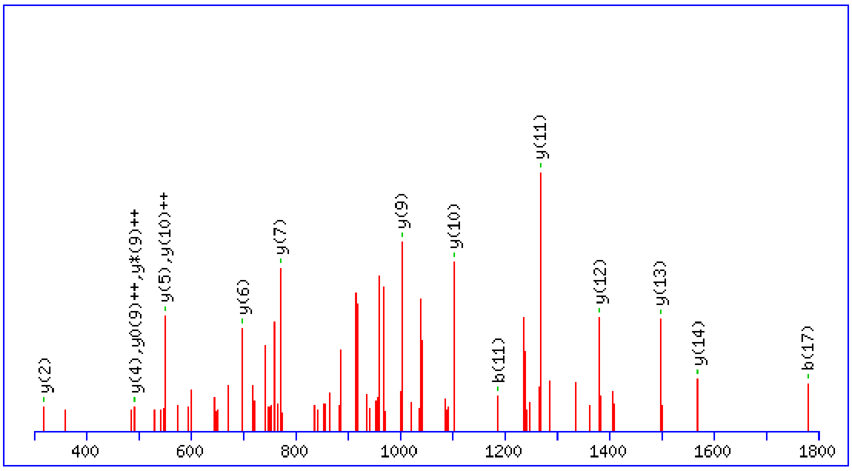
Peptide View

MS/MS Fragmentation of **LASLADLYVNDAFGTAHR**
Found in **AT3G12780.1** in **TAIR_Arabidopsis**, Symbols: PGK1 | PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase | chr3:4061134-4063147 REVERSE

Match to Query 9211: 1956.894112 from(979.454332,2+) index(8723)
Title: Elution from: 77.089 to 77.089 scan no 11629 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

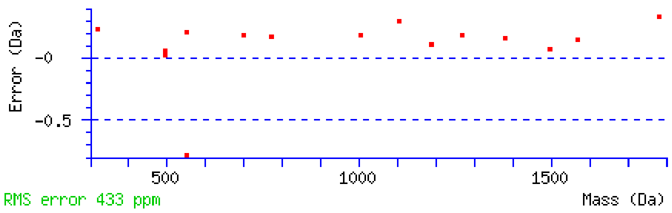
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

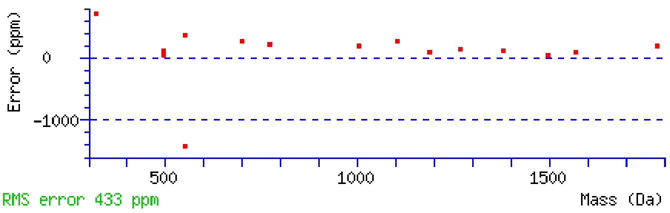


Monoisotopic mass of neutral peptide Mr(calc): 1956.8982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 107 **Expect:** 1.5e-010
Matches : 16/176 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							18
2	187.1225	94.0649					A	1843.8244	922.4158	1825.8008	913.4040	1825.8138	913.4106	17
3	275.1516	138.0794			257.1410	129.0741	S	1771.7902	886.3988	1753.7667	877.3870	1753.7797	877.3935	16
4	389.2327	195.1200			371.2221	186.1147	L	1683.7612	842.3842	1665.7376	833.3724	1665.7506	833.3789	15
5	461.2668	231.1371			443.2563	222.1318	A	***1569.6801***	785.3437	1551.6565	776.3319	1551.6695	776.3384	14
6	577.2908	289.1490			559.2802	280.1438	D	***1497.6459***	749.3266	1479.6223	740.3148	1479.6354	740.3213	13
7	691.3719	346.1896			673.3613	337.1843	L	***1381.6220***	691.3146	1363.5984	682.3028	1363.6114	682.3093	12
8	855.4323	428.2198			837.4217	419.2145	Y	***1267.5409***	634.2741	1249.5173	625.2623	1249.5303	625.2688	11
9	955.4977	478.2525			937.4872	469.2472	V	***1103.4805***	552.2439	1085.4569	543.2321	1085.4699	543.2386	10
10	1071.5347	536.2710	1053.5111	527.2592	1053.5242	527.2657	N	***1003.4150***	502.2112	985.3915	493.1994	985.4045	493.2059	9
11	**1187.5587**	594.2830	1169.5351	585.2712	1169.5481	585.2777	D	887.3780	444.1927	869.3545	435.1809	869.3675	435.1874	8
12	1259.5928	630.3001	1241.5693	621.2883	1241.5823	621.2948	A	***771.3541***	386.1807	753.3305	377.1689	753.3435	377.1754	7
13	1407.6583	704.3328	1389.6347	695.3210	1389.6477	695.3275	F	***699.3199***	350.1636	681.2963	341.1518	681.3094	341.1583	6
14	1465.6768	733.3420	1447.6532	724.3302	1447.6662	724.3368	G	***551.2545***	276.1309	533.2309	267.1191	533.2439	267.1256	5
15	1567.7215	784.3644	1549.6979	775.3526	1549.7109	775.3591	T	***493.2360***	247.1216	475.2124	238.1098	475.2254	238.1163	4
16	1639.7557	820.3815	1621.7321	811.3697	1621.7451	811.3762	A	391.1913	196.0993	373.1677	187.0875			3
17	**1779.8057**	890.4065	1761.7821	881.3947	1761.7951	881.4012	H	***319.1571***	160.0822	301.1335	151.0704			2
18							R	179.1071	90.0572	161.0835	81.0454			1

AT3G12780.1





NCBI **BLAST** search of LASLADLYVNDAFGTAHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
107.3	1956.8982	-0.0041	LASLADLYVNDAFGTAHR
4.9	1956.8987	-0.0046	PSESSYKVHRPAKSGGSR

Mascot: http://www.matrixscience.com/

AT3G13120.1

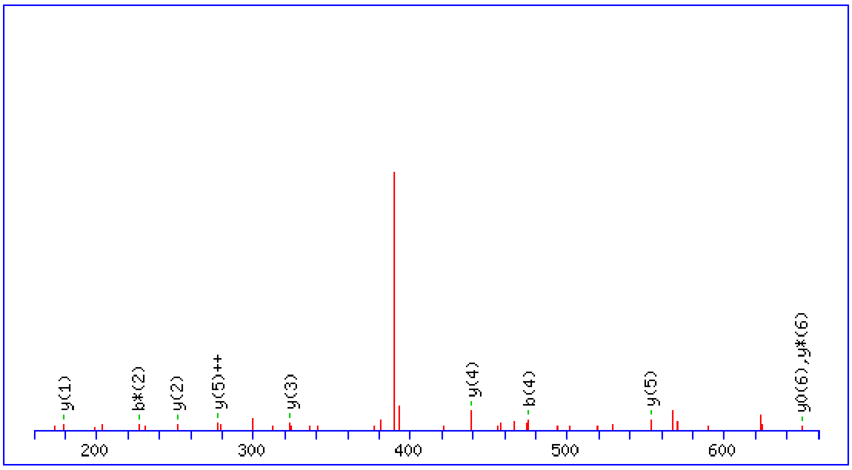
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QILDAAR**
Found in **AT3G13120.1** in **TAIR_Arabidopsis**, Symbols: | 30S ribosomal protein S10, chloroplast, putative | chr3:4220317-4221533 REVERSE

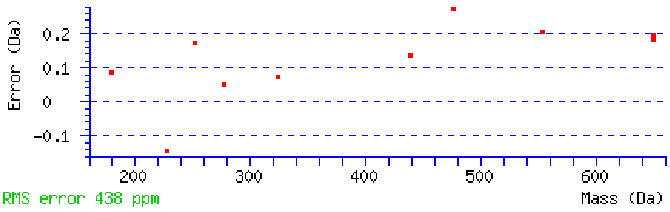
Match to Query 999: 796.405428 from(399.209990,2+) index(1181)
Title: Elution from: 17.893 to 17.893 scan no 1648 cid35.00 polarity:+
Data file D6h-3_1.mgf

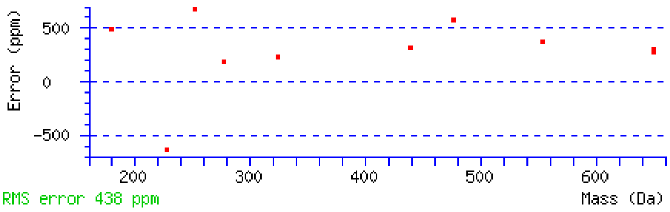
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 796.4069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.031
Matches : 10/60 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							7
2	245.1410	123.0741	227.1174	114.0624			I	667.3616	334.1844	649.3380	325.1726	649.3510	325.1791	6
3	359.2221	180.1147	341.1985	171.1029			L	***553.2805***	277.1439	535.2569	268.1321	535.2699	268.1386	5
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	D	***439.1994***	220.1033	421.1758	211.0915	421.1888	211.0980	4
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	A	***323.1754***	162.0913	305.1518	153.0795			3
6	619.3144	310.1608	601.2908	301.1490	601.3038	301.1556	A	***251.1412***	126.0743	233.1177	117.0625			2
7							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of QILDAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.9	796.4069	-0.0015	QILDAAR
13.7	796.4069	-0.0015	LDIQAAR
13.7	796.4069	-0.0015	NLIEAAR

AT3G13120.1

13.6	796.4069	-0.0015	ALVADAAR
12.6	796.4043	0.0012	ELLNTSL
12.6	796.4043	0.0012	DILEATK
10.8	796.4069	-0.0015	EIGSKPR
10.8	796.4069	-0.0015	KLDTGPR
9.8	796.4069	-0.0015	STLNPVR
9.7	796.4069	-0.0015	SKLADPR

AT3G13330.1

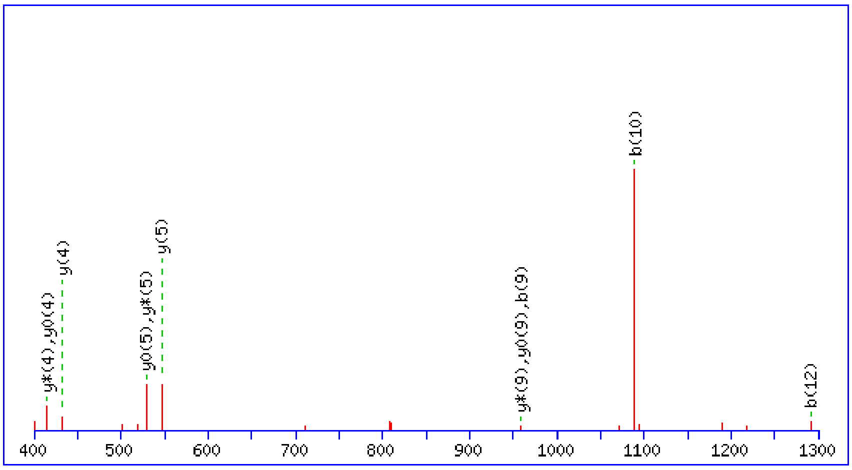
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAFLSAALIELSPPK**
Found in **AT3G13330.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr3:4319811-4330068 REVERSE

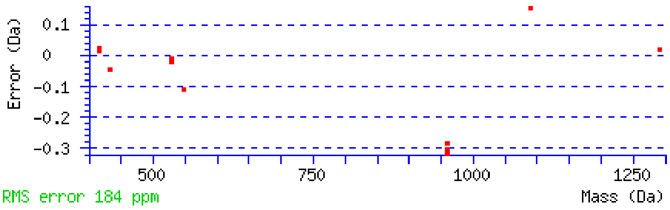
Match to Query 7422: 1634.846500 from(818.430526,2+) index(7966)
Title: Elution from: 71.416 to 71.416 scan no 10443 cid35.00 polarity:+
Data file D6h-2_2.mgf

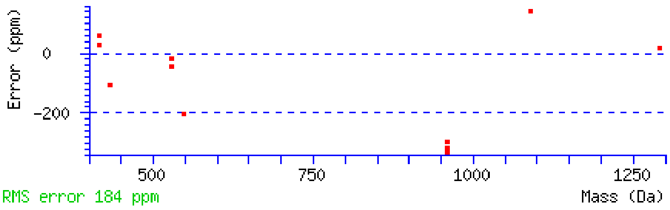
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1634.8496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.045
Matches : 11/126 fragment ions using 13 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	165.0676	83.0375			Y							15
2	237.1018	119.0545			A	1471.7965	736.4019	1453.7729	727.3901	1453.7860	727.3966	14
3	385.1672	193.0873			F	1399.7624	700.3848	1381.7388	691.3730	1381.7518	691.3795	13
4	499.2483	250.1278			L	1251.6969	626.3521	1233.6733	617.3403	1233.6864	617.3468	12
5	587.2774	294.1423	569.2668	285.1371	S	1137.6158	569.3115	1119.5922	560.2998	1119.6053	560.3063	11
6	659.3115	330.1594	641.3010	321.1541	A	1049.5868	525.2970	1031.5632	516.2852	1031.5762	516.2917	10
7	731.3457	366.1765	713.3351	357.1712	A	977.5526	489.2799	959.5290	480.2682	959.5420	480.2747	9
8	845.4268	423.2170	827.4162	414.2118	L	905.5185	453.2629	887.4949	444.2511	887.5079	444.2576	8
9	***959.5079***	480.2576	941.4973	471.2523	I	791.4374	396.2223	773.4138	387.2105	773.4268	387.2170	7
10	***1089.5475***	545.2774	1071.5370	536.2721	E	677.3563	339.1818	659.3327	330.1700	659.3457	330.1765	6
11	1203.6286	602.3179	1185.6181	593.3127	L	***547.3166***	274.1620	529.2930	265.1502	529.3061	265.1567	5
12	***1291.6577***	646.3325	1273.6471	637.3272	S	***433.2355***	217.1214	415.2120	208.1096	415.2250	208.1161	4
13	1389.7075	695.3574	1371.6969	686.3521	P	345.2065	173.1069	327.1829	164.0951			3
14	1487.7573	744.3823	1469.7467	735.3770	P	247.1567	124.0820	229.1331	115.0702			2
15					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YAFLSAALIELSPPK

AT3G13330.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.1	1634.8496	-0.0031	YAFLSAALIELSPPK
17.2	1634.8474	-0.0009	IDITVPTGAQIIYSK
4.3	1634.8453	0.0012	IIEWMELQKRIR

AT3G13470.1

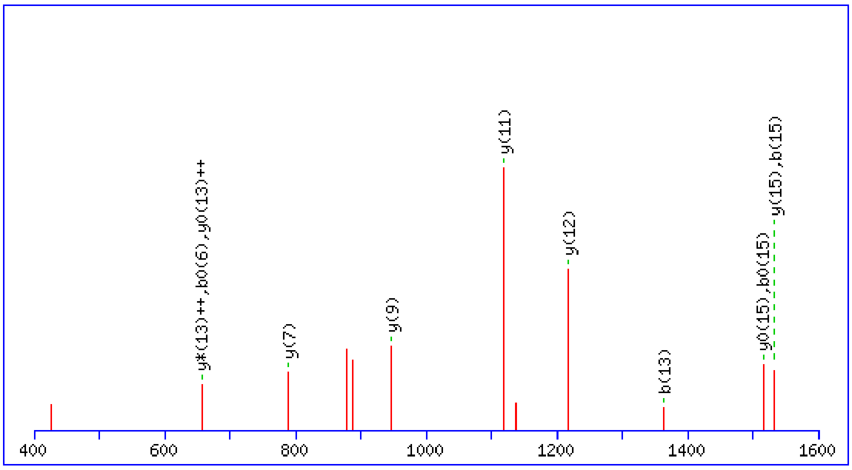
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EMTTIVGDGTTQEAVNK**
Found in **AT3G13470.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr3:4389692-4392631 FORWARD

Match to Query 8458: 1792.850062 from(897.432307,2+) index(3260)
Title: Elution from: 35.164 to 35.164 scan no 4188 cid35.00 polarity:+
Data file D1d-1_1.mgf

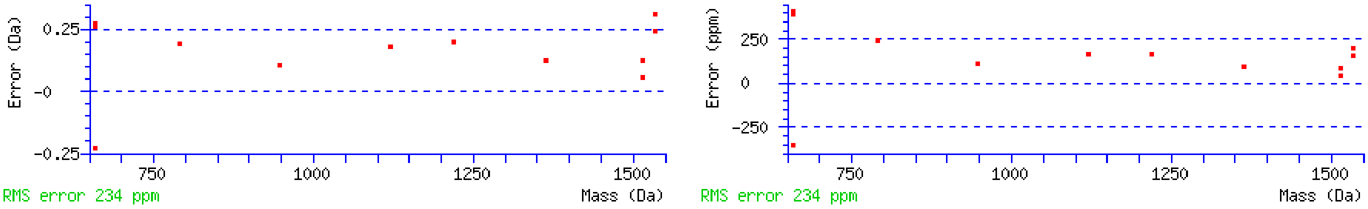
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1792.8513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00029
Matches : 12/162 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	261.0904	131.0488			243.0798	122.0435	M	1664.8160	832.9116	1647.7894	824.3984	1646.8054	823.9063	16
3	362.1380	181.5727			344.1275	172.5674	T	***1533.7755***	767.3914	1516.7489	758.8781	1515.7649	758.3861	15
4	463.1857	232.0965			445.1751	223.0912	T	1432.7278	716.8675	1415.7013	708.3543	1414.7173	707.8623	14
5	576.2698	288.6385			558.2592	279.6332	I	1331.6801	666.3437	1314.6536	657.8304	1313.6696	657.3384	13
6	675.3382	338.1727			657.3276	329.1675	V	***1218.5961***	609.8017	1201.5695	601.2884	1200.5855	600.7964	12
7	732.3597	366.6835			714.3491	357.6782	G	***1119.5277***	560.2675	1102.5011	551.7542	1101.5171	551.2622	11
8	847.3866	424.1969			829.3760	415.1917	D	1062.5062	531.7567	1045.4796	523.2435	1044.4956	522.7515	10
9	904.4081	452.7077			886.3975	443.7024	G	***947.4793***	474.2433	930.4527	465.7300	929.4687	465.2380	9
10	1005.4557	503.2315			987.4452	494.2262	T	890.4578	445.7325	873.4312	437.2193	872.4472	436.7272	8
11	1106.5034	553.7553			1088.4929	544.7501	T	***789.4101***	395.2087	772.3836	386.6954	771.3995	386.2034	7
12	1234.5620	617.7846	1217.5354	609.2714	1216.5514	608.7794	Q	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	6
13	**1363.6046**	682.3059	1346.5780	673.7927	1345.5940	673.3007	E	560.3039	280.6556	543.2773	272.1423	542.2933	271.6503	5
14	1434.6417	717.8245	1417.6152	709.3112	1416.6311	708.8192	A	431.2613	216.1343	414.2347	207.6210			4
15	**1533.7101**	767.3587	1516.6836	758.8454	1515.6996	758.3534	V	360.2241	180.6157	343.1976	172.1024			3
16	1647.7530	824.3802	1630.7265	815.8669	1629.7425	815.3749	N	261.1557	131.0815	244.1292	122.5682			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT3G13470.1



NCBI **BLAST** search of EMTTIVGDGTTQEAVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.1	1792.8513	-0.0012	EMTTIVGDGTTQEAVNK
2.4	1792.8488	0.0013	MATTLSRDQYVYMAK

Mascot: http://www.matrixscience.com/

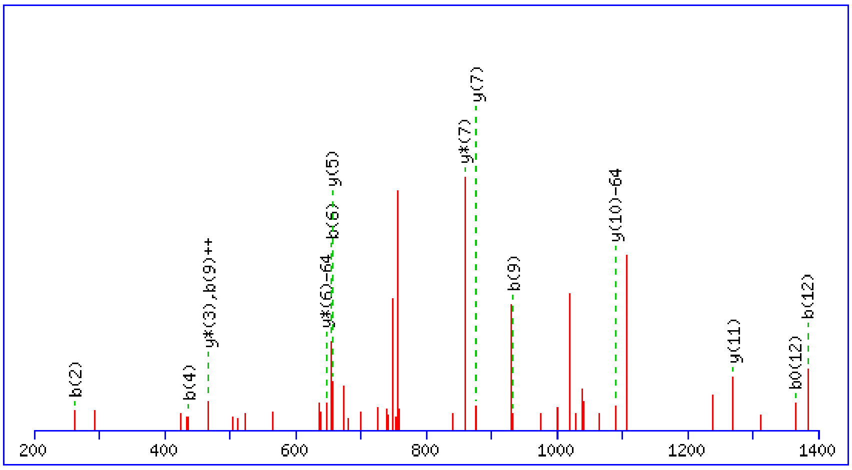
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEDGDTFAGLMWK**
Found in **AT3G13840.1** in **TAIR_Arabidopsis**, Symbols: | scarecrow transcription factor family protein | chr3:4555312-4556844 REVERSE

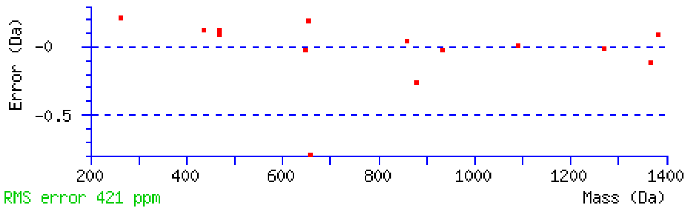
Match to Query 6686: 1530.594766 from(766.304659,2+) index(2188)
Title: Elution from: 25.858 to 25.858 scan no 2848 cid35.00 polarity:+
Data file 0-3_1.mgf

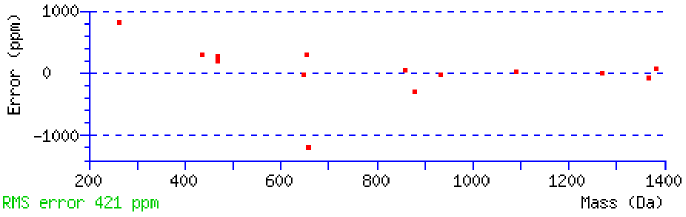
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1530.5929
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 18 **Expect:** 0.036
Matches : 14/162 fragment ions using 31 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	133.0448	67.0260			M							13
2	***263.0844***	132.0458	245.0739	123.0406	E	1399.5627	700.2850	1381.5391	691.2732	1381.5521	691.2797	12
3	379.1084	190.0578	361.0978	181.0526	D	**1269.5231**	635.2652	1251.4995	626.2534	1251.5125	626.2599	11
4	***437.1269***	219.0671	419.1163	210.0618	G	1153.4991	577.2532	1135.4755	568.2414	1135.4885	568.2479	10
5	553.1509	277.0791	535.1403	268.0738	D	1095.4806	548.2439	1077.4570	539.2321	1077.4700	539.2386	9
6	***655.1956***	328.1014	637.1850	319.0962	T	979.4566	490.2319	961.4330	481.2201	961.4460	481.2267	8
7	803.2610	402.1342	785.2505	393.1289	F	**877.4119**	439.2096	859.3883	430.1978			7
8	875.2952	438.1512	857.2846	429.1460	A	729.3464	365.1769	711.3229	356.1651			6
9	***933.3137***	467.1605	915.3031	458.1552	G	**657.3123**	329.1598	639.2887	320.1480			5
10	1047.3948	524.2010	1029.3842	515.1957	L	599.2938	300.1505	581.2702	291.1387			4
11	1195.4272	598.2172	1177.4167	589.2120	M	485.2127	243.1100	467.1891	234.0982			3
12	***1383.5006***	692.2539	1365.4900	683.2487	W	337.1803	169.0938	319.1567	160.0820			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MEDGDTFAGLMWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G13840.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.4	1530.5929	0.0019	MEDGDTFAGLMWK
8.6	1530.5929	0.0019	ECFLDMGAFPEGK
1.7	1530.5941	0.0007	SIMNADQMGMIEK
1.4	1530.5932	0.0016	EDATSGSTEEKSMK

AT3G13920.1

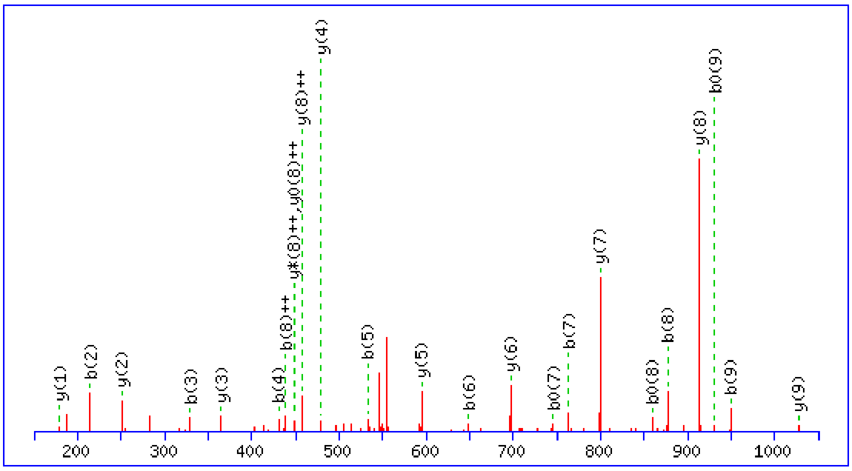
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLITTDLLAR**
Found in **AT3G13920.1** in **TAIR_Arabidopsis**, Symbols: RH4, TIF4A1, EIF4A1 | EIF4A1 (eukaryotic translation initiation factor 4A-1); ATP-dependent helicase | chr3:4592642-4594135 REVERSE

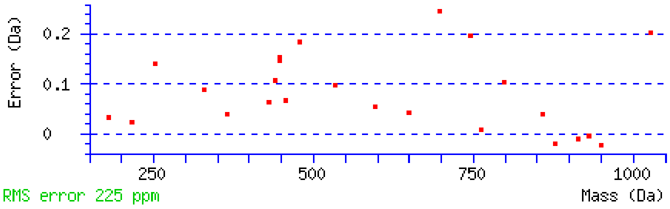
Match to Query 3091: 1126.635826 from(564.325189,2+) index(6765)
Title: Elution from: 62.555 to 62.555 scan no 8847 cid35.00 polarity:+
Data file D12h-2_2.mgf

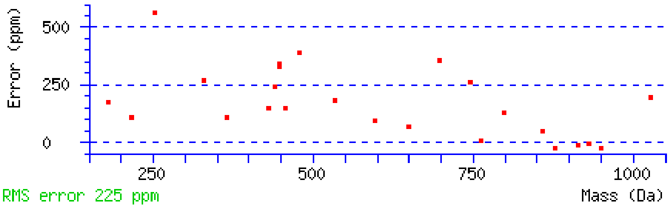
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1126.6372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 4.8e-008
Matches : 24/76 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400			V							10
2	**215.1538**	108.0805			L	***1027.5790***	514.2932	1009.5555	505.2814	1009.5685	505.2879	9
3	**329.2349**	165.1211			I	***913.4979***	457.2526	895.4744	448.2408	895.4874	448.2473	8
4	**431.2796**	216.1435	413.2691	207.1382	T	***799.4168***	400.2121	781.3933	391.2003	781.4063	391.2068	7
5	**533.3243**	267.1658	515.3138	258.1605	T	***697.3721***	349.1897	679.3485	340.1779	679.3616	340.1844	6
6	**649.3483**	325.1778	631.3378	316.1725	D	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	5
7	**763.4294**	382.2184	745.4189	373.2131	L	***479.3034***	240.1554	461.2799	231.1436			4
8	**877.5105**	439.2589	859.5000	430.2536	L	***365.2223***	183.1148	347.1988	174.1030			3
9	**949.5447**	475.2760	931.5341	466.2707	A	***251.1412***	126.0743	233.1177	117.0625			2
10					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VLITTDLLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G13920.1

Score	Mr(calc)	Delta	Sequence
77.8	1126.6372	-0.0014	VLITTDLLAR
2.1	1126.6372	-0.0014	VIAEAKKLDK
2.1	1126.6372	-0.0014	VLKKADEALK

AT3G13920.3

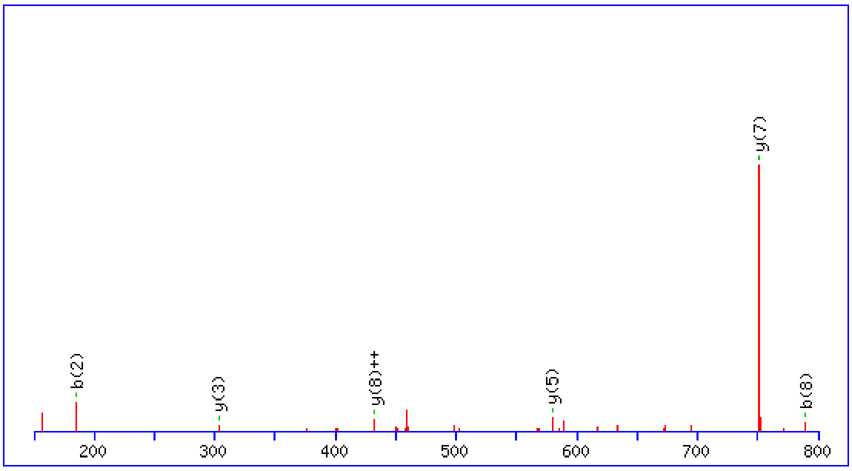
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGDYLGVK**
Found in **AT3G13920.3** in **TAIR_Arabidopsis**, Symbols: RH4, TIF4A1, EIF4A1 | EIF4A1 (eukaryotic translation initiation factor 4A-1) | chr3:4592642-4594101 REVERSE

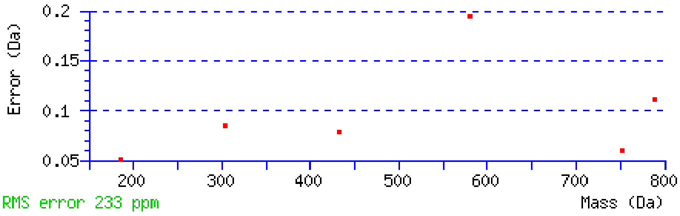
Match to Query 1880: 934.512690 from(468.263621,2+) index(5081)
Title: Elution from: 45.435 to 45.435 scan no 6482 cid35.00 polarity:+
Data file D12h-3_3.mgf

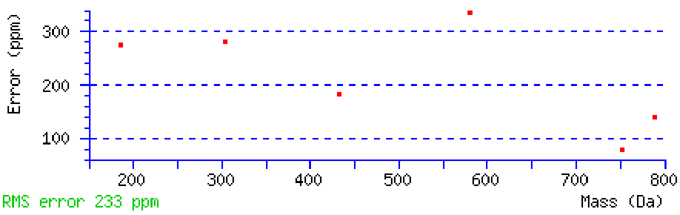
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 934.5124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.011
Matches : 6/64 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							9
2	***185.1285***	93.0679			L	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	8
3	242.1499	121.5786			G	***751.3985***	376.2029	734.3719	367.6896	733.3879	367.1976	7
4	357.1769	179.0921	339.1663	170.0868	D	694.3770	347.6921	677.3505	339.1789	676.3665	338.6869	6
5	520.2402	260.6237	502.2296	251.6185	Y	***579.3501***	290.1787	562.3235	281.6654			5
6	633.3243	317.1658	615.3137	308.1605	L	416.2867	208.6470	399.2602	200.1337			4
7	690.3457	345.6765	672.3352	336.6712	G	***303.2027***	152.1050	286.1761	143.5917			3
8	***789.4141***	395.2107	771.4036	386.2054	V	246.1812	123.5942	229.1547	115.0810			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ALGDYLGVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G13920.3

26.6	934.5124	0.0003	ALGDYLGVK
16.2	934.5123	0.0003	ALYEALQK
5.5	934.5124	0.0003	AIEIFTNK
5.4	934.5124	0.0003	LASSFSPVK
5.4	934.5124	0.0003	SPSVGFITK
2.7	934.5124	0.0003	AFLDVSGVK
2.3	934.5124	0.0003	ATAELFGVK

AT3G13930.1

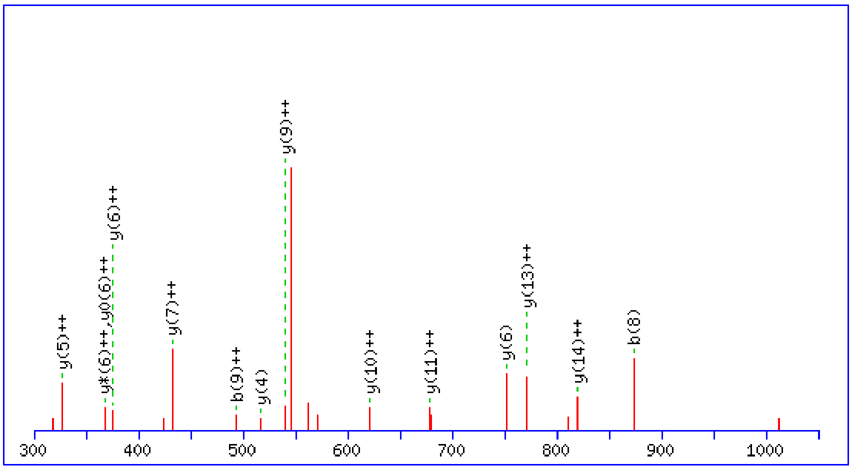
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPALDYVDIPHTQIR**
Found in **AT3G13930.1** in **TAIR_Arabidopsis**, Symbols: | dihydrolipoamide S-acetyltransferase, putative | chr3:4596247-4600150 FORWARD

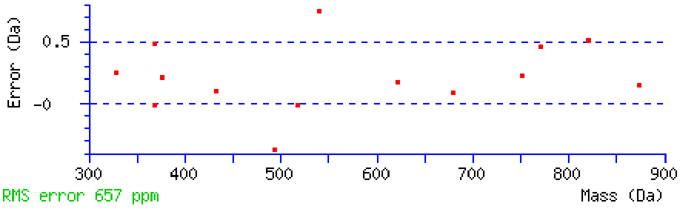
Match to Query 8253: 1735.925178 from(579.649002,3+) index(6765)
Title: Elution from: 60.059 to 60.059 scan no 8776 cid35.00 polarity:+
Data file 0-2_2.mgf

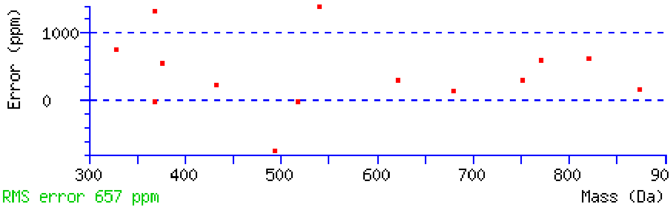
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1735.9257
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.3e-005
Matches : 14/130 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							15
2	197.1285	99.0679					P	1637.8646	819.4359	1620.8380	810.9227	1619.8540	810.4306	14
3	268.1656	134.5864					A	1540.8118	770.9095	1523.7853	762.3963	1522.8013	761.9043	13
4	381.2496	191.1285					L	1469.7747	735.3910	1452.7482	726.8777	1451.7641	726.3857	12
5	496.2766	248.6419			478.2660	239.6366	D	1356.6906	678.8490	1339.6641	670.3357	1338.6801	669.8437	11
6	659.3399	330.1736			641.3293	321.1683	Y	1241.6637	621.3355	1224.6371	612.8222	1223.6531	612.3302	10
7	758.4083	379.7078			740.3978	370.7025	V	1078.6004	539.8038	1061.5738	531.2905	1060.5898	530.7985	9
8	873.4353	437.2213			855.4247	428.2160	D	979.5320	490.2696	962.5054	481.7563	961.5214	481.2643	8
9	986.5193	493.7633			968.5088	484.7580	I	864.5050	432.7561	847.4785	424.2429	846.4944	423.7509	7
10	1083.5721	542.2897			1065.5615	533.2844	P	**751.4209**	376.2141	734.3944	367.7008	733.4104	367.2088	6
11	1220.6310	610.8191			1202.6204	601.8139	H	654.3682	327.6877	637.3416	319.1745	636.3576	318.6824	5
12	1321.6787	661.3430			1303.6681	652.3377	T	**517.3093**	259.1583	500.2827	250.6450	499.2987	250.1530	4
13	1449.7373	725.3723	1432.7107	716.8590	1431.7267	716.3670	Q	416.2616	208.6344	399.2350	200.1212			3
14	1562.8213	781.9143	1545.7948	773.4010	1544.8108	772.9090	I	288.2030	144.6051	271.1765	136.0919			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VPALDYVDIPHTQIR

AT3G13930.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.9	1735.9257	-0.0005	VPALDYVDIPHTQIR
10.4	1735.9291	-0.0039	SMKARDVISWTSIVK
2.2	1735.9217	0.0035	ARTEYLEASIGVSGRK

Mascot: http://www.matrixscience.com/

AT3G14067.1

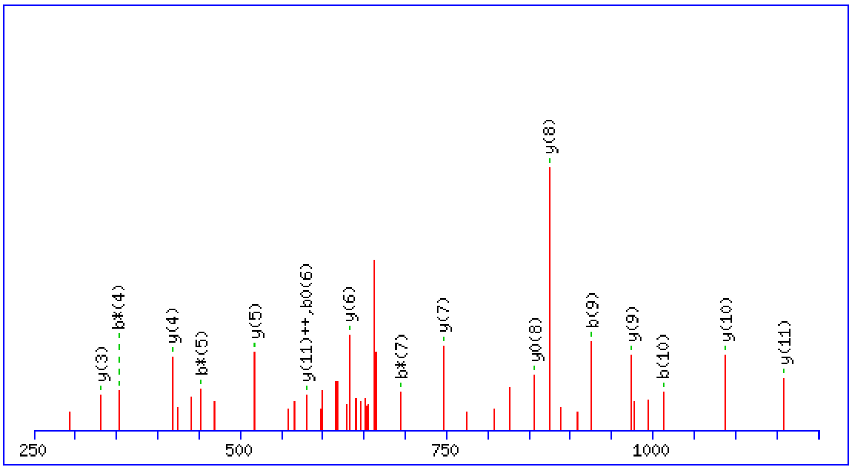
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPANVEIDVSPSK**
Found in **AT3G14067.1** in **TAIR_Arabidopsis**, Symbols: | subtilase family protein | chr3:4658428-4660761 REVERSE

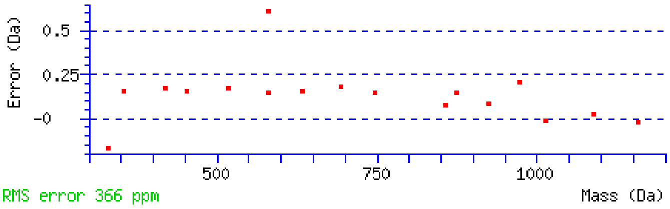
Match to Query 4849: 1341.675664 from(671.845108,2+) index(2969)
Title: Elution from: 32.152 to 32.152 scan no 3794 cid35.00 polarity:+
Data file D1d-2_1.mgf

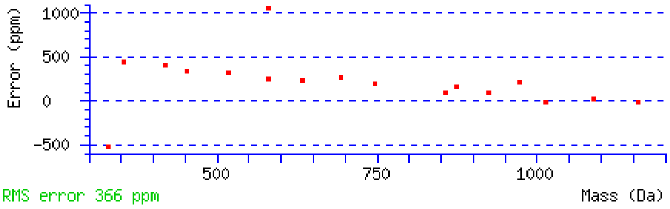
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1341.6776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 3.3e-010
Matches : 17/136 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	185.0921	93.0497			167.0815	84.0444	P	1255.6529	628.3301	1238.6263	619.8168	1237.6423	619.3248	12
3	256.1292	128.5682			238.1186	119.5629	A	***1158.6001***	579.8037	1141.5735	571.2904	1140.5895	570.7984	11
4	370.1721	185.5897	353.1456	177.0764	352.1615	176.5844	N	***1087.5630***	544.2851	1070.5364	535.7719	1069.5524	535.2798	10
5	469.2405	235.1239	452.2140	226.6106	451.2300	226.1186	V	***973.5201***	487.2637	956.4935	478.7504	955.5095	478.2584	9
6	598.2831	299.6452	581.2566	291.1319	580.2726	290.6399	E	***874.4516***	437.7295	857.4251	429.2162	856.4411	428.7242	8
7	711.3672	356.1872	694.3406	347.6740	693.3566	347.1819	I	***745.4090***	373.2082	728.3825	364.6949	727.3985	364.2029	7
8	826.3941	413.7007	809.3676	405.1874	808.3836	404.6954	D	***632.3250***	316.6661	615.2984	308.1529	614.3144	307.6608	6
9	**925.4625**	463.2349	908.4360	454.7216	907.4520	454.2296	V	***517.2980***	259.1527	500.2715	250.6394	499.2875	250.1474	5
10	**1012.4946**	506.7509	995.4680	498.2376	994.4840	497.7456	S	***418.2296***	209.6185	401.2031	201.1052	400.2191	200.6132	4
11	1109.5473	555.2773	1092.5208	546.7640	1091.5368	546.2720	P	***331.1976***	166.1024	314.1710	157.5892	313.1870	157.0972	3
12	1196.5794	598.7933	1179.5528	590.2800	1178.5688	589.7880	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SPANVEIDVSPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G14067.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
99.9	1341.6776	-0.0019	SPANVEIDVSPSK

Mascot: http://www.matrixscience.com/

AT3G14090.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSAMEAIFK**
Found in **AT3G14090.1** in **TAIR_Arabidopsis**, Symbols: ATEXO70D3 | ATEXO70D3 (exocyst subunit EXO70 family protein D3); protein binding | chr3:4669515-4671386 REVERSE

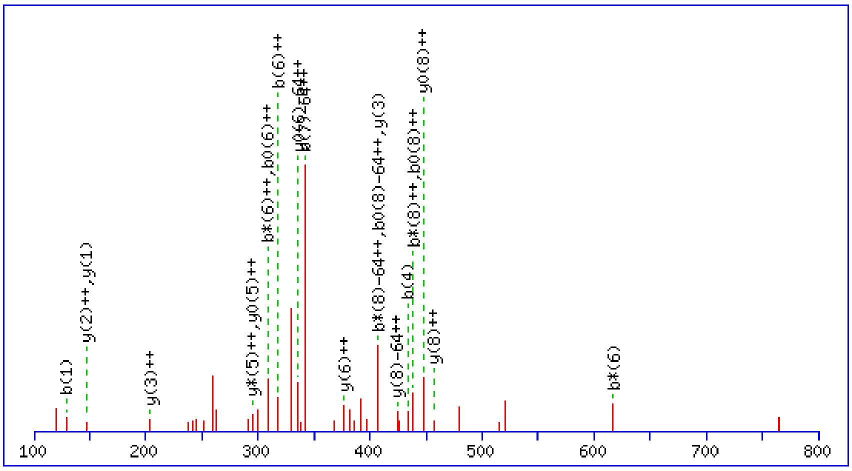
Match to Query 2696: 1039.535241 from(347.519023,3+) index(2168)
Title: Elution from: 24.128 to 24.128 scan no 2739 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

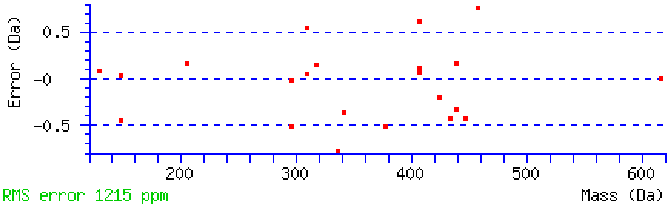
Label all possible matches ○ Label matches used for scoring ●

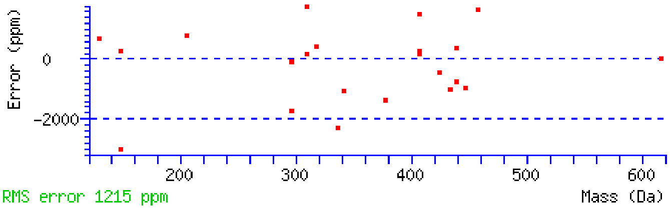
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1039.5372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.015
Matches : 23/134 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**129.1022**	65.0548	112.0757	56.5415			K							9
2	216.1343	108.5708	199.1077	100.0575	198.1237	99.5655	S	912.4495	456.7284	895.4230	448.2151	894.4390	447.7231	8
3	287.1714	144.0893	270.1448	135.5761	269.1608	135.0840	A	825.4175	413.2124	808.3910	404.6991	807.4069	404.2071	7
4	**434.2068**	217.6070	417.1802	209.0938	416.1962	208.6017	M	754.3804	377.6938	737.3538	369.1806	736.3698	368.6885	6
5	563.2494	282.1283	546.2228	273.6151	545.2388	273.1230	E	607.3450	304.1761	590.3184	295.6629	589.3344	295.1708	5
6	634.2865	**317.6469**	617.2599	309.1336	616.2759	308.6416	A	478.3024	239.6548	461.2758	231.1416			4
7	747.3706	374.1889	730.3440	365.6756	729.3600	365.1836	I	**407.2653**	204.1363	390.2387	195.6230			3
8	894.4390	**447.7231**	877.4124	439.2098	876.4284	438.7178	F	294.1812	147.5942	277.1547	139.0810			2
9							K	**147.1128**	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KSAMEAIFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14090.1

Score	Mr(calc)	Delta	Sequence
22.8	1039.5372	-0.0019	KSAMEAIFK
19.3	1039.5372	-0.0019	KIVEMYNK
17.6	1039.5338	0.0014	FKDENFIK
13.7	1039.5338	0.0014	STFPSLNFK
11.3	1039.5338	0.0014	YIFDKNQL
10.3	1039.5372	-0.0020	SALSYLCVK
5.5	1039.5372	-0.0020	LDLKYCTK
5.4	1039.5338	0.0014	FDLQNYLK
4.6	1039.5372	-0.0019	KTFEEMKK
3.1	1039.5372	-0.0020	METLQKFK

AT3G14210.1

Mascot Search Results

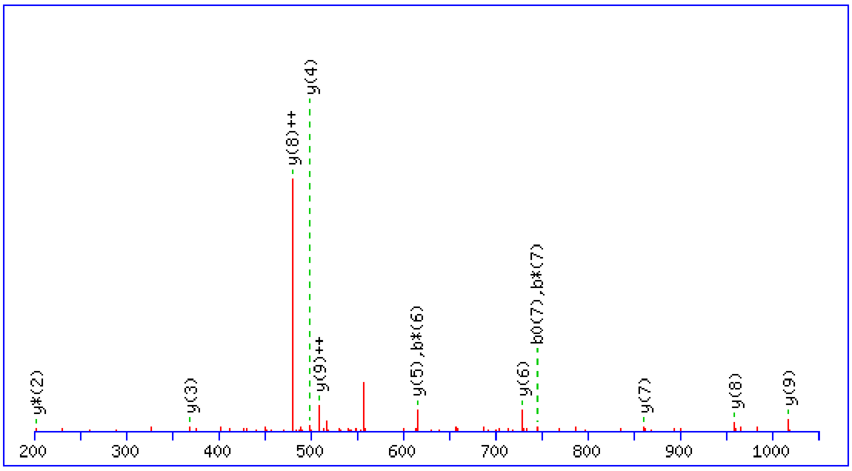
Peptide View

MS/MS Fragmentation of **IGPMLNEFAK**
Found in **AT3G14210.1** in **TAIR_Arabidopsis**, Symbols: ESM1 | ESM1 (EPITHIOSPECIFIER MODIFIER 1); carboxylesterase | chr3:4729893-4731569 FORWARD

Match to Query 3865: 1130.542720 from(566.278636,2+) index(6215)
Title: Elution from: 54.344 to 54.344 scan no 7746 cid35.00 polarity:+
Data file 0-1_1.mgf

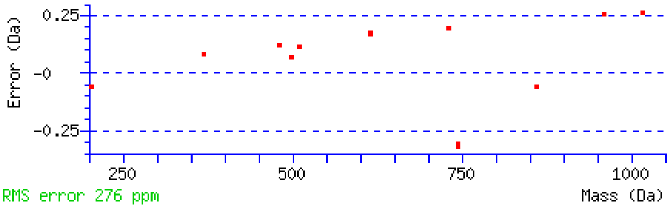
Click mouse within plot area to zoom in by factor of two about that point

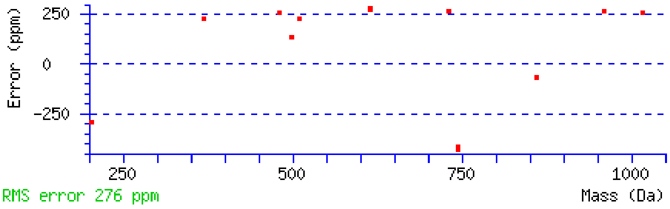
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1130.5438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.3e-005
Matches : 13/80 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							10
2	173.1069	87.0571					G	***1017.4700***	509.2386	999.4464	500.2269	999.4594	500.2334	9
3	271.1567	136.0820					P	***959.4515***	480.2294	941.4279	471.2176	941.4410	471.2241	8
4	403.1942	202.1007					M	***861.4017***	431.2045	843.3781	422.1927	843.3912	422.1992	7
5	517.2753	259.1413					L	***729.3642***	365.1857	711.3406	356.1739	711.3536	356.1805	6
6	633.3123	317.1598	615.2887	308.1480			N	***615.2831***	308.1452	597.2595	299.1334	597.2725	299.1399	5
7	763.3519	382.1796	745.3283	373.1678	745.3414	373.1743	E	***499.2461***	250.1267	481.2225	241.1149	481.2355	241.1214	4
8	911.4174	456.2123	893.3938	447.2005	893.4068	447.2070	F	***369.2065***	185.1069	351.1829	176.0951			3
9	983.4515	492.2294	965.4279	483.2176	965.4410	483.2241	A	221.1410	111.0741	203.1174	102.0624			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IGPMLNEFAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14210.1

Score	Mr(calc)	Delta	Sequence
57.9	1130.5438	-0.0011	IGPMLNEFAK
19.6	1130.5442	-0.0015	LGKVGCTQPR
12.4	1130.5416	0.0011	IGDQGLMSVAK
11.9	1130.5416	0.0011	AVGGLEMKEGK
9.8	1130.5416	0.0011	LNLEGCTALK
4.4	1130.5416	0.0011	LGETLGICAGK
4.3	1130.5416	0.0011	LGMSITSPQGK
4.1	1130.5416	0.0011	GIVQMISENK
3.7	1130.5405	0.0023	INLWFDPSK
3.5	1130.5438	-0.0011	AVWDEMIKK

AT3G14310.1

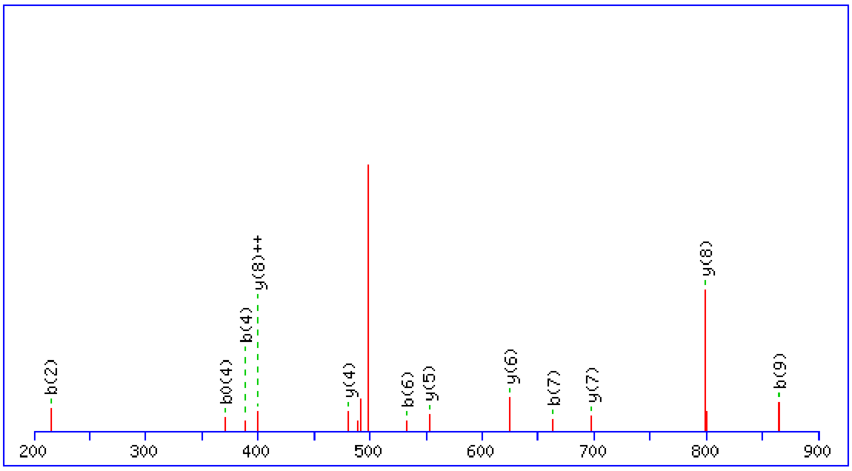
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VITAAAEAQK**
Found in **AT3G14310.1** in **TAIR_Arabidopsis**, Symbols: ATPME3 | ATPME3 (Arabidopsis thaliana pectin methylesterase 3) | chr3:4772221-4775102 REVERSE

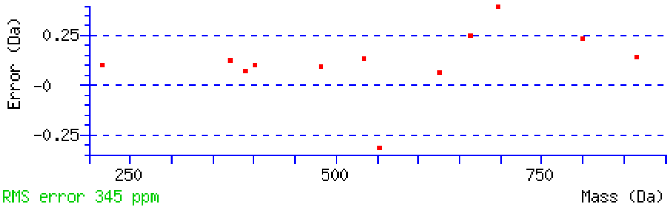
Match to Query 2736: 1012.519616 from(507.267084,2+) index(443)
Title: Elution from: 10.383 to 10.383 scan no 729 cid35.00 polarity:+
Data file C7-2_1.mgf

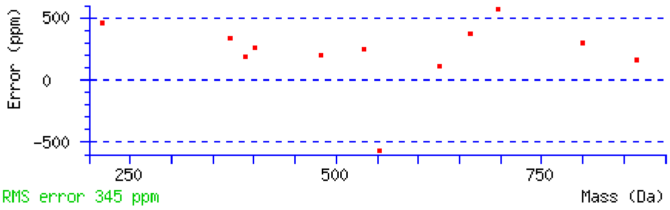
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1012.5197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 5e-005
Matches : 12/82 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							10
2	***215.1538***	108.0805					I	913.4616	457.2344	895.4380	448.2226	895.4510	448.2291	9
3	317.1985	159.1029			299.1880	150.0976	T	***799.3805***	400.1939	781.3569	391.1821	781.3699	391.1886	8
4	***389.2327***	195.1200			371.2221	186.1147	A	***697.3357***	349.1715	679.3122	340.1597	679.3252	340.1662	7
5	461.2668	231.1371			443.2563	222.1318	A	***625.3016***	313.1544	607.2780	304.1426	607.2910	304.1492	6
6	***533.3010***	267.1541			515.2904	258.1488	A	***553.2674***	277.1374	535.2439	268.1256	535.2569	268.1321	5
7	***663.3406***	332.1739			645.3300	323.1687	E	***481.2333***	241.1203	463.2097	232.1085	463.2227	232.1150	4
8	735.3748	368.1910			717.3642	359.1857	A	351.1937	176.1005	333.1701	167.0887			3
9	***865.4274***	433.2173	847.4038	424.2056	847.4168	424.2121	Q	279.1595	140.0834	261.1359	131.0716			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VITAAAEAQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14310.1

Score	Mr(calc)	Delta	Sequence
52.6	1012.5197	-0.0001	VITAAAEAQK
16.3	1012.5197	-0.0001	DPTTAQKIK
7.3	1012.5197	-0.0001	VIDREIEK
5.3	1012.5220	-0.0023	DPPKTIGFK
5.3	1012.5220	-0.0023	IVPNFDVAK
5.3	1012.5197	-0.0001	LVDVKGADGK
5.3	1012.5197	-0.0001	VLVQDDGKK
4.1	1012.5220	-0.0023	GAFLPAVAEK
4.1	1012.5220	-0.0023	IDLWEAKK
4.1	1012.5197	-0.0001	LDDALKAQK

AT3G14390.1

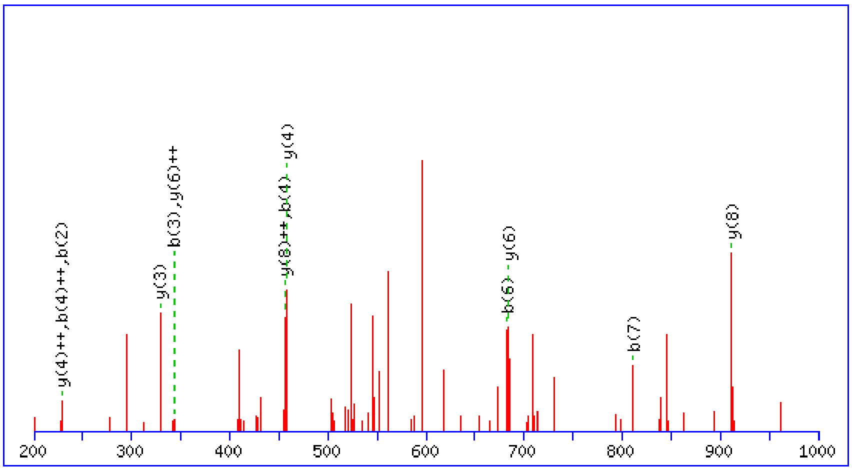
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLNLIIEPGR**
Found in **AT3G14390.1** in **TAIR_Arabidopsis**, Symbols: | diaminopimelate decarboxylase, putative / DAP carboxylase, putative | chr3:4806778-4808961 FORWARD

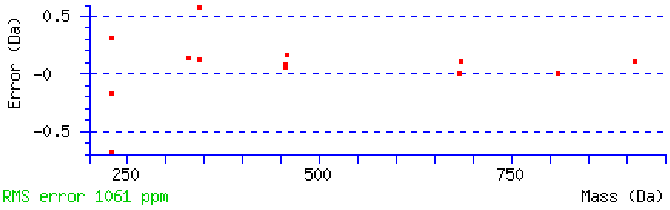
Match to Query 3854: 1138.634408 from(570.324480,2+) index(7354)
Title: Elution from: 65.333 to 65.333 scan no 9553 cid35.00 polarity:+
Data file D12h-3_1.mgf

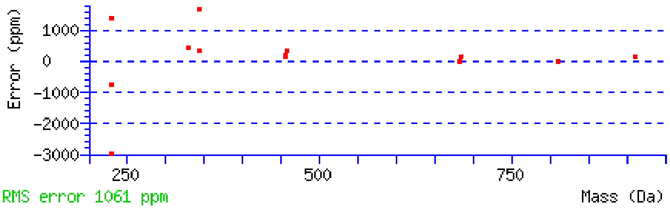
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1138.6346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0023
Matches : 13/98 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							10
2	***229.1183***	115.0628			211.1077	106.0575	L	1024.6150	512.8111	1007.5884	504.2978	1006.6044	503.8058	9
3	***343.1612***	172.0842	326.1347	163.5710	325.1506	163.0790	N	**911.5309**	456.2691	894.5043	447.7558	893.5203	447.2638	8
4	***456.2453***	228.6263	439.2187	220.1130	438.2347	219.6210	L	797.4880	399.2476	780.4614	390.7343	779.4774	390.2423	7
5	569.3293	285.1683	552.3028	276.6550	551.3188	276.1630	I	**684.4039**	342.7056	667.3774	334.1923	666.3933	333.7003	6
6	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	I	571.3198	286.1636	554.2933	277.6503	553.3093	277.1583	5
7	***811.4560***	406.2316	794.4294	397.7184	793.4454	397.2264	E	**458.2358**	229.6215	441.2092	221.1083	440.2252	220.6162	4
8	908.5088	454.7580	891.4822	446.2447	890.4982	445.7527	P	**329.1932**	165.1002	312.1666	156.5870			3
9	965.5302	483.2687	948.5037	474.7555	947.5197	474.2635	G	232.1404	116.5738	215.1139	108.0606			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DLNLIIEPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14390.1

Score	Mr(calc)	Delta	Sequence
29.7	1138.6346	-0.0002	DLNLIIEPGR
11.6	1138.6346	-0.0002	LIDLPGLDQR

AT3G14415.1

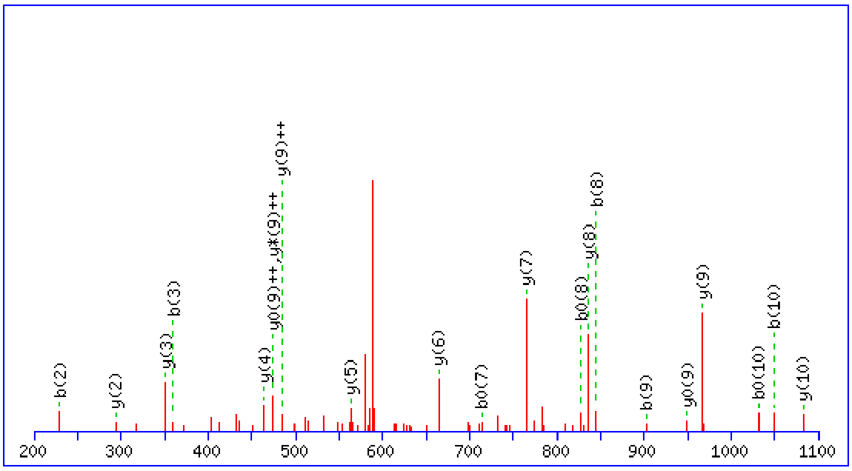
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDMATTVLGFK**
Found in **AT3G14415.1** in **TAIR_Arabidopsis**, Symbols: | (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative | chr3:4818674-4820755 FORWARD

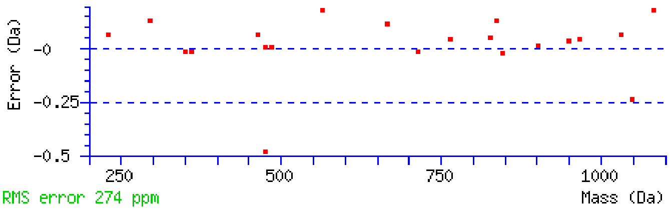
Match to Query 3878: 1194.632456 from(598.323504,2+) index(7868)
Title: Elution from: 68.515 to 68.515 scan no 10310 cid35.00 polarity:+
Data file D6h-3_3.mgf

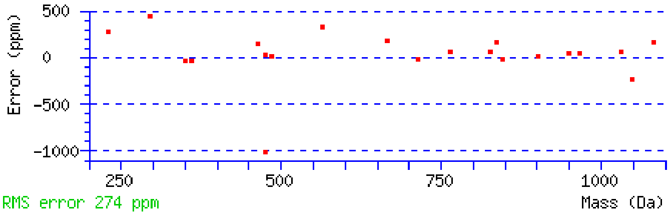
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1194.6319
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 1.6e-008
Matches : 21/88 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							11
2	**229.1183**	115.0628	211.1077	106.0575	D	***1082.5551***	541.7812	1065.5285	533.2679	1064.5445	532.7759	10
3	**360.1588**	180.5830	342.1482	171.5777	M	***967.5281***	484.2677	950.5016	475.7544	949.5176	475.2624	9
4	431.1959	216.1016	413.1853	207.0963	A	***836.4876***	418.7475	819.4611	410.2342	818.4771	409.7422	8
5	532.2436	266.6254	514.2330	257.6201	T	***765.4505***	383.2289	748.4240	374.7156	747.4400	374.2236	7
6	633.2912	317.1493	615.2807	308.1440	T	***664.4028***	332.7051	647.3763	324.1918	646.3923	323.6998	6
7	732.3597	366.6835	714.3491	357.6782	V	***563.3552***	282.1812	546.3286	273.6679			5
8	**845.4437**	423.2255	827.4332	414.2202	L	***464.2867***	232.6470	447.2602	224.1337			4
9	**902.4652**	451.7362	884.4546	442.7309	G	***351.2027***	176.1050	334.1761	167.5917			3
10	**1049.5336**	525.2704	1031.5230	516.2652	F	***294.1812***	147.5942	277.1547	139.0810			2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IDMATTVLGFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14415.1

Score	Mr(calc)	Delta	Sequence
83.2	1194.6319	0.0006	IDMATTVLGFK
11.8	1194.6318	0.0006	MDPAITKLYK
1.1	1194.6292	0.0033	MVRSFREVR
0.7	1194.6318	0.0006	DLITPSYKMK
0.3	1194.6318	0.0006	VGITSMPLYAK
0.2	1194.6318	0.0006	YNSILDMVLK

Mascot: http://www.matrixscience.com/

AT3G14420.1

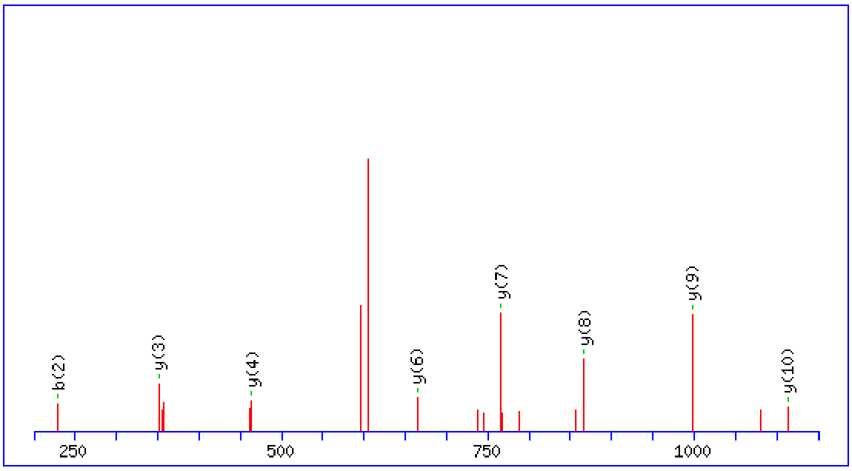
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDMTTTVLGFK**
Found in **AT3G14420.1** in **TAIR_Arabidopsis**, Symbols: | (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative | chr3:4821811-4823906 FORWARD

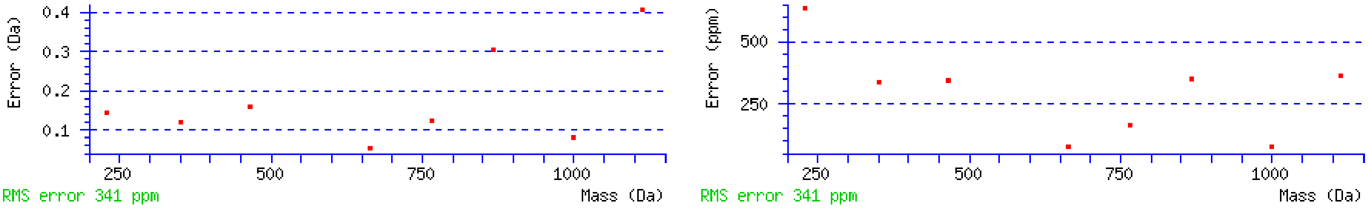
Match to Query 4269: 1224.640630 from(613.327591,2+) index(8146)
Title: Elution from: 71.918 to 71.918 scan no 10712 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1224.6424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 3.7e-007
Matches : 8/88 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			**I**							11
2	229.1183	115.0628	211.1077	106.0575	**D**	***1112.5656***	556.7865	1095.5391	548.2732	1094.5551	547.7812	10
3	360.1588	180.5830	342.1482	171.5777	**M**	***997.5387***	499.2730	980.5121	490.7597	979.5281	490.2677	9
4	461.2064	231.1069	443.1959	222.1016	**T**	***866.4982***	433.7527	849.4716	425.2395	848.4876	424.7475	8
5	562.2541	281.6307	544.2436	272.6254	**T**	***765.4505***	383.2289	748.4240	374.7156	747.4400	374.2236	7
6	663.3018	332.1545	645.2912	323.1493	**T**	***664.4028***	332.7051	647.3763	324.1918	646.3923	323.6998	6
7	762.3702	381.6887	744.3597	372.6835	**V**	563.3552	282.1812	546.3286	273.6679			5
8	875.4543	438.2308	857.4437	429.2255	**L**	***464.2867***	232.6470	447.2602	224.1337			4
9	932.4757	466.7415	914.4652	457.7362	**G**	***351.2027***	176.1050	334.1761	167.5917			3
10	1079.5442	540.2757	1061.5336	531.2704	**F**	294.1812	147.5942	277.1547	139.0810			2
11					**K**	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of IDMTTTVLGFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14420.1

Score	Mr(calc)	Delta	Sequence
68.3	1224.6424	-0.0018	IDMTTTVLGFK
14.1	1224.6391	0.0016	LDFADVATFVK
12.5	1224.6390	0.0016	LDQVFESLFK
8.6	1224.6397	0.0009	EVMQGHQRLK
5.3	1224.6424	-0.0018	FKETMETLVK
2.1	1224.6424	-0.0018	EVILYNVTMK
2.1	1224.6424	-0.0018	TGELFMALVTK
0.2	1224.6424	-0.0018	YTMISALDALK

AT3G14420.6

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVVEQLVR**
Found in **AT3G14420.6** in **TAIR_Arabidopsis**, Symbols: | (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative | chr3:4821906-4823906 FORWARD

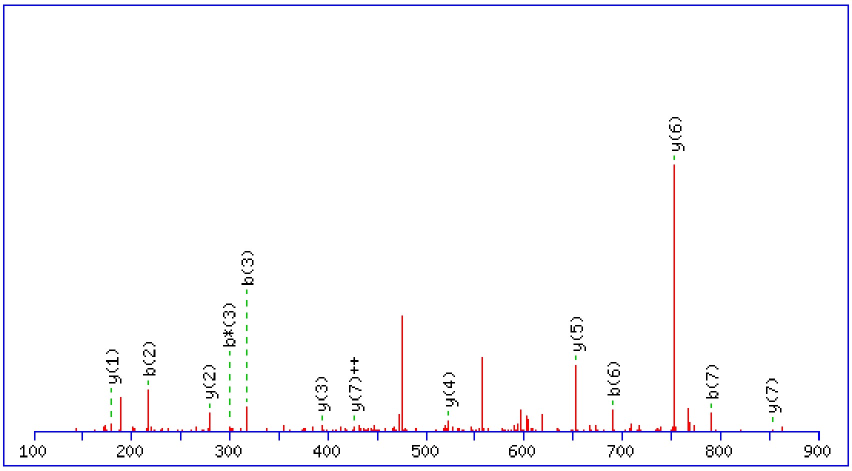
Match to Query 2394: 968.508070 from(485.261311,2+) index(4467)
Title: Elution from: 40.922 to 40.922 scan no 5512 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 900 Da Full range

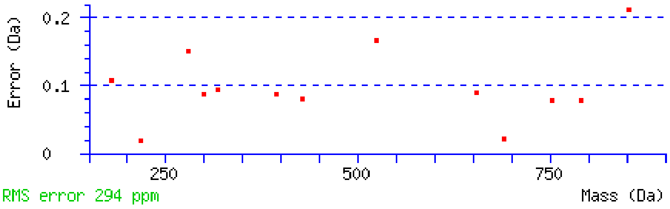
Label all possible matches ○ Label matches used for scoring ●

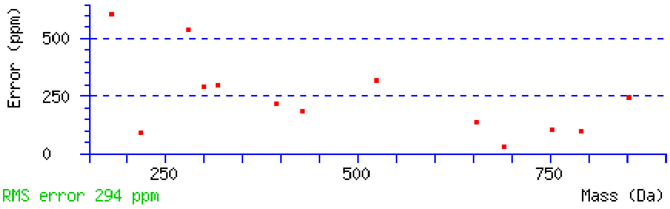
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.5065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00015
Matches : 13/70 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							8
2	**217.1097**	109.0585	199.0861	100.0467			V	***853.4768***	427.2420	835.4532	418.2303	835.4662	418.2368	7
3	**317.1752**	159.0912	299.1516	150.0794			V	***753.4114***	377.2093	735.3878	368.1975	735.4008	368.2040	6
4	447.2148	224.1110	429.1912	215.0992	429.2042	215.1058	E	***653.3459***	327.1766	635.3223	318.1648	635.3354	318.1713	5
5	577.2674	289.1374	559.2439	280.1256	559.2569	280.1321	Q	***523.3063***	262.1568	505.2827	253.1450			4
6	**691.3485**	346.1779	673.3250	337.1661	673.3380	337.1726	L	***393.2536***	197.1305	375.2301	188.1187			3
7	**791.4140**	396.2106	773.3904	387.1988	773.4034	387.2054	V	***279.1725***	140.0899	261.1490	131.0781			2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NVVEQLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.6	968.5065	0.0016	NVVEQLVR

AT3G14420.6

6.5	968.5065	0.0016	NVGLIGLDR
5.1	968.5065	0.0015	TNPEIVKR
4.3	968.5065	0.0015	LSVVATPNR
1.3	968.5065	0.0015	QQQISPKK
0.6	968.5065	0.0016	TLTVAAGPAR
0.3	968.5088	-0.0007	VPSLWTVR

AT3G14460.1

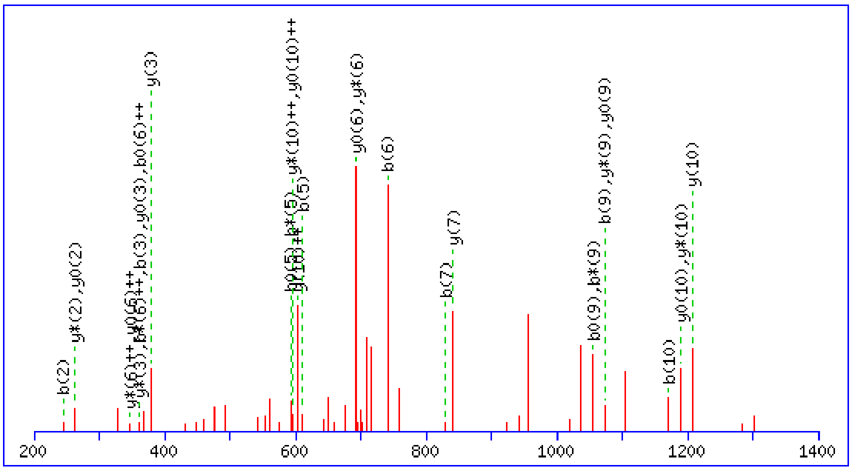
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLNFTESLQPTR**
Found in **AT3G14460.1** in **TAIR_Arabidopsis**, Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4851997-4856271 REVERSE

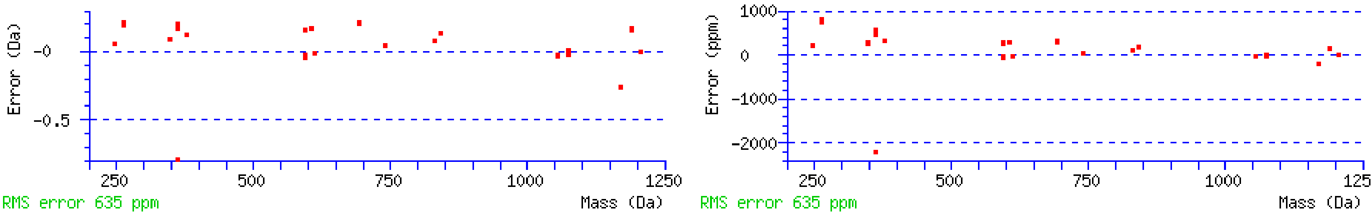
Match to Query 5326: 1450.714306 from(726.364429,2+) index(9724)
Title: Elution from: 95.296 to 95.296 scan no 13947 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1450.7141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0058
Matches : 31/122 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							12
2	***245.1774***	123.0923	227.1538	114.0805			L	1321.6323	661.3198	1303.6087	652.3080	1303.6217	652.3145	11
3	***361.2144***	181.1108	343.1908	172.0990			N	**1207.5512**	604.2792	1189.5276	595.2674	1189.5406	595.2740	10
4	509.2799	255.1436	491.2563	246.1318			F	1091.5142	546.2607	1073.4906	537.2489	1073.5036	537.2555	9
5	***611.3246***	306.1659	593.3010	297.1541	593.3140	297.1606	T	943.4488	472.2280	925.4252	463.2162	925.4382	463.2227	8
6	***741.3642***	371.1857	723.3406	362.1739	723.3536	362.1805	E	**841.4040**	421.2057	823.3805	412.1939	823.3935	412.2004	7
7	***829.3933***	415.2003	811.3697	406.1885	811.3827	406.1950	S	711.3644	356.1858	693.3408	347.1741	693.3538	347.1806	6
8	943.4744	472.2408	925.4508	463.2290	925.4638	463.2355	L	623.3353	312.1713	605.3118	303.1595	605.3248	303.1660	5
9	***1073.5270***	537.2671	1055.5034	528.2553	1055.5164	528.2619	Q	509.2543	255.1308	491.2307	246.1190	491.2437	246.1255	4
10	***1171.5768***	586.2920	1153.5532	577.2802	1153.5662	577.2868	P	**379.2016**	190.1044	361.1780	181.0926	361.1910	181.0992	3
11	1273.6215	637.3144	1255.5979	628.3026	1255.6110	628.3091	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
12							R	179.1071	90.0572	161.0835	81.0454			1



NCBI **BLAST** search of KLNFTESLQPTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G14460.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.4	1450.7141	0.0003	KLNFTESLQPTR
12.6	1450.7145	-0.0002	AWIGIFNMLLML
11.9	1450.7141	0.0003	DNFEVKTIPRSK
11.4	1450.7127	0.0016	MNKNVDKAMLLR
7.9	1450.7118	0.0025	SERETGIKTGNLK
4.0	1450.7118	0.0025	SAIAGANGESAKKTK
0.3	1450.7100	0.0043	MLDAGKSLCSLLK

AT3G14610.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVFNKVNDFEK**
Found in **AT3G14610.1** in **TAIR_Arabidopsis**, Symbols: CYP72A7 | CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7); oxygen binding | chr3:4912572-4914510 FORWARD

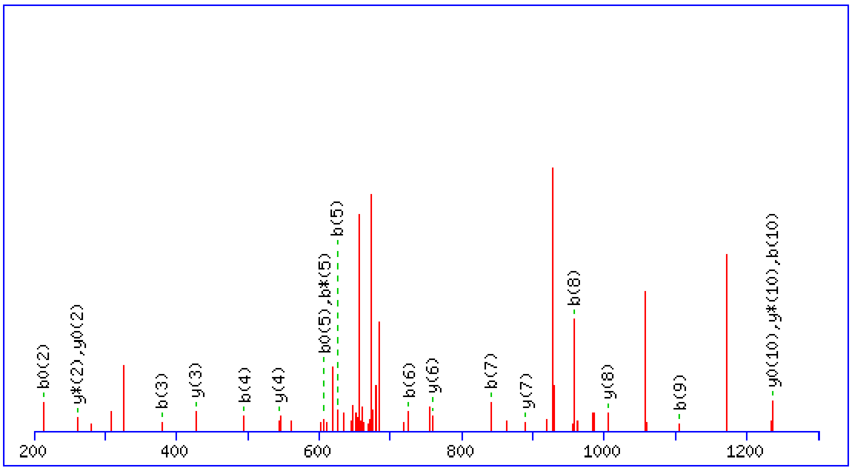
Match to Query 5704: 1382.629882 from(692.322217,2+) index(2420)
Title: Elution from: 26.929 to 26.929 scan no 3075 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

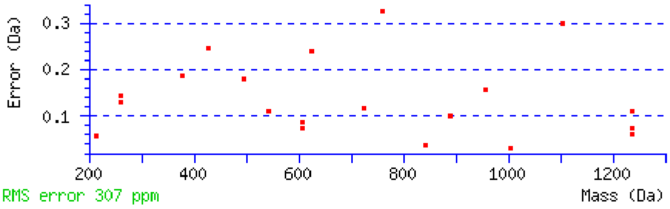
Label all possible matches ○ Label matches used for scoring ●

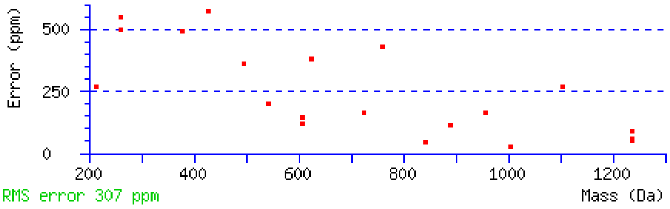
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.6276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0066
Matches : 20/112 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							11
2	231.1124	116.0598			213.1018	107.0545	V	1253.5953	627.3013	1235.5717	618.2895	1235.5847	618.2960	10
3	***379.1778***	190.0925			361.1672	181.0873	F	1153.5299	577.2686	1135.5063	568.2568	1135.5193	568.2633	9
4	***495.2148***	248.1110	477.1912	239.0992	477.2042	239.1058	N	**1005.4644**	503.2358	987.4408	494.2240	987.4538	494.2306	8
5	***625.3038***	313.1556	607.2802	304.1438	607.2933	304.1503	K	**889.4274**	445.2173	871.4038	436.2056	871.4168	436.2121	7
6	***725.3693***	363.1883	707.3457	354.1765	707.3587	354.1830	V	**759.3384**	380.1728	741.3148	371.1610	741.3278	371.1675	6
7	***841.4063***	421.2068	823.3827	412.1950	823.3957	412.2015	N	659.2729	330.1401	641.2493	321.1283	641.2624	321.1348	5
8	***957.4303***	479.2188	939.4067	470.2070	939.4197	470.2135	D	**543.2359**	272.1216	525.2123	263.1098	525.2254	263.1163	4
9	***1105.4957***	553.2515	1087.4721	544.2397	1087.4851	544.2462	F	**427.2120**	214.1096	409.1884	205.0978	409.2014	205.1043	3
10	***1235.5353***	618.2713	1217.5117	609.2595	1217.5248	609.2660	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EVFNKVNDFEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G14610.1

Score	Mr(calc)	Delta	Sequence
31.9	1382.6276	0.0022	EVFNKVNDFEK
8.0	1382.6288	0.0011	SSSAATLTLMNQK
5.3	1382.6276	0.0022	TWSFTQVPTSSK
3.7	1382.6330	-0.0031	FSSKSHGFRPGR
1.8	1382.6288	0.0011	VRDMLISSESSK
0.2	1382.6310	-0.0011	QTMSGEVGFGVLK

AT3G14900.1

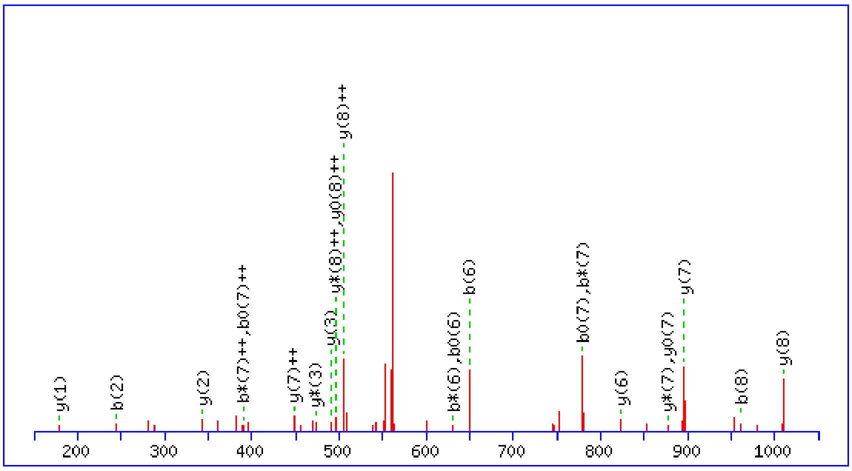
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLAESLFYR**
Found in **AT3G14900.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO39402.1); contains domain PTHR12839 (PTHR12839) | chr3:5013449-5015284 REVERSE

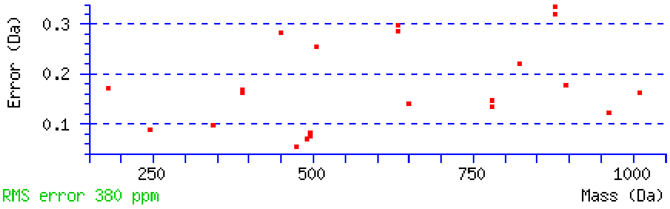
Match to Query 3283: 1138.581766 from(570.298159,2+) index(1601)
Title: Elution from: 23.643 to 23.643 scan no 2223 cid35.00 polarity:+
Data file D1d-1_1.mgf

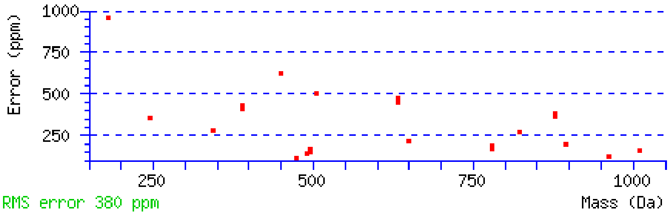
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1138.5797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.006
Matches : 22/82 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							9
2	**245.1774**	123.0923	227.1538	114.0805			L	***1009.4979***	505.2526	991.4744	496.2408	991.4874	496.2473	8
3	317.2116	159.1094	299.1880	150.0976			A	***895.4168***	448.2121	877.3933	439.2003	877.4063	439.2068	7
4	447.2512	224.1292	429.2276	215.1174	429.2406	215.1239	E	***823.3827***	412.1950	805.3591	403.1832	805.3721	403.1897	6
5	535.2802	268.1438	517.2567	259.1320	517.2697	259.1385	S	693.3431	347.1752	675.3195	338.1634	675.3325	338.1699	5
6	**649.3613**	325.1843	631.3378	316.1725	631.3508	316.1790	L	605.3140	303.1606	587.2904	294.1488			4
7	797.4268	399.2170	779.4032	390.2052	779.4162	390.2118	F	***491.2329***	246.1201	473.2093	237.1083			3
8	**961.4872**	481.2472	943.4636	472.2354	943.4766	472.2419	Y	***343.1675***	172.0874	325.1439	163.0756			2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KLAESLFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G14900.1

28.1	1138.5797	0.0021	KLAESLFYR
11.5	1138.5801	0.0016	ARGKSSFLTR
9.1	1138.5828	-0.0010	KQAHLRNPR
7.9	1138.5801	0.0016	QNLRPEIPR
7.7	1138.5801	0.0016	QLQHITNIR
3.8	1138.5797	0.0021	NVYLTFTIR
1.4	1138.5831	-0.0013	IPASICQLPK
0.8	1138.5801	0.0016	IGRPGSSLAHK
0.5	1138.5797	0.0021	IIVFTTNYR

AT3G14940.1

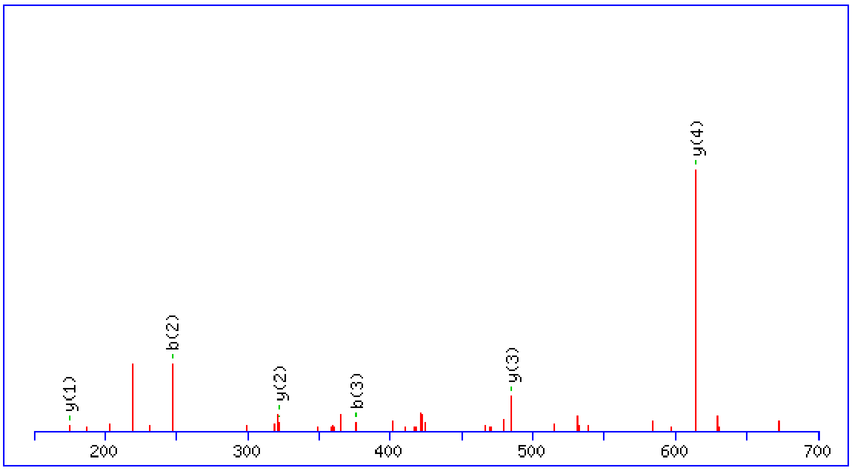
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVEYFR**
Found in **AT3G14940.1** in **TAIR_Arabidopsis**, Symbols: ATPPC3 | ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase | chr3:5025591-5029483 FORWARD

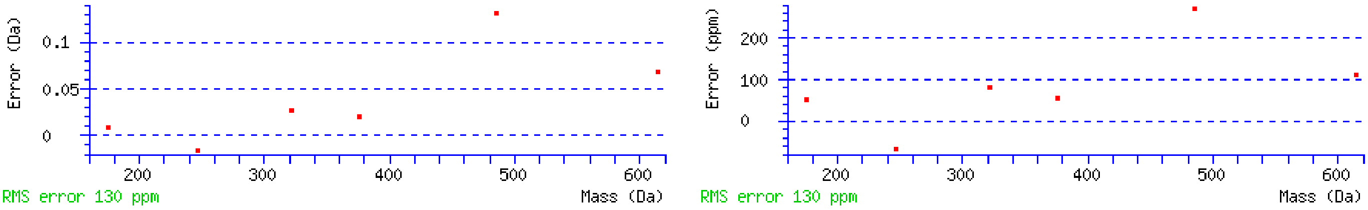
Match to Query 1335: 859.422570 from(430.718561,2+) index(4116)
Title: Elution from: 38.503 to 38.503 scan no 5167 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 859.4228
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.031
Matches : 6/40 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							6
2	**247.1441**	124.0757			V	713.3617	357.1845	696.3352	348.6712	695.3511	348.1792	5
3	**376.1867**	188.5970	358.1761	179.5917	E	***614.2933***	307.6503	597.2667	299.1370	596.2827	298.6450	4
4	539.2500	270.1287	521.2395	261.1234	Y	***485.2507***	243.1290	468.2241	234.6157			3
5	686.3184	343.6629	668.3079	334.6576	F	***322.1874***	161.5973	305.1608	153.0840			2
6					R	***175.1190***	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of FVEYFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.3	859.4228	-0.0003	FVEYFR
0.7	859.4222	0.0004	MLTNPER

AT3G14940.1

Mascot: http://www.matrixscience.com/

AT3G14990.1

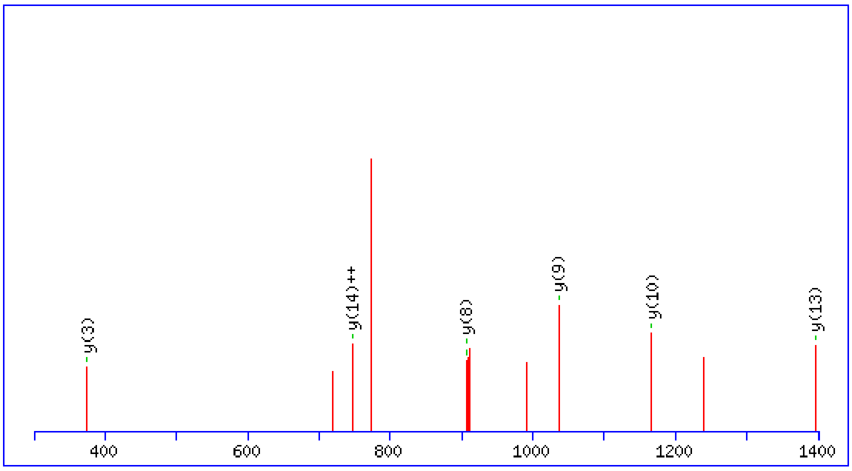
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APGTAMEFSLAIVEK**
Found in **AT3G14990.1** in **TAIR_Arabidopsis**, Symbols: | 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative | chr3:5047517-5049628 FORWARD

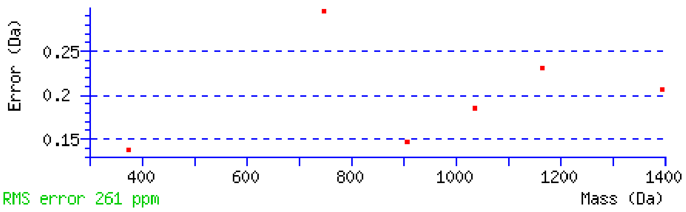
Match to Query 6837: 1562.799608 from(782.407080,2+) index(8759)
Title: Elution from: 80.429 to 80.429 scan no 11770 cid35.00 polarity:+
Data file D12h-2_1.mgf

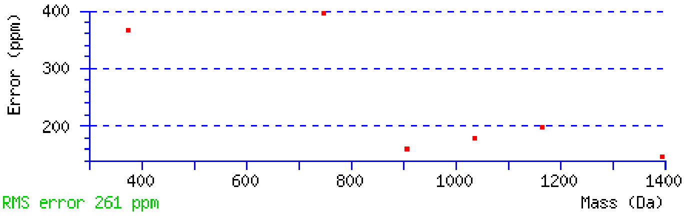
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1562.8014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0085
Matches : 6/132 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			**A**							**15**
2	169.0972	85.0522			**P**	1492.7716	746.8894	1475.7450	738.3762	1474.7610	737.8842	**14**
3	226.1186	113.5629			**G**	***1395.7188***	698.3631	1378.6923	689.8498	1377.7083	689.3578	**13**
4	327.1663	164.0868	309.1557	155.0815	**T**	1338.6974	669.8523	1321.6708	661.3390	1320.6868	660.8470	**12**
5	398.2034	199.6053	380.1928	190.6001	**A**	1237.6497	619.3285	1220.6231	610.8152	1219.6391	610.3232	**11**
6	529.2439	265.1256	511.2333	256.1203	**M**	***1166.6126***	583.8099	1149.5860	575.2967	1148.6020	574.8046	**10**
7	658.2865	329.6469	640.2759	320.6416	**E**	***1035.5721***	518.2897	1018.5455	509.7764	1017.5615	509.2844	**9**
8	805.3549	403.1811	787.3443	394.1758	**F**	***906.5295***	453.7684	889.5029	445.2551	888.5189	444.7631	**8**
9	892.3869	446.6971	874.3764	437.6918	**S**	759.4611	380.2342	742.4345	371.7209	741.4505	371.2289	**7**
10	1005.4710	503.2391	987.4604	494.2339	**L**	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	**6**
11	1076.5081	538.7577	1058.4975	529.7524	**A**	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	**5**
12	1189.5922	595.2997	1171.5816	586.2944	**I**	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	**4**
13	1288.6606	644.8339	1270.6500	635.8286	**V**	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
14	1417.7032	709.3552	1399.6926	700.3499	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
15					**K**	147.1128	74.0600	130.0863	65.5468			**1**





AT3G14990.1

NCBI **BLAST** search of APGTAMEFSLAIVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.4	1562.8014	-0.0018	APGTAMEFSLAIVEK
3.4	1562.7987	0.0009	APEVMETRKHTHK

Mascot: http://www.matrixscience.com/

AT3G15000.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLAQIVGSEDEAR**
Found in **AT3G15000.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Uncharacterized mitochondrial protein At3g15000 [Arabidopsis Thaliana] (GB:Q9LKA5); similar to plastid developmental protein DAG, putative [Arabidopsis thaliana] (TAIR:AT3G06790.2); similar to unnamed protein product [Vitis

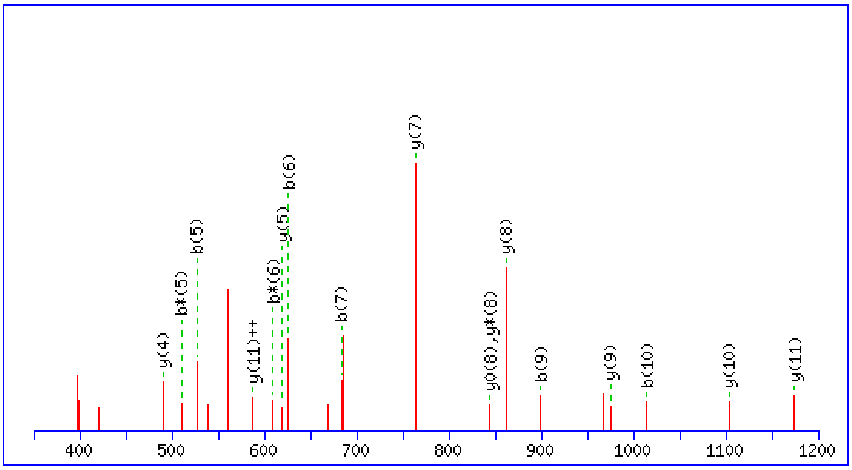
Match to Query 5507: 1387.693134 from(694.853843,2+) index(4438)
Title: Elution from: 41.474 to 41.474 scan no 5573 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1200 Da Full range

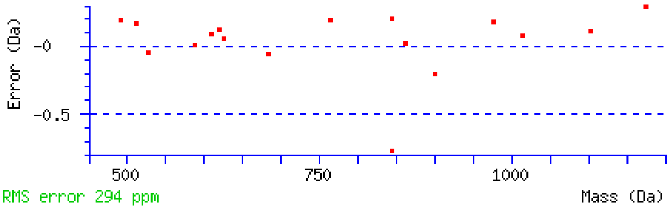
Label all possible matches ○ Label matches used for scoring ●

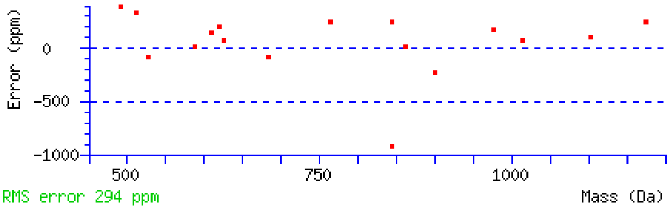
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1387.6943
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 2.2e-005
Matches : 17/134 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							13
2	215.1390	108.0731			197.1285	99.0679	L	1287.6539	644.3306	1270.6274	635.8173	1269.6434	635.3253	12
3	286.1761	143.5917			268.1656	134.5864	A	***1174.5699***	587.7886	1157.5433	579.2753	1156.5593	578.7833	11
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	Q	***1103.5327***	552.2700	1086.5062	543.7567	1085.5222	543.2647	10
5	***527.3188***	264.1630	510.2922	255.6498	509.3082	255.1577	I	***975.4742***	488.2407	958.4476	479.7274	957.4636	479.2354	9
6	***626.3872***	313.6972	609.3606	305.1840	608.3766	304.6920	V	***862.3901***	431.6987	845.3636	423.1854	844.3795	422.6934	8
7	***683.4087***	342.2080	666.3821	333.6947	665.3981	333.2027	G	***763.3217***	382.1645	746.2951	373.6512	745.3111	373.1592	7
8	770.4407	385.7240	753.4141	377.2107	752.4301	376.7187	S	706.3002	353.6537	689.2737	345.1405	688.2897	344.6485	6
9	***899.4833***	450.2453	882.4567	441.7320	881.4727	441.2400	E	***619.2682***	310.1377	602.2416	301.6245	601.2576	301.1325	5
10	***1014.5102***	507.7587	997.4837	499.2455	996.4997	498.7535	D	***490.2256***	245.6164	473.1991	237.1032	472.2150	236.6112	4
11	1143.5528	572.2800	1126.5263	563.7668	1125.5422	563.2748	E	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
12	1214.5899	607.7986	1197.5634	599.2853	1196.5794	598.7933	A	246.1561	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TLAQIVGSEDEAR

AT3G15000.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.5	1387.6943	-0.0012	TLAQIVGSEDEAR
0.0	1387.6943	-0.0012	RGGDDVAVETELK

AT3G15095.3

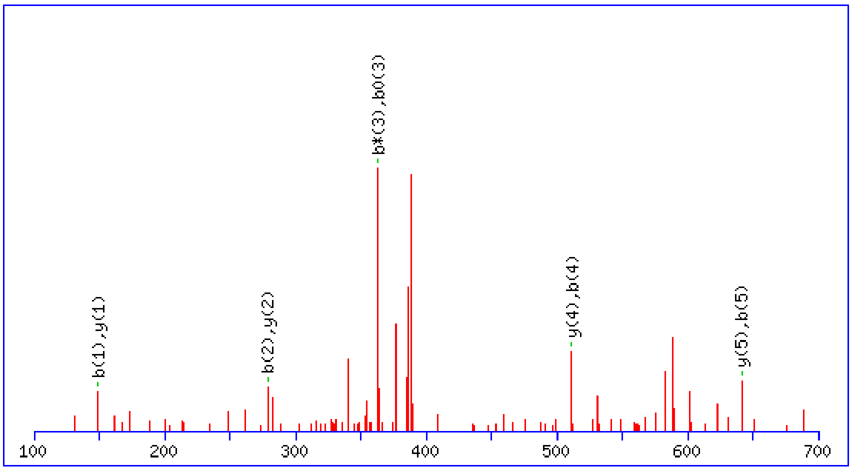
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKTEKK**
Found in **AT3G15095.3** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO39345.1) | chr3:5082837-5084057 FORWARD

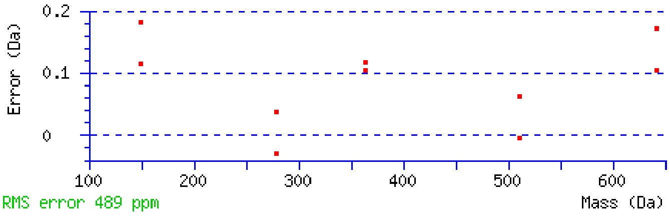
Match to Query 905: 788.396322 from(395.205437,2+) index(1478)
Title: Elution from: 18.865 to 18.865 scan no 1939 cid35.00 polarity:+
Data file D6h-3_3.mgf

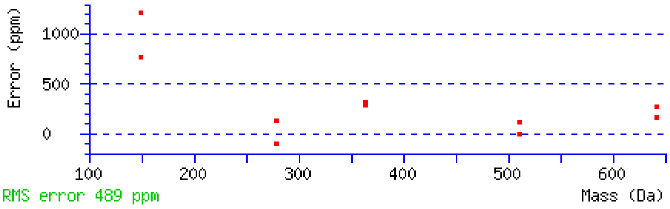
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 788.3944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 34 **Expect:** 0.0034
Matches : 10/74 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***149.0397***	75.0235					**M**							**6**
2	***279.1287***	140.0680	261.1052	131.0562			**K**	***641.3693***	321.1883	623.3457	312.1765	623.3587	312.1830	**5**
3	381.1735	191.0904	363.1499	182.0786	363.1629	182.0851	**T**	***511.2802***	256.1438	493.2567	247.1320	493.2697	247.1385	**4**
4	***511.2131***	256.1102	493.1895	247.0984	493.2025	247.1049	**E**	409.2355	205.1214	391.2120	196.1096	391.2250	196.1161	**3**
5	***641.3021***	321.1547	623.2785	312.1429	623.2916	312.1494	**K**	***279.1959***	140.1016	261.1723	131.0898			**2**
6							**K**	***149.1069***	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MKTEKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.9	788.3944	0.0019	MKTEKK
22.4	788.3944	0.0019	KMKTEK

AT3G15095.3

22.4	788.3945	0.0019	MASSLKK
22.4	788.3944	0.0019	MEKKTK
22.4	788.3944	0.0019	MKVTASK
22.4	788.3967	-0.0003	MQIFVK
20.3	788.3971	-0.0008	ARQMKK
20.3	788.3944	0.0019	ETKMKK
20.3	788.3944	0.0019	TEKMKK
17.8	788.3971	-0.0008	RMKSAGK

AT3G15140.1

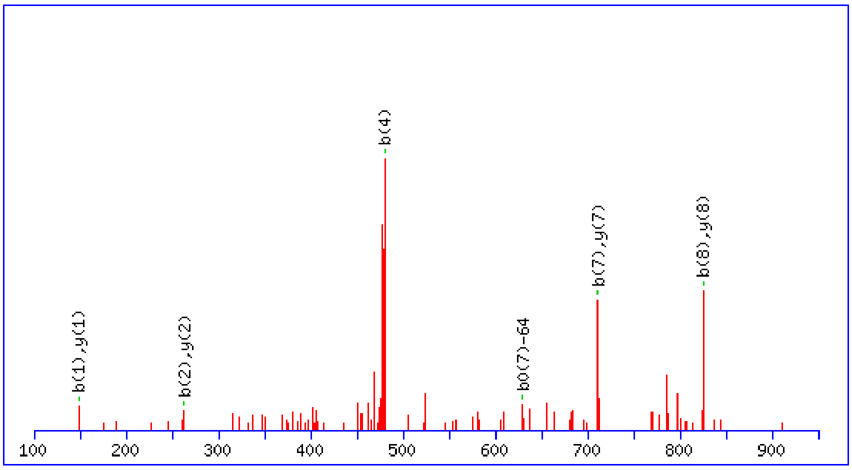
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLSEGAVLK**
Found in **AT3G15140.1** in **TAIR_Arabidopsis**, Symbols: | exonuclease family protein | chr3:5099719-5101724 REVERSE

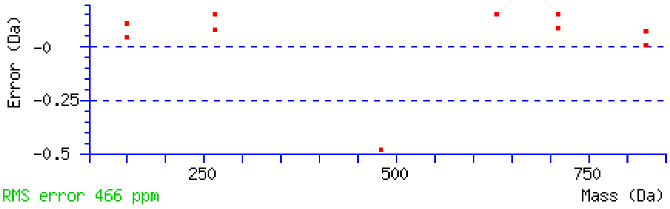
Match to Query 2195: 972.479654 from(487.247103,2+) index(1296)
Title: Elution from: 18.677 to 18.677 scan no 1792 cid35.00 polarity:+
Data file C7-1_2.mgf

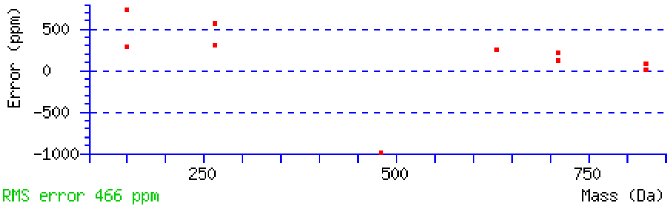
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0046
Matches : 10/94 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	*149.0397*	75.0235			M							9
2	*263.1208*	132.0640			L	**825.4559**	413.2316	807.4323	404.2198	807.4453	404.2263	8
3	351.1499	176.0786	333.1393	167.0733	S	**711.3748**	356.1910	693.3512	347.1792	693.3642	347.1857	7
4	*481.1895*	241.0984	463.1789	232.0931	E	623.3457	312.1765	605.3221	303.1647	605.3351	303.1712	6
5	539.2080	270.1076	521.1974	261.1024	G	493.3061	247.1567	475.2825	238.1449			5
6	611.2421	306.1247	593.2316	297.1194	A	435.2876	218.1474	417.2640	209.1356			4
7	*711.3076*	356.1574	693.2970	347.1522	V	363.2534	182.1303	345.2298	173.1186			3
8	*825.3887*	413.1980	807.3781	404.1927	L	**263.1880**	132.0976	245.1644	123.0858			2
9					K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MLSEGAVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G15140.1

35.3	972.4810	-0.0014	MLSEGAVLK
17.3	972.4810	-0.0014	EMEKLVSK
17.2	972.4776	0.0020	DFDVLNLK
17.2	972.4776	0.0020	IFTKPDDK
15.2	972.4810	-0.0014	MKESLLDK
15.2	972.4776	0.0020	VPYEQSLK
14.7	972.4799	-0.0002	LFEEWLK
12.0	972.4776	0.0020	FLGLDVGDK
12.0	972.4810	-0.0014	MAEDKILK
10.8	972.4810	-0.0013	EMTKEVVK

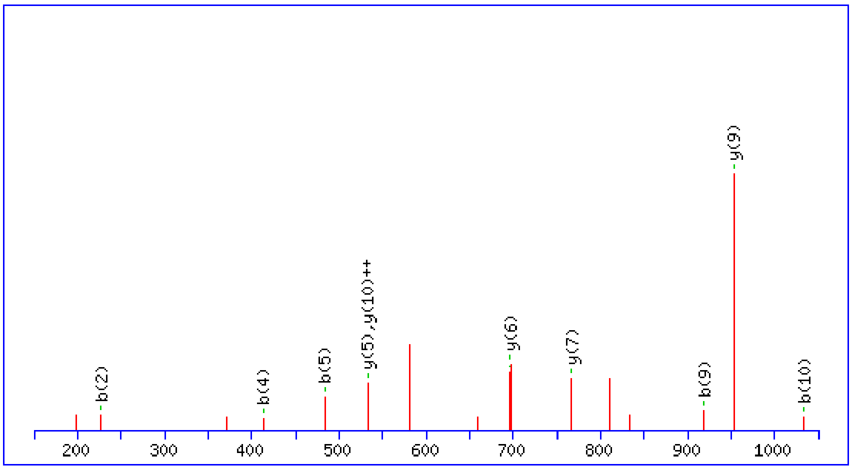
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIGEAYSAIDK**
Found in **AT3G15190.1** in **TAIR_Arabidopsis**, Symbols: | chloroplast 30S ribosomal protein S20, putative | chr3:5116223-5117419 FORWARD

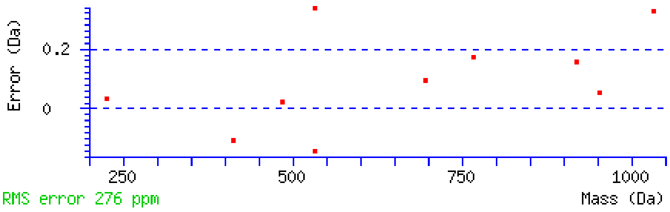
Match to Query 4255: 1178.615762 from(590.315157,2+) index(4496)
Title: Elution from: 41.572 to 41.572 scan no 5590 cid35.00 polarity:+
Data file 0-1_1.mgf

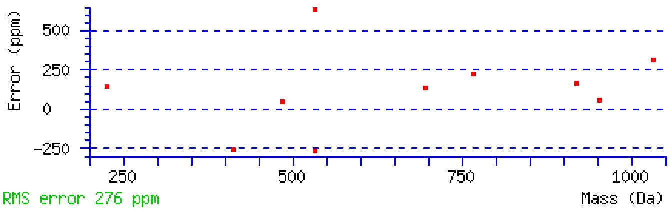
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1178.6183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0019
Matches : 10/92 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							11
2	***227.1754***	114.0913			I	1066.5415	533.7744	1049.5150	525.2611	1048.5310	524.7691	10
3	284.1969	142.6021			G	***953.4575***	477.2324	936.4309	468.7191	935.4469	468.2271	9
4	***413.2395***	207.1234	395.2289	198.1181	E	896.4360	448.7216	879.4094	440.2084	878.4254	439.7164	8
5	***484.2766***	242.6419	466.2660	233.6366	A	***767.3934***	384.2003	750.3668	375.6871	749.3828	375.1951	7
6	647.3399	324.1736	629.3293	315.1683	Y	***696.3563***	348.6818	679.3297	340.1685	678.3457	339.6765	6
7	734.3719	367.6896	716.3614	358.6843	S	***533.2930***	267.1501	516.2664	258.6368	515.2824	258.1448	5
8	805.4090	403.2082	787.3985	394.2029	A	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
9	***918.4931***	459.7502	900.4825	450.7449	I	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
10	***1033.5201***	517.2637	1015.5095	508.2584	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
11					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LIGEAYSAIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G15190.1

Score	Mr(calc)	Delta	Sequence
33.1	1178.6183	-0.0025	LIGEAYSAIDK
6.3	1178.6151	0.0006	IIEITMCRK
2.1	1178.6151	0.0006	LKILNMSGCK
1.0	1178.6183	-0.0025	LIDEFALSGSK
1.0	1178.6158	-0.0000	LLVYEFMHK

Mascot: http://www.matrixscience.com/

AT3G15340.1

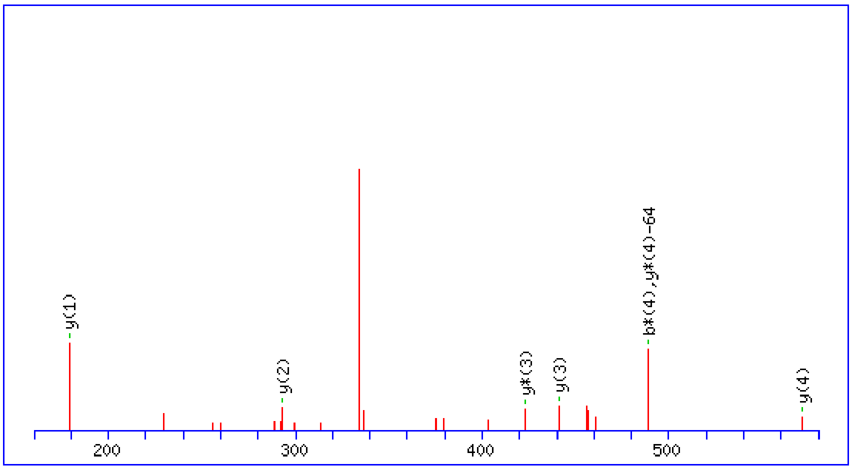
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IKMLR**
Found in **AT3G15340.1** in **TAIR_Arabidopsis**

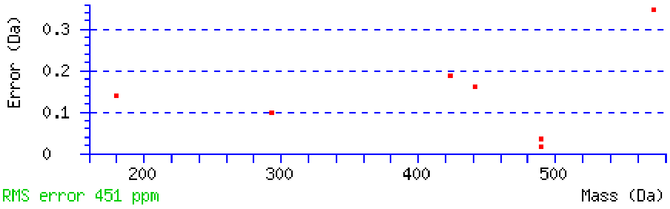
Match to Query 568: 684.383666 from(343.199109,2+) index(2870)
Title: Elution from: 28.884 to 28.884 scan no 3567 cid35.00 polarity:+
Data file D12h-1_3.mgf

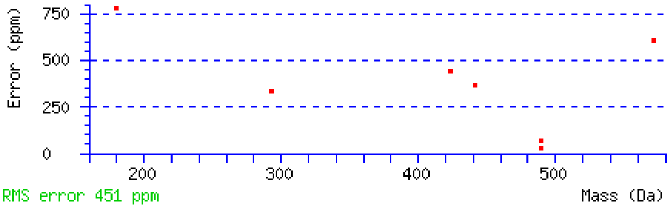
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 684.3835
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.018
Matches : 7/46 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	115.0884	58.0478			I					5
2	245.1774	123.0923	227.1538	114.0805	K	***571.3097***	286.1585	553.2861	277.1467	4
3	393.2098	197.1086	375.1863	188.0968	M	***441.2206***	221.1140	423.1970	212.1022	3
4	507.2909	254.1491	489.2674	245.1373	L	***293.1882***	147.0977	275.1646	138.0859	2
5					R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of IKMLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.3	684.3835	0.0002	IKMLR
25.3	684.3835	0.0002	LKMIR
25.3	684.3835	0.0002	LKMLR
22.8	684.3835	0.0002	LMKLR

AT3G15340.1

17.5	684.3835	0.0002	KLMLR
14.3	684.3835	0.0002	LKIMR
14.3	684.3835	0.0002	LKLMR
14.3	684.3835	0.0002	MIKIR
14.3	684.3835	0.0002	MLKLR
12.4	684.3835	0.0002	LMIKR

AT3G15350.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDEVLNKIDK**
Found in **AT3G15350.1** in **TAIR_Arabidopsis**, Symbols: | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein | chr3:5167257-5168889 FORWARD

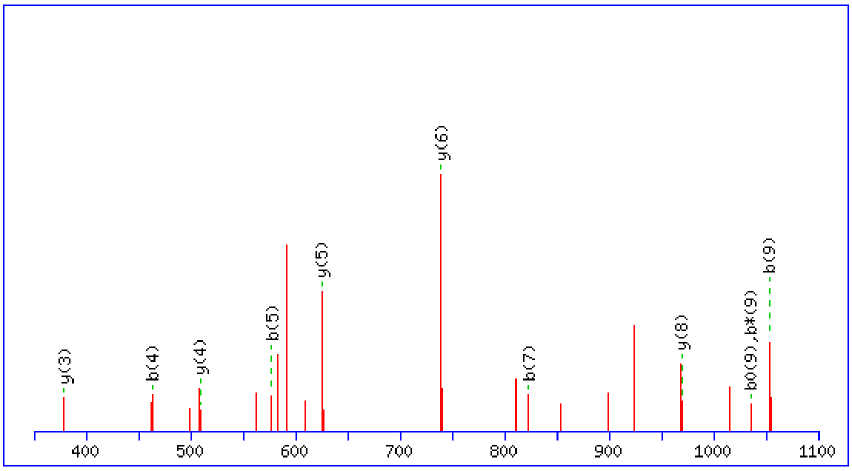
Match to Query 4297: 1200.566544 from(601.290548,2+) index(4013)
Title: Elution from: 37.724 to 37.724 scan no 4988 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1100 Da Full range

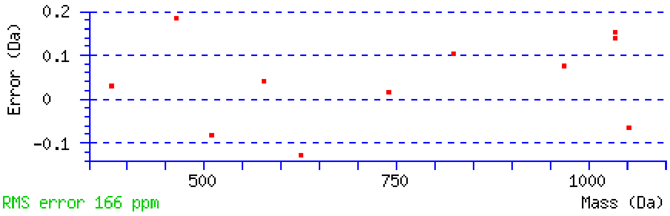
Label all possible matches ○ Label matches used for scoring ●

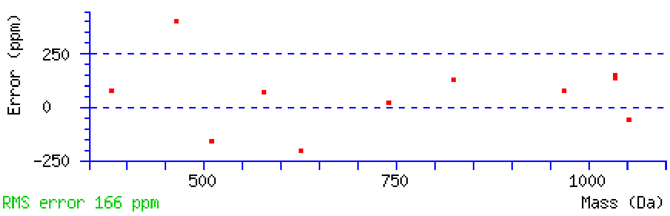
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1200.5648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.014
Matches : 11/96 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	**D**							**10**
2	233.0552	117.0313			215.0447	108.0260	**D**	1085.5481	543.2777	1067.5246	534.2659	1067.5376	534.2724	**9**
3	363.0949	182.0511			345.0843	173.0458	**E**	***969.5242***	485.2657	951.5006	476.2539	951.5136	476.2604	**8**
4	***463.1603***	232.0838			445.1497	223.0785	**V**	839.4845	420.2459	821.4609	411.2341	821.4740	411.2406	**7**
5	***577.2414***	289.1243			559.2308	280.1191	**L**	***739.4191***	370.2132	721.3955	361.2014	721.4085	361.2079	**6**
6	693.2784	347.1428	675.2548	338.1310	675.2678	338.1376	**N**	***625.3380***	313.1726	607.3144	304.1608	607.3274	304.1673	**5**
7	***823.3674***	412.1874	805.3439	403.1756	805.3569	403.1821	**K**	***509.3010***	255.1541	491.2774	246.1423	491.2904	246.1488	**4**
8	937.4485	469.2279	919.4250	460.2161	919.4380	460.2226	**I**	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	**3**
9	***1053.4725***	527.2399	1035.4489	518.2281	1035.4620	518.2346	**D**	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	**2**
10							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of DDEVLNKIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G15350.1

Score	Mr(calc)	Delta	Sequence
26.4	1200.5648	0.0017	DDEVLNKIDK
15.2	1200.5648	0.0017	VQASLGEELDK
9.3	1200.5648	0.0017	TDEIIEALER
8.1	1200.5648	0.0017	KLEEANEEVK
5.2	1200.5675	-0.0010	DRPSANLIDGK
2.1	1200.5671	-0.0005	FEIVQPEEAK
2.0	1200.5646	0.0020	VFEMFFNKK
1.3	1200.5648	0.0017	LEDSLQEINK
0.7	1200.5693	-0.0028	EYSKIFFEK
0.4	1200.5675	-0.0010	ATKSKEHEQK

AT3G15360.1

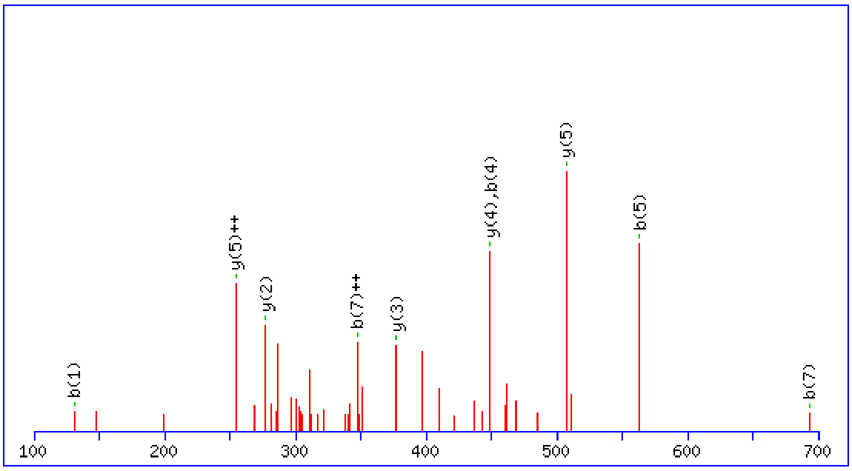
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSIIGAVPR**
Found in **AT3G15360.1** in **TAIR_Arabidopsis**, Symbols: ATM4, TRX-M4, ATHM4 | ATHM4 (Arabidopsis thioredoxin M-type 4); thiol-disulfide exchange intermediate | chr3:5188455-5189464 FORWARD

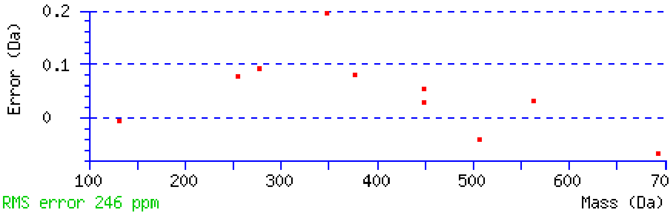
Match to Query 2987: 1068.572988 from(357.198272,3+) index(2151)
Title: Elution from: 24.784 to 24.784 scan no 2757 cid35.00 polarity:+
Data file C7-1_3.mgf

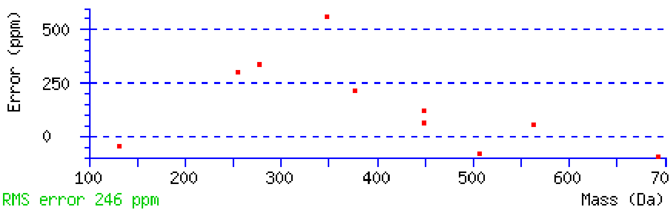
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1068.5720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0046
Matches : 10/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	***131.0963***	66.0518	113.0727	57.0400			K							10
2	247.1203	124.0638	229.0967	115.0520	229.1097	115.0585	D	939.4902	470.2488	921.4666	461.2370	921.4797	461.2435	9
3	335.1493	168.0783	317.1258	159.0665	317.1388	159.0730	S	823.4662	412.2368	805.4427	403.2250	805.4557	403.2315	8
4	***449.2304***	225.1189	431.2069	216.1071	431.2199	216.1136	I	735.4372	368.2222	717.4136	359.2104			7
5	***563.3115***	282.1594	545.2880	273.1476	545.3010	273.1541	I	621.3561	311.1817	603.3325	302.1699			6
6	621.3300	311.1687	603.3065	302.1569	603.3195	302.1634	G	***507.2750***	254.1411	489.2514	245.1293			5
7	***693.3642***	347.1857	675.3406	338.1739	675.3536	338.1805	A	***449.2565***	225.1319	431.2329	216.1201			4
8	793.4296	397.2185	775.4061	388.2067	775.4191	388.2132	V	***377.2223***	189.1148	359.1988	180.1030			3
9	891.4794	446.2434	873.4559	437.2316	873.4689	437.2381	P	***277.1569***	139.0821	259.1333	130.0703			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KDSIIGAVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G15360.1

Score	Mr(calc)	Delta	Sequence
30.8	1068.5720	0.0010	KDSIIGAVPR
9.3	1068.5746	-0.0017	KNKHVTGLR
4.1	1068.5720	0.0010	DGQAVIIALR
3.6	1068.5720	0.0010	LLKDSPNLR
2.6	1068.5749	-0.0019	IPSMLLEIK
1.5	1068.5720	0.0010	SIPRTPEKK

AT3G15730.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEGPIAWDVMYNFEQR**
Found in **AT3G15730.1** in **TAIR_Arabidopsis**, Symbols: PLD, PLDALPHA1 | PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D | chr3:5330842-5333481 FORWARD

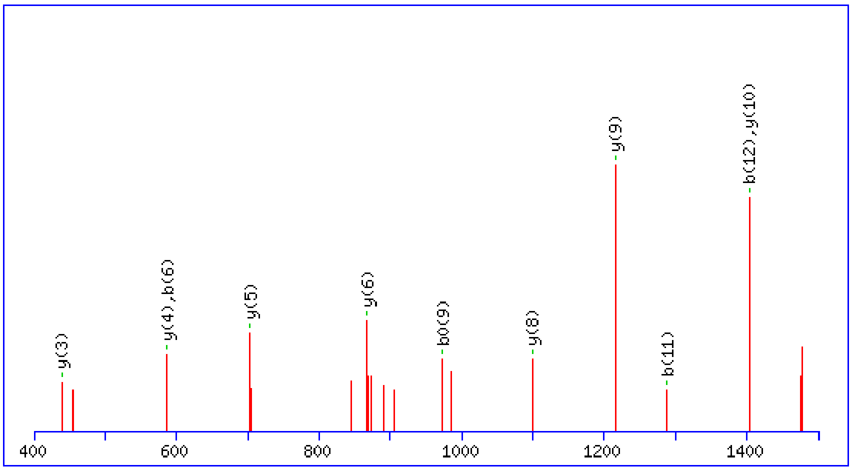
Match to Query 9275: 1988.854740 from(995.434646,2+) index(10386)
Title: Elution from: 98.645 to 98.645 scan no 14785 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

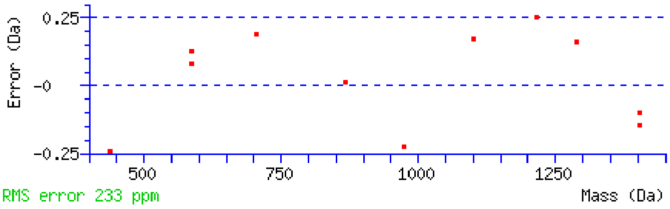
Show Y-axis ☐

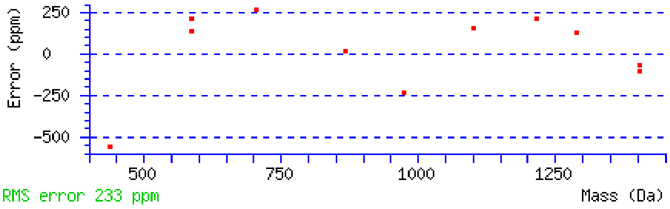


Monoisotopic mass of neutral peptide Mr(calc): 1988.8595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 5.7e-006
Matches : 11/152 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							16
2	245.1280	123.0676			227.1174	114.0624	E	1875.7857	938.3965	1857.7621	929.3847	1857.7751	929.3912	15
3	303.1465	152.0769			285.1359	143.0716	G	1745.7461	873.3767	1727.7225	864.3649	1727.7355	864.3714	14
4	401.1963	201.1018			383.1857	192.0965	P	1687.7276	844.3674	1669.7040	835.3556	1669.7170	835.3621	13
5	515.2774	258.1423			497.2668	249.1371	I	1589.6778	795.3425	1571.6542	786.3307	1571.6672	786.3372	12
6	**587.3115**	294.1594			569.3010	285.1541	A	1475.5967	738.3020	1457.5731	729.2902	1457.5861	729.2967	11
7	775.3849	388.1961			757.3744	379.1908	W	***1403.5625***	702.2849	1385.5389	693.2731	1385.5519	693.2796	10
8	891.4089	446.2081			873.3983	437.2028	D	***1215.4891***	608.2482	1197.4655	599.2364	1197.4786	599.2429	9
9	991.4744	496.2408			973.4638	487.2355	V	***1099.4651***	550.2362	1081.4416	541.2244	1081.4546	541.2309	8
10	1123.5119	562.2596			1105.5013	553.2543	M	999.3997	500.2035	981.3761	491.1917	981.3891	491.1982	7
11	**1287.5722**	644.2898			1269.5617	635.2845	Y	***867.3622***	434.1847	849.3386	425.1729	849.3516	425.1794	6
12	**1403.6092**	702.3083	1385.5857	693.2965	1385.5987	693.3030	N	***703.3018***	352.1545	685.2782	343.1428	685.2912	343.1493	5
13	1551.6747	776.3410	1533.6511	767.3292	1533.6641	767.3357	F	***587.2648***	294.1360	569.2412	285.1243	569.2543	285.1308	4
14	1681.7143	841.3608	1663.6907	832.3490	1663.7038	832.3555	E	***439.1994***	220.1033	421.1758	211.0915	421.1888	211.0980	3
15	1811.7670	906.3871	1793.7434	897.3753	1793.7564	897.3818	Q	309.1597	155.0835	291.1362	146.0717			2
16							R	179.1071	90.0572	161.0835	81.0454			1

AT3G15730.1





NCBI **BLAST** search of LEGPIAWDVMYNFEQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.3	1988.8595	-0.0047	LEGPIAWDVMYNFEQR
0.7	1988.8573	-0.0025	SSSTSWSIMFRTEYLR

Mascot: http://www.matrixscience.com/

AT3G16330.1

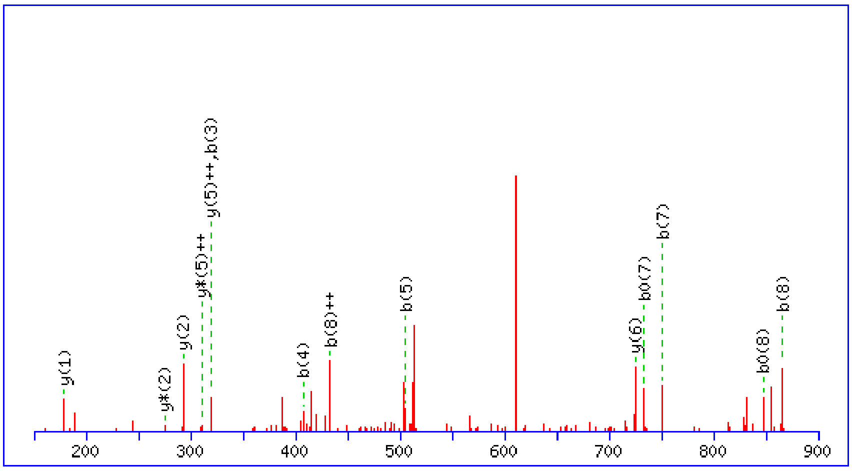
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTDSPFPLR**
Found in **AT3G16330.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52140.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64915.1) | chr3:5535269-5535886 FORWARD

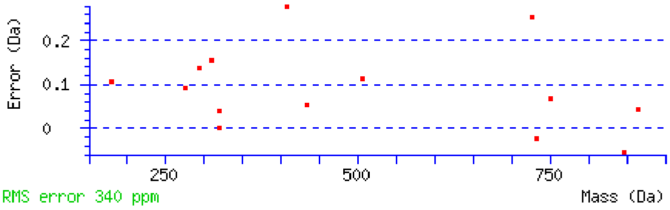
Match to Query 2829: 1042.511668 from(522.263110,2+) index(4454)
Title: Elution from: 42.043 to 42.043 scan no 5630 cid35.00 polarity:+
Data file 0-3_1.mgf

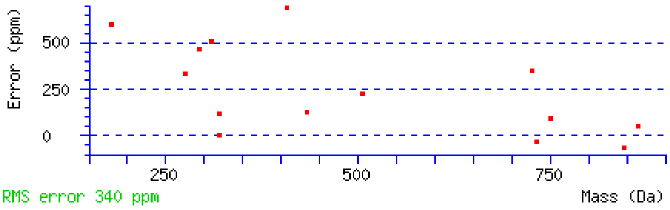
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1042.5092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.026
Matches : 14/68 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							9
2	203.1174	102.0624	185.1069	93.0571	T	943.4510	472.2291	925.4274	463.2173	925.4404	463.2239	8
3	***319.1414***	160.0743	301.1309	151.0691	D	841.4063	421.2068	823.3827	412.1950	823.3957	412.2015	7
4	***407.1705***	204.0889	389.1599	195.0836	S	**725.3823**	363.1948	707.3587	354.1830	707.3717	354.1895	6
5	***505.2203***	253.1138	487.2097	244.1085	P	637.3532	319.1803	619.3297	310.1685			5
6	653.2857	327.1465	635.2752	318.1412	F	539.3034	270.1554	521.2799	261.1436			4
7	***751.3355***	376.1714	733.3250	367.1661	P	391.2380	196.1226	373.2144	187.1108			3
8	***865.4166***	433.2120	847.4061	424.2067	L	**293.1882**	147.0977	275.1646	138.0859			2
9					R	**179.1071**	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VTDSPFPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G16330.1

23.9	1042.5092	0.0025	VTDSPFPLR
12.2	1042.5125	-0.0009	VSISPMEIR
10.0	1042.5125	-0.0009	SLDLAKPCK
7.5	1042.5118	-0.0002	FTQHNLLR
6.8	1042.5125	-0.0009	GPLESLMIR
6.7	1042.5125	-0.0009	ELGLALEMR
6.6	1042.5125	-0.0009	EMELQILR
6.2	1042.5125	-0.0009	LEELQLMR
5.2	1042.5092	0.0025	EEWVISIR
5.0	1042.5096	0.0021	SINQNAKPR

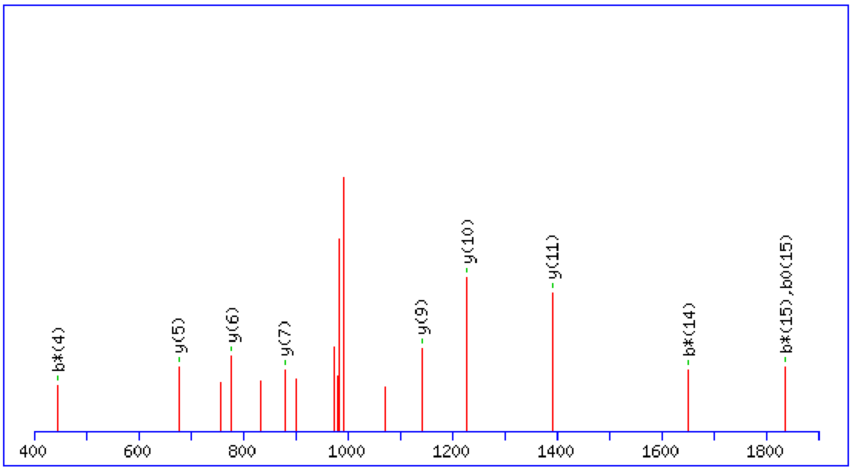
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYNGFYSFDTTTNEWK**
Found in **AT3G16400.1** in **TAIR_Arabidopsis**, Symbols: ATMLP-470 | ATMLP-470 (MYROSINASE-BINDING PROTEIN-LIKE PROTEIN-470) | chr3:5566522-5568336 FORWARD

Match to Query 9298: 1999.856156 from(1000.935354,2+) index(7989)
Title: Elution from: 71.602 to 71.602 scan no 10590 cid35.00 polarity:+
Data file 0-1_2.mgf

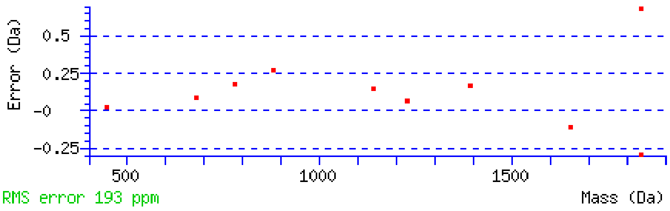
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

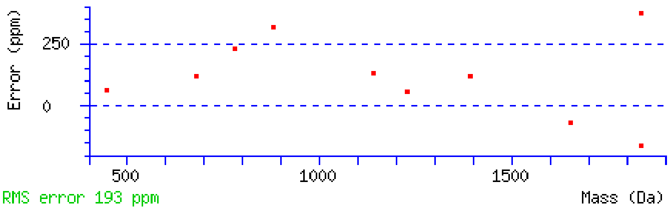


Monoisotopic mass of neutral peptide Mr(calc): 1999.8588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00011
Matches : 10/164 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							16
2	292.1292	146.5682	275.1026	138.0550			Y	1872.8075	936.9074	1855.7810	928.3941	1854.7970	927.9021	15
3	406.1721	203.5897	389.1456	195.0764			N	1709.7442	855.3757	1692.7176	846.8625	1691.7336	846.3705	14
4	463.1936	232.1004	446.1670	223.5872			G	1595.7013	798.3543	1578.6747	789.8410	1577.6907	789.3490	13
5	610.2620	305.6346	593.2354	297.1214			F	1538.6798	769.8435	1521.6533	761.3303	1520.6692	760.8383	12
6	773.3253	387.1663	756.2988	378.6530			Y	***1391.6114***	696.3093	1374.5848	687.7961	1373.6008	687.3040	11
7	860.3573	430.6823	843.3308	422.1690	842.3468	421.6770	S	***1228.5481***	614.7777	1211.5215	606.2644	1210.5375	605.7724	10
8	1007.4258	504.2165	990.3992	495.7032	989.4152	495.2112	F	***1141.5160***	571.2617	1124.4895	562.7484	1123.5055	562.2564	9
9	1122.4527	561.7300	1105.4262	553.2167	1104.4421	552.7247	D	994.4476	497.7274	977.4211	489.2142	976.4371	488.7222	8
10	1223.5004	612.2538	1206.4738	603.7406	1205.4898	603.2485	T	***879.4207***	440.2140	862.3941	431.7007	861.4101	431.2087	7
11	1324.5481	662.7777	1307.5215	654.2644	1306.5375	653.7724	T	***778.3730***	389.6901	761.3464	381.1769	760.3624	380.6849	6
12	1425.5957	713.3015	1408.5692	704.7882	1407.5852	704.2962	T	***677.3253***	339.1663	660.2988	330.6530	659.3148	330.1610	5
13	1539.6387	770.3230	1522.6121	761.8097	1521.6281	761.3177	N	576.2776	288.6425	559.2511	280.1292	558.2671	279.6372	4
14	1668.6813	834.8443	1651.6547	826.3310	1650.6707	825.8390	E	462.2347	231.6210	445.2082	223.1077	444.2241	222.6157	3
15	1854.7606	927.8839	1837.7340	919.3706	1836.7500	918.8786	W	333.1921	167.0997	316.1656	158.5864			2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT3G16400.1





NCBI **BLAST** search of QYNGFYSFDTTTNEWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.1	1999.8588	-0.0027	QYNGFYSFDTTTNEWK

Mascot: http://www.matrixscience.com/

AT3G16410.1

{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WTQVETFGVRPSER**
Found in **AT3G16410.1** in **TAIR_Arabidopsis**, Symbols: | jacalin lectin family protein | chr3:5572151-5574365 FORWARD

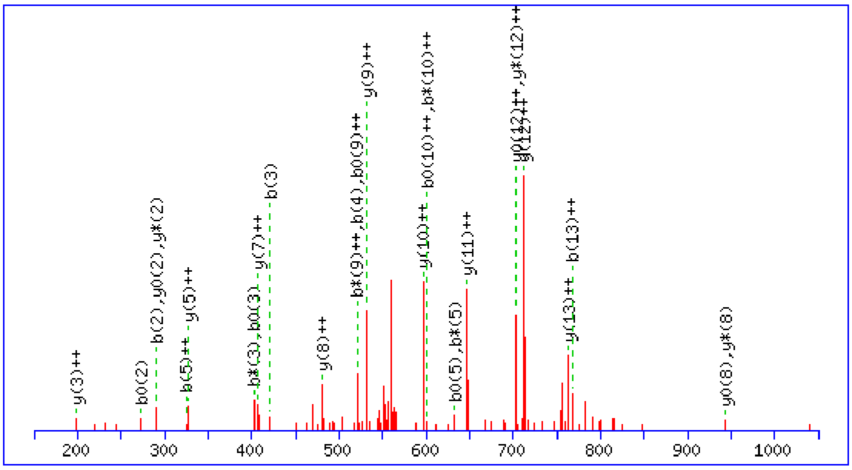
Match to Query 8033: 1712.773668 from(571.931832,3+) index(4273)
Title: Elution from: 39.537 to 39.537 scan no 5369 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1050 Da Full range

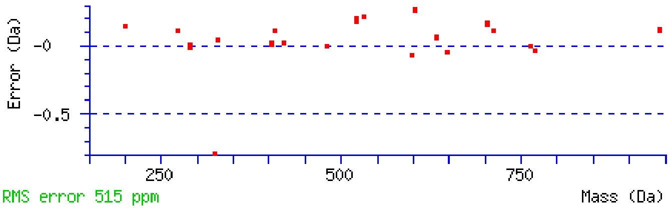
Label all possible matches ○ Label matches used for scoring ●

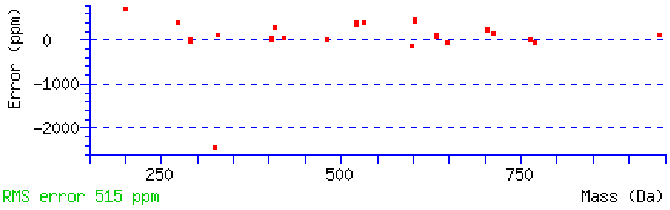
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1712.7775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 4.6e-005
Matches : 30/148 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	189.0807	95.0440					**W**							**14**
2	**291.1254**	146.0663			273.1148	137.0610	**T**	1525.7114	763.3593	1507.6878	754.3475	1507.7008	754.3540	**13**
3	**421.1780**	211.0926	403.1544	202.0809	403.1675	202.0874	**Q**	1423.6667	712.3370	1405.6431	703.3252	1405.6561	703.3317	**12**
4	**521.2435**	261.1254	503.2199	252.1136	503.2329	252.1201	**V**	1293.6140	647.3106	1275.5904	638.2989	1275.6035	638.3054	**11**
5	651.2831	**326.1452**	633.2595	317.1334	633.2725	317.1399	**E**	1193.5486	597.2779	1175.5250	588.2661	1175.5380	588.2726	**10**
6	753.3278	377.1675	735.3042	368.1558	735.3172	368.1623	**T**	1063.5089	532.2581	1045.4854	523.2463	1045.4984	523.2528	**9**
7	901.3933	451.2003	883.3697	442.1885	883.3827	442.1950	**F**	961.4642	481.2358	943.4406	472.2240	943.4537	472.2305	**8**
8	959.4118	480.2095	941.3882	471.1977	941.4012	471.2042	**G**	813.3988	407.2030	795.3752	398.1912	795.3882	398.1977	**7**
9	1059.4772	530.2422	1041.4536	521.2304	1041.4666	521.2370	**V**	755.3803	378.1938	737.3567	369.1820	737.3697	369.1885	**6**
10	1219.5665	610.2869	1201.5429	601.2751	1201.5559	601.2816	**R**	655.3148	328.1611	637.2912	319.1493	637.3043	319.1558	**5**
11	1317.6163	659.3118	1299.5927	650.3000	1299.6057	650.3065	**P**	495.2256	248.1164	477.2020	239.1046	477.2150	239.1111	**4**
12	1405.6453	**703.3263**	1387.6217	694.3145	1387.6348	694.3210	**S**	397.1758	199.0915	379.1522	190.0797	379.1652	190.0862	**3**
13	1535.6849	**768.3461**	1517.6614	759.3343	1517.6744	759.3408	**E**	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	**2**
14							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of WTQVETFGVRPSER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G16410.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.3	1712.7775	-0.0038	WTQVETFGVRPSER
15.5	1712.7752	-0.0016	ANTKTAENGSDRLWK
13.8	1712.7752	-0.0016	REEQPRDLYLSER
4.5	1712.7759	-0.0023	SVMEEGSEIGEKVRK
3.9	1712.7703	0.0034	DSVDLDTNVSGSRVTK

Mascot: http://www.matrixscience.com/

AT3G16420.1

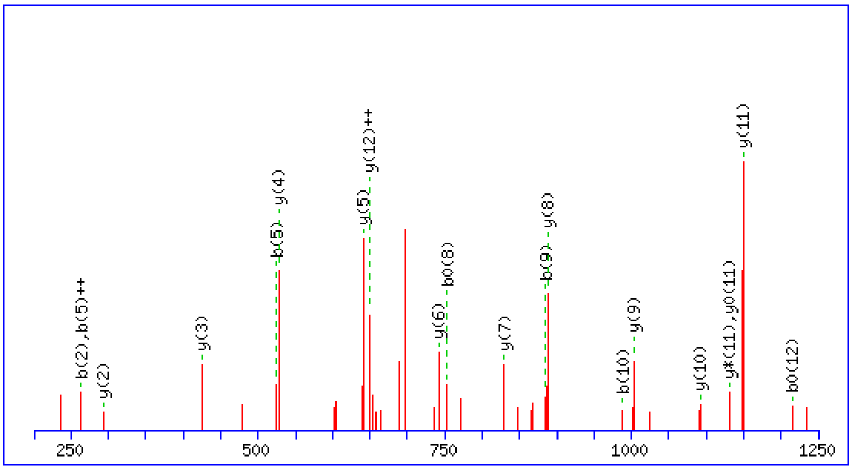
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFGSDGSVITMLR**
Found in **AT3G16420.1** in **TAIR_Arabidopsis**, Symbols: PBP1 | PBP1 (PYK10-BINDING PROTEIN 1) | chr3:5579566-5580680 FORWARD

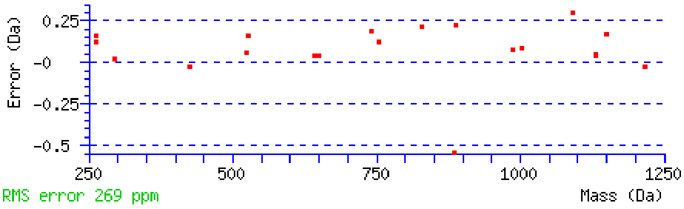
Match to Query 5625: 1410.676246 from(706.345399,2+) index(8748)
Title: Elution from: 77.227 to 77.227 scan no 11596 cid35.00 polarity:+
Data file C7-2_2.mgf

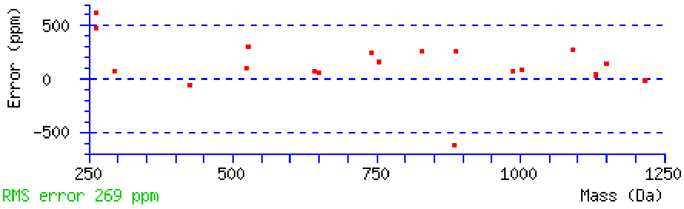
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1410.6753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 6.5e-009
Matches : 20/108 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			I							13
2	**263.1538**	132.0805			F	1297.6015	649.3044	1279.5779	640.2926	1279.5910	640.2991	12
3	321.1723	161.0898			G	***1149.5361***	575.2717	1131.5125	566.2599	1131.5255	566.2664	11
4	409.2014	205.1043	391.1908	196.0990	S	***1091.5176***	546.2624	1073.4940	537.2506	1073.5070	537.2571	10
5	**525.2254**	263.1163	507.2148	254.1110	D	***1003.4885***	502.2479	985.4649	493.2361	985.4779	493.2426	9
6	583.2439	292.1256	565.2333	283.1203	G	***887.4645***	444.2359	869.4409	435.2241	869.4540	435.2306	8
7	671.2729	336.1401	653.2624	327.1348	S	***829.4460***	415.2267	811.4225	406.2149	811.4355	406.2214	7
8	771.3384	386.1728	753.3278	377.1675	V	***741.4170***	371.2121	723.3934	362.2003	723.4064	362.2068	6
9	**885.4195**	443.2134	867.4089	434.2081	I	***641.3515***	321.1794	623.3279	312.1676	623.3410	312.1741	5
10	**987.4642**	494.2357	969.4536	485.2304	T	***527.2704***	264.1389	509.2468	255.1271	509.2599	255.1336	4
11	1119.5017	560.2545	1101.4911	551.2492	M	***425.2257***	213.1165	407.2021	204.1047			3
12	1233.5828	617.2950	1215.5722	608.2898	L	***293.1882***	147.0977	275.1646	138.0859			2
13					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IFGSDGSVITMLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G16420.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.2	1410.6753	0.0009	IFGSDGSVITMLR
10.7	1410.6787	-0.0025	LMSVITGRDMIK
9.4	1410.6740	0.0023	MMIELLCKGKR
9.4	1410.6740	0.0023	MMIELLCKGKR
8.7	1410.6780	-0.0017	VRFEDIGRCLK
8.3	1410.6724	0.0039	EFSGVGRQEVRK
7.0	1410.6724	0.0038	KLEEYRGNLNR
3.8	1410.6796	-0.0033	FLPSSRWRWR
1.5	1410.6758	0.0005	EAGIMTSSGRRVK
0.3	1410.6746	0.0016	KEGYKITGFHGR

AT3G16450.1

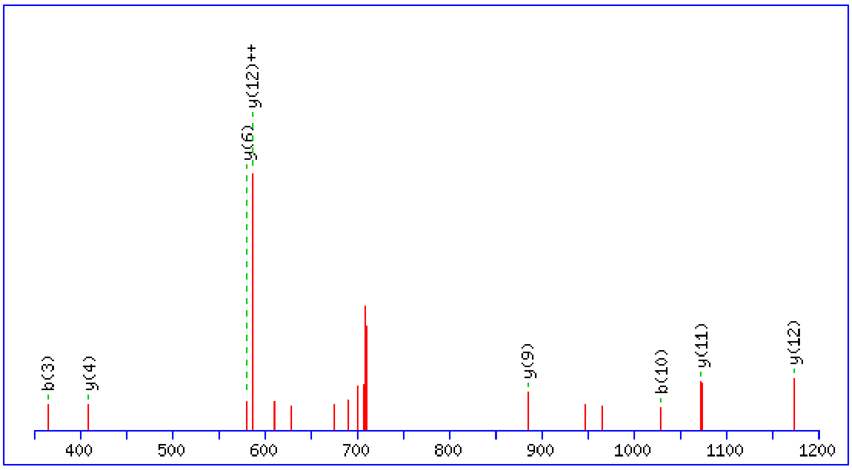
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYVGQGQDGISAVK**
Found in **AT3G16450.1** in **TAIR_Arabidopsis**, Symbols: | jacalin lectin family protein | chr3:5588599-5589798 FORWARD

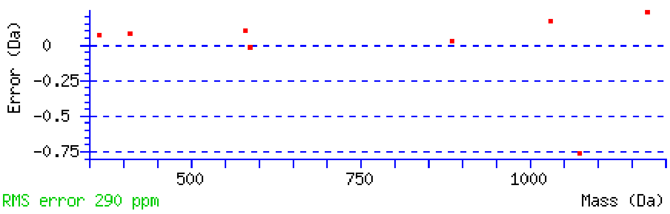
Match to Query 5620: 1436.686480 from(719.350516,2+) index(2821)
Title: Elution from: 31.760 to 31.760 scan no 3650 cid35.00 polarity:+
Data file D12h-2_1.mgf

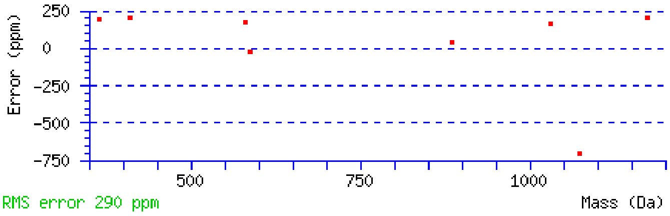
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1436.6853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0023
Matches : 8/128 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							14
2	265.1331	133.0702					Y	1337.6272	669.3172	1319.6036	660.3055	1319.6167	660.3120	13
3	**365.1985**	183.1029					V	***1173.5669***	587.2871	1155.5433	578.2753	1155.5563	578.2818	12
4	423.2170	212.1122					G	***1073.5014***	537.2543	1055.4778	528.2425	1055.4908	528.2491	11
5	553.2697	277.1385	535.2461	268.1267			Q	1015.4829	508.2451	997.4593	499.2333	997.4723	499.2398	10
6	611.2882	306.1477	593.2646	297.1359			G	***885.4303***	443.2188	867.4067	434.2070	867.4197	434.2135	9
7	741.3408	371.1741	723.3172	362.1623			Q	827.4118	414.2095	809.3882	405.1977	809.4012	405.2042	8
8	857.3648	429.1860	839.3412	420.1743	839.3542	420.1808	D	697.3591	349.1832	679.3355	340.1714	679.3485	340.1779	7
9	915.3833	458.1953	897.3597	449.1835	897.3727	449.1900	G	***581.3351***	291.1712	563.3115	282.1594	563.3246	282.1659	6
10	**1029.4644**	515.2358	1011.4408	506.2240	1011.4538	506.2306	I	523.3166	262.1620	505.2930	253.1502	505.3061	253.1567	5
11	1117.4935	559.2504	1099.4699	550.2386	1099.4829	550.2451	S	***409.2355***	205.1214	391.2120	196.1096	391.2250	196.1161	4
12	1189.5276	595.2674	1171.5040	586.2557	1171.5171	586.2622	A	321.2065	161.1069	303.1829	152.0951			3
13	1289.5931	645.3002	1271.5695	636.2884	1271.5825	636.2949	V	249.1723	125.0898	231.1487	116.0780			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VYVGQGQDGISAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G16450.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.6	1436.6853	0.0011	VYVGQGQDGISAVK
7.7	1436.6858	0.0007	RSASNTTPSAAVVR
6.5	1436.6840	0.0025	GMLMNGTEIAVKR
4.4	1436.6833	0.0032	DFVGALRMAHKR
3.7	1436.6903	-0.0038	NFLSHIQKEFR
3.3	1436.6888	-0.0023	MIEKIARDVSDK
3.0	1436.6858	0.0007	RNSSGAVTTAIPSR
2.1	1436.6863	0.0002	KYMALVIGCPPR
1.8	1436.6876	-0.0011	LLSEYGQALWNK
1.5	1436.6880	-0.0016	RVFNELQAGLDR

AT3G16460.1

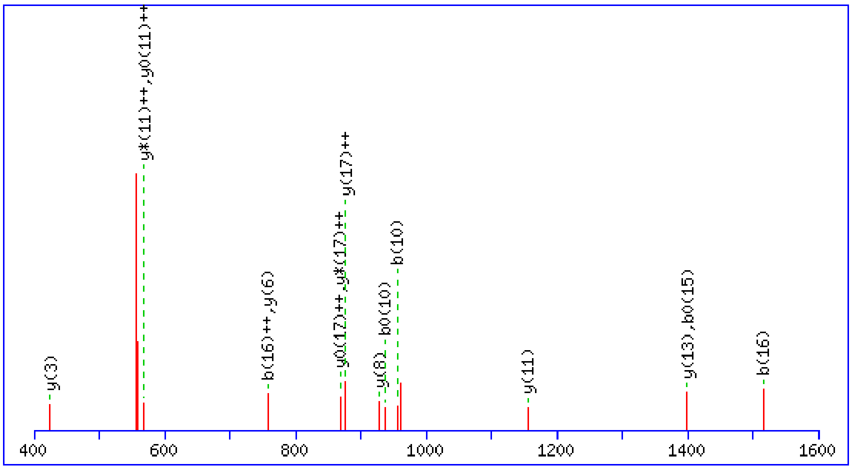
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVGQAQDGIGAVSFVYDK**
Found in **AT3G16460.1** in **TAIR_Arabidopsis**, Symbols: | jacalin lectin family protein | chr3:5593035-5595528 FORWARD

Match to Query 9023: 1938.968902 from(970.491727,2+) index(7471)
Title: Elution from: 66.567 to 66.567 scan no 9845 cid35.00 polarity:+
Data file 0-2_2.mgf

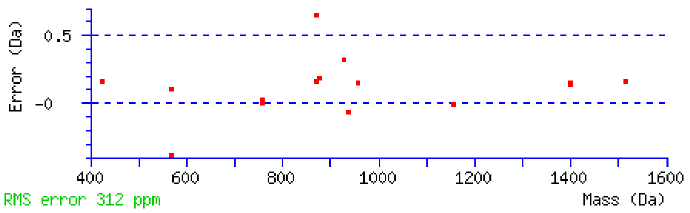
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

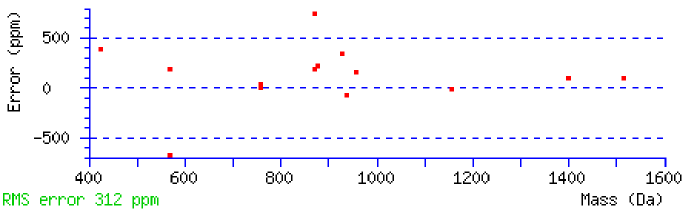


Monoisotopic mass of neutral peptide Mr(calc): 1938.9687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.002
Matches : 15/204 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							19
2	187.1077	94.0575			169.0972	85.0522	S	1840.9076	920.9574	1823.8810	912.4441	1822.8970	911.9521	18
3	286.1761	143.5917			268.1656	134.5864	V	1753.8755	877.4414	1736.8490	868.9281	1735.8650	868.4361	17
4	343.1976	172.1024			325.1870	163.0972	G	1654.8071	827.9072	1637.7806	819.3939	1636.7966	818.9019	16
5	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	Q	1597.7857	799.3965	1580.7591	790.8832	1579.7751	790.3912	15
6	542.2933	271.6503	525.2667	263.1370	524.2827	262.6450	A	1469.7271	735.3672	1452.7005	726.8539	1451.7165	726.3619	14
7	670.3519	335.6796	653.3253	327.1663	652.3413	326.6743	Q	***1398.6900***	699.8486	1381.6634	691.3354	1380.6794	690.8433	13
8	785.3788	393.1930	768.3523	384.6798	767.3682	384.1878	D	1270.6314	635.8193	1253.6048	627.3061	1252.6208	626.8141	12
9	842.4003	421.7038	825.3737	413.1905	824.3897	412.6985	G	***1155.6045***	578.3059	1138.5779	569.7926	1137.5939	569.3006	11
10	**955.4843**	478.2458	938.4578	469.7325	937.4738	469.2405	I	1098.5830	549.7951	1081.5564	541.2819	1080.5724	540.7898	10
11	1012.5058	506.7565	995.4793	498.2433	994.4952	497.7513	G	985.4989	493.2531	968.4724	484.7398	967.4884	484.2478	9
12	1083.5429	542.2751	1066.5164	533.7618	1065.5324	533.2698	A	***928.4775***	464.7424	911.4509	456.2291	910.4669	455.7371	8
13	1182.6113	591.8093	1165.5848	583.2960	1164.6008	582.8040	V	857.4403	429.2238	840.4138	420.7105	839.4298	420.2185	7
14	1269.6434	635.3253	1252.6168	626.8120	1251.6328	626.3200	S	***758.3719***	379.6896	741.3454	371.1763	740.3614	370.6843	6
15	1416.7118	708.8595	1399.6852	700.3462	1398.7012	699.8542	F	671.3399	336.1736	654.3134	327.6603	653.3293	327.1683	5
16	**1515.7802**	758.3937	1498.7536	749.8805	1497.7696	749.3884	V	524.2715	262.6394	507.2449	254.1261	506.2609	253.6341	4
17	1678.8435	839.9254	1661.8170	831.4121	1660.8329	830.9201	Y	***425.2031***	213.1052	408.1765	204.5919	407.1925	204.0999	3
18	1793.8705	897.4389	1776.8439	888.9256	1775.8599	888.4336	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT3G16460.1





NCBI **BLAST** search of VSVGQAQDGIGAVSFVYDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.2	1938.9687	0.0002	VSVGQAQDGIGAVSFVYDK
1.7	1938.9647	0.0042	ASGIVEGGGSLSDVYSSAKR

Mascot: http://www.matrixscience.com/

AT3G16470.1

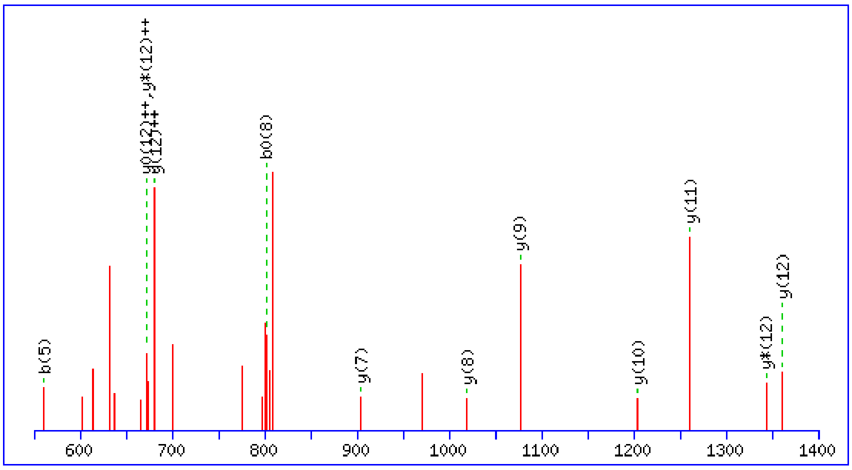
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYVGQGDSCVTYFK**
Found in **AT3G16470.1** in **TAIR_Arabidopsis**, Symbols: JR1 | JR1 (Jacalin lectin family protein) | chr3:5596102-5597715 REVERSE

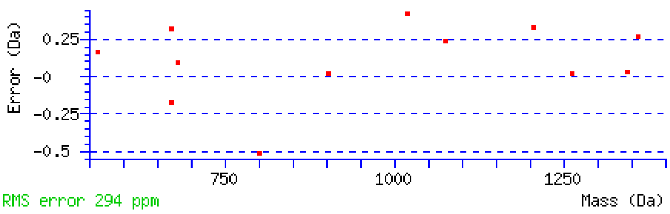
Match to Query 7326: 1635.756804 from(818.885678,2+) index(5453)
Title: Elution from: 51.972 to 51.972 scan no 7048 cid35.00 polarity:+
Data file D1d-1_1.mgf

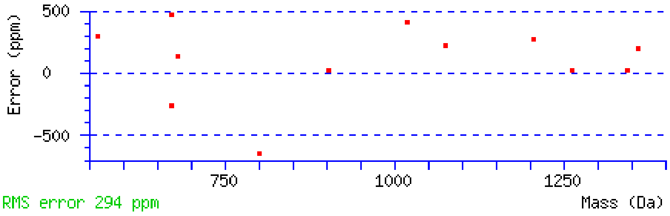
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1635.7603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00027
Matches : 14/130 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							14
2	277.1547	139.0810					Y	1523.6835	762.3454	1506.6570	753.8321	1505.6729	753.3401	13
3	376.2231	188.6152					V	***1360.6202***	680.8137	1343.5936	672.3005	1342.6096	671.8084	12
4	433.2445	217.1259					G	***1261.5518***	631.2795	1244.5252	622.7662	1243.5412	622.2742	11
5	**561.3031**	281.1552	544.2766	272.6419			Q	***1204.5303***	602.7688	1187.5038	594.2555	1186.5197	593.7635	10
6	618.3246	309.6659	601.2980	301.1527			G	***1076.4717***	538.7395	1059.4452	530.2262	1058.4612	529.7342	9
7	733.3515	367.1794	716.3250	358.6661	715.3410	358.1741	D	***1019.4503***	510.2288	1002.4237	501.7155	1001.4397	501.2235	8
8	820.3836	410.6954	803.3570	402.1821	802.3730	401.6901	S	***904.4233***	452.7153	887.3968	444.2020	886.4128	443.7100	7
9	980.4142	490.7107	963.3877	482.1975	962.4036	481.7055	C	817.3913	409.1993	800.3647	400.6860	799.3807	400.1940	6
10	1079.4826	540.2449	1062.4561	531.7317	1061.4721	531.2397	V	657.3606	329.1840	640.3341	320.6707	639.3501	320.1787	5
11	1180.5303	590.7688	1163.5038	582.2555	1162.5197	581.7635	T	558.2922	279.6498	541.2657	271.1365	540.2817	270.6445	4
12	**1343.5936**	672.3005	1326.5671	663.7872	1325.5831	663.2952	Y	457.2445	229.1259	440.2180	220.6126			3
13	1490.6620	745.8347	1473.6355	737.3214	1472.6515	736.8294	F	294.1812	147.5942	277.1547	139.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IYVGQGDSCVTYFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G16470.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.9	1635.7603	-0.0035	IYVGQGDSCVTYFK
1.2	1635.7562	0.0006	KNSSSGSASNMFYIK
1.1	1635.7542	0.0026	FEWWAKGNNNNTR

AT3G16640.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSEEDQAVFKK**
Found in **AT3G16640.1** in **TAIR_Arabidopsis**, Symbols: TCTP | TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) | chr3:5669715-5670735 REVERSE

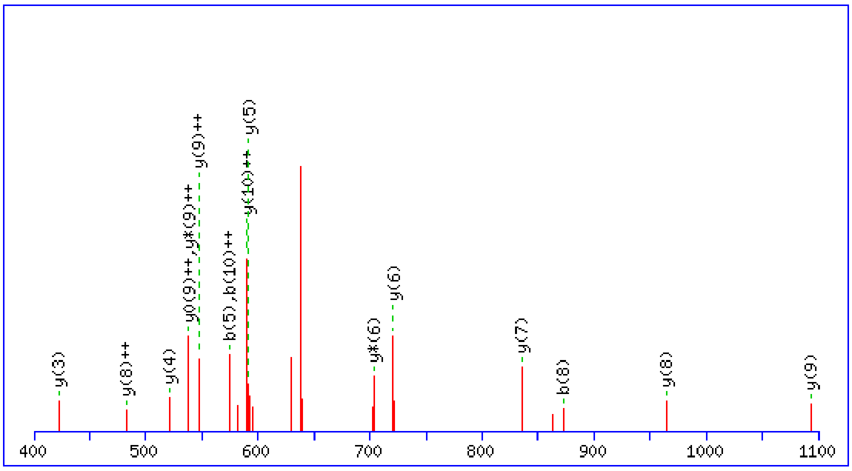
Match to Query 4760: 1292.658974 from(647.336763,2+) index(1838)
Title: Elution from: 22.394 to 22.394 scan no 2394 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1100 Da Full range

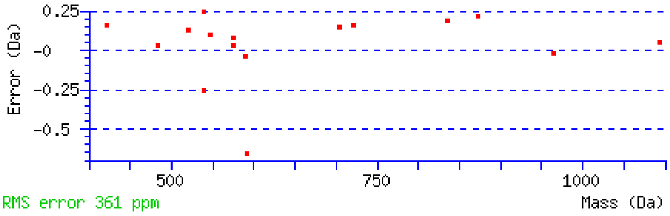
Label all possible matches ○ Label matches used for scoring ●

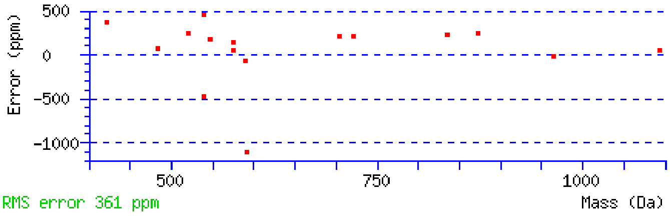
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1292.6612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 4.4e-007
Matches : 16/96 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	201.1234	101.0653			183.1128	92.0600	S	1180.5844	590.7959	1163.5579	582.2826	1162.5739	581.7906	10
3	330.1660	165.5866			312.1554	156.5813	E	***1093.5524***	547.2798	1076.5259	538.7666	1075.5419	538.2746	9
4	459.2086	230.1079			441.1980	221.1026	E	***964.5098***	482.7585	947.4833	474.2453	946.4993	473.7533	8
5	**574.2355**	287.6214			556.2249	278.6161	D	***835.4672***	418.2373	818.4407	409.7240	817.4567	409.2320	7
6	702.2941	351.6507	685.2675	343.1374	684.2835	342.6454	Q	***720.4403***	360.7238	703.4137	352.2105			6
7	773.3312	387.1692	756.3046	378.6560	755.3206	378.1640	A	***592.3817***	296.6945	575.3552	288.1812			5
8	**872.3996**	436.7034	855.3731	428.1902	854.3890	427.6982	V	***521.3446***	261.1759	504.3180	252.6627			4
9	1019.4680	510.2376	1002.4415	501.7244	1001.4575	501.2324	F	***422.2762***	211.6417	405.2496	203.1285			3
10	1147.5630	574.2851	1130.5364	565.7719	1129.5524	565.2798	K	275.2078	138.1075	258.1812	129.5942			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LSEEDQAVFKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G16640.1

Score	Mr(calc)	Delta	Sequence
70.0	1292.6612	-0.0022	LSEEDQAVFKK
20.8	1292.6612	-0.0022	TVEEIFSALER
11.4	1292.6580	0.0009	ATKMAGAAMNLAK
3.2	1292.6580	0.0009	ATKMAGAAMNLAK
3.1	1292.6612	-0.0022	SFLDEKAQDLK
2.6	1292.6560	0.0029	NHWHVVMARK
0.8	1292.6612	-0.0022	AEPTPAPPKEEK

Mascot Search Results

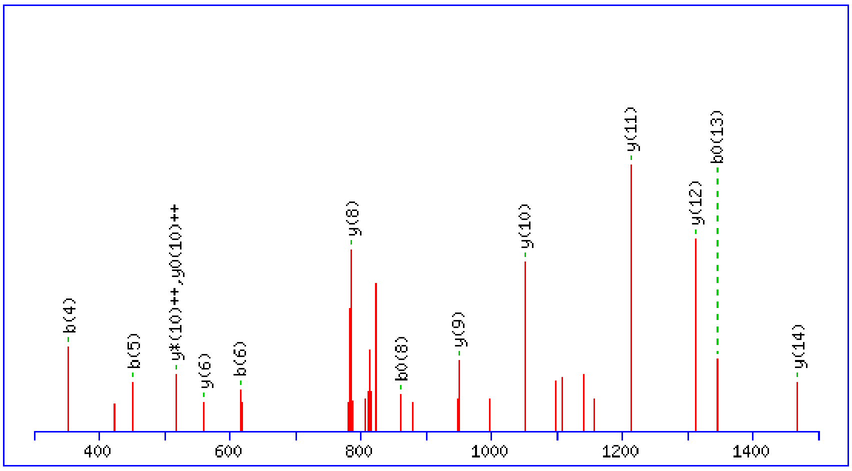
Peptide View

MS/MS Fragmentation of **VPGVVYTYPEVASVGK**
Found in **AT3G17240.1** in **TAIR_Arabidopsis**, Symbols: LPD2 | LPD2 (LIPOAMIDE DEHYDROGENASE 2); FAD binding / dihydrolipoyl dehydrogenase/ oxidoreductase | chr3:5890284-5892172 REVERSE

Match to Query 7763: 1663.880756 from(832.947654,2+) index(6328)
Title: Elution from: 58.134 to 58.134 scan no 8196 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

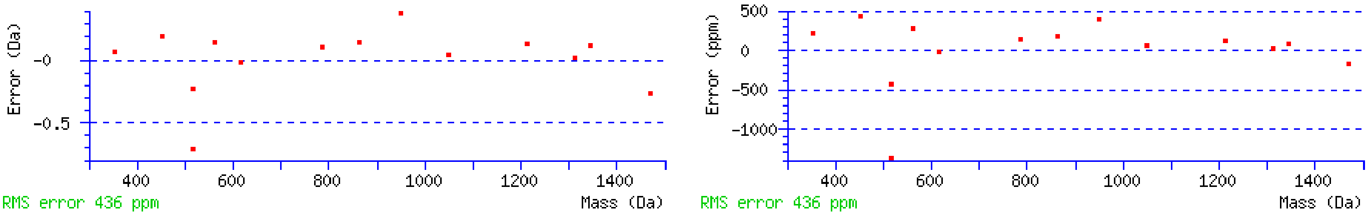
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1663.8821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 2.3e-005
Matches : 14/132 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415			**V**							**16**
2	197.1285	99.0679			**P**	1565.8210	783.4141	1548.7944	774.9009	1547.8104	774.4088	**15**
3	254.1499	127.5786			**G**	***1468.7682***	734.8878	1451.7417	726.3745	1450.7577	725.8825	**14**
4	**353.2183**	177.1128			**V**	1411.7468	706.3770	1394.7202	697.8637	1393.7362	697.3717	**13**
5	**452.2867**	226.6470			**V**	***1312.6783***	656.8428	1295.6518	648.3295	1294.6678	647.8375	**12**
6	**615.3501**	308.1787			**Y**	***1213.6099***	607.3086	1196.5834	598.7953	1195.5994	598.3033	**11**
7	716.3978	358.7025	698.3872	349.6972	**T**	***1050.5466***	525.7769	1033.5201	517.2637	1032.5360	516.7717	**10**
8	879.4611	440.2342	861.4505	431.2289	**Y**	***949.4989***	475.2531	932.4724	466.7398	931.4884	466.2478	**9**
9	976.5138	488.7606	958.5033	479.7553	**P**	***786.4356***	393.7214	769.4090	385.2082	768.4250	384.7162	**8**
10	1105.5564	553.2819	1087.5459	544.2766	**E**	689.3828	345.1951	672.3563	336.6818	671.3723	336.1898	**7**
11	1204.6249	602.8161	1186.6143	593.8108	**V**	***560.3402***	280.6738	543.3137	272.1605	542.3297	271.6685	**6**
12	1275.6620	638.3346	1257.6514	629.3293	**A**	461.2718	231.1396	444.2453	222.6263	443.2613	222.1343	**5**
13	1362.6940	681.8506	1344.6834	672.8454	**S**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
14	1461.7624	731.3848	1443.7518	722.3796	**V**	303.2027	152.1050	286.1761	143.5917			**3**
15	1518.7839	759.8956	1500.7733	750.8903	**G**	204.1343	102.5708	187.1077	94.0575			**2**
16					**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT3G17240.1



NCBI **BLAST** search of VPGVVYTYPEVASVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.0	1663.8821	-0.0014	VPGVVYTYPEVASVGK

AT3G17390.1

MATRIX SCIENCE Mascot Search Results

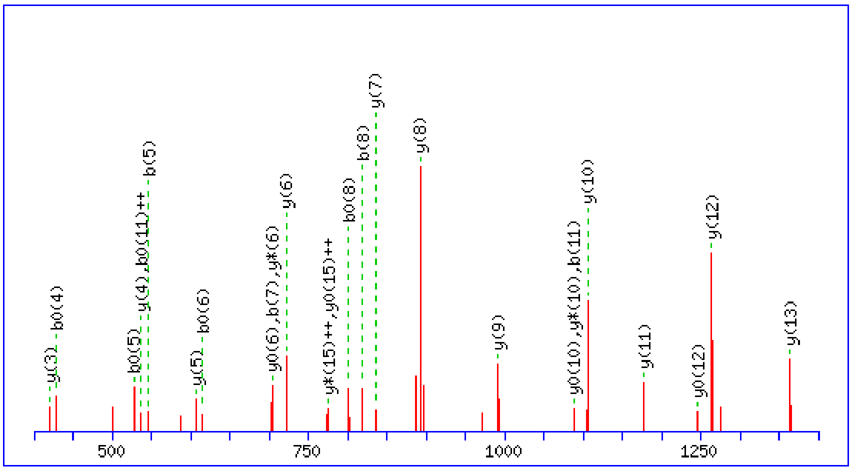
Peptide View

MS/MS Fragmentation of **EIGFVSADVGLDADNCK**
Found in **AT3G17390.1** in **TAIR_Arabidopsis**, Symbols: SAMS3, MAT4, MTO3 | MTO3 (S-adenosylmethionine synthase 3); methionine adenosyltransferase | chr3:5952490-5953671 REVERSE

Match to Query 8159: 1808.823268 from(905.418910,2+) index(6637)
Title: Elution from: 62.664 to 62.664 scan no 8772 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

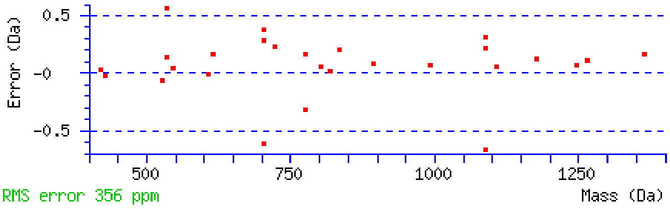
Or, Plot from 400 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

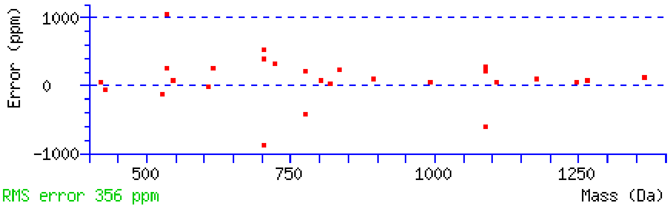


Monoisotopic mass of neutral peptide Mr(calc): 1808.8251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 3e-008
Matches : 27/158 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	243.1339	122.0706			225.1234	113.0653	I	1680.7898	840.8985	1663.7632	832.3852	1662.7792	831.8932	16
3	300.1554	150.5813			282.1448	141.5761	G	1567.7057	784.3565	1550.6792	775.8432	1549.6951	775.3512	15
4	447.2238	224.1155			429.2132	215.1103	F	1510.6842	755.8458	1493.6577	747.3325	1492.6737	746.8405	14
5	**546.2922**	273.6498			528.2817	264.6445	V	***1363.6158***	682.3115	1346.5893	673.7983	1345.6053	673.3063	13
6	633.3243	317.1658			615.3137	308.1605	S	***1264.5474***	632.7773	1247.5209	624.2641	1246.5368	623.7721	12
7	**704.3614**	352.6843			686.3508	343.6790	A	***1177.5154***	589.2613	1160.4888	580.7481	1159.5048	580.2560	11
8	**819.3883**	410.1978			801.3777	401.1925	D	***1106.4783***	553.7428	1089.4517	545.2295	1088.4677	544.7375	10
9	918.4567	459.7320			900.4462	450.7267	V	***991.4513***	496.2293	974.4248	487.7160	973.4408	487.2240	9
10	975.4782	488.2427			957.4676	479.2374	G	***892.3829***	446.6951	875.3564	438.1818	874.3723	437.6898	8
11	**1088.5623**	544.7848			1070.5517	535.7795	L	***835.3614***	418.1844	818.3349	409.6711	817.3509	409.1791	7
12	1203.5892	602.2982			1185.5786	593.2930	D	***722.2774***	361.6423	705.2508	353.1291	704.2668	352.6370	6
13	1274.6263	637.8168			1256.6157	628.8115	A	***607.2504***	304.1289	590.2239	295.6156	589.2399	295.1236	5
14	1389.6533	695.3303			1371.6427	686.3250	D	***536.2133***	268.6103	519.1868	260.0970	518.2028	259.6050	4
15	1503.6962	752.3517	1486.6696	743.8385	1485.6856	743.3464	N	***421.1864***	211.0968	404.1598	202.5836			3
16	1663.7268	832.3671	1646.7003	823.8538	1645.7163	823.3618	C	307.1435	154.0754	290.1169	145.5621			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT3G17390.1





NCBI **BLAST** search of EIGFVSADVGLDADNCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.8	1808.8251	-0.0018	EIGFVSADVGLDADNCK

Mascot: http://www.matrixscience.com/

AT3G18190.1

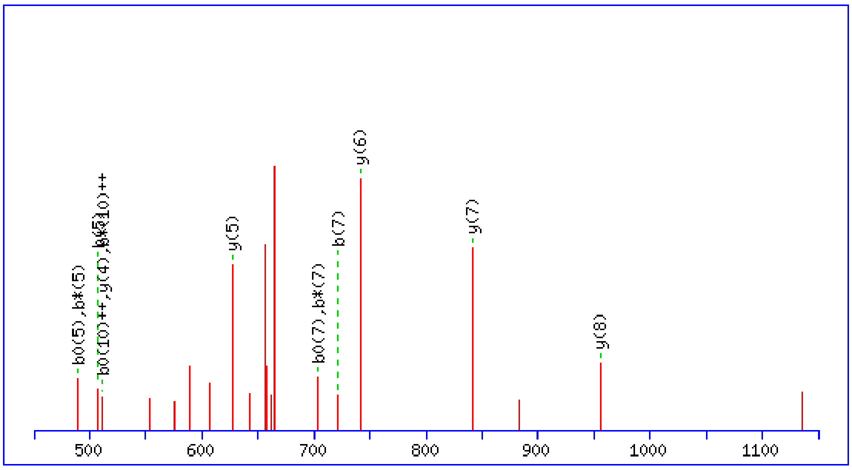
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSNQLVLDEAER**
Found in **AT3G18190.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr3:6232232-6233842 FORWARD

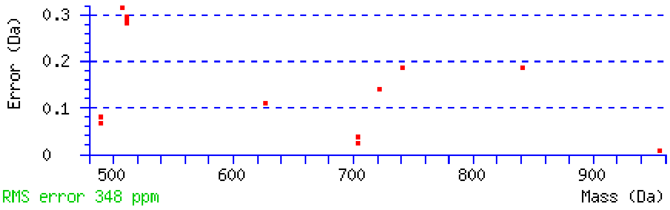
Match to Query 4891: 1346.601464 from(674.308008,2+) index(3082)
Title: Elution from: 32.903 to 32.903 scan no 3920 cid35.00 polarity:+
Data file D1d-2_1.mgf

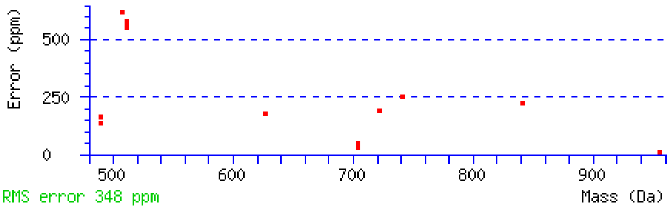
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1346.6020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00052
Matches : 13/124 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							12
2	147.0548	74.0311			129.0443	65.0258	S	1289.5908	645.2991	1271.5672	636.2873	1271.5803	636.2938	11
3	263.0918	132.0496	245.0683	123.0378	245.0813	123.0443	N	1201.5618	601.2845	1183.5382	592.2727	1183.5512	592.2792	10
4	393.1445	197.0759	375.1209	188.0641	375.1339	188.0706	Q	1085.5248	543.2660	1067.5012	534.2542	1067.5142	534.2607	9
5	**507.2256**	254.1164	489.2020	245.1046	489.2150	245.1111	L	***955.4721***	478.2397	937.4485	469.2279	937.4616	469.2344	8
6	607.2910	304.1492	589.2674	295.1374	589.2805	295.1439	V	***841.3910***	421.1991	823.3674	412.1874	823.3805	412.1939	7
7	**721.3721**	361.1897	703.3485	352.1779	703.3616	352.1844	L	***741.3256***	371.1664	723.3020	362.1546	723.3150	362.1611	6
8	837.3961	419.2017	819.3725	410.1899	819.3855	410.1964	D	***627.2445***	314.1259	609.2209	305.1141	609.2339	305.1206	5
9	967.4357	484.2215	949.4122	475.2097	949.4252	475.2162	E	***511.2205***	256.1139	493.1969	247.1021	493.2099	247.1086	4
10	1039.4699	520.2386	1021.4463	511.2268	1021.4593	511.2333	A	381.1809	191.0941	363.1573	182.0823	363.1703	182.0888	3
11	1169.5095	585.2584	1151.4859	576.2466	1151.4989	576.2531	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GSNQLVLDEAER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G18190.1

Score	Mr(calc)	Delta	Sequence
40.5	1346.6020	-0.0006	GSNQLVLDEAER
12.4	1346.5995	0.0019	QAGRYMAVYQK
5.1	1346.5995	0.0019	STCIASLWQHK
1.8	1346.6043	-0.0028	IFQELNSEHSK

AT3G18240.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANKIAEDIR**
Found in **AT3G18240.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21460.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68106.1) | chr3:6255816-6257701 FORWARD

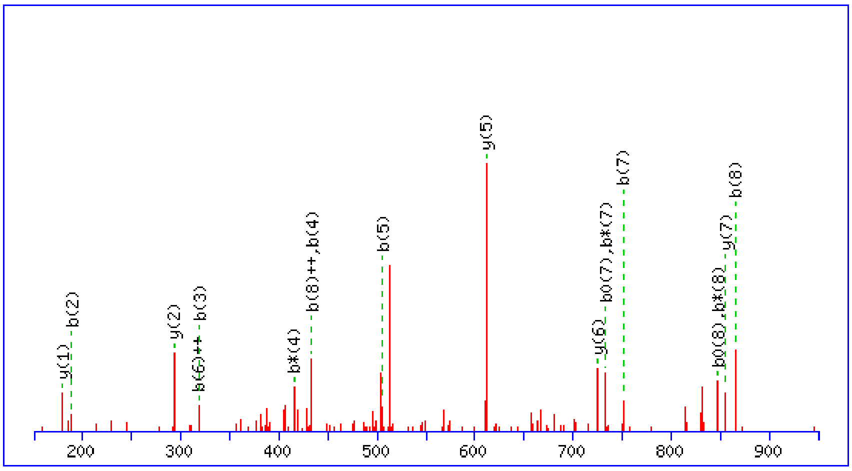
Match to Query 2523: 1042.518528 from(522.266540,2+) index(4376)
Title: Elution from: 42.673 to 42.673 scan no 5591 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

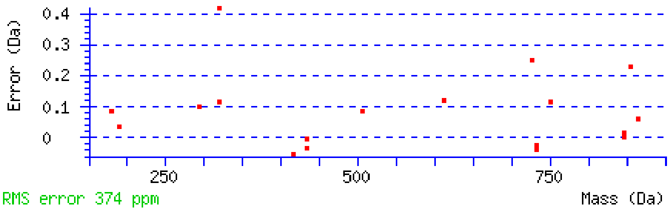
Label all possible matches ○ Label matches used for scoring ●

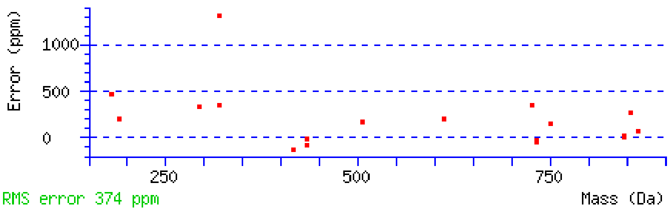
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1042.5199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00024
Matches : 18/80 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244					A							9
2	***189.0784***	95.0428	171.0548	86.0311			N	971.4931	486.2502	953.4695	477.2384	953.4825	477.2449	8
3	***319.1675***	160.0874	301.1439	151.0756			K	**855.4561**	428.2317	837.4325	419.2199	837.4455	419.2264	7
4	***433.2486***	217.1279	415.2250	208.1161			I	**725.3670**	363.1872	707.3435	354.1754	707.3565	354.1819	6
5	***505.2827***	253.1450	487.2591	244.1332			A	**611.2859**	306.1466	593.2624	297.1348	593.2754	297.1413	5
6	635.3223	**318.1648**	617.2987	309.1530	617.3118	309.1595	E	539.2518	270.1295	521.2282	261.1177	521.2412	261.1243	4
7	***751.3463***	376.1768	733.3227	367.1650	733.3357	367.1715	D	409.2122	205.1097	391.1886	196.0979	391.2016	196.1044	3
8	***865.4274***	**433.2173**	847.4038	424.2056	847.4168	424.2121	I	**293.1882**	147.0977	275.1646	138.0859			2
9							R	**179.1071**	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ANKIAEDIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G18240.1

46.4	1042.5199	-0.0014	ANKIAEDIR
21.7	1042.5199	-0.0014	NVVDADKLR
19.7	1042.5199	-0.0014	LVTDNSKPR
14.1	1042.5199	-0.0014	NEQEKLLR
11.8	1042.5199	-0.0014	GGASIQVELR
11.2	1042.5199	-0.0014	GEGGIAEKLR
11.2	1042.5199	-0.0014	AGQIGILDSR
11.2	1042.5199	-0.0014	AKQVDDVVR
11.2	1042.5199	-0.0014	VKEAGLQER
10.3	1042.5199	-0.0014	RDDEILLR

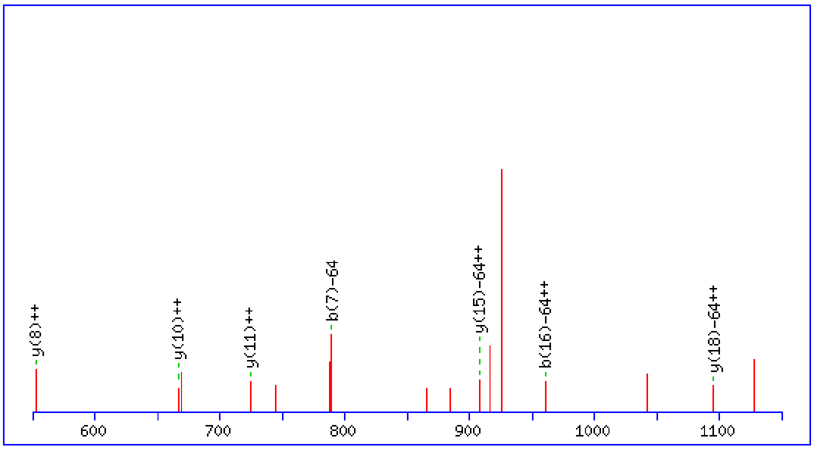
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDMKAMLTDKTFHSQWQDR**
Found in **AT3G18310.1** in **TAIR_Arabidopsis**, Symbols: | similar to hypothetical protein [Vitis vinifera] (GB:CAN64638.1) | chr3:6284529-6287150 REVERSE

Match to Query 9823: 2400.101127 from(801.040985,3+) index(10178)
Title: Elution from: 101.804 to 101.804 scan no 14962 cid35.00 polarity:+
Data file D1d-1_3.mgf

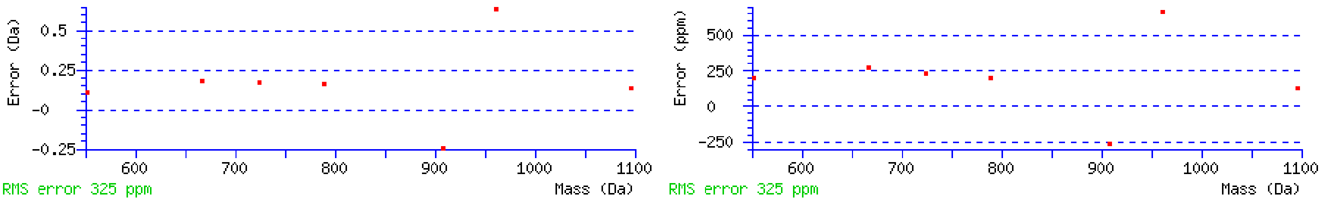
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2400.0991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 16 **Expect:** 0.049
Matches : 7/314 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							19
2	263.1026	132.0550			245.0921	123.0497	D	2190.0397	1095.5235	2173.0131	1087.0102	2172.0291	1086.5182	18
3	394.1431	197.5752			376.1326	188.5699	M	2075.0127	1038.0100	2057.9862	1029.4967	2057.0022	1029.0047	17
4	522.2381	261.6227	505.2115	253.1094	504.2275	252.6174	K	1943.9722	972.4898	1926.9457	963.9765	1925.9617	963.4845	16
5	593.2752	297.1412	576.2486	288.6280	575.2646	288.1360	A	1815.8773	908.4423	1798.8507	899.9290	1797.8667	899.4370	15
6	676.3123	338.6598	659.2858	330.1465	658.3017	329.6545	M	1744.8402	872.9237	1727.8136	864.4104	1726.8296	863.9184	14
7	789.3964	395.2018	772.3698	386.6886	771.3858	386.1965	L	1661.8030	831.4052	1644.7765	822.8919	1643.7925	822.3999	13
8	890.4441	445.7257	873.4175	437.2124	872.4335	436.7204	T	1548.7190	774.8631	1531.6924	766.3499	1530.7084	765.8578	12
9	1005.4710	503.2391	988.4444	494.7259	987.4604	494.2339	D	1447.6713	724.3393	1430.6448	715.8260	1429.6607	715.3340	11
10	1133.5660	567.2866	1116.5394	558.7733	1115.5554	558.2813	K	1332.6444	666.8258	1315.6178	658.3125	1314.6338	657.8205	10
11	1234.6136	617.8105	1217.5871	609.2972	1216.6031	608.8052	T	1204.5494	602.7783	1187.5228	594.2651	1186.5388	593.7731	9
12	1381.6821	691.3447	1364.6555	682.8314	1363.6715	682.3394	F	1103.5017	552.2545	1086.4752	543.7412	1085.4912	543.2492	8
13	1518.7410	759.8741	1501.7144	751.3608	1500.7304	750.8688	H	956.4333	478.7203	939.4068	470.2070	938.4227	469.7150	7
14	1605.7730	803.3901	1588.7464	794.8769	1587.7624	794.3849	S	819.3744	410.1908	802.3478	401.6776	801.3638	401.1856	6
15	1733.8316	867.4194	1716.8050	858.9061	1715.8210	858.4141	Q	732.3424	366.6748	715.3158	358.1615	714.3318	357.6695	5
16	1919.9109	960.4591	1902.8843	951.9458	1901.9003	951.4538	W	604.2838	302.6455	587.2572	294.1323	586.2732	293.6402	4
17	2047.9695	1024.4884	2030.9429	1015.9751	2029.9589	1015.4831	Q	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
18	2162.9964	1082.0018	2145.9699	1073.4886	2144.9858	1072.9966	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT3G18310.1



NCBI **BLAST** search of FDMKAMLTDKTFHSQWQDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
16.0	2400.0991	0.0020	FDMKAMLTDKTFHSQWQDR	Oxidation M6 89.66%
6.6	2400.0991	0.0020	FDMKAMLTDKTFHSQWQDR	Oxidation M3 10.34%
4.8	2400.0944	0.0067	GLMSFPLDGNNSTDFIEDWVK	
4.5	2400.1016	-0.0005	DSLDGENMEILVNSYHHQGVK	
4.0	2400.0946	0.0066	MAVEGMMKKHGGFSNIVEMEK	
4.0	2400.0946	0.0066	MAVEGMMKKHGGFSNIVEMEK	
3.5	2400.0946	0.0066	MAVEGMMKKHGGFSNIVEMEK	
2.8	2400.1049	-0.0038	EMESRLKGFLSGEGTPESMSGR	
1.6	2400.0964	0.0047	RRPFVTHFTGCQPCSGDHNK	
0.9	2400.1036	-0.0025	SSSTEATLLLVDTAGCDMEEKK	

Mascot: http://www.matrixscience.com/

AT3G18330.1

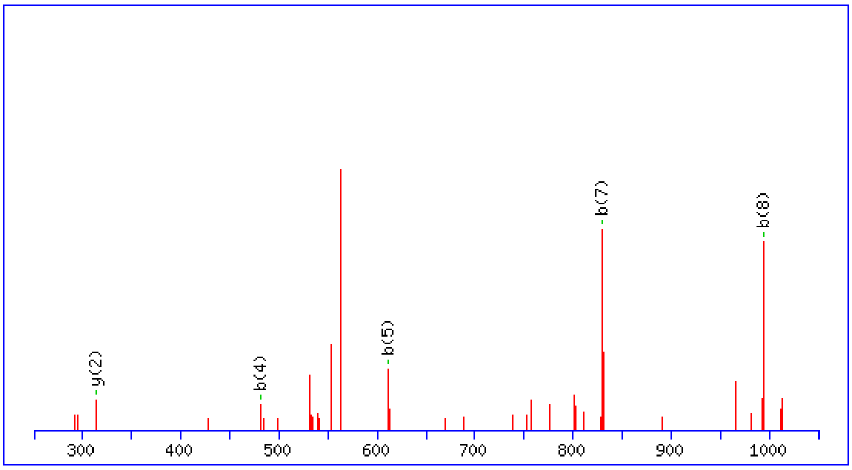
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NISCKKSYK**
Found in **AT3G18330.1** in **TAIR_Arabidopsis**, Symbols: | F-box family protein | chr3:6291133-6292263 REVERSE

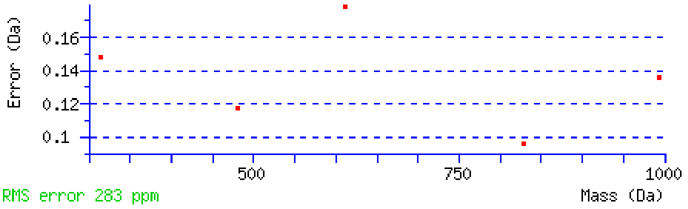
Match to Query 4021: 1140.540520 from(571.277536,2+) index(1757)
Title: Elution from: 21.599 to 21.599 scan no 2317 cid35.00 polarity:+
Data file D1d-3_1.mgf

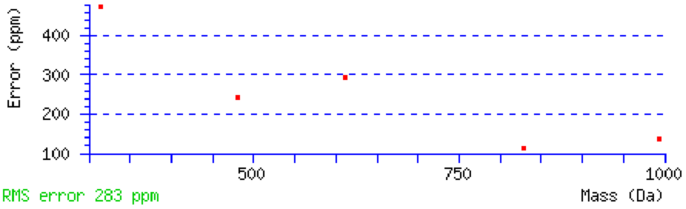
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1140.5390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.024
Matches : 5/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	231.1254	116.0663	213.1018	107.0545			I	1025.5092	513.2583	1007.4857	504.2465	1007.4987	504.2530	8
3	319.1544	160.0809	301.1309	151.0691	301.1439	151.0756	S	911.4281	456.2177	893.4046	447.2059	893.4176	447.2124	7
4	***481.1792***	241.0932	463.1556	232.0814	463.1686	232.0879	C	823.3991	412.2032	805.3755	403.1914	805.3885	403.1979	6
5	***611.2682***	306.1377	593.2446	297.1259	593.2576	297.1324	K	661.3744	331.1908	643.3508	322.1790	643.3638	322.1855	5
6	741.3572	371.1822	723.3336	362.1705	723.3467	362.1770	K	531.2853	266.1463	513.2617	257.1345	513.2748	257.1410	4
7	***829.3863***	415.1968	811.3627	406.1850	811.3757	406.1915	S	401.1963	201.1018	383.1727	192.0900	383.1857	192.0965	3
8	***993.4466***	497.2270	975.4231	488.2152	975.4361	488.2217	Y	313.1672	157.0873	295.1437	148.0755			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NISCKKSYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.4	1140.5390	0.0015	NISCKKSYK

AT3G18330.1

6.2	1140.5412	-0.0007	YFAILSMQR
2.5	1140.5390	0.0015	INSVMTRYK
1.5	1140.5434	-0.0029	FTMYIWLR
1.0	1140.5385	0.0020	LLVFDYMSK
0.3	1140.5437	-0.0032	GKPGPESLTDK

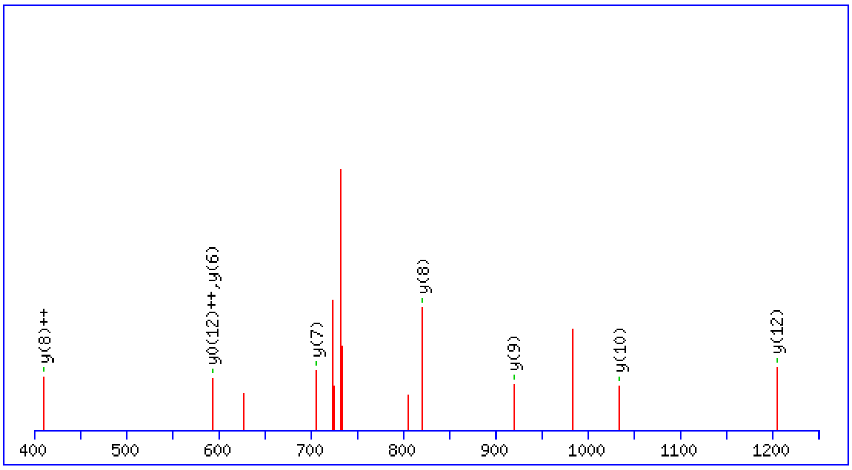
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNGNNVDLGTACGK**
Found in **AT3G18740.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L30 (RPL30C) | chr3:6453443-6453876 FORWARD

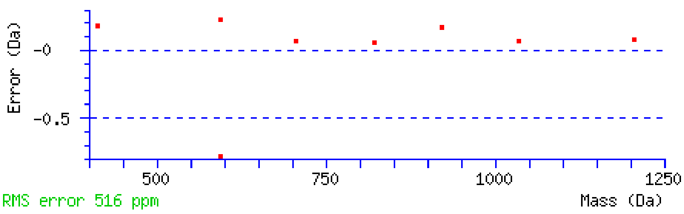
Match to Query 6114: 1481.654458 from(741.834505,2+) index(1964)
Title: Elution from: 23.379 to 23.379 scan no 2547 cid35.00 polarity:+
Data file 0-2_2.mgf

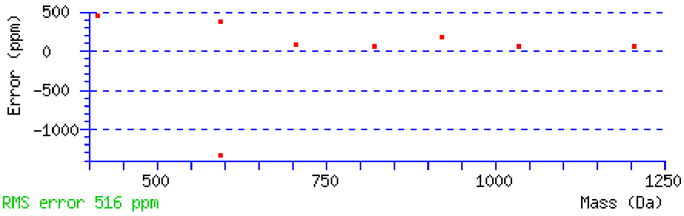
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1481.6569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 8.3e-005
Matches : 8/134 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							14
2	278.1135	139.5604	261.0870	131.0471			N	1319.6008	660.3041	1302.5743	651.7908	1301.5903	651.2988	13
3	335.1350	168.0711	318.1084	159.5579			G	**1205.5579**	603.2826	1188.5314	594.7693	1187.5473	594.2773	12
4	449.1779	225.0926	432.1514	216.5793			N	1148.5364	574.7719	1131.5099	566.2586	1130.5259	565.7666	11
5	563.2209	282.1141	546.1943	273.6008			N	**1034.4935**	517.7504	1017.4670	509.2371	1016.4830	508.7451	10
6	662.2893	331.6483	645.2627	323.1350			V	**920.4506**	460.7289	903.4240	452.2157	902.4400	451.7237	9
7	777.3162	389.1617	760.2897	380.6485	759.3056	380.1565	D	**821.3822**	411.1947	804.3556	402.6815	803.3716	402.1894	8
8	890.4003	445.7038	873.3737	437.1905	872.3897	436.6985	L	**706.3552**	353.6813	689.3287	345.1680	688.3447	344.6760	7
9	947.4217	474.2145	930.3952	465.7012	929.4112	465.2092	G	**593.2712**	297.1392	576.2446	288.6260	575.2606	288.1339	6
10	1048.4694	524.7383	1031.4429	516.2251	1030.4588	515.7331	T	536.2497	268.6285	519.2232	260.1152	518.2391	259.6232	5
11	1119.5065	560.2569	1102.4800	551.7436	1101.4960	551.2516	A	435.2020	218.1047	418.1755	209.5914			4
12	1279.5372	640.2722	1262.5106	631.7590	1261.5266	631.2669	C	364.1649	182.5861	347.1384	174.0728			3
13	1336.5586	668.7830	1319.5321	660.2697	1318.5481	659.7777	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YNGNNVDLGTACGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G18740.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.4	1481.6569	-0.0024	YNGNNVDLGTACGK

Mascot: http://www.matrixscience.com/

AT3G18940.1

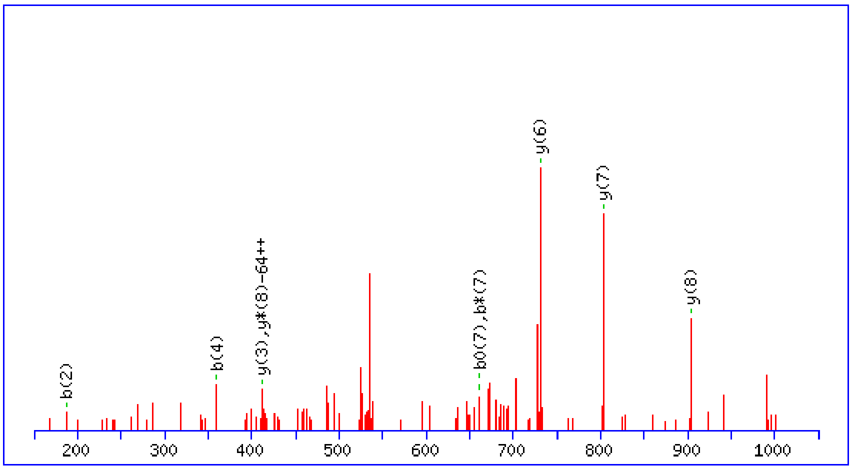
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPVAKGMMIK**
Found in **AT3G18940.1** in **TAIR_Arabidopsis**, Symbols: | clast3-related | chr3:6527087-6529056 REVERSE

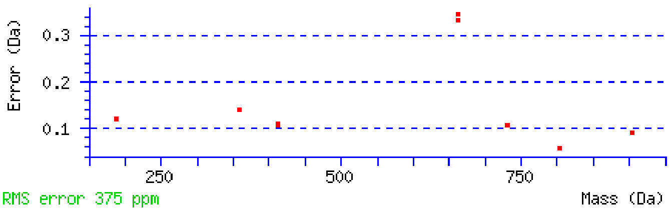
Match to Query 3489: 1088.536180 from(545.275366,2+) index(6578)
Title: Elution from: 57.363 to 57.363 scan no 8379 cid35.00 polarity:+
Data file D6h-1_1.mgf

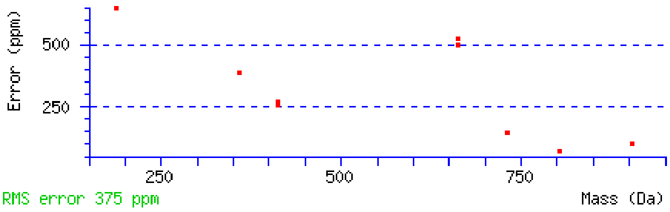
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1088.5367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.007
Matches : 9/122 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	89.0363	45.0218			71.0258	36.0165	S					10
2	**187.0861**	94.0467			169.0756	85.0414	P	1001.5149	501.2611	983.4913	492.2493	9
3	287.1516	144.0794			269.1410	135.0741	V	***903.4651***	452.2362	885.4415	443.2244	8
4	**359.1857**	180.0965			341.1752	171.0912	A	***803.3996***	402.2034	785.3760	393.1917	7
5	489.2748	245.1410	471.2512	236.1292	471.2642	236.1357	K	***731.3655***	366.1864	713.3419	357.1746	6
6	547.2933	274.1503	529.2697	265.1385	529.2827	265.1450	G	601.2764	301.1419	583.2528	292.1301	5
7	679.3308	340.1690	661.3072	331.1572	661.3202	331.1637	M	543.2579	272.1326	525.2343	263.1208	4
8	827.3632	414.1852	809.3396	405.1735	809.3527	405.1800	M	***411.2204***	206.1138	393.1968	197.1020	3
9	941.4443	471.2258	923.4207	462.2140	923.4338	462.2205	I	263.1880	132.0976	245.1644	123.0858	2
10							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of SPVAKGMMIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G18940.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
31.5	1088.5367	-0.0005	SPVAKGMMIK	Oxidation M8 96.31%
17.3	1088.5367	-0.0005	SPVAKGMMIK	Oxidation M7 3.69%
8.5	1088.5380	-0.0018	IAVEGVDTFK	
5.2	1088.5359	0.0003	VRVTMGFHK	
0.1	1088.5385	-0.0023	KKPSSTSSPR	

AT3G19170.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFAQAIDVVR**
Found in **AT3G19170.1** in **TAIR_Arabidopsis**, Symbols: ATPREP1, ATZNMP | ATPREP1/ATZNMP (PRESEQUENCE PROTEASE 1); metalloendopeptidase | chr3:6625584-6631880 REVERSE

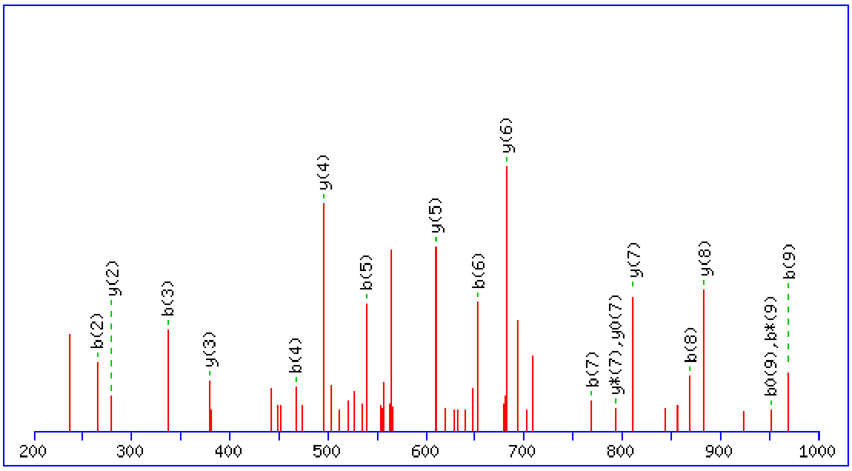
Match to Query 3973: 1146.543566 from(574.279059,2+) index(7135)
Title: Elution from: 62.709 to 62.709 scan no 9170 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1000 Da Full range

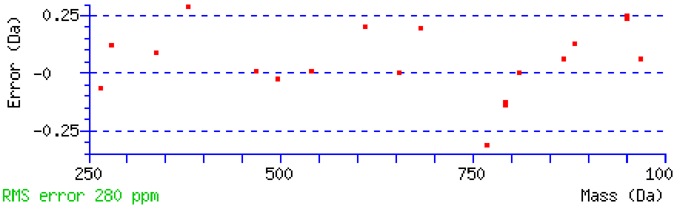
Label all possible matches ○ Label matches used for scoring ●

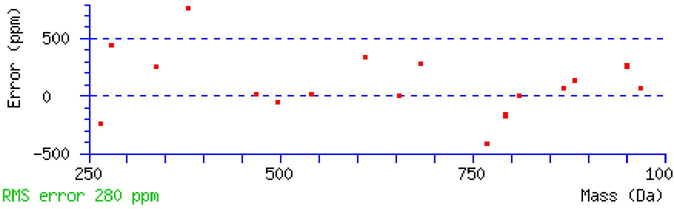
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1146.5461
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 7e-007
Matches : 19/96 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							10
2	***265.0967***	133.0520			247.0861	124.0467	F	1031.5295	516.2684	1013.5059	507.2566	1013.5189	507.2631	9
3	***337.1309***	169.0691			319.1203	160.0638	A	**883.4640**	442.2356	865.4404	433.2239	865.4534	433.2304	8
4	***467.1835***	234.0954	449.1599	225.0836	449.1729	225.0901	Q	**811.4299**	406.2186	793.4063	397.2068	793.4193	397.2133	7
5	***539.2176***	270.1125	521.1941	261.1007	521.2071	261.1072	A	**681.3772**	341.1922	663.3536	332.1805	663.3667	332.1870	6
6	***653.2987***	327.1530	635.2752	318.1412	635.2882	318.1477	I	**609.3431**	305.1752	591.3195	296.1634	591.3325	296.1699	5
7	***769.3227***	385.1650	751.2991	376.1532	751.3122	376.1597	D	**495.2620**	248.1346	477.2384	239.1228	477.2514	239.1293	4
8	***869.3882***	435.1977	851.3646	426.1859	851.3776	426.1924	V	**379.2380**	190.1226	361.2144	181.1108			3
9	***969.4536***	485.2304	951.4300	476.2187	951.4431	476.2252	V	**279.1725**	140.0899	261.1490	131.0781			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DFAQAIDVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G19170.1

Score	Mr(calc)	Delta	Sequence
70.9	1146.5461	-0.0026	DFAQAIDVVR
25.0	1146.5462	-0.0026	GYLKNPEANK
12.8	1146.5462	-0.0026	YANLPASEIR
9.5	1146.5462	-0.0026	NIFLNEDLR
6.6	1146.5461	-0.0026	FAEDNGILVR
4.9	1146.5414	0.0022	VFPGCQIVGR
4.8	1146.5435	0.0001	LYVEAGEVEK
3.4	1146.5461	-0.0026	DTSAVQLPFR
0.6	1146.5414	0.0022	AGFSVCVHKK
0.6	1146.5435	0.0001	EIKFELDDK

AT3G19710.1

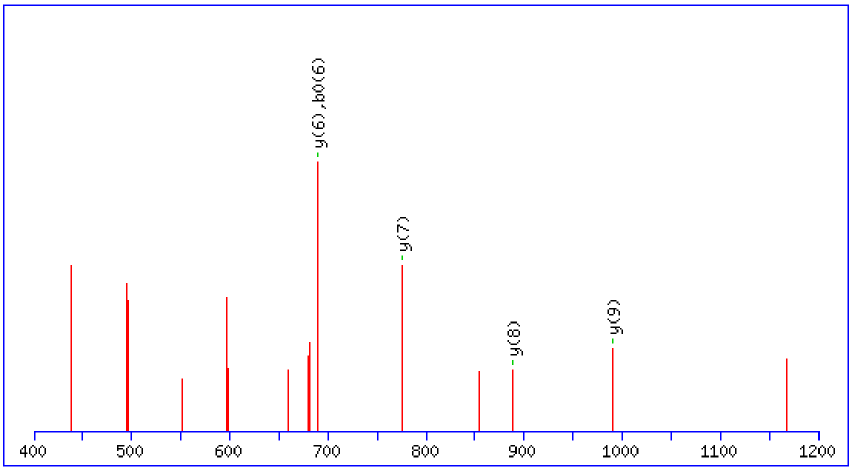
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYETLSDIQTGR**
Found in **AT3G19710.1** in **TAIR_Arabidopsis**, Symbols: BCAT4 | BCAT4 (BRANCHED-CHAIN AMINOTRANSFERASE4); catalytic/ methionine-oxo-acid transaminase | chr3:6847208-6849435 REVERSE

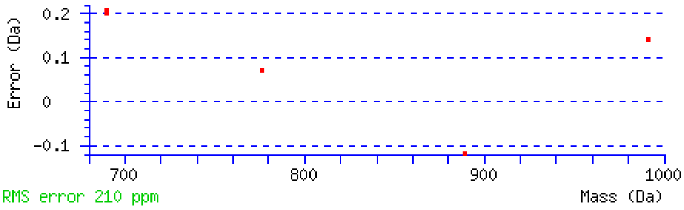
Match to Query 5148: 1394.703414 from(698.358983,2+) index(4954)
Title: Elution from: 44.111 to 44.111 scan no 6222 cid35.00 polarity:+
Data file 0-3_3.mgf

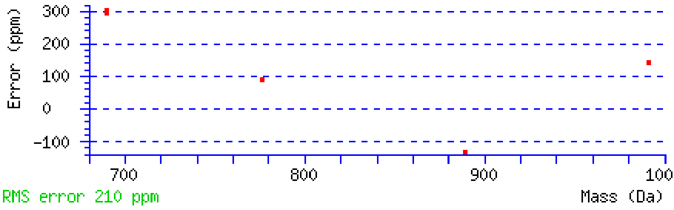
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1394.7041
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.027
Matches : 5/108 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							12
2	277.1547	139.0810					Y	1282.6274	641.8173	1265.6008	633.3041	1264.6168	632.8120	11
3	406.1973	203.6023			388.1867	194.5970	E	1119.5640	560.2857	1102.5375	551.7724	1101.5535	551.2804	10
4	507.2449	254.1261			489.2344	245.1208	T	***990.5215***	495.7644	973.4949	487.2511	972.5109	486.7591	9
5	620.3290	310.6681			602.3184	301.6629	L	***889.4738***	445.2405	872.4472	436.7272	871.4632	436.2352	8
6	707.3610	354.1842			689.3505	345.1789	S	***776.3897***	388.6985	759.3632	380.1852	758.3791	379.6932	7
7	822.3880	411.6976			804.3774	402.6923	D	***689.3577***	345.1825	672.3311	336.6692	671.3471	336.1772	6
8	935.4720	468.2397			917.4615	459.2344	I	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	5
9	1063.5306	532.2689	1046.5041	523.7557	1045.5201	523.2637	Q	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	4
10	1164.5783	582.7928	1147.5517	574.2795	1146.5677	573.7875	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
11	1221.5998	611.3035	1204.5732	602.7902	1203.5892	602.2982	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LYETLSDIQTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G19710.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.5	1394.7041	-0.0007	LYETLSDIQTGR
2.6	1394.7041	-0.0007	FEETKKISEER
1.3	1394.7016	0.0018	SGGYMPSLLFAPR
1.1	1394.7055	-0.0021	YRSDSPPVRYR
0.7	1394.7041	-0.0007	LSKSSGQGEVEFK
0.2	1394.7010	0.0024	DTMEALRRIMK

AT3G19820.1

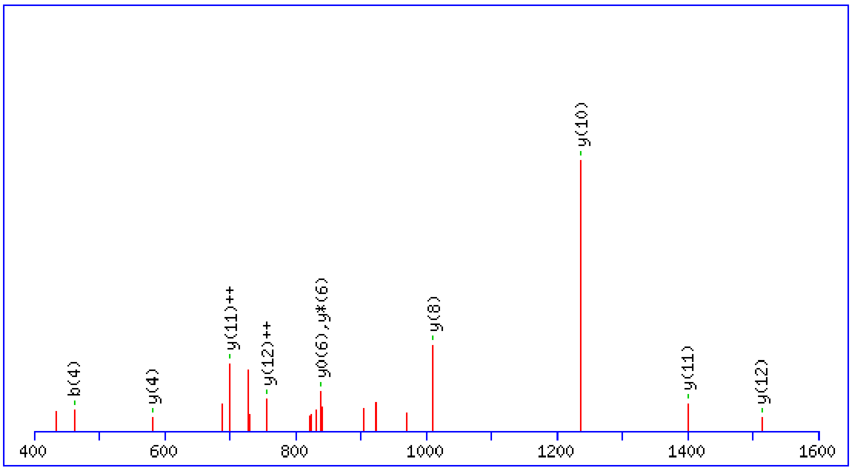
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQIYPEPGFEYENR**
Found in **AT3G19820.1** in **TAIR_Arabidopsis**, Symbols: DIM, EVE1, DW1, DIM1, CBB1, DWF1 | DWF1 (DIMINUTO 1); catalytic | chr3:6879841-6881622 REVERSE

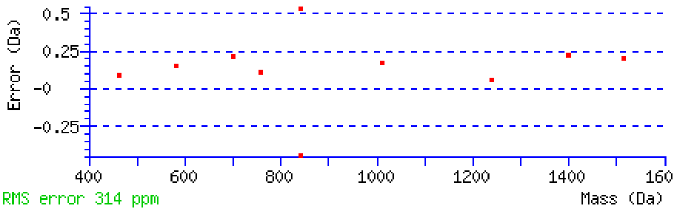
Match to Query 8008: 1697.767090 from(849.890821,2+) index(5408)
Title: Elution from: 49.322 to 49.322 scan no 6804 cid35.00 polarity:+
Data file D6h-2_2.mgf

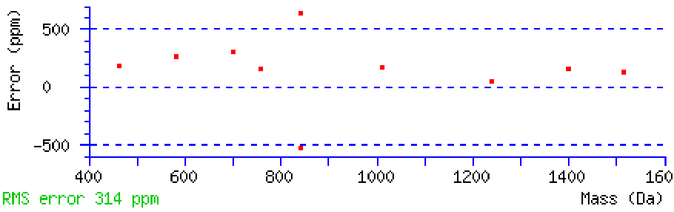
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1697.7685
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00022
Matches : 10/140 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**14**
2	186.0873	93.5473	169.0608	85.0340			**Q**	1641.7544	821.3808	1624.7278	812.8675	1623.7438	812.3755	**13**
3	299.1714	150.0893	282.1448	141.5761			**I**	***1513.6958***	757.3515	1496.6692	748.8383	1495.6852	748.3462	**12**
4	462.2347	231.6210	445.2082	223.1077			**Y**	***1400.6117***	700.8095	1383.5852	692.2962	1382.6012	691.8042	**11**
5	559.2875	280.1474	542.2609	271.6341			**P**	***1237.5484***	619.2778	1220.5218	610.7646	1219.5378	610.2726	**10**
6	688.3301	344.6687	671.3035	336.1554	670.3195	335.6634	**E**	1140.4956	570.7515	1123.4691	562.2382	1122.4851	561.7462	**9**
7	785.3828	393.1951	768.3563	384.6818	767.3723	384.1898	**P**	***1011.4530***	506.2302	994.4265	497.7169	993.4425	497.2249	**8**
8	842.4043	421.7058	825.3777	413.1925	824.3937	412.7005	**G**	914.4003	457.7038	897.3737	449.1905	896.3897	448.6985	**7**
9	989.4727	495.2400	972.4462	486.7267	971.4621	486.2347	**F**	857.3788	429.1930	840.3523	420.6798	839.3682	420.1878	**6**
10	1118.5153	559.7613	1101.4888	551.2480	1100.5047	550.7560	**E**	710.3104	355.6588	693.2838	347.1456	692.2998	346.6536	**5**
11	1281.5786	641.2930	1264.5521	632.7797	1263.5681	632.2877	**Y**	***581.2678***	291.1375	564.2413	282.6243	563.2572	282.1323	**4**
12	1410.6212	705.8143	1393.5947	697.3010	1392.6107	696.8090	**E**	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	**3**
13	1524.6642	762.8357	1507.6376	754.3224	1506.6536	753.8304	**N**	289.1619	145.0846	272.1353	136.5713			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GQIYPEPGFEYENR

AT3G19820.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.5	1697.7685	-0.0014	GQIYPEPGFEYENR
1.0	1697.7640	0.0031	GLMSEAEKVWEEMK

AT3G19960.1

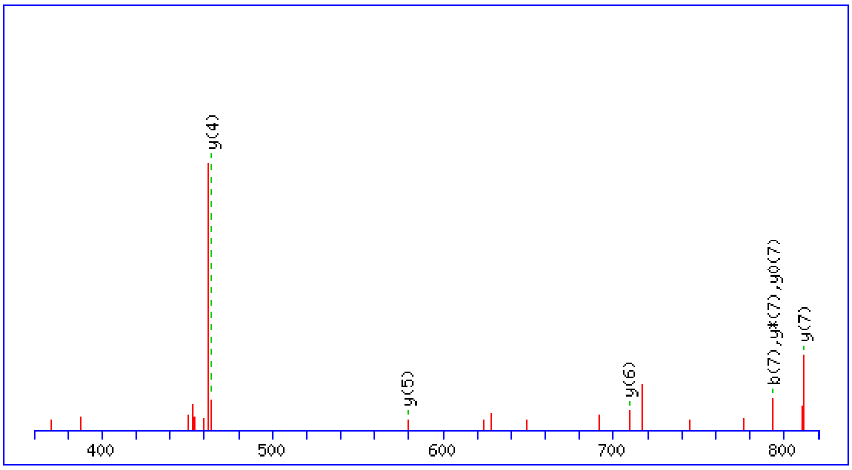
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETKLILSK**
Found in **AT3G19960.1** in **TAIR_Arabidopsis**, Symbols: ATM1 | ATATM (myosin 1); motor | chr3:6949793-6956742 FORWARD

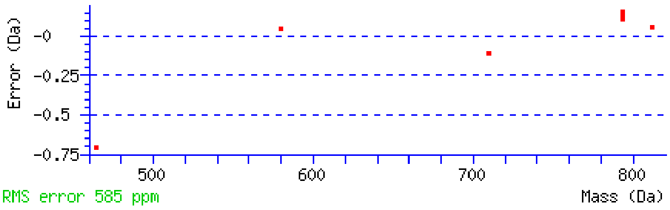
Match to Query 2134: 940.544812 from(471.279682,2+) index(733)
Title: Elution from: 12.052 to 12.052 scan no 1028 cid35.00 polarity:+
Data file D1d-3_2.mgf

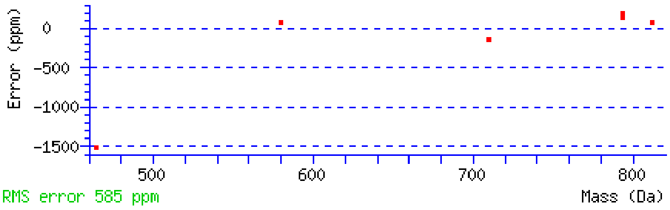
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 360 to 820 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 940.5453
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.001
Matches : 7/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							8
2	233.0916	117.0494			215.0811	108.0442	T	***811.5130***	406.2601	793.4894	397.2483	793.5024	397.2548	7
3	363.1806	182.0940	345.1571	173.0822	345.1701	173.0887	K	***709.4683***	355.2378	691.4447	346.2260	691.4577	346.2325	6
4	477.2617	239.1345	459.2382	230.1227	459.2512	230.1292	L	***579.3792***	290.1933	561.3556	281.1815	561.3687	281.1880	5
5	591.3428	296.1751	573.3193	287.1633	573.3323	287.1698	I	***465.2981***	233.1527	447.2746	224.1409	447.2876	224.1474	4
6	705.4239	353.2156	687.4004	344.2038	687.4134	344.2103	L	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
7	793.4530	397.2301	775.4294	388.2184	775.4424	388.2249	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ETKLILSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.6	940.5453	-0.0005	ETKLILSK
26.4	940.5453	-0.0005	KTEVLLTK

AT3G19960.1

13.4	940.5476	-0.0027	AIFEIVLK
13.4	940.5476	-0.0028	YSLPIVIK
12.0	940.5453	-0.0005	KELSLITK
2.9	940.5453	-0.0005	SELKTLLK
2.3	940.5453	-0.0005	DITIKITK
2.3	940.5453	-0.0005	IIKELSTK
1.1	940.5476	-0.0027	LIIDFLAK

AT3G19990.1

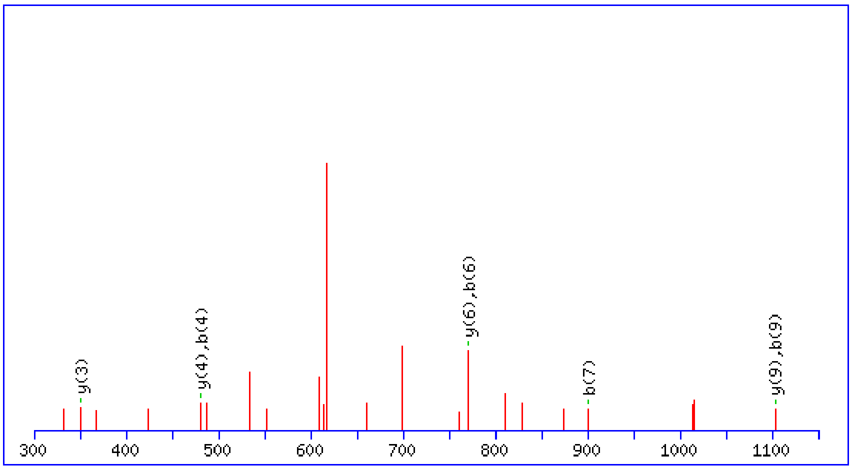
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FKEAEREAEK**
Found in **AT3G19990.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr3:6965677-6967108 FORWARD

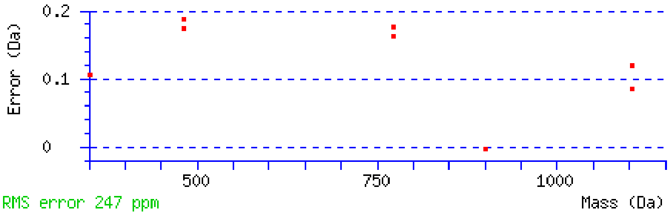
Match to Query 4208: 1250.572090 from(626.293321,2+) index(2192)
Title: Elution from: 27.332 to 27.332 scan no 2894 cid35.00 polarity:+
Data file D12h-2_1.mgf

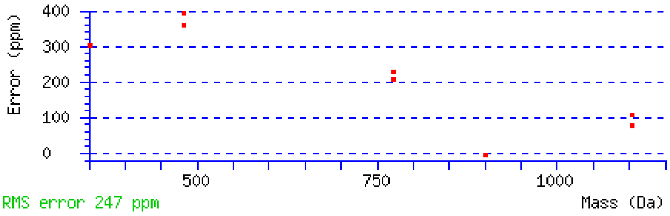
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1250.5701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.02
Matches : 8/100 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					**F**							**10**
2	279.1618	140.0845	261.1382	131.0727			**K**	***1103.5120***	552.2596	1085.4884	543.2478	1085.5014	543.2543	**9**
3	409.2014	205.1043	391.1778	196.0925	391.1908	196.0990	**E**	973.4229	487.2151	955.3994	478.2033	955.4124	478.2098	**8**
4	***481.2355***	241.1214	463.2120	232.1096	463.2250	232.1161	**A**	843.3833	422.1953	825.3597	413.1835	825.3727	413.1900	**7**
5	611.2752	306.1412	593.2516	297.1294	593.2646	297.1359	**E**	***771.3492***	386.1782	753.3256	377.1664	753.3386	377.1729	**6**
6	***771.3644***	386.1858	753.3408	377.1741	753.3538	377.1806	**R**	641.3095	321.1584	623.2859	312.1466	623.2990	312.1531	**5**
7	***901.4040***	451.2057	883.3805	442.1939	883.3935	442.2004	**E**	***481.2203***	241.1138	463.1967	232.1020	463.2097	232.1085	**4**
8	973.4382	487.2227	955.4146	478.2109	955.4276	478.2175	**A**	***351.1807***	176.0940	333.1571	167.0822	333.1701	167.0887	**3**
9	***1103.4778***	552.2425	1085.4542	543.2308	1085.4673	543.2373	**E**	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	**2**
10							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of FKEAEREAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G19990.1

27.7	1250.5701	0.0020	FKEAEREAEK
27.5	1250.5701	0.0020	EEAFRKEEAK
20.3	1250.5735	-0.0014	MRTDLEEAKK
14.3	1250.5701	0.0020	FEVTAIANTDR
12.6	1250.5724	-0.0003	FSIPEFQDVR
12.1	1250.5688	0.0033	EIQTCMGRIK
11.2	1250.5701	0.0020	FTSEVAELQGR
10.5	1250.5688	0.0033	MRELQMTAQK
10.5	1250.5758	-0.0037	SMIPQNLGSFK
8.8	1250.5757	-0.0036	VAVICGYGDVGK

AT3G20210.1

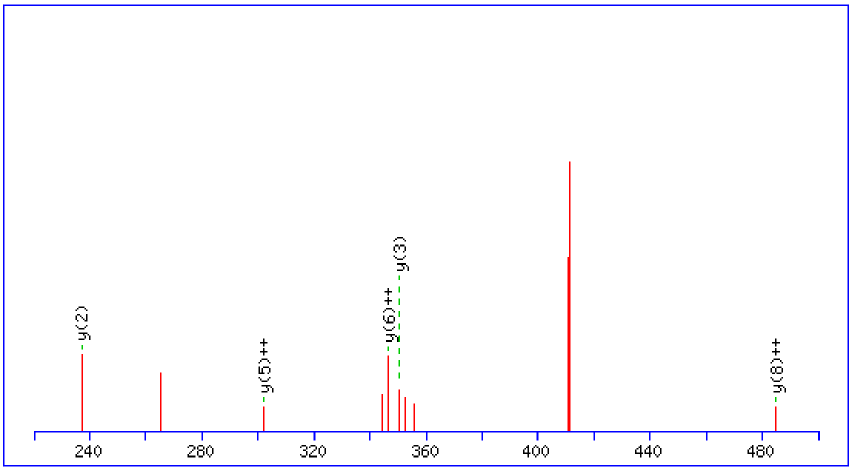
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DYLSSYIGR**
Found in **AT3G20210.1** in **TAIR_Arabidopsis**, Symbols: DELTAVPE, DELTA-VPE | DELTA-VPE (delta vacuolar processing enzyme); cysteine-type endopeptidase | chr3:7052488-7054531 FORWARD

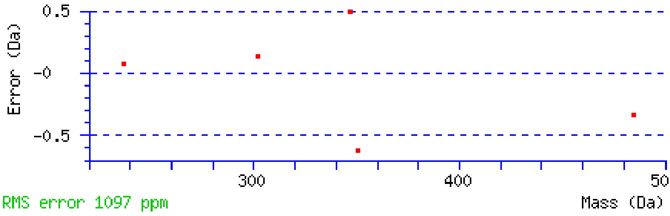
Match to Query 3299: 1084.483287 from(362.501705,3+) index(4670)
Title: Elution from: 41.233 to 41.233 scan no 5838 cid35.00 polarity:+
Data file D1d-3_3.mgf

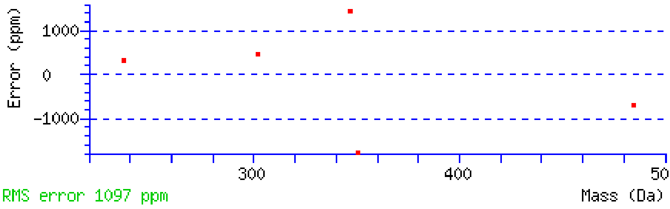
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1084.4833
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.047
Matches : 5/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							9
2	281.0916	141.0494	263.0811	132.0442	Y	969.4666	485.2370	951.4431	476.2252	951.4561	476.2317	8
3	395.1727	198.0900	377.1622	189.0847	L	805.4063	403.2068	787.3827	394.1950	787.3957	394.2015	7
4	483.2018	242.1045	465.1912	233.0992	S	691.3252	346.1662	673.3016	337.1544	673.3146	337.1609	6
5	571.2308	286.1191	553.2203	277.1138	S	603.2961	302.1517	585.2725	293.1399	585.2856	293.1464	5
6	735.2912	368.1492	717.2806	359.1440	Y	515.2671	258.1372	497.2435	249.1254			4
7	849.3723	425.1898	831.3617	416.1845	I	***351.2067***	176.1070	333.1831	167.0952			3
8	907.3908	454.1990	889.3802	445.1938	G	***237.1256***	119.0664	219.1020	110.0546			2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DYLSSYIGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G20210.1

19.4	1084.4833	-0.0001	DYLSSYIGR
11.1	1084.4833	-0.0000	DFIHDIGEK
9.7	1084.4838	-0.0005	SYSGERKSR
6.3	1084.4833	-0.0000	SFGFSGTKDK
4.5	1084.4865	-0.0032	SSSFNRRGR
3.9	1084.4838	-0.0005	SEKHGGVGGNK
3.9	1084.4833	-0.0000	VHEFLADDK
3.9	1084.4833	-0.0000	TFVYTNSGGK

AT3G20350.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SESMNLREEVDDER**
Found in **AT3G20350.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50660.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO38960.1) | chr3:7096608-7099378 FORWARD

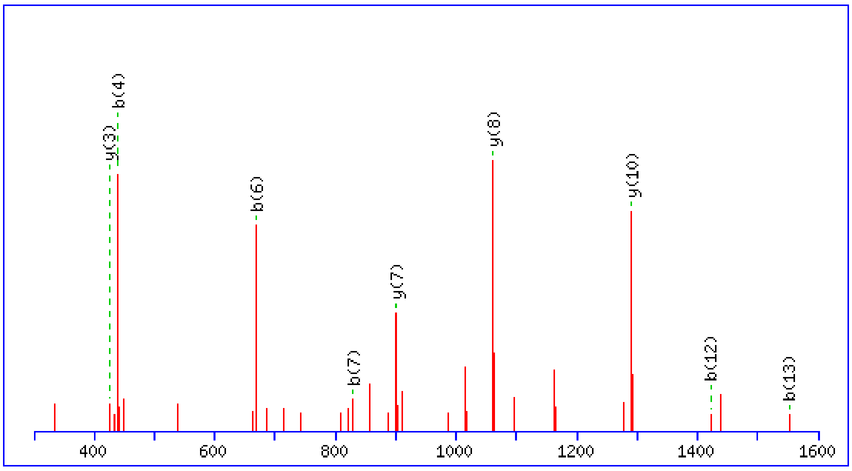
Match to Query 7923: 1728.677536 from(865.346044,2+) index(7082)
Title: Elution from: 62.499 to 62.499 scan no 9284 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1600 Da Full range

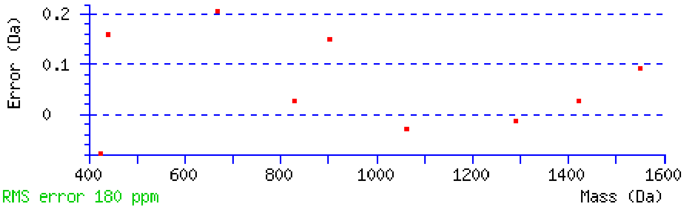
Label all possible matches ○ Label matches used for scoring ●

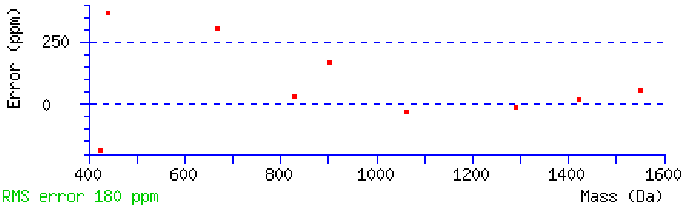
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1728.6747
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0007
Matches : 9/146 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							14
2	219.0760	110.0416			201.0654	101.0363	E	1641.6529	821.3301	1623.6294	812.3183	1623.6424	812.3248	13
3	307.1050	154.0562			289.0945	145.0509	S	1511.6133	756.3103	1493.5897	747.2985	1493.6027	747.3050	12
4	***439.1425***	220.0749			421.1320	211.0696	M	1423.5842	712.2958	1405.5607	703.2840	1405.5737	703.2905	11
5	555.1795	278.0934	537.1560	269.0816	537.1690	269.0881	N	***1291.5467***	646.2770	1273.5231	637.2652	1273.5362	637.2717	10
6	***669.2606***	335.1340	651.2371	326.1222	651.2501	326.1287	L	1175.5097	588.2585	1157.4861	579.2467	1157.4992	579.2532	9
7	***829.3499***	415.1786	811.3263	406.1668	811.3393	406.1733	R	***1061.4286***	531.2180	1043.4050	522.2062	1043.4181	522.2127	8
8	959.3895	480.1984	941.3659	471.1866	941.3790	471.1931	E	***901.3394***	451.1733	883.3158	442.1615	883.3288	442.1680	7
9	1089.4292	545.2182	1071.4056	536.2064	1071.4186	536.2129	E	771.2998	386.1535	753.2762	377.1417	753.2892	377.1482	6
10	1189.4946	595.2509	1171.4710	586.2391	1171.4840	586.2457	V	641.2601	321.1337	623.2365	312.1219	623.2496	312.1284	5
11	1305.5186	653.2629	1287.4950	644.2511	1287.5080	644.2576	D	541.1947	271.1010	523.1711	262.0892	523.1841	262.0957	4
12	***1421.5426***	711.2749	1403.5190	702.2631	1403.5320	702.2696	D	***425.1707***	213.0890	407.1471	204.0772	407.1601	204.0837	3
13	***1551.5822***	776.2947	1533.5586	767.2829	1533.5716	767.2894	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SESMNLREEVDDER

AT3G20350.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.1	1728.6747	0.0028	SESMNLREEVDDER
2.6	1728.6826	-0.0050	VFEPGCSNPTGMASEK
2.1	1728.6747	0.0028	MESSPKQQNTEEER
2.1	1728.6821	-0.0046	RALADDGSSSSDGSPER
1.8	1728.6776	-0.0001	DMDDSALGTEGMVEVK

AT3G20390.1

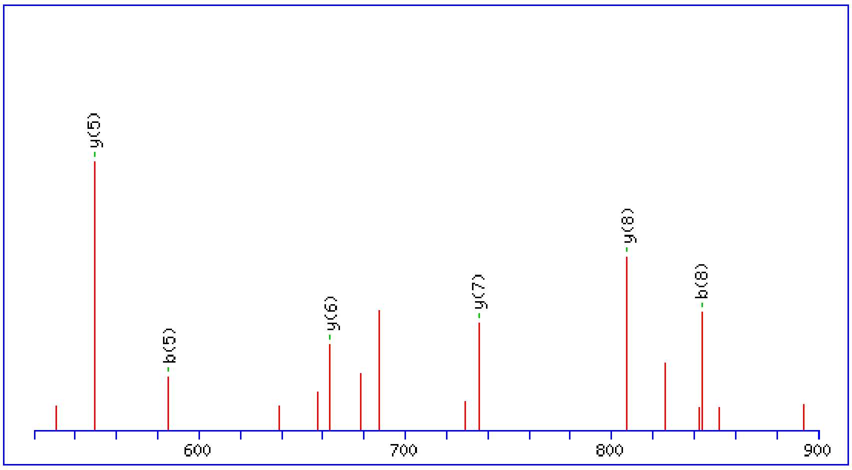
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STYQVAALPLNAK**
Found in **AT3G20390.1** in **TAIR_Arabidopsis**, Symbols: | endoribonuclease L-PSP family protein | chr3:7110233-7111701 REVERSE

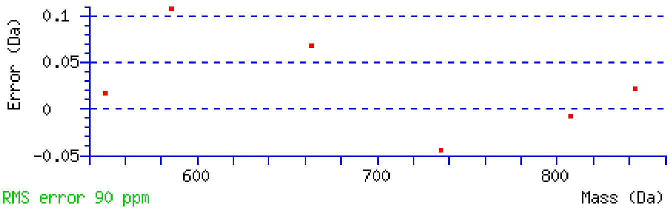
Match to Query 5442: 1390.700630 from(696.357591,2+) index(5167)
Title: Elution from: 45.682 to 45.682 scan no 6482 cid35.00 polarity:+
Data file C7-3_2.mgf

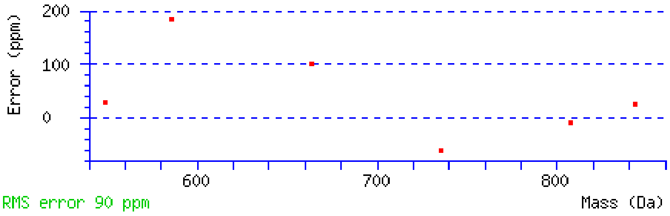
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 520 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1390.7033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0037
Matches : 6/116 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							13
2	191.0811	96.0442			173.0705	87.0389	T	1303.6815	652.3444	1285.6579	643.3326	1285.6709	643.3391	12
3	355.1414	178.0743			337.1309	169.0691	Y	1201.6368	601.3220	1183.6132	592.3102			11
4	485.1941	243.1007	467.1705	234.0889	467.1835	234.0954	Q	1037.5764	519.2918	1019.5528	510.2801			10
5	**585.2595**	293.1334	567.2359	284.1216	567.2489	284.1281	V	907.5238	454.2655	889.5002	445.2537			9
6	657.2937	329.1505	639.2701	320.1387	639.2831	320.1452	A	***807.4583***	404.2328	789.4347	395.2210			8
7	729.3278	365.1675	711.3042	356.1558	711.3172	356.1623	A	***735.4242***	368.2157	717.4006	359.2039			7
8	**843.4089**	422.2081	825.3853	413.1963	825.3983	413.2028	L	***663.3900***	332.1986	645.3664	323.1869			6
9	941.4587	471.2330	923.4351	462.2212	923.4481	462.2277	P	***549.3089***	275.1581	531.2853	266.1463			5
10	1055.5398	528.2735	1037.5162	519.2617	1037.5292	519.2683	L	451.2591	226.1332	433.2355	217.1214			4
11	1171.5768	586.2920	1153.5532	577.2802	1153.5662	577.2868	N	337.1780	169.0926	319.1544	160.0809			3
12	1243.6110	622.3091	1225.5874	613.2973	1225.6004	613.3038	A	221.1410	111.0741	203.1174	102.0624			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of STYQVAALPLNAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G20390.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.5	1390.7033	-0.0026	STYQVAALPLNAK
5.8	1390.7010	-0.0004	AGKTIALVGESGSGK

AT3G20820.1

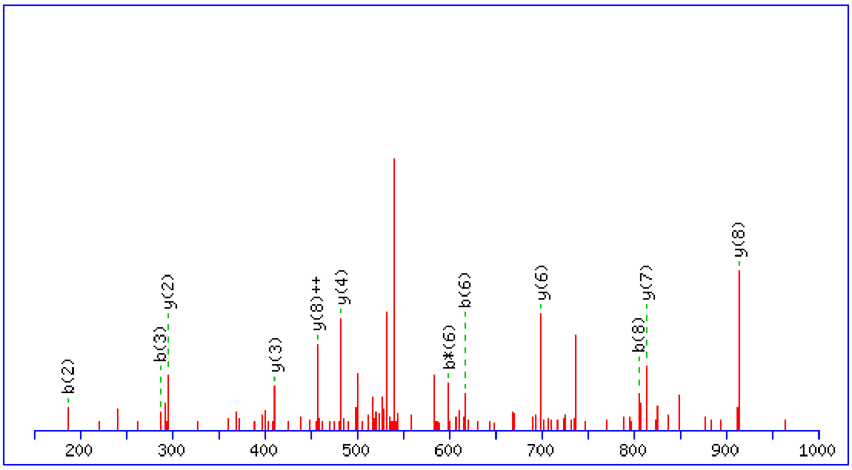
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVLNVADNR**
Found in **AT3G20820.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat family protein | chr3:7280936-7282033 FORWARD

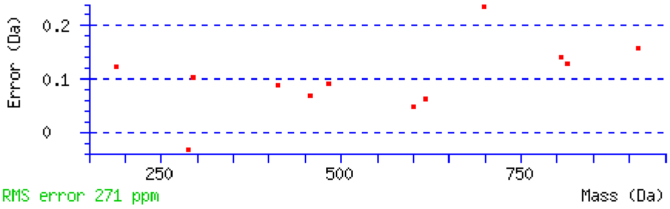
Match to Query 3608: 1098.556790 from(550.285671,2+) index(4474)
Title: Elution from: 40.964 to 40.964 scan no 5520 cid35.00 polarity:+
Data file D12h-1_1.mgf

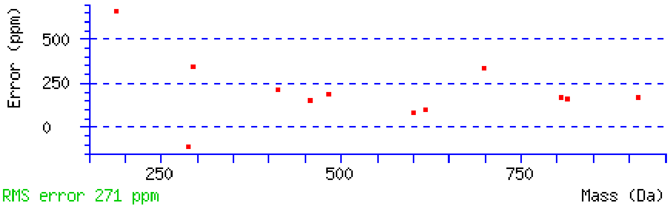
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1098.5592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00067
Matches : 12/82 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							10
2	**187.1225**	94.0649					A	985.4854	493.2463	967.4618	484.2345	967.4748	484.2410	9
3	**287.1880**	144.0976					V	***913.4512***	457.2292	895.4276	448.2175	895.4406	448.2240	8
4	401.2691	201.1382					L	***813.3858***	407.1965	795.3622	398.1847	795.3752	398.1912	7
5	517.3061	259.1567	499.2825	250.1449			N	***699.3047***	350.1560	681.2811	341.1442	681.2941	341.1507	6
6	**617.3715**	309.1894	599.3479	300.1776			V	583.2677	292.1375	565.2441	283.1257	565.2571	283.1322	5
7	689.4057	345.2065	671.3821	336.1947			A	***483.2022***	242.1047	465.1786	233.0930	465.1917	233.0995	4
8	**805.4296**	403.2185	787.4061	394.2067	787.4191	394.2132	D	***411.1681***	206.0877	393.1445	197.0759	393.1575	197.0824	3
9	921.4666	461.2370	903.4431	452.2252	903.4561	452.2317	N	***295.1441***	148.0757	277.1205	139.0639			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LAVLNVADNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G20820.1

40.2	1098.5592	-0.0024	LAVLNVADNR
1.1	1098.5592	-0.0024	LAVEGPGKASR
0.6	1098.5592	-0.0024	SPIVNIQASR

AT3G21055.1

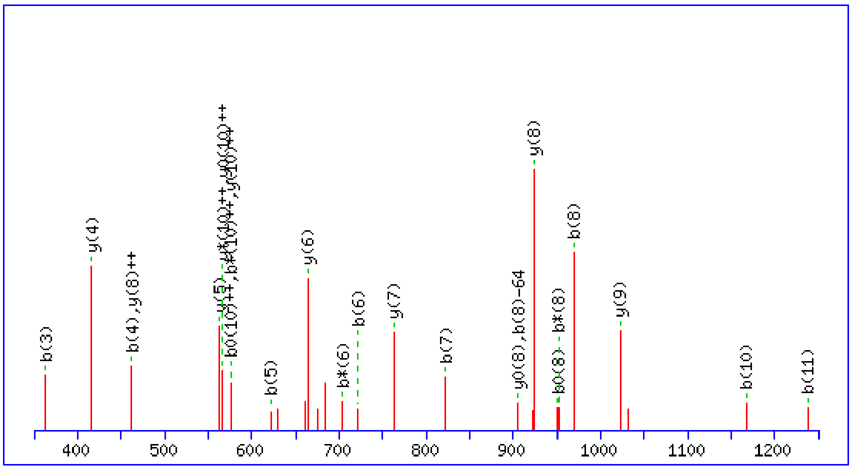
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAQVCVTMPTAK**
Found in **AT3G21055.1** in **TAIR_Arabidopsis**, Symbols: PSBTN | PSBTN (photosystem II subunit T) | chr3:7376767-7377078 REVERSE

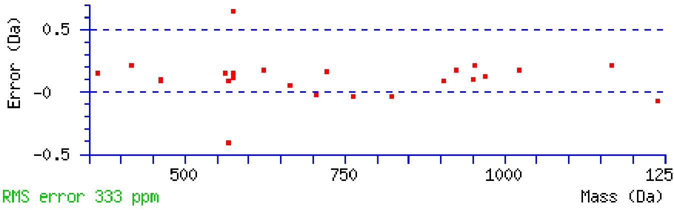
Match to Query 5387: 1383.650452 from(692.832502,2+) index(2105)
Title: Elution from: 25.786 to 25.786 scan no 2766 cid35.00 polarity:+
Data file D6h-2_1.mgf

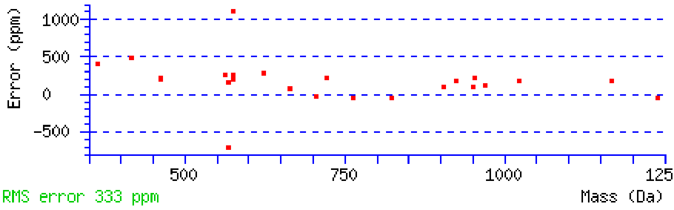
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1383.6527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 78 **Expect:** 2.9e-008
Matches : 25/178 fragment ions using 27 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							12
2	235.1077	118.0575					A	1221.5966	611.3019	1204.5701	602.7887	1203.5860	602.2967	11
3	***363.1663***	182.0868	346.1397	173.5735			Q	1150.5595	575.7834	1133.5329	567.2701	1132.5489	566.7781	10
4	***462.2347***	231.6210	445.2082	223.1077			V	**1022.5009**	511.7541	1005.4744	503.2408	1004.4904	502.7488	9
5	***622.2654***	311.6363	605.2388	303.1230			C	**923.4325**	462.2199	906.4060	453.7066	905.4219	453.2146	8
6	***721.3338***	361.1705	704.3072	352.6573			V	**763.4019**	382.2046	746.3753	373.6913	745.3913	373.1993	7
7	***822.3815***	411.6944	805.3549	403.1811	804.3709	402.6891	T	**664.3334**	332.6704	647.3069	324.1571	646.3229	323.6651	6
8	***969.4169***	485.2121	952.3903	476.6988	951.4063	476.2068	M	**563.2858**	282.1465	546.2592	273.6332	545.2752	273.1412	5
9	1066.4696	533.7384	1049.4431	525.2252	1048.4591	524.7332	P	**416.2504**	208.6288	399.2238	200.1155	398.2398	199.6235	4
10	***1167.5173***	584.2623	1150.4907	575.7490	1149.5067	575.2570	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
11	***1238.5544***	619.7808	1221.5279	611.2676	1220.5438	610.7756	A	218.1499	109.5786	201.1234	101.0653			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YAQVCVTMPTAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G21055.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.3	1383.6527	-0.0022	YAQVCVTMPTAK
0.8	1383.6500	0.0005	GCRFCNVKTSR

Mascot: http://www.matrixscience.com/

AT3G21150.1

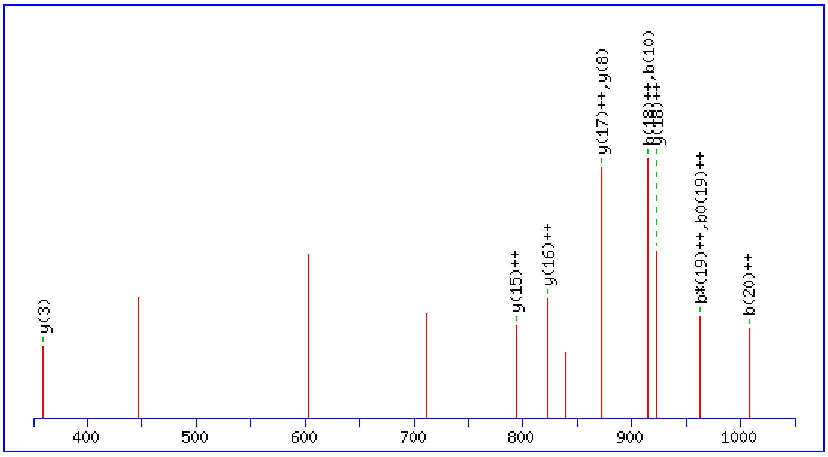
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEDVTGVSAGMIRAVESKLAR**
Found in **AT3G21150.1** in **TAIR_Arabidopsis**, Symbols: | zinc finger (B-box type) family protein | chr3:7412719-7413396 REVERSE

Match to Query 9535: 2187.169398 from(730.063742,3+) index(9667)
Title: Elution from: 89.310 to 89.310 scan no 13443 cid35.00 polarity:+
Data file D12h-3_2.mgf

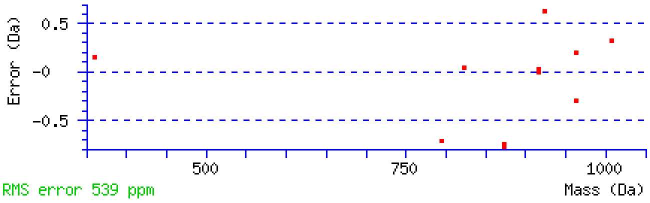
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

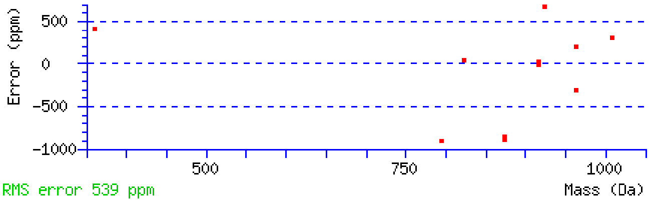


Monoisotopic mass of neutral peptide Mr(calc): 2187.1681
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.048
Matches : 11/206 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							21
2	229.1183	115.0628			211.1077	106.0575	E	2089.1070	1045.0571	2072.0805	1036.5439	2071.0964	1036.0519	20
3	344.1452	172.5763			326.1347	163.5710	D	1960.0644	980.5358	1943.0379	972.0226	1942.0539	971.5306	19
4	443.2136	222.1105			425.2031	213.1052	V	1845.0375	923.0224	1828.0109	914.5091	1827.0269	914.0171	18
5	544.2613	272.6343			526.2508	263.6290	T	1745.9691	873.4882	1728.9425	864.9749	1727.9585	864.4829	17
6	601.2828	301.1450			583.2722	292.1397	G	1644.9214	822.9643	1627.8948	814.4511	1626.9108	813.9590	16
7	700.3512	350.6792			682.3406	341.6740	V	1587.8999	794.4536	1570.8734	785.9403	1569.8894	785.4483	15
8	787.3832	394.1953			769.3727	385.1900	S	1488.8315	744.9194	1471.8050	736.4061	1470.8209	735.9141	14
9	858.4203	429.7138			840.4098	420.7085	A	1401.7995	701.4034	1384.7729	692.8901	1383.7889	692.3981	13
10	915.4418	458.2245			897.4312	449.2193	G	1330.7624	665.8848	1313.7358	657.3715	1312.7518	656.8795	12
11	1046.4823	523.7448			1028.4717	514.7395	M	1273.7409	637.3741	1256.7144	628.8608	1255.7303	628.3688	11
12	1159.5664	580.2868			1141.5558	571.2815	I	1142.7004	571.8538	1125.6739	563.3406	1124.6899	562.8486	10
13	1315.6675	658.3374	1298.6409	649.8241	1297.6569	649.3321	R	1029.6164	515.3118	1012.5898	506.7985	1011.6058	506.3065	9
14	1386.7046	693.8559	1369.6780	685.3427	1368.6940	684.8506	A	**873.5152**	437.2613	856.4887	428.7480	855.5047	428.2560	8
15	1485.7730	743.3901	1468.7464	734.8769	1467.7624	734.3849	V	802.4781	401.7427	785.4516	393.2294	784.4676	392.7374	7
16	1614.8156	807.9114	1597.7890	799.3982	1596.8050	798.9061	E	703.4097	352.2085	686.3832	343.6952	685.3991	343.2032	6
17	1701.8476	851.4274	1684.8211	842.9142	1683.8370	842.4222	S	574.3671	287.6872	557.3406	279.1739	556.3566	278.6819	5
18	1829.9426	**915.4749**	1812.9160	906.9617	1811.9320	906.4696	K	487.3351	244.1712	470.3085	235.6579			4
19	1943.0266	972.0170	1926.0001	963.5037	1925.0161	963.0117	L	**359.2401**	180.1237	342.2136	171.6104			3
20	2014.0638	**1007.5355**	1997.0372	999.0222	1996.0532	998.5302	A	246.1561	123.5817	229.1295	115.0684			2
21							R	175.1190	88.0631	158.0924	79.5498			1

AT3G21150.1





NCBI **BLAST** search of VEDVTGVSAGMIRAVESKLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.7	2187.1681	0.0013	VEDVTGVSAGMIRAVESKLAR
2.9	2187.1648	0.0046	TTAQHLSQVHGLQVELGELK
1.5	2187.1730	-0.0036	SMISMLRKPPKHFEMLVK
1.5	2187.1730	-0.0036	SMISMLRKPPKHFEMLVK
0.2	2187.1647	0.0046	QDLLLTQRESIYGSKPSPR
0.2	2187.1688	0.0006	HVYVDFSQLNVTLPKKDGK
0.1	2187.1647	0.0046	ATELKDPNGQVLRLLDYSR

AT3G22110.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAAVGANNQAAQSILK**
Found in **AT3G22110.1** in **TAIR_Arabidopsis**, Symbols: PAC1 | PAC1 (20S proteasome alpha subunit C1); peptidase | chr3:7792826-7793578 REVERSE

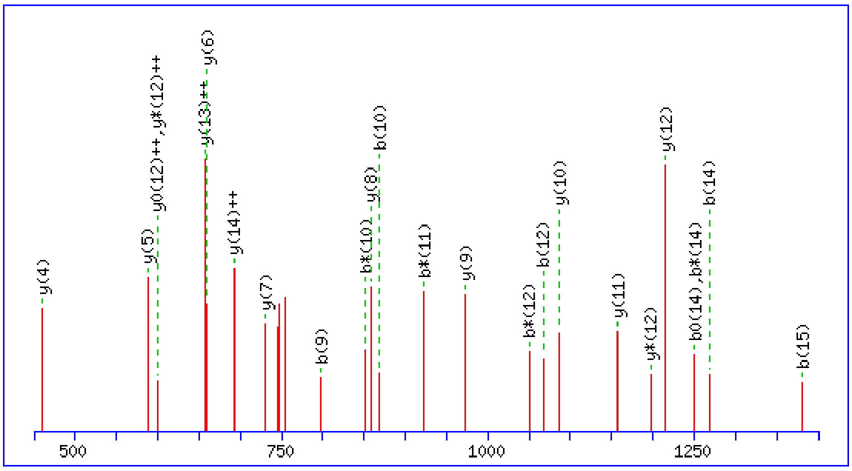
Match to Query 6462: 1525.821410 from(763.917981,2+) index(3146)
Title: Elution from: 31.009 to 31.009 scan no 3915 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1400 Da Full range

Label all possible matches ○ Label matches used for scoring ●

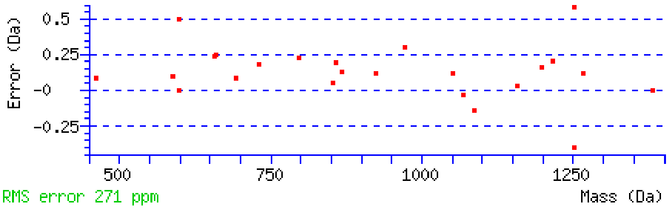
Show Y-axis ☐

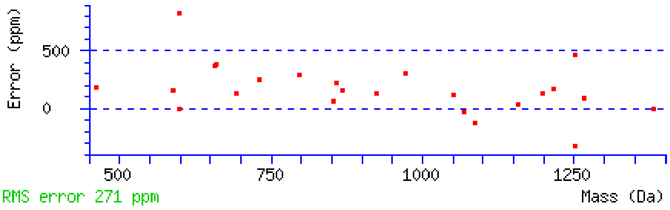


Monoisotopic mass of neutral peptide Mr(calc): 1525.8212
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 96 **Expect:** 8.4e-010
Matches : 24/138 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							16
2	143.0815	72.0444					A	1455.7914	728.3993	1438.7649	719.8861	1437.7809	719.3941	15
3	214.1186	107.5629					A	1384.7543	692.8808	1367.7278	684.3675	1366.7437	683.8755	14
4	313.1870	157.0972					V	1313.7172	657.3622	1296.6906	648.8490	1295.7066	648.3570	13
5	370.2085	185.6079					G	***1214.6488***	607.8280	1197.6222	599.3148	1196.6382	598.8227	12
6	441.2456	221.1264					A	***1157.6273***	579.3173	1140.6008	570.8040	1139.6167	570.3120	11
7	555.2885	278.1479	538.2620	269.6346			N	***1086.5902***	543.7987	1069.5636	535.2855	1068.5796	534.7935	10
8	669.3315	335.1694	652.3049	326.6561			N	***972.5473***	486.7773	955.5207	478.2640	954.5367	477.7720	9
9	**797.3900**	399.1987	780.3635	390.6854			Q	***858.5043***	429.7558	841.4778	421.2425	840.4938	420.7505	8
10	**868.4272**	434.7172	851.4006	426.2039			A	***730.4458***	365.7265	713.4192	357.2132	712.4352	356.7212	7
11	939.4643	470.2358	922.4377	461.7225			A	***659.4087***	330.2080	642.3821	321.6947	641.3981	321.2027	6
12	**1067.5228**	534.2651	1050.4963	525.7518			Q	***588.3715***	294.6894	571.3450	286.1761	570.3610	285.6841	5
13	1154.5549	577.7811	1137.5283	569.2678	1136.5443	568.7758	S	***460.3130***	230.6601	443.2864	222.1468	442.3024	221.6548	4
14	**1267.6389**	634.3231	1250.6124	625.8098	1249.6284	625.3178	I	373.2809	187.1441	356.2544	178.6308			3
15	**1380.7230**	690.8651	1363.6965	682.3519	1362.7124	681.8599	L	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT3G22110.1





NCBI **BLAST** search of AAAVGANNQAAQSILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.0	1525.8212	0.0002	AAAVGANNQAAQSILK
5.3	1525.8239	-0.0025	LPEGITGEELDIIK

Mascot: http://www.matrixscience.com/

AT3G22190.1

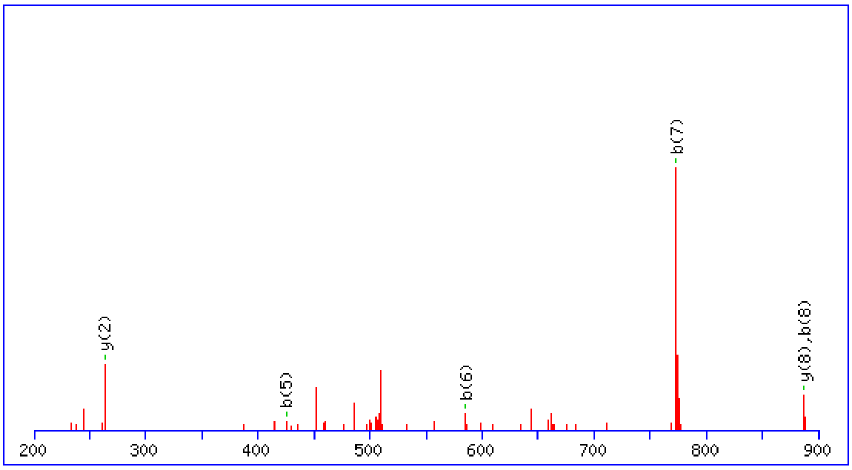
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGASGRWIK**
Found in **AT3G22190.1** in **TAIR_Arabidopsis**, Symbols: IQD5 | IQD5 (IQ-domain 5); calmodulin binding | chr3:7831668-7833519 REVERSE

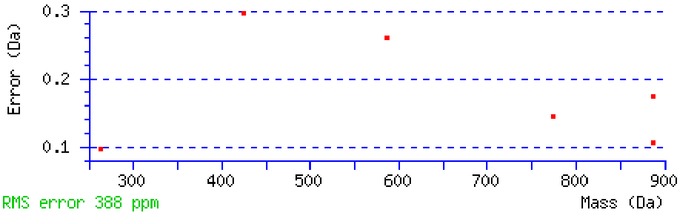
Match to Query 2950: 1034.476636 from(518.245594,2+) index(1679)
Title: Elution from: 21.947 to 21.947 scan no 2247 cid35.00 polarity:+
Data file C7-2_1.mgf

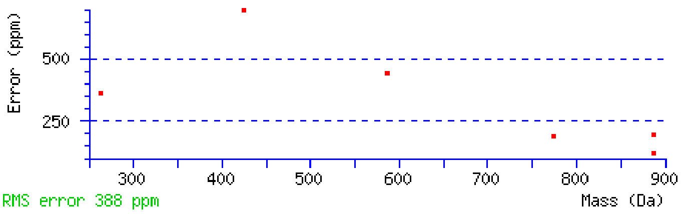
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1034.4760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 **Expect:** 0.0048
Matches : 6/102 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							9
2	207.0582	104.0327					G	**887.4508**	444.2290	869.4272	435.2173	869.4403	435.2238	8
3	279.0924	140.0498					A	829.4323	415.2198	811.4087	406.2080	811.4218	406.2145	7
4	367.1214	184.0643			349.1109	175.0591	S	757.3982	379.2027	739.3746	370.1909	739.3876	370.1974	6
5	***425.1399***	213.0736			407.1294	204.0683	G	669.3691	335.1882	651.3455	326.1764			5
6	***585.2292***	293.1182	567.2056	284.1064	567.2186	284.1129	R	611.3506	306.1789	593.3270	297.1671			4
7	***773.3026***	387.1549	755.2790	378.1431	755.2920	378.1496	W	451.2614	226.1343	433.2378	217.1225			3
8	***887.3837***	444.1955	869.3601	435.1837	869.3731	435.1902	I	**263.1880**	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MGASGRWIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G22190.1

32.6	1034.4760	0.0007	MGASGRWIK
14.2	1034.4789	-0.0023	EMKMVPYK
14.2	1034.4793	-0.0027	MKQREMAK
11.9	1034.4764	0.0002	QMQNKRGR
10.7	1034.4767	-0.0000	LKESMICK
8.7	1034.4793	-0.0027	KMQQMSLR
8.4	1034.4785	-0.0018	SRSSSELQK
8.3	1034.4737	0.0029	SNGKVISCR
3.9	1034.4760	0.0007	MLFSSHKR
3.9	1034.4793	-0.0027	MLREMIGR

AT3G22200.1

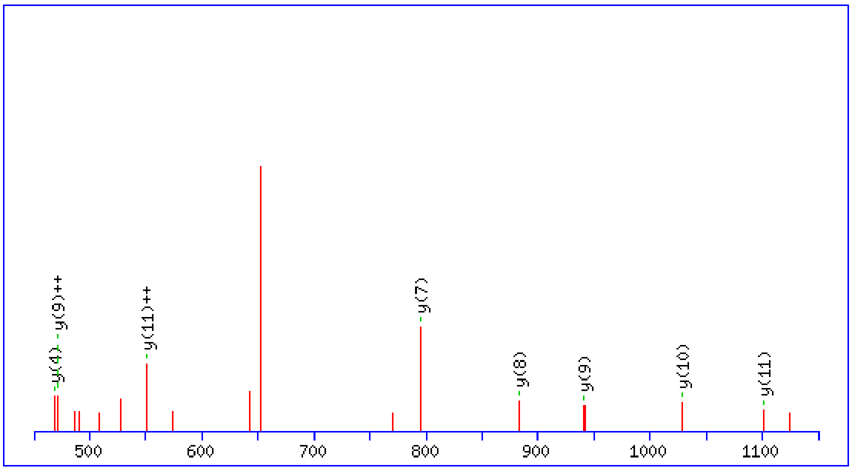
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFASGSPIIGETR**
Found in **AT3G22200.1** in **TAIR_Arabidopsis**, Symbols: HER1, POP2, GABA-T | POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase | chr3:7835293-7838870 FORWARD

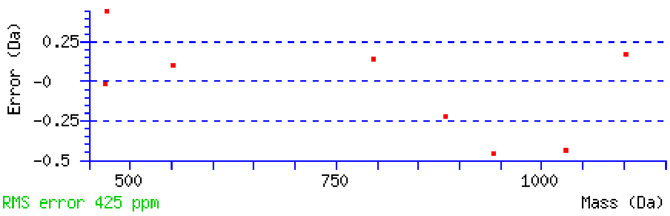
Match to Query 5053: 1320.621274 from(661.317913,2+) index(4133)
Title: Elution from: 38.608 to 38.608 scan no 5137 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

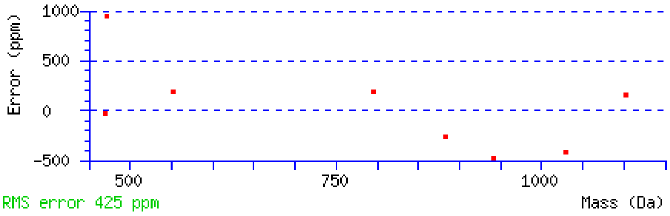


Monoisotopic mass of neutral peptide Mr(calc): 1320.6250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00032
Matches : 8/112 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							13
2	221.1069	111.0571			F	1249.5982	625.3027	1231.5746	616.2909	1231.5876	616.2974	12
3	293.1410	147.0741			A	***1101.5327***	551.2700	1083.5091	542.2582	1083.5221	542.2647	11
4	381.1701	191.0887	363.1595	182.0834	S	***1029.4986***	515.2529	1011.4750	506.2411	1011.4880	506.2476	10
5	439.1886	220.0979	421.1780	211.0926	G	***941.4695***	471.2384	923.4459	462.2266	923.4589	462.2331	9
6	527.2176	264.1125	509.2071	255.1072	S	***883.4510***	442.2291	865.4274	433.2173	865.4404	433.2239	8
7	625.2674	313.1374	607.2569	304.1321	P	***795.4219***	398.2146	777.3983	389.2028	777.4114	389.2093	7
8	739.3485	370.1779	721.3380	361.1726	I	697.3721	349.1897	679.3485	340.1779	679.3616	340.1844	6
9	853.4296	427.2185	835.4191	418.2132	I	583.2910	292.1492	565.2674	283.1374	565.2805	283.1439	5
10	911.4481	456.2277	893.4376	447.2224	G	***469.2099***	235.1086	451.1863	226.0968	451.1994	226.1033	4
11	1041.4878	521.2475	1023.4772	512.2422	E	411.1914	206.0994	393.1678	197.0876	393.1809	197.0941	3
12	1143.5325	572.2699	1125.5219	563.2646	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
13					R	179.1071	90.0572	161.0835	81.0454			1



RMS error 425 ppm



RMS error 425 ppm

NCBI **BLAST** search of AFASGSPIIGETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G22200.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.3	1320.6250	-0.0037	AFASGSPIIGETR
4.8	1320.6228	-0.0015	IRSDSEPKSSAK
2.6	1320.6180	0.0032	RNQAAIGTDVMK
2.4	1320.6207	0.0006	EQRMSQIRPR
2.4	1320.6250	-0.0037	VFGRGELVDDAK
2.2	1320.6228	-0.0015	EVLDTESRSRL
1.9	1320.6232	-0.0020	VMFDKMPLPAK
1.7	1320.6228	-0.0015	DDTSLETIVRR
1.7	1320.6228	-0.0015	LQTDQSSLEKR
1.7	1320.6180	0.0032	AALESMRQEIR

AT3G22460.1

Mascot Search Results

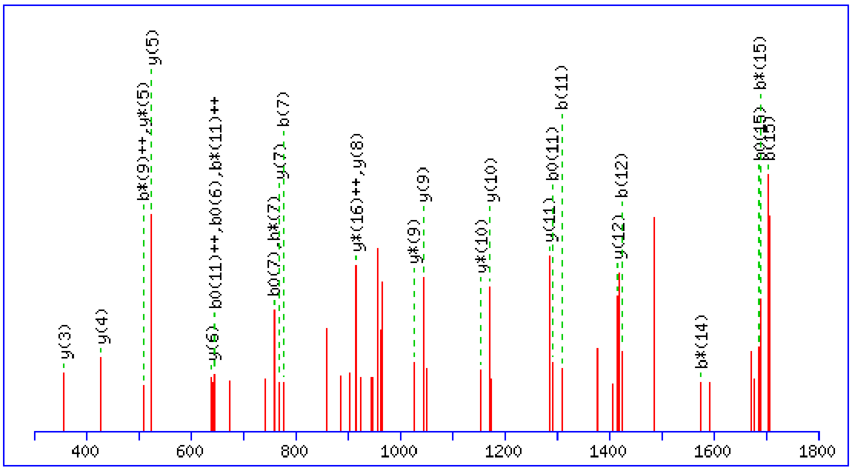
Peptide View

MS/MS Fragmentation of **TPNGYMLQQFENPANPK**
Found in **AT3G22460.1** in **TAIR_Arabidopsis**, Symbols: | cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative | chr3:7963862-7964776 FORWARD

Match to Query 8633: 1947.914126 from(974.964339,2+) index(6052)
Title: Elution from: 56.018 to 56.018 scan no 7895 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

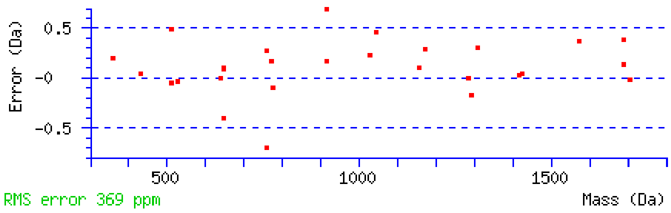
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

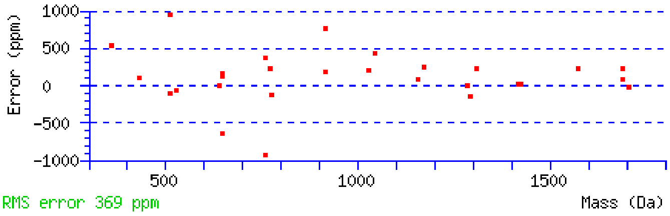


Monoisotopic mass of neutral peptide Mr(calc): 1947.9149
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 6.7e-007
Matches : 28/176 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**17**
2	199.1077	100.0575			181.0972	91.0522	**P**	1847.8745	924.4409	1830.8479	915.9276	1829.8639	915.4356	**16**
3	313.1506	157.0790	296.1241	148.5657	295.1401	148.0737	**N**	1750.8217	875.9145	1733.7952	867.4012	1732.8112	866.9092	**15**
4	370.1721	185.5897	353.1456	177.0764	352.1615	176.5844	**G**	1636.7788	818.8930	1619.7523	810.3798	1618.7682	809.8878	**14**
5	533.2354	267.1214	516.2089	258.6081	515.2249	258.1161	**Y**	1579.7573	790.3823	1562.7308	781.8690	1561.7468	781.3770	**13**
6	664.2759	332.6416	647.2494	324.1283	646.2654	323.6363	**M**	***1416.6940***	708.8506	1399.6675	700.3374	1398.6834	699.8454	**12**
7	**777.3600**	389.1836	760.3334	380.6704	759.3494	380.1783	**L**	***1285.6535***	643.3304	1268.6270	634.8171	1267.6430	634.3251	**11**
8	905.4186	453.2129	888.3920	444.6996	887.4080	444.2076	**Q**	***1172.5695***	586.7884	1155.5429	578.2751	1154.5589	577.7831	**10**
9	1033.4771	517.2422	1016.4506	508.7289	1015.4666	508.2369	**Q**	***1044.5109***	522.7591	1027.4843	514.2458	1026.5003	513.7538	**9**
10	1180.5456	590.7764	1163.5190	582.2631	1162.5350	581.7711	**F**	***916.4523***	458.7298	899.4258	450.2165	898.4417	449.7245	**8**
11	**1309.5882**	655.2977	1292.5616	646.7844	1291.5776	646.2924	**E**	***769.3839***	385.1956	752.3573	376.6823	751.3733	376.1903	**7**
12	**1423.6311**	712.3192	1406.6045	703.8059	1405.6205	703.3139	**N**	***640.3413***	320.6743	623.3148	312.1610			**6**
13	1520.6838	760.8456	1503.6573	752.3323	1502.6733	751.8403	**P**	***526.2984***	263.6528	509.2718	255.1396			**5**
14	1591.7210	796.3641	1574.6944	787.8508	1573.7104	787.3588	**A**	***429.2456***	215.1264	412.2191	206.6132			**4**
15	**1705.7639**	853.3856	1688.7373	844.8723	1687.7533	844.3803	**N**	***358.2085***	179.6079	341.1819	171.0946			**3**
16	1802.8166	901.9120	1785.7901	893.3987	1784.8061	892.9067	**P**	244.1656	122.5864	227.1390	114.0731			**2**
17							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT3G22460.1





NCBI **BLAST** search of TPNGYMLQQFENPANPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.3	1947.9149	-0.0007	TPNGYMLQQFENPANPK
0.3	1947.9104	0.0037	MSDLAQSLGMPPGLSEGMK

Mascot: http://www.matrixscience.com/

AT3G22790.1

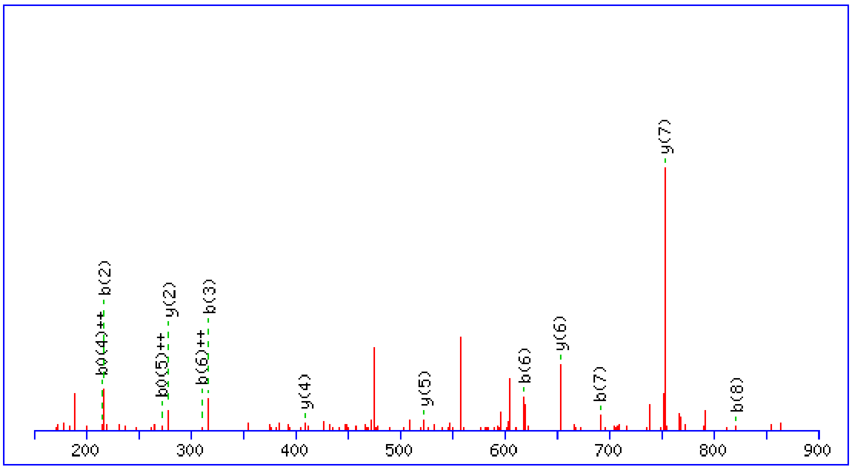
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLVELGAEK**
Found in **AT3G22790.1** in **TAIR_Arabidopsis**, Symbols: | kinase interacting family protein | chr3:8052453-8057895 REVERSE

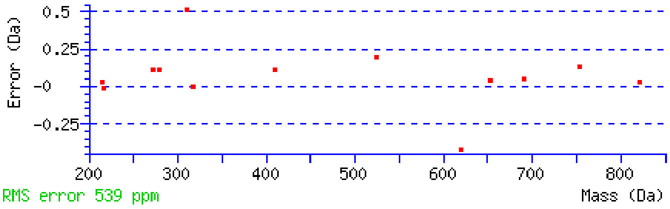
Match to Query 2396: 968.501400 from(485.257976,2+) index(4262)
Title: Elution from: 38.770 to 38.770 scan no 5273 cid35.00 polarity:+
Data file D1d-3_1.mgf

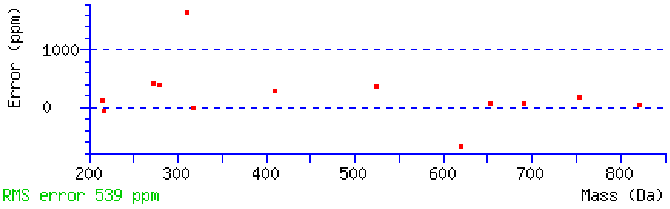
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.5038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.036
Matches : 13/78 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							9
2	***217.1331***	109.0702	199.1225	100.0649	L	867.4664	434.2369	849.4428	425.2251	849.4559	425.2316	8
3	***317.1985***	159.1029	299.1880	150.0976	V	***753.3853***	377.1963	735.3617	368.1845	735.3748	368.1910	7
4	447.2382	224.1227	429.2276	215.1174	E	***653.3199***	327.1636	635.2963	318.1518	635.3093	318.1583	6
5	561.3193	281.1633	543.3087	272.1580	L	***523.2802***	262.1438	505.2567	253.1320	505.2697	253.1385	5
6	***619.3378***	310.1725	601.3272	301.1672	G	***409.1991***	205.1032	391.1756	196.0914	391.1886	196.0979	4
7	***691.3719***	346.1896	673.3613	337.1843	A	351.1807	176.0940	333.1571	167.0822	333.1701	167.0887	3
8	***821.4115***	411.2094	803.4010	402.2041	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TLVELGAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.0	968.5038	-0.0024	TLVELGAEK

AT3G22790.1

14.6	968.4991	0.0023	LTMIPLDR
10.0	968.5039	-0.0025	TLNILEEK
5.8	968.5039	-0.0025	EAISLGLEK
5.1	968.5039	-0.0025	EALLEKEK
4.1	968.5038	-0.0024	LAEVTGLEK
4.0	968.5018	-0.0004	KAIMALHR
3.9	968.5038	-0.0024	GLEAVETLK
3.1	968.4991	0.0023	VTLEMLPR
2.2	968.5038	-0.0024	DTQEIILK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSDLLAFSGPAPER**
Found in **AT3G22840.1** in **TAIR_Arabidopsis**, Symbols: ELIP, ELIP1 | ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chlorophyll binding | chr3:8084635-8085452 REVERSE

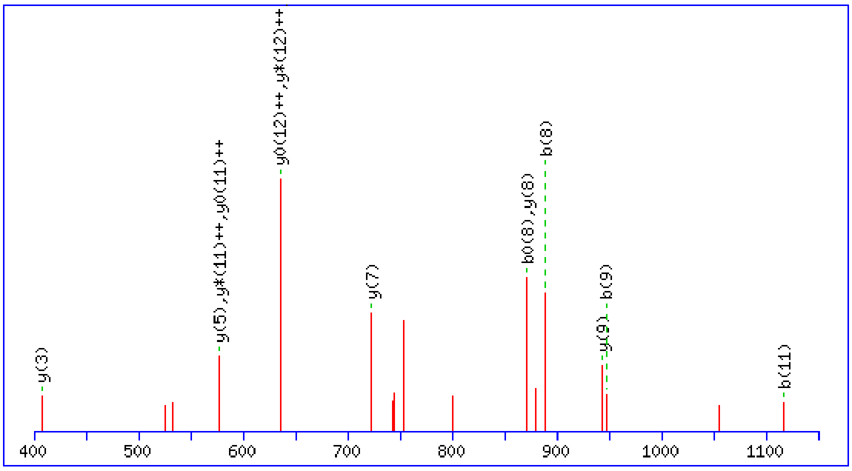
Match to Query 6392: 1522.704458 from(762.359505,2+) index(7591)
Title: Elution from: 66.360 to 66.360 scan no 9969 cid35.00 polarity:+
Data file C7-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1150 Da Full range

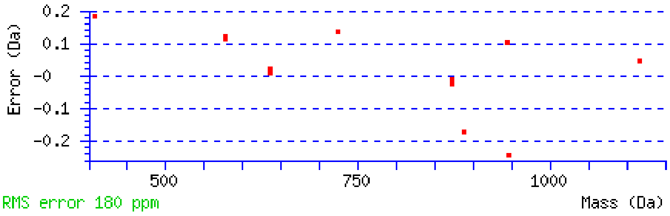
Label all possible matches ○ Label matches used for scoring ●

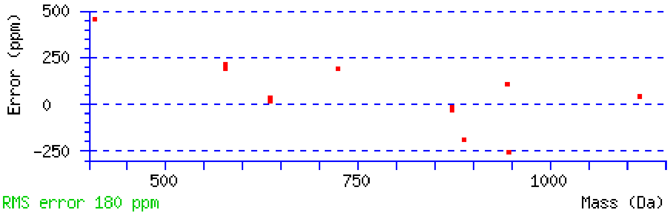
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1522.7010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 7.6e-005
Matches : 15/126 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400			**F**							**14**
2	237.1018	119.0545	219.0912	110.0492	**S**	1375.6429	688.3251	1357.6193	679.3133	1357.6323	679.3198	**13**
3	353.1258	177.0665	335.1152	168.0612	**D**	1287.6138	644.3105	1269.5902	635.2987	1269.6032	635.3053	**12**
4	467.2069	234.1071	449.1963	225.1018	**L**	1171.5898	586.2986	1153.5662	577.2868	1153.5793	577.2933	**11**
5	581.2880	291.1476	563.2774	282.1423	**L**	1057.5087	529.2580	1039.4851	520.2462	1039.4982	520.2527	**10**
6	653.3221	327.1647	635.3115	318.1594	**A**	***943.4276***	472.2175	925.4040	463.2057	925.4171	463.2122	**9**
7	801.3876	401.1974	783.3770	392.1921	**F**	***871.3935***	436.2004	853.3699	427.1886	853.3829	427.1951	**8**
8	**889.4166**	445.2120	871.4061	436.2067	**S**	***723.3280***	362.1677	705.3044	353.1559	705.3175	353.1624	**7**
9	**947.4351**	474.2212	929.4246	465.2159	**G**	***635.2990***	318.1531	617.2754	309.1413	617.2884	309.1478	**6**
10	1045.4849	523.2461	1027.4744	514.2408	**P**	***577.2805***	289.1439	559.2569	280.1321	559.2699	280.1386	**5**
11	**1117.5191**	559.2632	1099.5085	550.2579	**A**	479.2307	240.1190	461.2071	231.1072	461.2201	231.1137	**4**
12	1215.5689	608.2881	1197.5583	599.2828	**P**	***407.1965***	204.1019	389.1729	195.0901	389.1860	195.0966	**3**
13	1345.6085	673.3079	1327.5979	664.3026	**E**	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	**2**
14					**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of FSDLLAFSGPAPER

AT3G22840.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.5	1522.7010	0.0034	FSDLLAFSGPAPER
1.7	1522.7041	0.0003	ATNNFSRHNIIGR
0.1	1522.7010	0.0034	EHSYQFIDINLK

AT3G22890.1

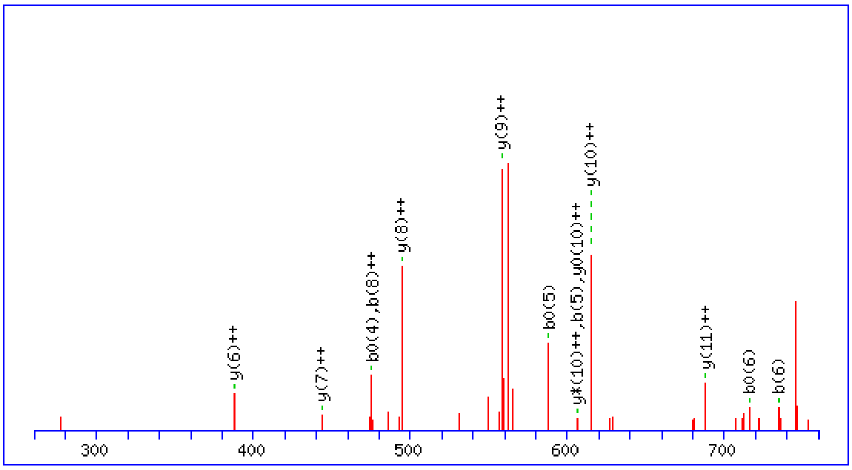
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESEFLQTLHFNSLR**
Found in **AT3G22890.1** in **TAIR_Arabidopsis**, Symbols: APS1 | APS1 (ATP sulfurylase 3) | chr3:8112844-8114741 FORWARD

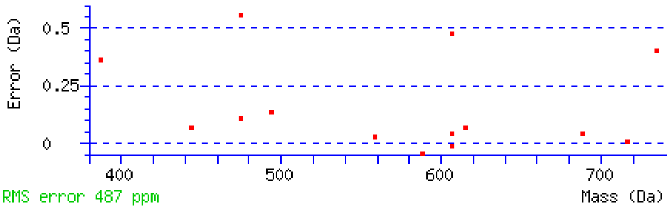
Match to Query 7877: 1719.853062 from(574.291630,3+) index(7709)
Title: Elution from: 68.042 to 68.042 scan no 10189 cid35.00 polarity:+
Data file 0-3_3.mgf

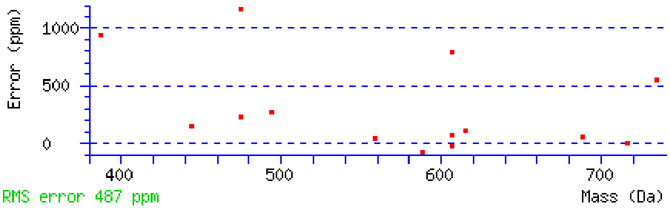
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 260 to 760 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1719.8580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0016
Matches : 14/142 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	217.0819	109.0446			199.0713	100.0393	S	1591.8227	796.4150	1574.7962	787.9017	1573.8122	787.4097	13
3	346.1245	173.5659			328.1139	164.5606	E	1504.7907	752.8990	1487.7641	744.3857	1486.7801	743.8937	12
4	493.1929	247.1001			475.1823	238.0948	F	1375.7481	688.3777	1358.7215	679.8644	1357.7375	679.3724	11
5	**606.2770**	303.6421			588.2664	294.6368	L	1228.6797	614.8435	1211.6531	606.3302	1210.6691	605.8382	10
6	**734.3355**	367.6714	717.3090	359.1581	716.3250	358.6661	Q	1115.5956	558.3014	1098.5691	549.7882	1097.5851	549.2962	9
7	835.3832	418.1953	818.3567	409.6820	817.3727	409.1900	T	987.5370	494.2722	970.5105	485.7589	969.5265	485.2669	8
8	948.4673	474.7373	931.4407	466.2240	930.4567	465.7320	L	886.4894	443.7483	869.4628	435.2350	868.4788	434.7430	7
9	1085.5262	543.2667	1068.4997	534.7535	1067.5156	534.2615	H	773.4053	387.2063	756.3787	378.6930	755.3947	378.2010	6
10	1232.5946	616.8009	1215.5681	608.2877	1214.5841	607.7957	F	636.3464	318.6768	619.3198	310.1636	618.3358	309.6715	5
11	1346.6375	673.8224	1329.6110	665.3091	1328.6270	664.8171	N	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
12	1433.6696	717.3384	1416.6430	708.8251	1415.6590	708.3331	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	1546.7536	773.8805	1529.7271	765.3672	1528.7431	764.8752	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ESEFLQTLHFNSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G22890.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.3	1719.8580	-0.0050	ESEFLQTLHFNSLR
5.5	1719.8540	-0.0010	GGSRVFEVNLVTDDGR
2.1	1719.8500	0.0031	TETAEARQTNSRAGTK
1.0	1719.8502	0.0029	SITSTAPLNGWMDSIK
0.1	1719.8527	0.0004	SSSTAVSVPISVNTDEK

AT3G23020.1

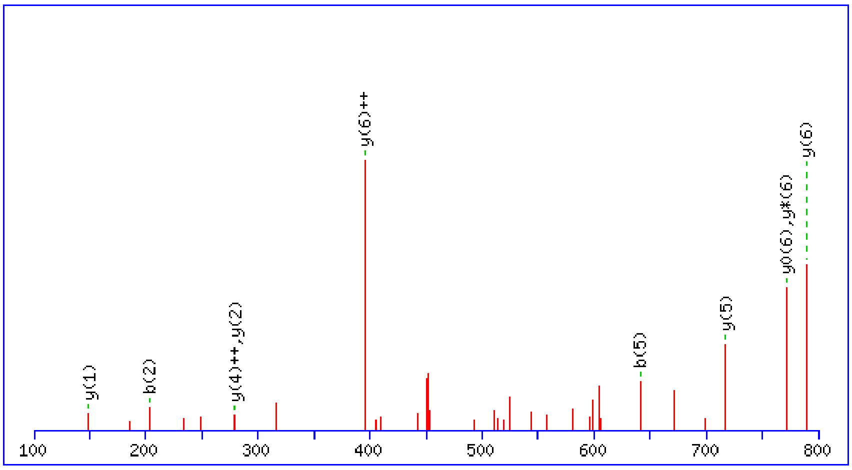
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAREFQK**
Found in **AT3G23020.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:8177222-8179750 REVERSE

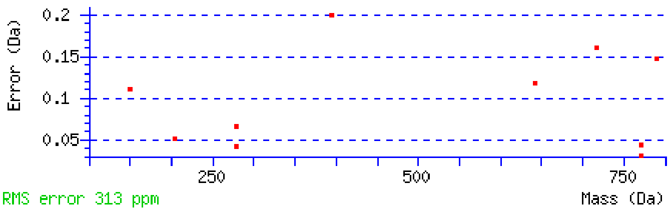
Match to Query 1865: 918.468370 from(460.241461,2+) index(7597)
Title: Elution from: 65.989 to 65.989 scan no 9675 cid35.00 polarity:+
Data file 0-1_1.mgf

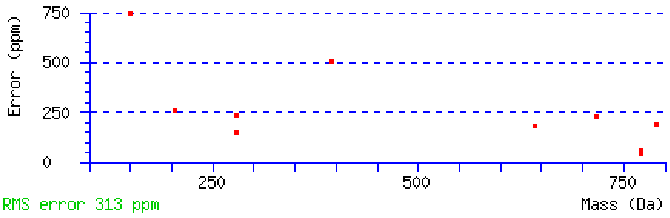
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 918.4697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0084
Matches : 11/60 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							7
2	**203.1305**	102.0689	185.1069	93.0571			A	***789.3880***	395.1976	771.3644	386.1858	771.3774	386.1924	6
3	363.2197	182.1135	345.1961	173.1017			R	***717.3538***	359.1806	699.3303	350.1688	699.3433	350.1753	5
4	493.2593	247.1333	475.2358	238.1215	475.2488	238.1280	E	557.2646	279.1359	539.2410	270.1241	539.2540	270.1307	4
5	**641.3248**	321.1660	623.3012	312.1542	623.3142	312.1607	F	427.2250	214.1161	409.2014	205.1043			3
6	**771.3774**	386.1924	753.3538	377.1806	753.3669	377.1871	Q	***279.1595***	140.0834	261.1359	131.0716			2
7							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KAREFQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.5	918.4697	-0.0014	KAREFQK
27.8	918.4693	-0.0009	GAFEFLVK
24.6	918.4671	0.0013	KFEETKK

AT3G23020.1

24.6	918.4671	0.0013	KYLTEAGK
23.9	918.4697	-0.0014	QFAKREK
21.2	918.4671	0.0013	KTFEEKK
19.6	918.4697	-0.0014	KAFGQTVR
18.7	918.4671	0.0013	KTKEFEK
16.8	918.4671	0.0013	KFSEASLK
16.7	918.4671	0.0013	ETQYLKK

AT3G23160.1

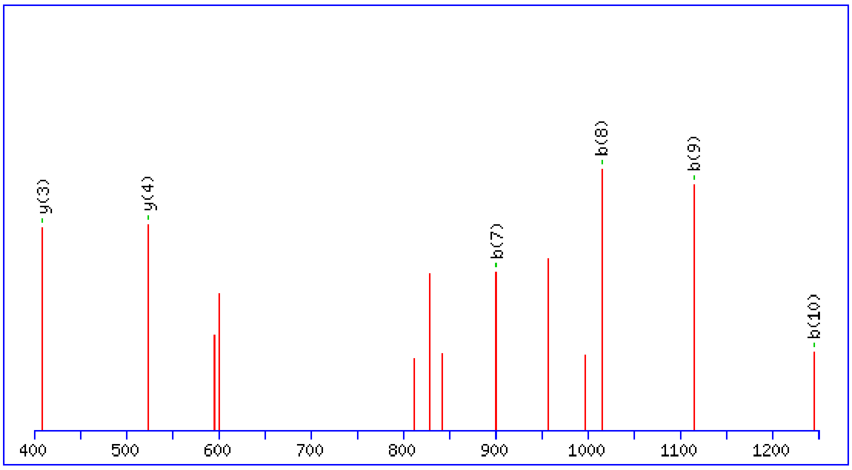
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFEQQNQIVKR**
Found in **AT3G23160.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04550.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71334.1); contains InterPro domain Protein of unknown function DUF668 (InterPro:IPR007700) | chr3:8260066-8

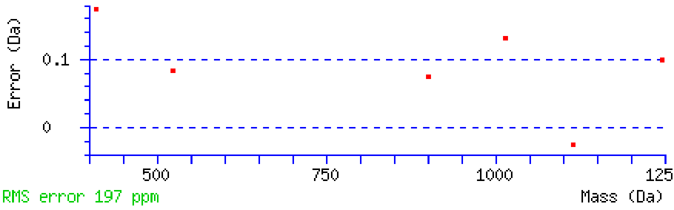
Match to Query 5608: 1422.670324 from(712.342438,2+) index(10886)
Title: Elution from: 108.718 to 108.718 scan no 15895 cid35.00 polarity:+
Data file C7-1_2.mgf

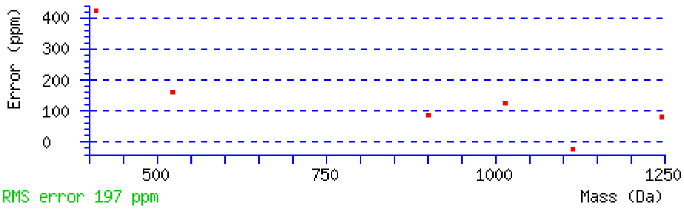
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1422.6724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0062
Matches : 6/100 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							11
2	265.1097	133.0585	247.0861	124.0467			F	1307.6427	654.3250	1289.6191	645.3132	1289.6321	645.3197	10
3	395.1493	198.0783	377.1258	189.0665	377.1388	189.0730	E	1159.5772	580.2923	1141.5537	571.2805	1141.5667	571.2870	9
4	525.2020	263.1046	507.1784	254.0928	507.1914	254.0994	Q	1029.5376	515.2724	1011.5140	506.2607			8
5	655.2546	328.1310	637.2311	319.1192	637.2441	319.1257	Q	899.4850	450.2461	881.4614	441.2343			7
6	771.2916	386.1495	753.2681	377.1377	753.2811	377.1442	N	769.4323	385.2198	751.4087	376.2080			6
7	***901.3443***	451.1758	883.3207	442.1640	883.3337	442.1705	Q	653.3953	327.2013	635.3717	318.1895			5
8	***1015.4254***	508.2163	997.4018	499.2045	997.4148	499.2110	I	**523.3427**	262.1750	505.3191	253.1632			4
9	***1115.4908***	558.2491	1097.4673	549.2373	1097.4803	549.2438	V	**409.2616**	205.1344	391.2380	196.1226			3
10	***1245.5799***	623.2936	1227.5563	614.2818	1227.5693	614.2883	K	309.1961	155.1017	291.1725	146.0899			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NFEQQNQIVKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G23160.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.3	1422.6724	-0.0021	NFEQQNQIVKR
20.7	1422.6697	0.0006	GSDAVASVFAVLDR
19.4	1422.6720	-0.0016	FWKSVVEEVER
4.9	1422.6697	0.0006	IFDQGTGTPSKQK
4.2	1422.6683	0.0020	DRMMLLDDIRK
4.0	1422.6720	-0.0016	KDYKPPVFEER
3.9	1422.6720	-0.0016	SIGFWTEGNGLVK
3.4	1422.6677	0.0027	LCYRHIEKQR
3.3	1422.6675	0.0028	QASLSTDKALSER
3.3	1422.6697	0.0006	DQYEKGALVEVR

Mascot: http://www.matrixscience.com/

AT3G23310.1

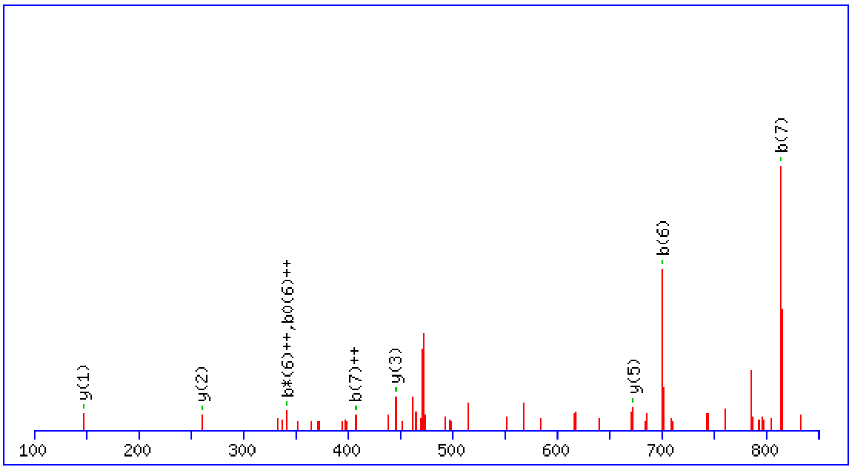
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTARAWLK**
Found in **AT3G23310.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase, putative | chr3:8339806-8343362 FORWARD

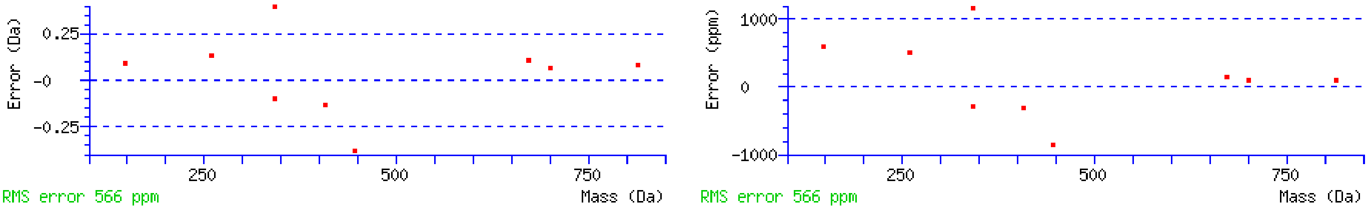
Match to Query 2317: 959.518778 from(480.766665,2+) index(1467)
Title: Elution from: 20.499 to 20.499 scan no 2023 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 959.5188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.035
Matches : 9/66 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							8
2	217.0819	109.0446			199.0713	100.0393	T	845.4992	423.2532	828.4727	414.7400	827.4886	414.2480	7
3	288.1190	144.5631			270.1084	135.5579	A	744.4515	372.7294	727.4250	364.2161			6
4	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	R	***673.4144***	337.2108	656.3879	328.6976			5
5	515.2572	258.1323	498.2307	249.6190	497.2467	249.1270	A	517.3133	259.1603	500.2867	250.6470			4
6	**701.3365**	351.1719	684.3100	342.6586	683.3260	342.1666	W	***446.2762***	223.6417	429.2496	215.1285			3
7	**814.4206**	407.7139	797.3941	399.2007	796.4100	398.7087	L	***260.1969***	130.6021	243.1703	122.0888			2
8							K	***147.1128***	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of DTARAWLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	959.5188	-0.0001	DTARAWLK
19.3	959.5175	0.0013	LETEVEIK

AT3G23310.1

16.4	959.5188	-0.0001	RSSPSWLK
15.3	959.5175	0.0013	LETDIEIK
7.5	959.5188	-0.0001	DWDRKIK
7.5	959.5175	0.0013	LELEESLK
7.5	959.5175	0.0013	SEEIIELK
4.9	959.5175	0.0013	LTELLDEK
3.3	959.5175	0.0013	DLLEELTK
0.3	959.5188	-0.0001	WLREGTAK

AT3G23400.1

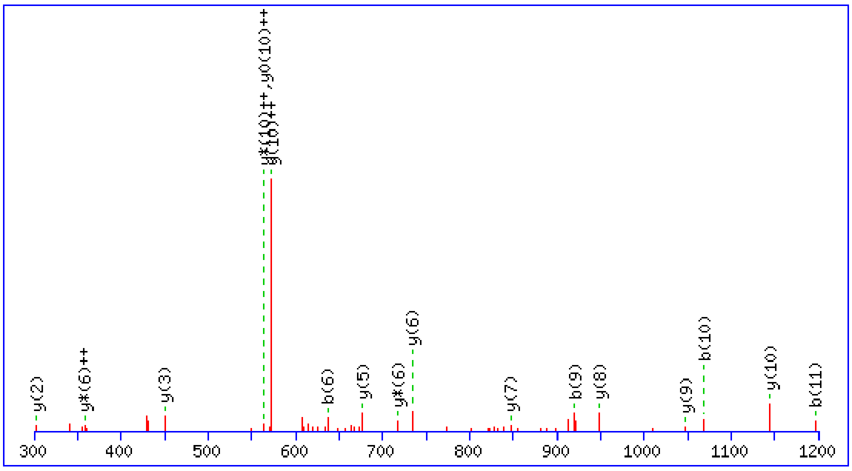
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIPVTLGQVFQR**
Found in **AT3G23400.1** in **TAIR_Arabidopsis**, Symbols: | plastid-lipid associated protein PAP / fibrillin family protein | chr3:8376643-8378232 REVERSE

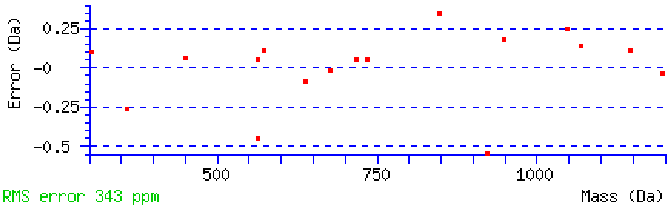
Match to Query 5051: 1369.805300 from(685.909926,2+) index(8358)
Title: Elution from: 74.881 to 74.881 scan no 11337 cid35.00 polarity:+
Data file D12h-3_3.mgf

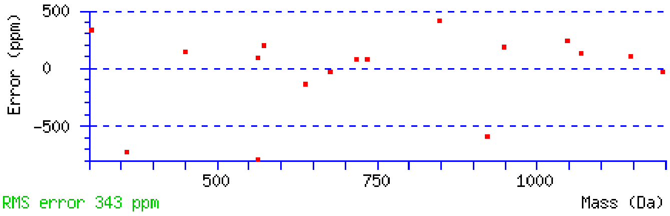
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1369.8082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 5.7e-006
Matches : 17/96 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							12
2	227.1754	114.0913					I	1257.7314	629.3693	1240.7048	620.8561	1239.7208	620.3640	11
3	324.2282	162.6177					P	***1144.6473***	572.8273	1127.6208	564.3140	1126.6368	563.8220	10
4	423.2966	212.1519					V	***1047.5946***	524.3009	1030.5680	515.7876	1029.5840	515.2956	9
5	524.3443	262.6758			506.3337	253.6705	T	***948.5261***	474.7667	931.4996	466.2534	930.5156	465.7614	8
6	**637.4283**	319.2178			619.4178	310.2125	L	***847.4785***	424.2429	830.4519	415.7296			7
7	694.4498	347.7285			676.4392	338.7233	G	***734.3944***	367.7008	717.3679	359.1876			6
8	822.5084	411.7578	805.4818	403.2445	804.4978	402.7525	Q	***677.3729***	339.1901	660.3464	330.6768			5
9	**921.5768**	461.2920	904.5502	452.7788	903.5662	452.2867	V	549.3144	275.1608	532.2878	266.6475			4
10	**1068.6452**	534.8262	1051.6186	526.3130	1050.6346	525.8210	F	***450.2459***	225.6266	433.2194	217.1133			3
11	**1196.7038**	598.8555	1179.6772	590.3423	1178.6932	589.8502	Q	***303.1775***	152.0924	286.1510	143.5791			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LIPVTLGQVFQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G23400.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.2	1369.8082	-0.0029	LIPVTLGQVFQR
1.7	1369.8041	0.0012	LNIKKTEQQLR
0.5	1369.8041	0.0012	NIELVSRAVLTR

AT3G23600.1

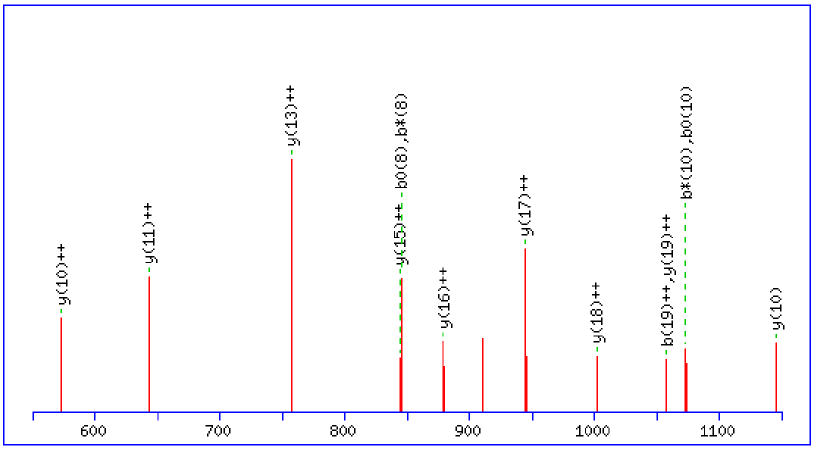
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EELIQAAVLLHPSFVNVDDIK**
Found in **AT3G23600.1** in **TAIR_Arabidopsis**, Symbols: | dienelactone hydrolase family protein | chr3:8473840-8475662 FORWARD

Match to Query 10012: 2375.175042 from(792.732290,3+) index(9860)
Title: Elution from: 92.654 to 92.654 scan no 13887 cid35.00 polarity:+
Data file C7-1_3.mgf

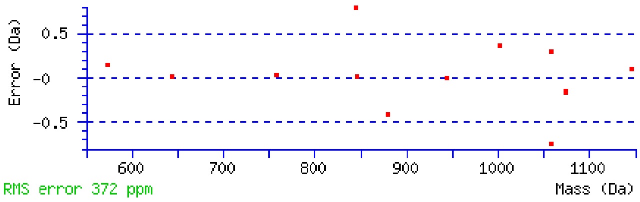
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

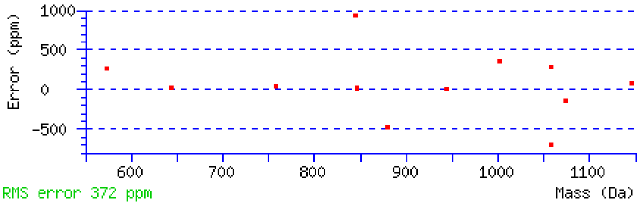


Monoisotopic mass of neutral peptide Mr(calc): 2375.1809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 1.9e-005
Matches : 14/228 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							21
2	261.0865	131.0469			243.0760	122.0416	E	2246.1486	1123.5779	2228.1250	1114.5661	2228.1380	1114.5726	20
3	375.1676	188.0875			357.1571	179.0822	L	2116.1089	1058.5581	2098.0854	1049.5463	2098.0984	1049.5528	19
4	489.2487	245.1280			471.2382	236.1227	I	2002.0278	1001.5176	1984.0043	992.5058	1984.0173	992.5123	18
5	619.3014	310.1543	601.2778	301.1425	601.2908	301.1490	Q	1887.9467	944.4770	1869.9232	935.4652	1869.9362	935.4717	17
6	691.3355	346.1714	673.3119	337.1596	673.3250	337.1661	A	1757.8941	879.4507	1739.8705	870.4389	1739.8835	870.4454	16
7	763.3697	382.1885	745.3461	373.1767	745.3591	373.1832	A	1685.8599	843.4336	1667.8364	834.4218	1667.8494	834.4283	15
8	863.4351	432.2212	845.4115	423.2094	845.4246	423.2159	V	1613.8258	807.4165	1595.8022	798.4047	1595.8152	798.4113	14
9	977.5162	489.2617	959.4926	480.2500	959.5057	480.2565	L	1513.7603	757.3838	1495.7368	748.3720	1495.7498	748.3785	13
10	1091.5973	546.3023	1073.5737	537.2905	1073.5868	537.2970	L	1399.6793	700.3433	1381.6557	691.3315	1381.6687	691.3380	12
11	1231.6473	616.3273	1213.6238	607.3155	1213.6368	607.3220	H	1285.5982	643.3027	1267.5746	634.2909	1267.5876	634.2974	11
12	1329.6971	665.3522	1311.6736	656.3404	1311.6866	656.3469	P	1145.5481	573.2777	1127.5246	564.2659	1127.5376	564.2724	10
13	1417.7262	709.3667	1399.7026	700.3549	1399.7156	700.3615	S	1047.4983	524.2528	1029.4748	515.2410	1029.4878	515.2475	9
14	1565.7916	783.3995	1547.7681	774.3877	1547.7811	774.3942	F	959.4693	480.2383	941.4457	471.2265	941.4587	471.2330	8
15	1665.8571	833.4322	1647.8335	824.4204	1647.8465	824.4269	V	811.4038	406.2056	793.3802	397.1938	793.3933	397.2003	7
16	1781.8941	891.4507	1763.8705	882.4389	1763.8835	882.4454	N	711.3384	356.1728	693.3148	347.1610	693.3278	347.1675	6
17	1881.9595	941.4834	1863.9360	932.4716	1863.9490	932.4781	V	595.3014	298.1543	577.2778	289.1425	577.2908	289.1490	5
18	1997.9835	999.4954	1979.9599	990.4836	1979.9730	990.4901	D	495.2359	248.1216	477.2123	239.1098	477.2254	239.1163	4
19	2114.0075	1057.5074	2095.9839	1048.4956	2095.9969	1048.5021	D	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
20	2228.0886	1114.5479	2210.0650	1105.5361	2210.0780	1105.5427	I	263.1880	132.0976	245.1644	123.0858			2
21							K	149.1069	75.0571	131.0833	66.0453			1

AT3G23600.1





NCBI **BLAST** search of EELIQAAVLLHPSFVNVDDIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.2	2375.1809	-0.0059	EELIQAAVLLHPSFVNVDDIK
2.3	2375.1710	0.0040	GAVPHGNLKATNILLDGAELNAR

Mascot: http://www.matrixscience.com/

AT3G23810.1

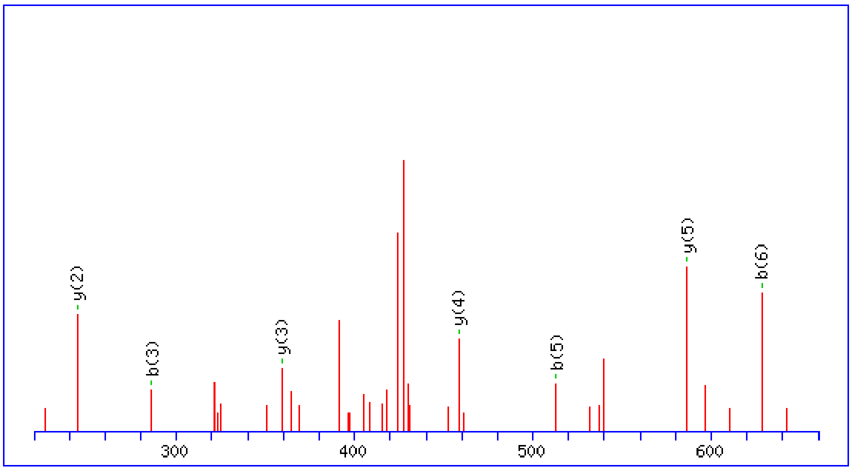
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGLQVDPK**
Found in **AT3G23810.1** in **TAIR_Arabidopsis**, Symbols: SAHH2 | SAHH2 (S-ADENOSYL-L-HOMOCYSTEINE (SAH) HYDROLASE 2); adenosylhomocysteinase | chr3:8588020-8589678 REVERSE

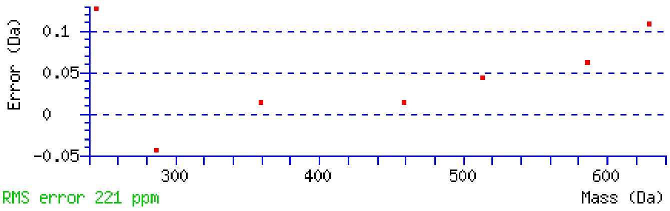
Match to Query 1445: 870.443890 from(436.229221,2+) index(1299)
Title: Elution from: 17.826 to 17.826 scan no 1759 cid35.00 polarity:+
Data file C7-3_2.mgf

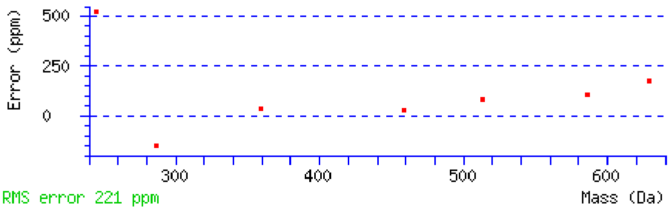
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 870.4447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.008
Matches : 7/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							8
2	173.0557	87.0315			155.0451	78.0262	G	756.4250	378.7162	739.3985	370.2029	738.4145	369.7109	7
3	**286.1397**	143.5735			268.1292	134.5682	L	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	6
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	Q	***586.3195***	293.6634	569.2930	285.1501	568.3089	284.6581	5
5	**513.2667**	257.1370	496.2402	248.6237	495.2562	248.1317	V	***458.2609***	229.6341	441.2344	221.1208	440.2504	220.6288	4
6	**628.2937**	314.6505	611.2671	306.1372	610.2831	305.6452	D	***359.1925***	180.0999	342.1660	171.5866	341.1819	171.0946	3
7	725.3464	363.1769	708.3199	354.6636	707.3359	354.1716	P	***244.1656***	122.5864	227.1390	114.0731			2
8							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DGLQVDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.0	870.4447	-0.0008	DGLQVDPK

AT3G23810.1

Mascot: http://www.matrixscience.com/

AT3G23940.1

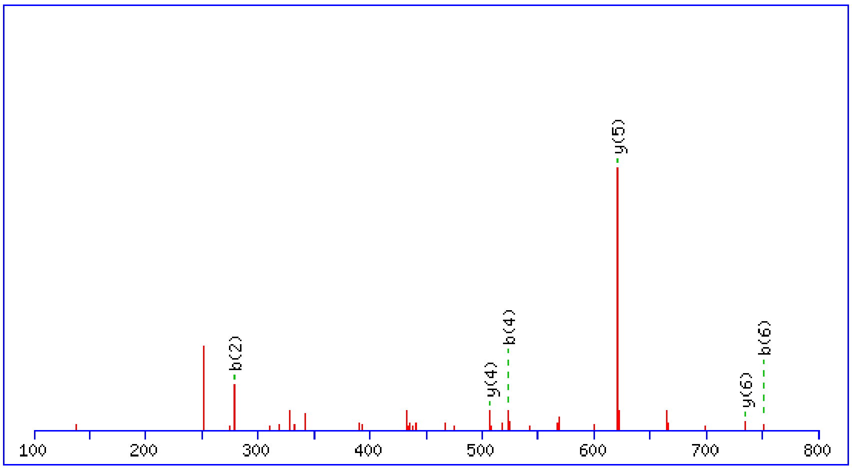
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLLELLK**
Found in **AT3G23940.1** in **TAIR_Arabidopsis**, Symbols: | dehydratase family | chr3:8648787-8652330 FORWARD

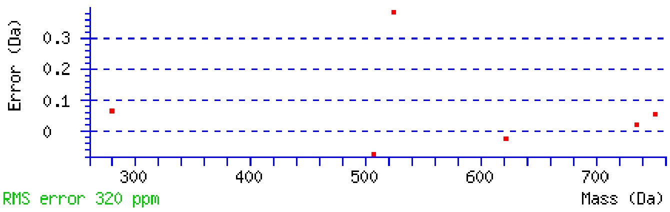
Match to Query 1501: 898.523816 from(450.269184,2+) index(7809)
Title: Elution from: 69.539 to 69.539 scan no 10274 cid35.00 polarity:+
Data file C7-1_3.mgf

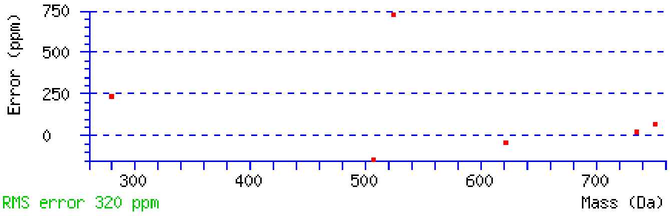
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 898.5240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.02
Matches : 6/48 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375			Y							7
2	*279.1487*	140.0780			L	*735.4709*	368.2391	717.4473	359.2273	717.4603	359.2338	6
3	393.2298	197.1186			L	*621.3898*	311.1985	603.3662	302.1867	603.3792	302.1933	5
4	*523.2695*	262.1384	505.2589	253.1331	E	*507.3087*	254.1580	489.2851	245.1462	489.2981	245.1527	4
5	637.3506	319.1789	619.3400	310.1736	L	377.2691	189.1382	359.2455	180.1264			3
6	*751.4317*	376.2195	733.4211	367.2142	L	263.1880	132.0976	245.1644	123.0858			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YLLELLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	898.5240	-0.0002	YLLELLK
22.6	898.5244	-0.0006	SKIGNLKK
20.0	898.5240	-0.0002	IYLLIEK

AT3G23940.1

19.5	898.5244	-0.0006	RKTIIEK
15.3	898.5240	-0.0002	IYLELLK
14.0	898.5244	-0.0006	SIINKGKK
9.6	898.5244	-0.0006	KKPASTKK
8.7	898.5244	-0.0006	RTLLKEK
5.5	898.5244	-0.0006	KPASTKKK
3.6	898.5244	-0.0006	LGLNKSKK

AT3G23990.1

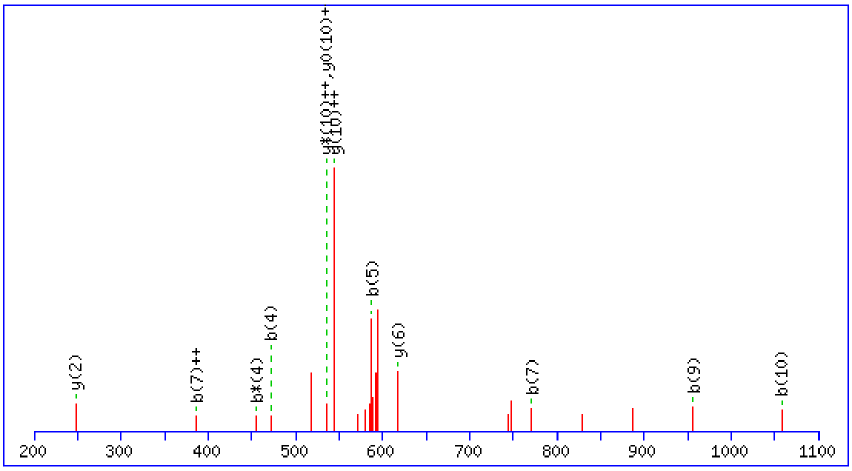
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRVTDALNATK**
Found in **AT3G23990.1** in **TAIR_Arabidopsis**, Symbols: HSP60 | HSP60 (Heat shock protein 60); ATP binding / protein binding / unfolded protein binding | chr3:8669020-8672285 FORWARD

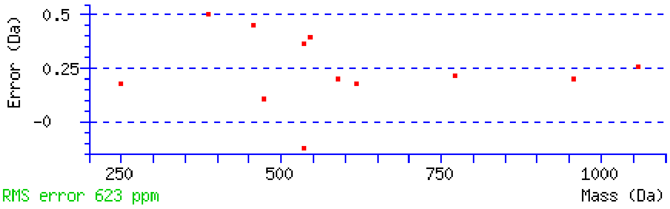
Match to Query 3842: 1202.623232 from(602.318892,2+) index(2644)
Title: Elution from: 29.999 to 29.999 scan no 3428 cid35.00 polarity:+
Data file D1d-2_1.mgf

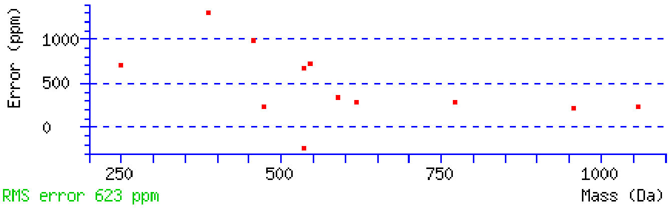
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1202.6255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0059
Matches : 12/116 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							11
2	272.1353	136.5713	255.1088	128.0580	254.1248	127.5660	R	1088.6058	544.8066	1071.5793	536.2933	1070.5953	535.8013	10
3	371.2037	186.1055	354.1772	177.5922	353.1932	177.1002	V	932.5047	466.7560	915.4782	458.2427	914.4942	457.7507	9
4	***472.2514***	236.6293	455.2249	228.1161	454.2409	227.6241	T	833.4363	417.2218	816.4098	408.7085	815.4258	408.2165	8
5	***587.2784***	294.1428	570.2518	285.6295	569.2678	285.1375	D	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	7
6	658.3155	329.6614	641.2889	321.1481	640.3049	320.6561	A	**617.3617**	309.1845	600.3352	300.6712	599.3511	300.1792	6
7	***771.3995***	386.2034	754.3730	377.6901	753.3890	377.1981	L	546.3246	273.6659	529.2980	265.1527	528.3140	264.6606	5
8	885.4425	443.2249	868.4159	434.7116	867.4319	434.2196	N	433.2405	217.1239	416.2140	208.6106	415.2300	208.1186	4
9	***956.4796***	478.7434	939.4530	470.2302	938.4690	469.7381	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
10	***1057.5273***	529.2673	1040.5007	520.7540	1039.5167	520.2620	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DRVTDALNATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G23990.1

Score	Mr(calc)	Delta	Sequence
29.4	1202.6255	-0.0023	DRVTDALNATK
5.4	1202.6255	-0.0023	EQDTLVRQSK
2.7	1202.6255	-0.0022	QESAERKVEK
2.2	1202.6255	-0.0022	LEESKEQGKR
1.5	1202.6196	0.0036	LRWPDFVDR
1.3	1202.6255	-0.0022	LAGESESNLRK
1.2	1202.6255	-0.0023	GLKEASTQNQK
0.7	1202.6255	-0.0023	NSSSDQVVVLR
0.5	1202.6255	-0.0023	IVQSSDQKNGK
0.4	1202.6264	-0.0031	GMNILRPQMK

AT3G24170.1

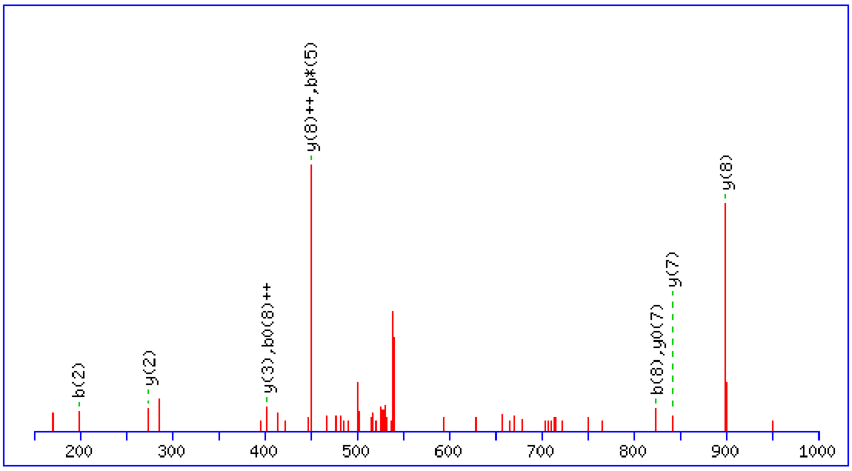
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGPNEVEVR**
Found in **AT3G24170.1** in **TAIR_Arabidopsis**, Symbols: ATGR1 | ATGR1 (GLUTATHIONE-DISULFIDE REDUCTASE); glutathione-disulfide reductase | chr3:8729769-8734122 REVERSE

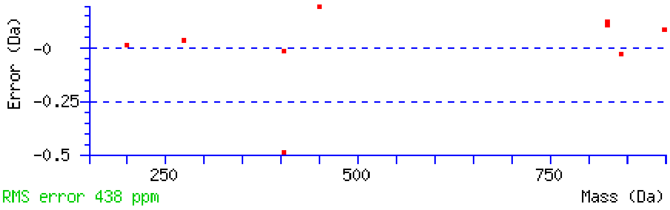
Match to Query 3475: 1096.586030 from(549.300291,2+) index(2285)
Title: Elution from: 25.793 to 25.793 scan no 2911 cid35.00 polarity:+
Data file 0-2_1.mgf

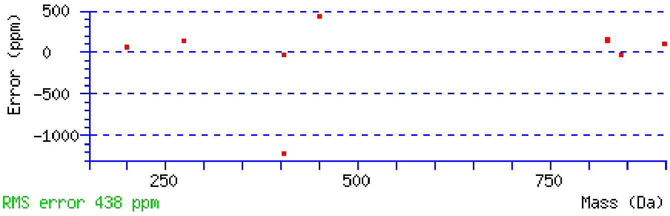
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1096.5877
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.015
Matches : 10/86 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							10
2	**199.1441**	100.0757					V	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	9
3	256.1656	128.5864					G	***899.4581***	450.2327	882.4316	441.7194	881.4476	441.2274	8
4	353.2183	177.1128					P	***842.4367***	421.7220	825.4101	413.2087	824.4261	412.7167	7
5	467.2613	234.1343	450.2347	225.6210			N	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	6
6	596.3039	298.6556	579.2773	290.1423	578.2933	289.6503	E	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	5
7	695.3723	348.1898	678.3457	339.6765	677.3617	339.1845	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
8	**824.4149**	412.7111	807.3883	404.1978	806.4043	403.7058	E	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	923.4833	462.2453	906.4567	453.7320	905.4727	453.2400	V	***274.1874***	137.5973	257.1608	129.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VVGPNEVEVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G24170.1

Score	Mr(calc)	Delta	Sequence
21.9	1096.5877	-0.0016	VVGPNEVEVR
5.2	1096.5877	-0.0016	LGLGDHSTAVK

Mascot: http://www.matrixscience.com/

AT3G24320.1

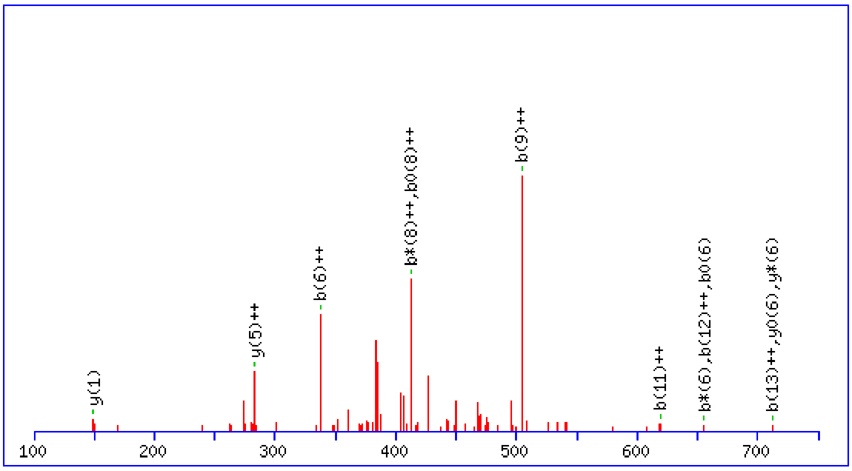
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLLLNPPAYDIALK**
Found in **AT3G24320.1** in **TAIR_Arabidopsis**, Symbols: MSH1, CHM1, ATMSH1, CHM | ATMSH1/CHM/CHM1/MSH1 (MUTL PROTEIN HOMOLOG 1); ATP binding / damaged DNA binding | chr3:8823236-8829578 REVERSE

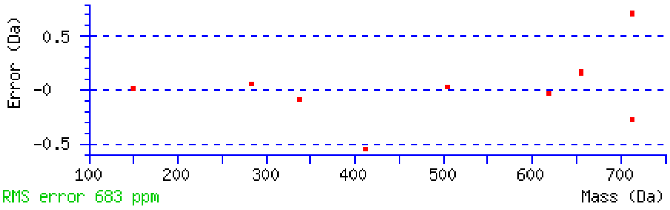
Match to Query 6927: 1570.822820 from(393.712981,4+) index(1949)
Title: Elution from: 23.288 to 23.288 scan no 2531 cid35.00 polarity:+
Data file 0-2_2.mgf

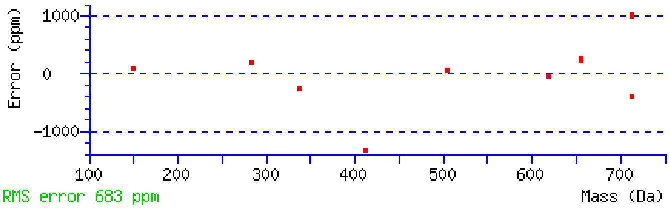
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1570.8183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.012
Matches : 13/140 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							14
2	231.1124	116.0598			213.1018	107.0545	L	1455.8016	728.4044	1437.7780	719.3926	1437.7910	719.3992	13
3	345.1935	173.1004			327.1829	164.0951	L	1341.7205	671.3639	1323.6969	662.3521	1323.7099	662.3586	12
4	459.2746	230.1409			441.2640	221.1356	L	1227.6394	614.3233	1209.6158	605.3115	1209.6288	605.3181	11
5	575.3115	288.1594	557.2880	279.1476	557.3010	279.1541	N	1113.5583	557.2828	1095.5347	548.2710	1095.5477	548.2775	10
6	673.3613	***337.1843***	655.3378	328.1725	655.3508	328.1790	P	997.5213	499.2643	979.4977	490.2525	979.5107	490.2590	9
7	771.4111	386.2092	753.3876	377.1974	753.4006	377.2039	P	899.4715	450.2394	881.4479	441.2276	881.4609	441.2341	8
8	843.4453	422.2263	825.4217	413.2145	825.4347	413.2210	A	801.4217	401.2145	783.3981	392.2027	783.4111	392.2092	7
9	1007.5057	***504.2565***	989.4821	495.2447	989.4951	495.2512	Y	729.3876	365.1974	711.3640	356.1856	711.3770	356.1921	6
10	1123.5296	562.2685	1105.5061	553.2567	1105.5191	553.2632	D	565.3272	283.1672	547.3036	274.1554	547.3166	274.1620	5
11	1237.6107	***619.3090***	1219.5872	610.2972	1219.6002	610.3037	I	449.3032	225.1552	431.2796	216.1435			4
12	1309.6449	***655.3261***	1291.6213	646.3143	1291.6343	646.3208	A	335.2221	168.1147	317.1985	159.1029			3
13	1423.7260	***712.3666***	1405.7024	703.3548	1405.7154	703.3613	L	263.1880	132.0976	245.1644	123.0858			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DLLLNPPAYDIALK

AT3G24320.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	1570.8183	0.0045	DLLLNPPAYDIALK
8.7	1570.8237	-0.0008	KLPIHHIPGPEGVR
3.0	1570.8187	0.0041	VSRTHDPILSLVSK
2.1	1570.8188	0.0040	HLKNLSLNPSSTLK
1.8	1570.8210	0.0018	LKNNGPSPPPPPPLK
1.1	1570.8187	0.0041	LQLGSKLSDVIHNK
0.8	1570.8266	-0.0038	LYIKELVMRNFK

AT3G24490.1

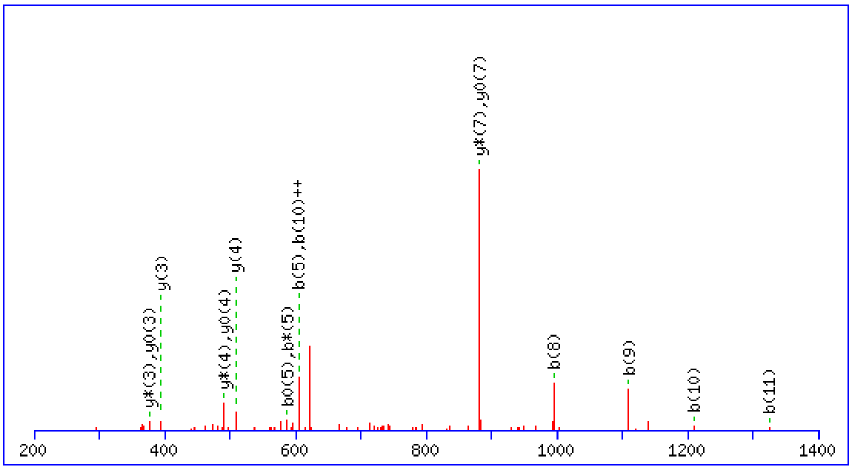
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLELQKKQIVDR**
Found in **AT3G24490.1** in **TAIR_Arabidopsis**, Symbols: | transcription factor | chr3:8911029-8912030 FORWARD

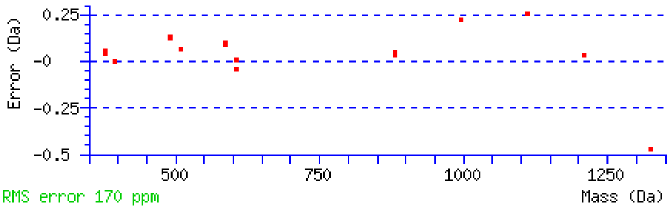
Match to Query 5838: 1502.776928 from(752.395740,2+) index(8492)
Title: Elution from: 79.859 to 79.859 scan no 11570 cid35.00 polarity:+
Data file D1d-1-2.mgf

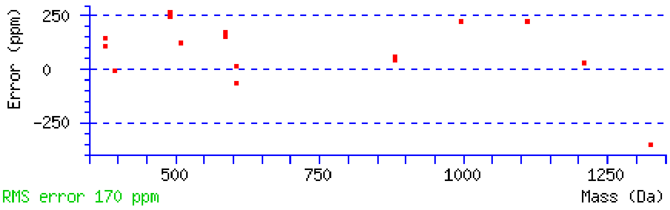
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1502.7795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0019
Matches : 16/122 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							12
2	231.1124	116.0598			213.1018	107.0545	L	1387.7628	694.3850	1369.7392	685.3732	1369.7522	685.3798	11
3	361.1520	181.0796			343.1414	172.0743	E	1273.6817	637.3445	1255.6581	628.3327	1255.6711	628.3392	10
4	475.2331	238.1202			457.2225	229.1149	L	1143.6421	572.3247	1125.6185	563.3129	1125.6315	563.3194	9
5	***605.2857***	303.1465	587.2621	294.1347	587.2752	294.1412	Q	1029.5610	515.2841	1011.5374	506.2723	1011.5504	506.2788	8
6	735.3748	368.1910	717.3512	359.1792	717.3642	359.1857	K	899.5083	450.2578	881.4847	441.2460	881.4978	441.2525	7
7	865.4638	433.2355	847.4402	424.2237	847.4532	424.2303	K	769.4193	385.2133	751.3957	376.2015	751.4087	376.2080	6
8	***995.5164***	498.2619	977.4929	489.2501	977.5059	489.2566	Q	639.3303	320.1688	621.3067	311.1570	621.3197	311.1635	5
9	***1109.5975***	555.3024	1091.5740	546.2906	1091.5870	546.2971	I	**509.2776**	255.1424	491.2540	246.1307	491.2671	246.1372	4
10	***1209.6630***	605.3351	1191.6394	596.3233	1191.6524	596.3298	V	**395.1965**	198.1019	377.1729	189.0901	377.1860	189.0966	3
11	***1325.6870***	663.3471	1307.6634	654.3353	1307.6764	654.3418	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DLELQKKQIVDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G24490.1

Score	Mr(calc)	Delta	Sequence
33.3	1502.7795	-0.0026	DLELQKKQIVDR
5.9	1502.7795	-0.0026	VLGPKSNVTSLNQK

AT3G24503.1

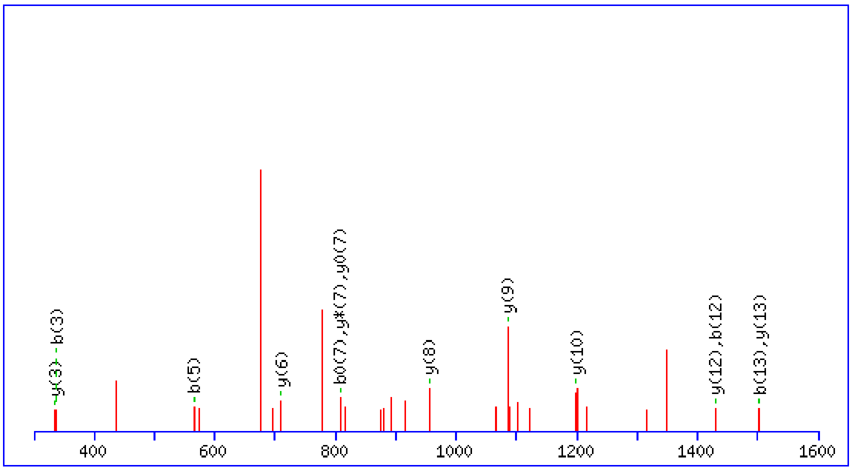
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FADLIEENIEELAK**
Found in **AT3G24503.1** in **TAIR_Arabidopsis**, Symbols: ALDH1A, REF1, ALDH2C4 | ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD) | chr3:8919739-8923036 REVERSE

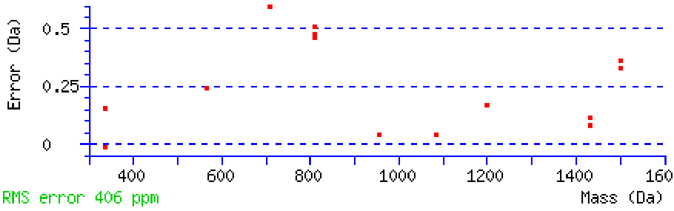
Match to Query 7321: 1648.780570 from(825.397561,2+) index(9800)
Title: Elution from: 92.662 to 92.662 scan no 13946 cid35.00 polarity:+
Data file D6h-2_3.mgf

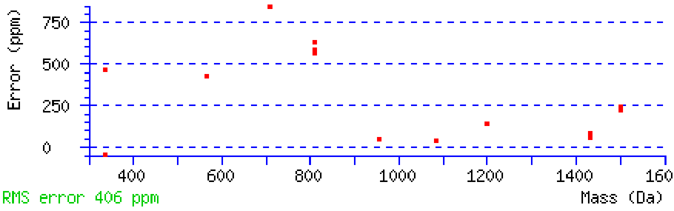
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1648.7772
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0028
Matches : 14/132 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							14
2	221.1069	111.0571					A	***1501.7191***	751.3632	1483.6955	742.3514	1483.7085	742.3579	13
3	**337.1309**	169.0691			319.1203	160.0638	D	***1429.6849***	715.3461	1411.6613	706.3343	1411.6743	706.3408	12
4	451.2120	226.1096			433.2014	217.1043	L	1313.6609	657.3341	1295.6373	648.3223	1295.6504	648.3288	11
5	**565.2930**	283.1502			547.2825	274.1449	I	***1199.5798***	600.2936	1181.5562	591.2818	1181.5693	591.2883	10
6	695.3327	348.1700			677.3221	339.1647	E	***1085.4987***	543.2530	1067.4751	534.2412	1067.4882	534.2477	9
7	825.3723	413.1898			807.3617	404.1845	E	***955.4591***	478.2332	937.4355	469.2214	937.4485	469.2279	8
8	941.4093	471.2083	923.3857	462.1965	923.3987	462.2030	N	825.4195	413.2134	807.3959	404.2016	807.4089	404.2081	7
9	1055.4904	528.2488	1037.4668	519.2370	1037.4798	519.2436	I	***709.3825***	355.1949	691.3589	346.1831	691.3719	346.1896	6
10	1185.5300	593.2687	1167.5064	584.2569	1167.5195	584.2634	E	595.3014	298.1543	577.2778	289.1425	577.2908	289.1490	5
11	1315.5697	658.2885	1297.5461	649.2767	1297.5591	649.2832	E	465.2618	233.1345	447.2382	224.1227	447.2512	224.1292	4
12	**1429.6508**	715.3290	1411.6272	706.3172	1411.6402	706.3237	L	***335.2221***	168.1147	317.1985	159.1029			3
13	**1501.6849**	751.3461	1483.6613	742.3343	1483.6743	742.3408	A	221.1410	111.0741	203.1174	102.0624			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FADLIEENIEELAK

AT3G24503.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.5	1648.7772	0.0033	FADLIEENIEELAK
3.3	1648.7799	0.0007	DLQDPVTDPIAYRK

AT3G24830.1

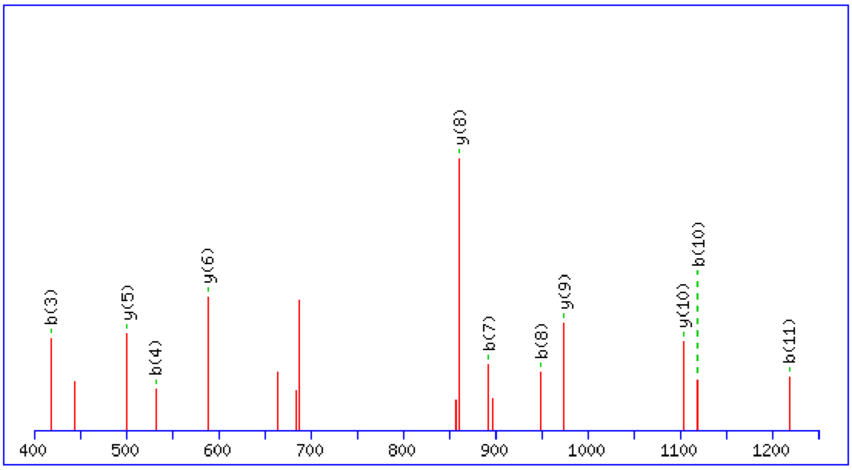
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CEEICLSGGLVR**
Found in **AT3G24830.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L13A (RPL13aB) | chr3:9064620-9065878 FORWARD

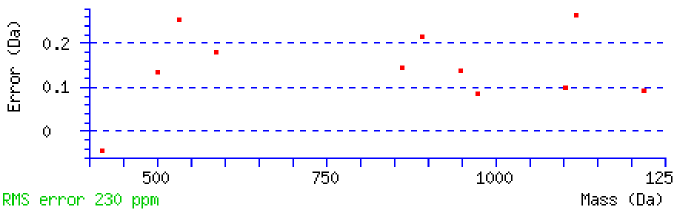
Match to Query 5761: 1391.652010 from(696.833281,2+) index(6015)
Title: Elution from: 52.732 to 52.732 scan no 7522 cid35.00 polarity:+
Data file D12h-1_1.mgf

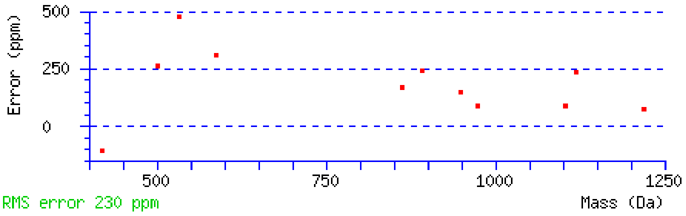
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [400] to [1250] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1391.6537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 9.5e-007
Matches : 11/98 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	161.0379	81.0226			**C**							**12**
2	290.0805	145.5439	272.0700	136.5386	**E**	1232.6303	616.8188	1215.6038	608.3055	1214.6198	607.8135	**11**
3	***419.1231***	210.0652	401.1125	201.0599	**E**	***1103.5878***	552.2975	1086.5612	543.7842	1085.5772	543.2922	**10**
4	***532.2072***	266.6072	514.1966	257.6019	**I**	***974.5452***	487.7762	957.5186	479.2629	956.5346	478.7709	**9**
5	692.2378	346.6226	674.2273	337.6173	**C**	***861.4611***	431.2342	844.4346	422.7209	843.4505	422.2289	**8**
6	805.3219	403.1646	787.3113	394.1593	**L**	701.4305	351.2189	684.4039	342.7056	683.4199	342.2136	**7**
7	***892.3539***	446.6806	874.3434	437.6753	**S**	***588.3464***	294.6768	571.3198	286.1636	570.3358	285.6715	**6**
8	***949.3754***	475.1913	931.3648	466.1860	**G**	***501.3144***	251.1608	484.2878	242.6475			**5**
9	1006.3968	503.7021	988.3863	494.6968	**G**	444.2929	222.6501	427.2663	214.1368			**4**
10	***1119.4809***	560.2441	1101.4703	551.2388	**L**	387.2714	194.1394	370.2449	185.6261			**3**
11	***1218.5493***	609.7783	1200.5388	600.7730	**V**	274.1874	137.5973	257.1608	129.0840			**2**
12					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of CEEICLSGGLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G24830.1

Score	Mr(calc)	Delta	Sequence
64.5	1391.6537	-0.0017	CEEICLSGGLVR
11.0	1391.6503	0.0017	FSPSNSPSSVPMR
4.7	1391.6503	0.0017	TDWEGEAVKAMR
3.0	1391.6528	-0.0008	VKSESNEDIESR
2.1	1391.6542	-0.0022	ISGSNERWSNSR
0.4	1391.6503	0.0017	AVAEAMEWGVASR
0.2	1391.6503	0.0017	TLMVAADWADQR

AT3G25220.1

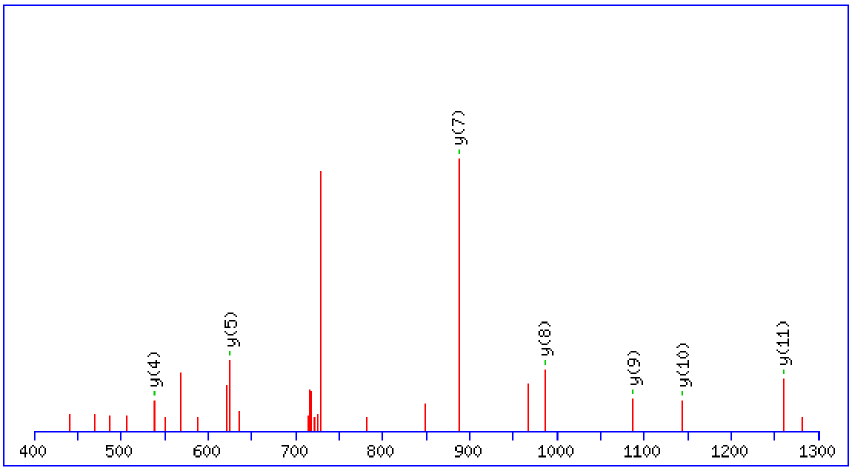
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTDGTVFDSSFER**
Found in **AT3G25220.1** in **TAIR_Arabidopsis**, Symbols: FKBP15-1 | FKBP15-1 (FK506-binding protein 15 kD-1); FK506 binding / peptidyl-prolyl cis-trans isomerase | chr3:9183928-9185700 FORWARD

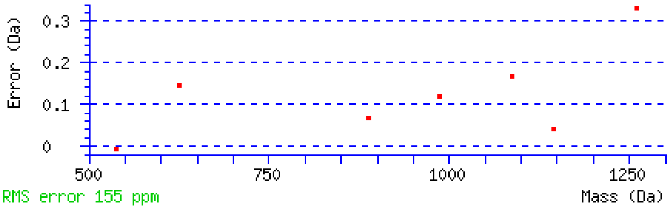
Match to Query 5998: 1472.678426 from(737.346489,2+) index(5911)
Title: Elution from: 52.477 to 52.477 scan no 7547 cid35.00 polarity:+
Data file 0-1_3.mgf

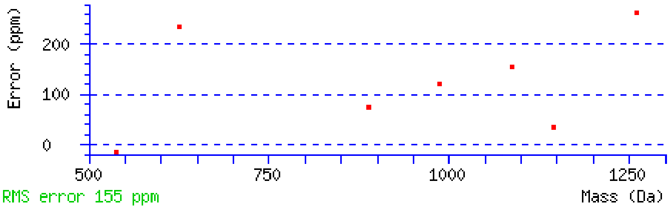
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1472.6784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 8.3e-007
Matches : 7/116 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							13
2	215.1390	108.0731	197.1285	99.0679	T	1360.6016	680.8044	1343.5750	672.2911	1342.5910	671.7991	12
3	330.1660	165.5866	312.1554	156.5813	D	***1259.5539***	630.2806	1242.5273	621.7673	1241.5433	621.2753	11
4	387.1874	194.0974	369.1769	185.0921	G	***1144.5269***	572.7671	1127.5004	564.2538	1126.5164	563.7618	10
5	488.2351	244.6212	470.2245	235.6159	T	***1087.5055***	544.2564	1070.4789	535.7431	1069.4949	535.2511	9
6	587.3035	294.1554	569.2930	285.1501	V	***986.4578***	493.7325	969.4312	485.2193	968.4472	484.7272	8
7	734.3719	367.6896	716.3614	358.6843	F	***887.3894***	444.1983	870.3628	435.6850	869.3788	435.1930	7
8	849.3989	425.2031	831.3883	416.1978	D	740.3210	370.6641	723.2944	362.1508	722.3104	361.6588	6
9	936.4309	468.7191	918.4203	459.7138	S	***625.2940***	313.1506	608.2675	304.6374	607.2835	304.1454	5
10	1023.4629	512.2351	1005.4524	503.2298	S	***538.2620***	269.6346	521.2354	261.1214	520.2514	260.6293	4
11	1170.5313	585.7693	1152.5208	576.7640	F	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
12	1299.5739	650.2906	1281.5634	641.2853	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LTDGTVFDSSFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G25220.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.0	1472.6784	0.0001	LTDGTVFDSSFER
2.5	1472.6817	-0.0033	GMEELTDIVDHAK

AT3G25230.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILAVGEK**
Found in **AT3G25230.1** in **TAIR_Arabidopsis**, Symbols: ROF1 | ROF1 (ROTAMASE FKBP 1); FK506 binding / calmodulin binding / peptidyl-prolyl cis-trans isomerase | chr3:9189494-9192374 FORWARD

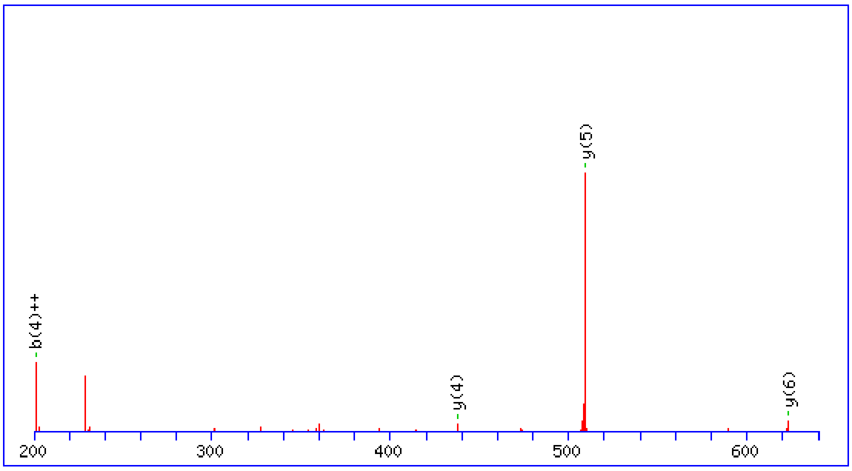
Match to Query 732: 736.419552 from(369.217052,2+) index(4047)
Title: Elution from: 37.900 to 37.900 scan no 5102 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 640 Da Full range

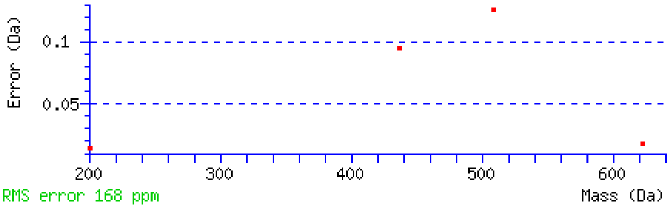
Label all possible matches ○ Label matches used for scoring ●

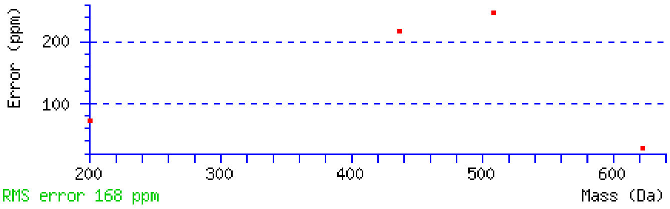
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 736.4195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.019
Matches : 4/48 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							7
2	229.1695	115.0884			L	***623.3457***	312.1765	605.3221	303.1647	605.3351	303.1712	6
3	301.2036	151.1054			A	***509.2646***	255.1359	491.2410	246.1241	491.2540	246.1307	5
4	401.2691	201.1382			V	***437.2304***	219.1189	419.2069	210.1071	419.2199	210.1136	4
5	459.2876	230.1474			G	337.1650	169.0861	319.1414	160.0743	319.1544	160.0809	3
6	589.3272	295.1672	571.3166	286.1620	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ILAVGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	736.4195	0.0000	ILAVGEK
17.6	736.4195	0.0000	LIPSTAK

AT3G25230.1

16.5	736.4195	0.0000	ILNEIK
16.5	736.4195	0.0000	LINEIK
16.5	736.4195	0.0000	LLNLEK
16.5	736.4195	0.0000	LLPTASK
16.3	736.4195	0.0000	LLLQDK
15.3	736.4195	0.0000	ILQEVK
15.3	736.4195	0.0000	LIEQVK
14.6	736.4195	0.0000	ILENLK

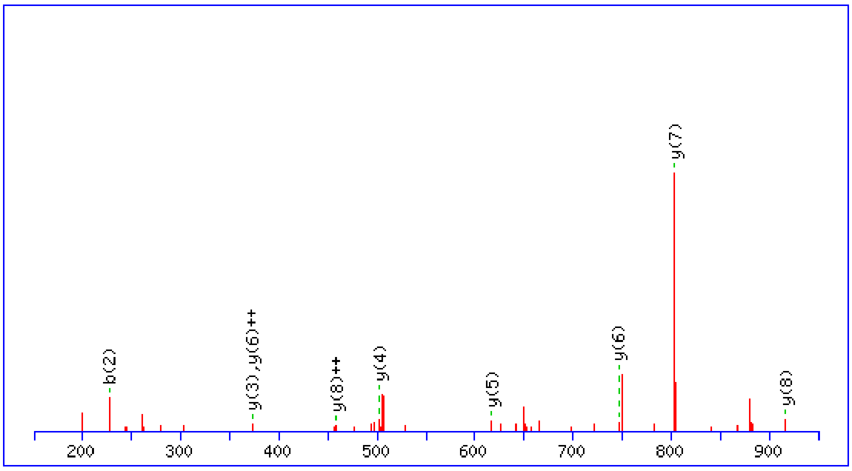
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLGEDEPEK**
Found in **AT3G25520.1** in **TAIR_Arabidopsis**, Symbols: ATL5, PGY3 | ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); structural constituent of ribosome | chr3:9270810-9272564 REVERSE

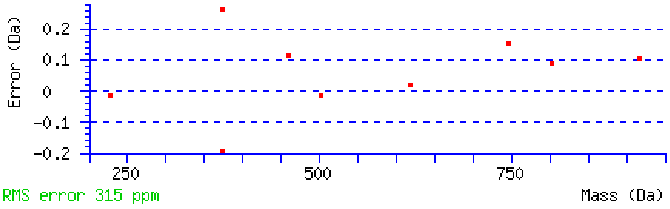
Match to Query 2834: 1028.500250 from(515.257401,2+) index(1512)
Title: Elution from: 20.045 to 20.045 scan no 2028 cid35.00 polarity:+
Data file C7-2_2.mgf

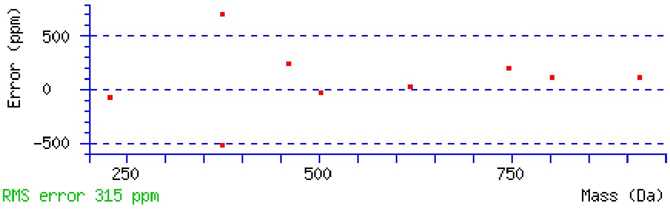
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1028.5026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.00072
Matches : 9/72 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							9
2	227.1754	114.0913			L	***916.4258***	458.7165	899.3993	450.2033	898.4153	449.7113	8
3	284.1969	142.6021			G	***803.3418***	402.1745	786.3152	393.6612	785.3312	393.1692	7
4	413.2395	207.1234	395.2289	198.1181	E	***746.3203***	373.6638	729.2937	365.1505	728.3097	364.6585	6
5	528.2664	264.6368	510.2558	255.6316	D	***617.2777***	309.1425	600.2511	300.6292	599.2671	300.1372	5
6	657.3090	329.1581	639.2984	320.1529	E	***502.2508***	251.6290	485.2242	243.1157	484.2402	242.6237	4
7	754.3618	377.6845	736.3512	368.6792	P	***373.2082***	187.1077	356.1816	178.5944	355.1976	178.1024	3
8	883.4044	442.2058	865.3938	433.2005	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LLGEDEPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G25520.1

32.9	1028.5026	-0.0023	LLGEDEPEK

Mascot: http://www.matrixscience.com/

AT3G25530.1

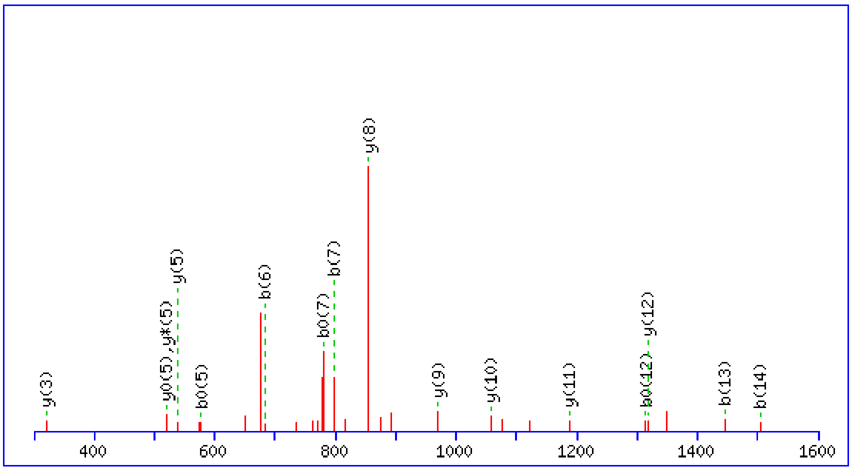
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALFEESIPAFDVLGK**
Found in **AT3G25530.1** in **TAIR_Arabidopsis**, Symbols: GHBDH, ATGHBDH | ATGHBDH/GHBDH; 3-hydroxybutyrate dehydrogenase/ phosphogluconate dehydrogenase (decarboxylating) | chr3:9273186-9274751 REVERSE

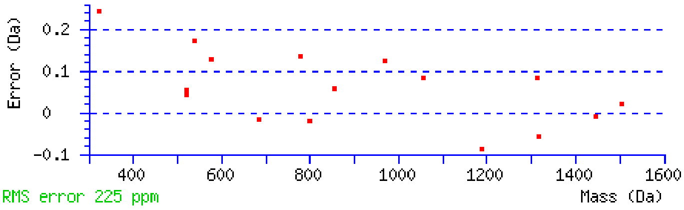
Match to Query 7545: 1650.808308 from(826.411430,2+) index(10221)
Title: Elution from: 96.280 to 96.280 scan no 14472 cid35.00 polarity:+
Data file 0-3_2.mgf

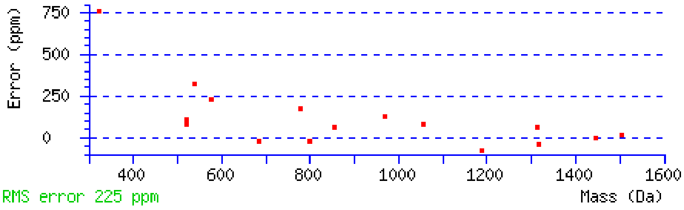
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1650.8081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00037
Matches : 16/126 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244			**A**							**15**
2	187.1225	94.0649			**L**	1579.7813	790.3943	1561.7577	781.3825	1561.7707	781.3890	**14**
3	335.1880	168.0976			**F**	1465.7002	733.3537	1447.6766	724.3419	1447.6896	724.3484	**13**
4	465.2276	233.1174	447.2170	224.1122	**E**	***1317.6347***	659.3210	1299.6111	650.3092	1299.6241	650.3157	**12**
5	595.2672	298.1373	577.2567	289.1320	**E**	***1187.5951***	594.3012	1169.5715	585.2894	1169.5845	585.2959	**11**
6	***683.2963***	342.1518	665.2857	333.1465	**S**	***1057.5555***	529.2814	1039.5319	520.2696	1039.5449	520.2761	**10**
7	***797.3774***	399.1923	779.3668	390.1871	**I**	***969.5264***	485.2668	951.5028	476.2550	951.5158	476.2616	**9**
8	895.4272	448.2172	877.4166	439.2120	**P**	***855.4453***	428.2263	837.4217	419.2145	837.4347	419.2210	**8**
9	967.4613	484.2343	949.4508	475.2290	**A**	757.3955	379.2014	739.3719	370.1896	739.3849	370.1961	**7**
10	1115.5268	558.2670	1097.5162	549.2617	**F**	685.3613	343.1843	667.3378	334.1725	667.3508	334.1790	**6**
11	1231.5508	616.2790	1213.5402	607.2737	**D**	***537.2959***	269.1516	519.2723	260.1398	519.2853	260.1463	**5**
12	1331.6162	666.3117	1313.6056	657.3065	**V**	421.2719	211.1396	403.2483	202.1278			**4**
13	***1445.6973***	723.3523	1427.6867	714.3470	**L**	***321.2065***	161.1069	303.1829	152.0951			**3**
14	***1503.7158***	752.3615	1485.7052	743.3563	**G**	207.1254	104.0663	189.1018	95.0545			**2**
15					**K**	149.1069	75.0571	131.0833	66.0453			**1**





AT3G25530.1

NCBI **BLAST** search of ALFEESIPAFDVLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.9	1650.8081	0.0002	ALFEESIPAFDVLGK
11.6	1650.8063	0.0020	ETSEQLRIQAEKAK
8.5	1650.8063	0.0020	GSDVTKAENKQNLVK
5.0	1650.8046	0.0038	IPVMVNMASSSLALGK
4.8	1650.8059	0.0024	AAEAVEEFGGILTSIK
3.9	1650.8094	-0.0011	MAPLRNMFPNLVTK
3.9	1650.8046	0.0038	IPVMVNMASSSLALGK
2.7	1650.8036	0.0047	TLSETQEILKDTQK
2.4	1650.8119	-0.0036	MVATKRVVEVEQDK
1.7	1650.8072	0.0011	RMIGESGCIPLLIR

AT3G25680.1

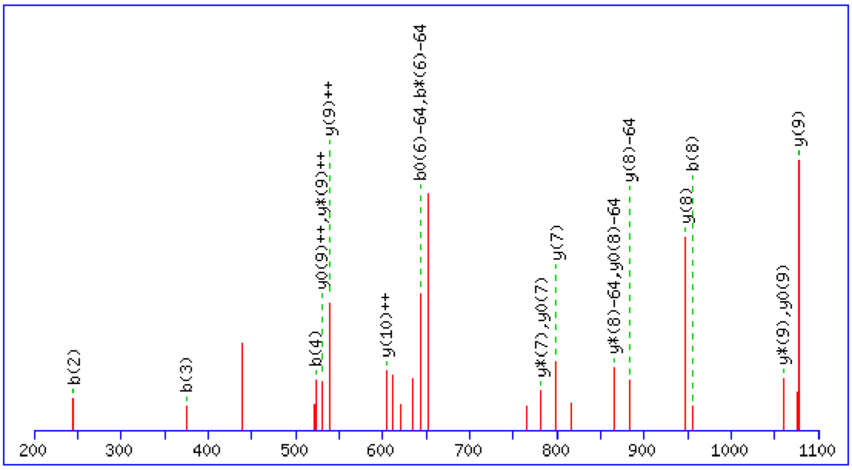
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQEMLSDLQSK**
Found in **AT3G25680.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42077.1); contains InterPro domain S-layer homology region (InterPro:IPR001119) | chr3:9350930-9353495 FORW

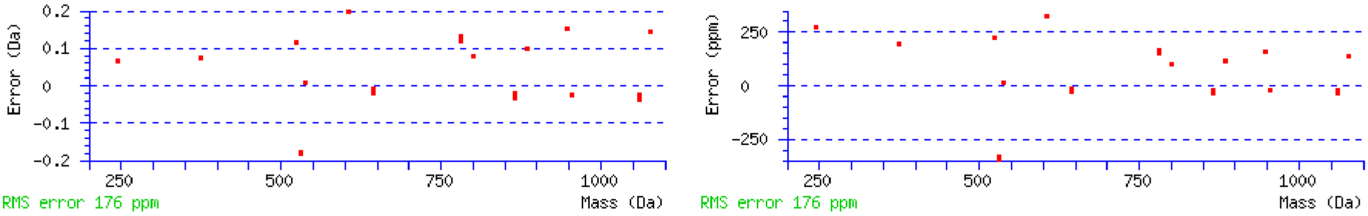
Match to Query 4804: 1320.601862 from(661.308207,2+) index(2835)
Title: Elution from: 29.073 to 29.073 scan no 3549 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.6024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.03
Matches : 20/172 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							11
2	***245.1410***	123.0741	227.1174	114.0624			Q	1207.5285	604.2679	1189.5049	595.2561	1189.5180	595.2626	10
3	***375.1806***	188.0940	357.1571	179.0822	357.1701	179.0887	E	**1077.4759**	539.2416	1059.4523	530.2298	1059.4653	530.2363	9
4	***523.2131***	262.1102	505.1895	253.0984	505.2025	253.1049	M	**947.4363**	474.2218	929.4127	465.2100	929.4257	465.2165	8
5	637.2942	319.1507	619.2706	310.1389	619.2836	310.1454	L	**799.4038**	400.2055	781.3802	391.1938	781.3933	391.2003	7
6	725.3232	363.1653	707.2997	354.1535	707.3127	354.1600	S	685.3227	343.1650	667.2991	334.1532	667.3122	334.1597	6
7	841.3472	421.1773	823.3236	412.1655	823.3367	412.1720	D	597.2937	299.1505	579.2701	290.1387	579.2831	290.1452	5
8	***955.4283***	478.2178	937.4047	469.2060	937.4178	469.2125	L	481.2697	241.1385	463.2461	232.1267	463.2591	232.1332	4
9	1085.4810	543.2441	1067.4574	534.2323	1067.4704	534.2388	Q	367.1886	184.0979	349.1650	175.0861	349.1780	175.0926	3
10	1173.5100	587.2587	1155.4864	578.2469	1155.4995	578.2534	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
11							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of LQEMLSDLQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G25680.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.8	1320.6024	-0.0005	LQEMLSDLQSK
18.2	1320.6050	-0.0032	LEKACAEAREK
12.7	1320.5994	0.0025	QLSDDLSDVRR
9.7	1320.6017	0.0002	GQSPEYQNLLR
6.0	1320.5994	0.0024	NSANQKEKADAK
4.6	1320.5994	0.0025	QIEESEERRK
4.0	1320.6043	-0.0024	QLENHFTRTR
3.3	1320.5994	0.0025	KQIEESEERR
3.2	1320.5990	0.0029	ELFSEIGEVER
2.7	1320.6017	0.0002	RNFPDQLESAK

AT3G25860.1

Mascot Search Results

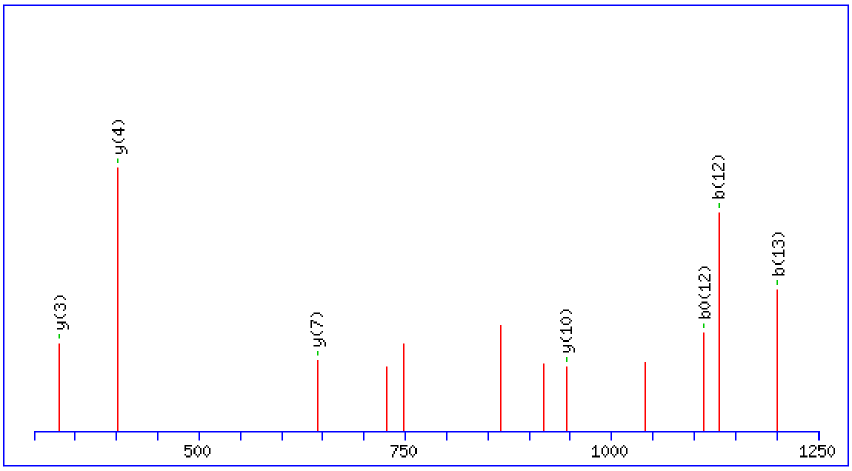
Peptide View

MS/MS Fragmentation of **ITASDVETAAGIAPSK**
Found in **AT3G25860.1** in **TAIR_Arabidopsis**, Symbols: PLE2, LTA2 | LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE); dihydrolipoyllysine-residue acetyltransferase | chr3:9461869-9463822 FORWARD

Match to Query 6498: 1529.794036 from(765.904294,2+) index(5877)
Title: Elution from: 54.427 to 54.427 scan no 7575 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

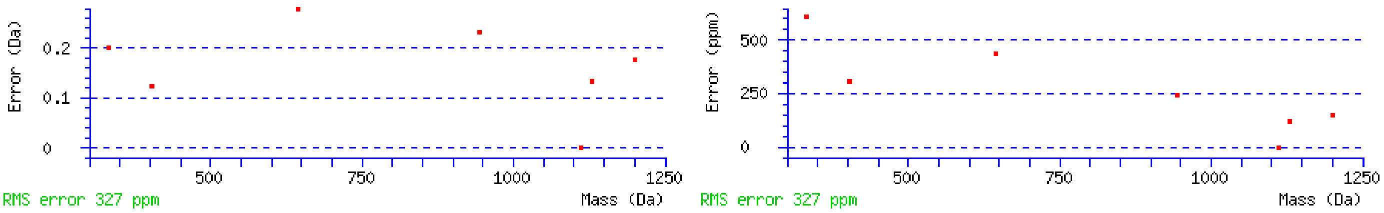
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1529.7937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.013
Matches : 7/146 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							16
2	215.1390	108.0731	197.1285	99.0679	T	1417.7169	709.3621	1400.6904	700.8488	1399.7064	700.3568	15
3	286.1761	143.5917	268.1656	134.5864	A	1316.6692	658.8383	1299.6427	650.3250	1298.6587	649.8330	14
4	373.2082	187.1077	355.1976	178.1024	S	1245.6321	623.3197	1228.6056	614.8064	1227.6216	614.3144	13
5	488.2351	244.6212	470.2245	235.6159	D	1158.6001	579.8037	1141.5735	571.2904	1140.5895	570.7984	12
6	587.3035	294.1554	569.2930	285.1501	V	1043.5732	522.2902	1026.5466	513.7769	1025.5626	513.2849	11
7	716.3461	358.6767	698.3355	349.6714	E	***944.5047***	472.7560	927.4782	464.2427	926.4942	463.7507	10
8	817.3938	409.2005	799.3832	400.1953	T	815.4621	408.2347	798.4356	399.7214	797.4516	399.2294	9
9	888.4309	444.7191	870.4203	435.7138	A	714.4145	357.7109	697.3879	349.1976	696.4039	348.7056	8
10	959.4680	480.2376	941.4575	471.2324	A	***643.3774***	322.1923	626.3508	313.6790	625.3668	313.1870	7
11	1016.4895	508.7484	998.4789	499.7431	G	572.3402	286.6738	555.3137	278.1605	554.3297	277.6685	6
12	**1129.5735**	565.2904	1111.5630	556.2851	I	515.3188	258.1630	498.2922	249.6498	497.3082	249.1577	5
13	**1200.6107**	600.8090	1182.6001	591.8037	A	***402.2347***	201.6210	385.2082	193.1077	384.2241	192.6157	4
14	1297.6634	649.3354	1279.6529	640.3301	P	***331.1976***	166.1024	314.1710	157.5892	313.1870	157.0972	3
15	1384.6955	692.8514	1366.6849	683.8461	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
16					K	147.1128	74.0600	130.0863	65.5468			1

AT3G25860.1



NCBI **BLAST** search of ITASDVETAAGIAPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	1529.7937	0.0004	ITASDVETAAGIAPSK
4.2	1529.7950	-0.0010	HPSPSPSPSASPVRK

Mascot: http://www.matrixscience.com/

AT3G25920.1

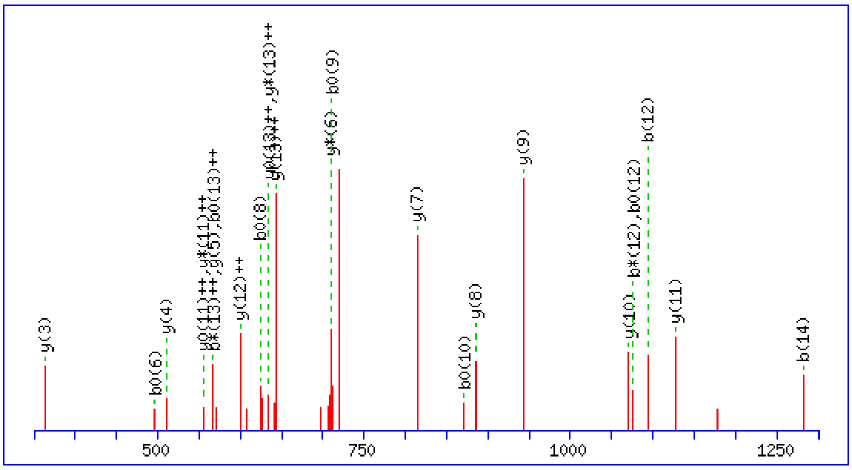
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GISAGQGASCGFGMR**
Found in **AT3G25920.1** in **TAIR_Arabidopsis**, Symbols: RPL15 | RPL15 (ribosomal protein L15) | chr3:9492505-9493795 REVERSE

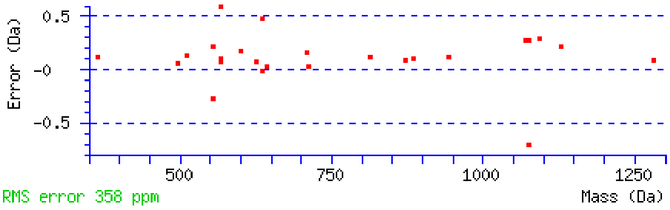
Match to Query 5324: 1454.637916 from(728.326234,2+) index(2953)
Title: Elution from: 31.511 to 31.511 scan no 3754 cid35.00 polarity:+
Data file D1d-1_3.mgf

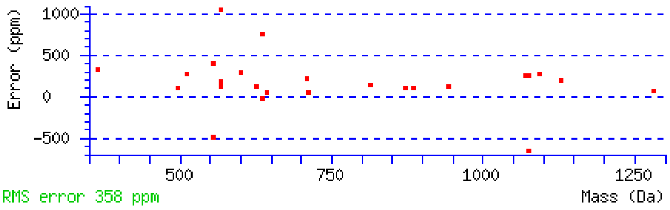
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1454.6395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 2e-008
Matches : 25/142 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							15
2	171.1128	86.0600					I	1398.6253	699.8163	1381.5987	691.3030	1380.6147	690.8110	14
3	258.1448	129.5761			240.1343	120.5708	S	1285.5412	643.2742	1268.5147	634.7610	1267.5307	634.2690	13
4	329.1819	165.0946			311.1714	156.0893	A	1198.5092	599.7582	1181.4826	591.2450	1180.4986	590.7530	12
5	386.2034	193.6053			368.1928	184.6001	G	***1127.4721***	564.2397	1110.4455	555.7264	1109.4615	555.2344	11
6	514.2620	257.6346	497.2354	249.1214	496.2514	248.6293	Q	***1070.4506***	535.7289	1053.4241	527.2157	1052.4400	526.7237	10
7	571.2835	286.1454	554.2569	277.6321	553.2729	277.1401	G	***942.3920***	471.6997	925.3655	463.1864	924.3815	462.6944	9
8	642.3206	321.6639	625.2940	313.1506	624.3100	312.6586	A	***885.3706***	443.1889	868.3440	434.6756	867.3600	434.1836	8
9	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	S	***814.3335***	407.6704	797.3069	399.1571	796.3229	398.6651	7
10	889.3832	445.1953	872.3567	436.6820	871.3727	436.1900	C	727.3014	364.1544	710.2749	355.6411			6
11	946.4047	473.7060	929.3782	465.1927	928.3941	464.7007	G	***567.2708***	284.1390	550.2442	275.6258			5
12	**1093.4731**	547.2402	1076.4466	538.7269	1075.4626	538.2349	F	***510.2493***	255.6283	493.2228	247.1150			4
13	1150.4946	575.7509	1133.4680	567.2377	1132.4840	566.7456	G	***363.1809***	182.0941	346.1544	173.5808			3
14	**1281.5351**	641.2712	1264.5085	632.7579	1263.5245	632.2659	M	306.1594	153.5834	289.1329	145.0701			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GISAGQGASCGFGMR

AT3G25920.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.8	1454.6395	-0.0016	GISAGQGASCGFGMR
0.1	1454.6381	-0.0002	QEKETEMEIMR

AT3G26060.1

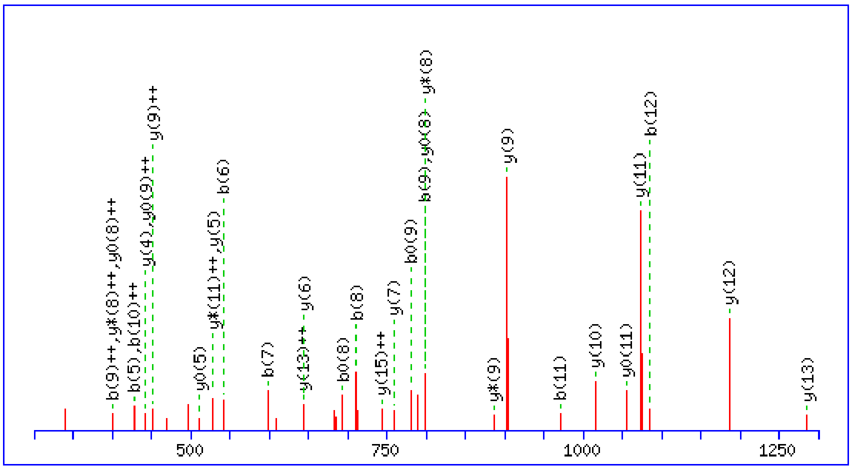
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGAEVIGISGDDSASHK**
Found in **AT3G26060.1** in **TAIR_Arabidopsis**, Symbols: ATPRX Q | ATPRX Q; antioxidant/ peroxiredoxin | chr3:9526044-9527360 FORWARD

Match to Query 7791: 1612.773080 from(807.393816,2+) index(2341)
Title: Elution from: 26.397 to 26.397 scan no 2983 cid35.00 polarity:+
Data file 0-1_1.mgf

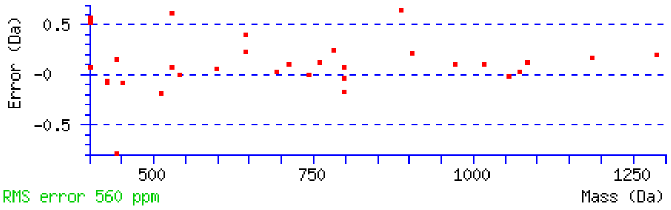
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

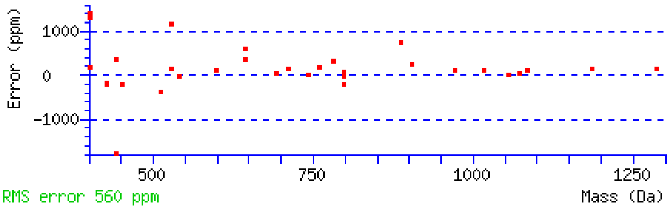


Monoisotopic mass of neutral peptide Mr(calc): 1612.7693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 1.8e-006
Matches : 32/150 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							17
2	129.0659	65.0366			G	1542.7394	771.8734	1525.7129	763.3601	1524.7289	762.8681	16
3	200.1030	100.5551			A	1485.7180	743.3626	1468.6914	734.8494	1467.7074	734.3573	15
4	329.1456	165.0764	311.1350	156.0711	E	1414.6809	707.8441	1397.6543	699.3308	1396.6703	698.8388	14
5	**428.2140**	214.6106	410.2034	205.6053	V	***1285.6383***	643.3228	1268.6117	634.8095	1267.6277	634.3175	13
6	**541.2980**	271.1527	523.2875	262.1474	I	***1186.5699***	593.7886	1169.5433	585.2753	1168.5593	584.7833	12
7	**598.3195**	299.6634	580.3089	290.6581	G	***1073.4858***	537.2465	1056.4592	528.7333	1055.4752	528.2413	11
8	**711.4036**	356.2054	693.3930	347.2001	I	***1016.4643***	508.7358	999.4378	500.2225	998.4538	499.7305	10
9	**798.4356**	399.7214	780.4250	390.7162	S	***903.3803***	452.1938	886.3537	443.6805	885.3697	443.1885	9
10	855.4571	428.2322	837.4465	419.2269	G	816.3482	408.6778	799.3217	400.1645	798.3377	399.6725	8
11	**970.4840**	485.7456	952.4734	476.7404	D	***759.3268***	380.1670	742.3002	371.6537	741.3162	371.1617	7
12	**1085.5109**	543.2591	1067.5004	534.2538	D	***644.2998***	322.6536	627.2733	314.1403	626.2893	313.6483	6
13	1172.5430	586.7751	1154.5324	577.7698	S	***529.2729***	265.1401	512.2463	256.6268	511.2623	256.1348	5
14	1243.5801	622.2937	1225.5695	613.2884	A	***442.2409***	221.6241	425.2143	213.1108	424.2303	212.6188	4
15	1330.6121	665.8097	1312.6016	656.8044	S	371.2037	186.1055	354.1772	177.5922	353.1932	177.1002	3
16	1467.6710	734.3392	1449.6605	725.3339	H	284.1717	142.5895	267.1452	134.0762			2
17					K	147.1128	74.0600	130.0863	65.5468			1

AT3G26060.1





NCBI **BLAST** search of AGAEVIGISGDDSASHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.1	1612.7693	0.0038	AGAEVIGISGDDSASHK

Mascot: http://www.matrixscience.com/

AT3G26070.1

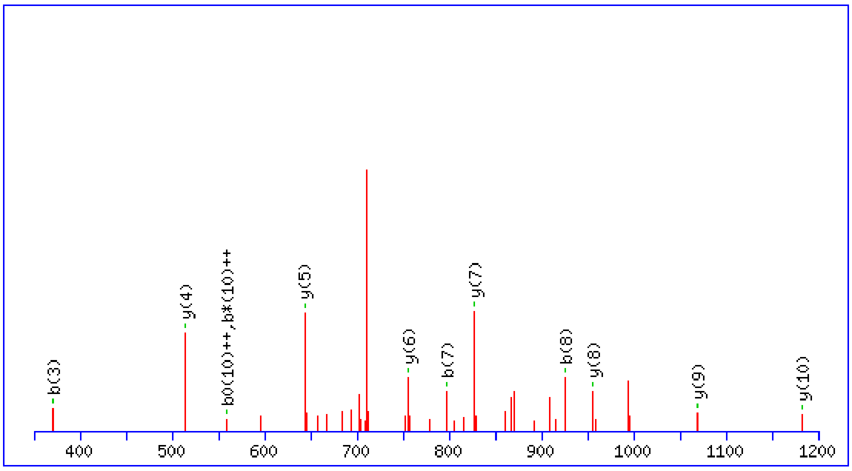
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QELLEAIEPLER**
Found in **AT3G26070.1** in **TAIR_Arabidopsis**, Symbols: | plastid-lipid associated protein PAP / fibrillin family protein | chr3:9528141-9529436 FORWARD

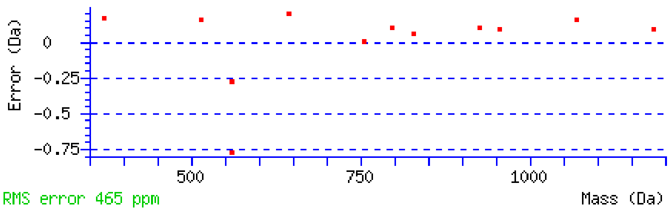
Match to Query 5209: 1438.766738 from(720.390645,2+) index(7744)
Title: Elution from: 72.384 to 72.384 scan no 10366 cid35.00 polarity:+
Data file D1d-1-2.mgf

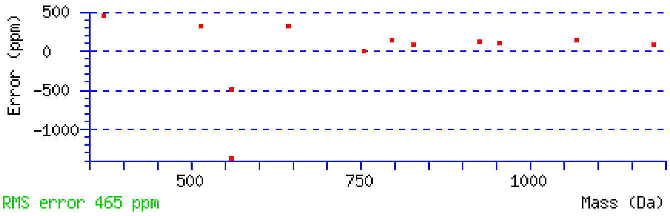
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1438.7667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 1.6e-006
Matches : 12/128 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							12
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	E	1311.7155	656.3614	1294.6889	647.8481	1293.7049	647.3561	11
3	**371.1925**	186.0999	354.1660	177.5866	353.1819	177.0946	L	***1182.6729***	591.8401	1165.6463	583.3268	1164.6623	582.8348	10
4	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	L	***1069.5888***	535.2980	1052.5623	526.7848	1051.5782	526.2928	9
5	613.3192	307.1632	596.2926	298.6499	595.3086	298.1579	E	***956.5047***	478.7560	939.4782	470.2427	938.4942	469.7507	8
6	684.3563	342.6818	667.3297	334.1685	666.3457	333.6765	A	***827.4621***	414.2347	810.4356	405.7214	809.4516	405.2294	7
7	**797.4403**	399.2238	780.4138	390.7105	779.4298	390.2185	I	***756.4250***	378.7162	739.3985	370.2029	738.4145	369.7109	6
8	**926.4829**	463.7451	909.4564	455.2318	908.4724	454.7398	E	***643.3410***	322.1741	626.3144	313.6608	625.3304	313.1688	5
9	1023.5357	512.2715	1006.5092	503.7582	1005.5251	503.2662	P	***514.2984***	257.6528	497.2718	249.1395	496.2878	248.6475	4
10	1136.6198	568.8135	1119.5932	560.3002	1118.6092	559.8082	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
11	1265.6624	633.3348	1248.6358	624.8215	1247.6518	624.3295	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QELLEAIEPLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G26070.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.7	1438.7667	0.0000	QELLEAIEPLER
0.3	1438.7708	-0.0040	IEGFTALLDGYIK

Mascot: http://www.matrixscience.com/

AT3G26450.1

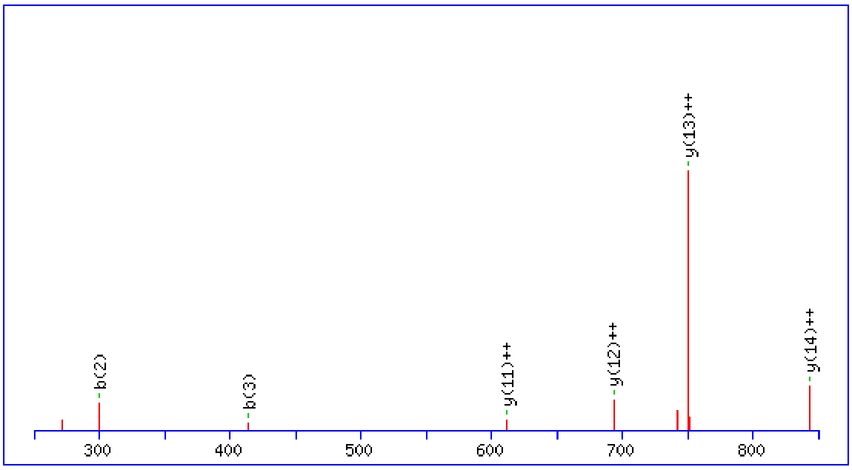
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IWNYTLGDGKEEVFK**
Found in **AT3G26450.1** in **TAIR_Arabidopsis**, Symbols: | major latex protein-related / MLP-related | chr3:9682830-9684536 REVERSE

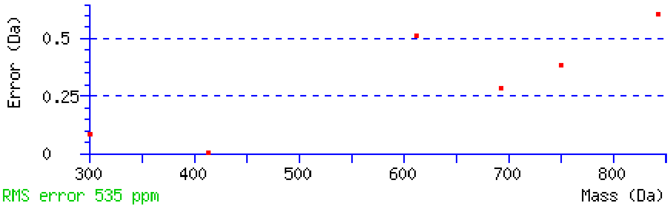
Match to Query 8752: 1797.897858 from(600.306562,3+) index(7050)
Title: Elution from: 62.447 to 62.447 scan no 9078 cid35.00 polarity:+
Data file D12h-3_1.mgf

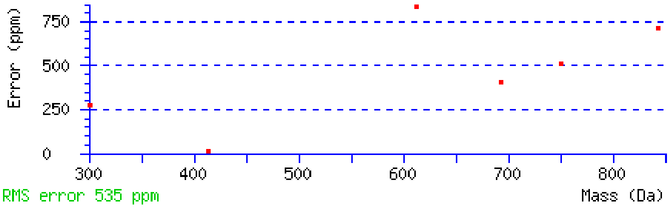
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1797.8937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0029
Matches : 6/150 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							15
2	**300.1707**	150.5890					W	1685.8170	843.4121	1668.7904	834.8988	1667.8064	834.4068	14
3	**414.2136**	207.6104	397.1870	199.0972			N	1499.7377	750.3725	1482.7111	741.8592	1481.7271	741.3672	13
4	577.2769	289.1421	560.2504	280.6288			Y	1385.6947	693.3510	1368.6682	684.8377	1367.6842	684.3457	12
5	678.3246	339.6659	661.2980	331.1527	660.3140	330.6606	T	1222.6314	611.8193	1205.6048	603.3061	1204.6208	602.8141	11
6	791.4087	396.2080	774.3821	387.6947	773.3981	387.2027	L	1121.5837	561.2955	1104.5572	552.7822	1103.5732	552.2902	10
7	848.4301	424.7187	831.4036	416.2054	830.4196	415.7134	G	1008.4997	504.7535	991.4731	496.2402	990.4891	495.7482	9
8	963.4571	482.2322	946.4305	473.7189	945.4465	473.2269	D	951.4782	476.2427	934.4516	467.7295	933.4676	467.2374	8
9	1020.4785	510.7429	1003.4520	502.2296	1002.4680	501.7376	G	836.4512	418.7293	819.4247	410.2160	818.4407	409.7240	7
10	1148.5735	574.7904	1131.5469	566.2771	1130.5629	565.7851	K	779.4298	390.2185	762.4032	381.7053	761.4192	381.2132	6
11	1277.6161	639.3117	1260.5895	630.7984	1259.6055	630.3064	E	651.3348	326.1710	634.3083	317.6578	633.3243	317.1658	5
12	1406.6587	703.8330	1389.6321	695.3197	1388.6481	694.8277	E	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
13	1505.7271	753.3672	1488.7005	744.8539	1487.7165	744.3619	V	393.2496	197.1285	376.2231	188.6152			3
14	1652.7955	826.9014	1635.7690	818.3881	1634.7849	817.8961	F	294.1812	147.5942	277.1547	139.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IWNYTLGDGKEEVFK

AT3G26450.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	1797.8937	0.0041	IWNYTLGDGKEEVFK
6.7	1797.8996	-0.0017	LALEAAAAAEDATPLDEK
6.6	1797.9023	-0.0044	GEIRRGGPSFEFRPGH
4.6	1797.8978	0.0000	MVCQSAGQTRFRTLK

AT3G26520.1

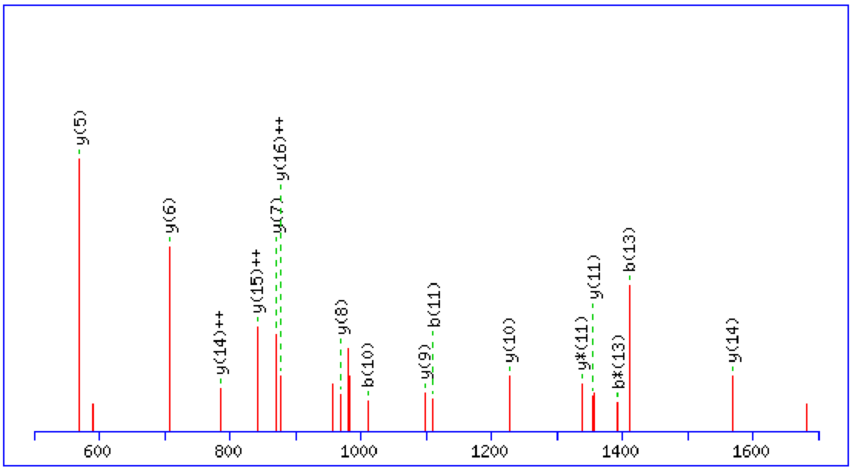
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIAIGGVQEEVYHPNALR**
Found in **AT3G26520.1** in **TAIR_Arabidopsis**, Symbols: SITIP, GAMMA-TIP2, TIP1;2, TIP2 | TIP2 (TONOPLAST INTRINSIC PROTEIN 2); water channel | chr3:9724007-9724940 REVERSE

Match to Query 9247: 1979.020872 from(990.517712,2+) index(5882)
Title: Elution from: 52.762 to 52.762 scan no 7515 cid35.00 polarity:+
Data file D6h-1_2.mgf

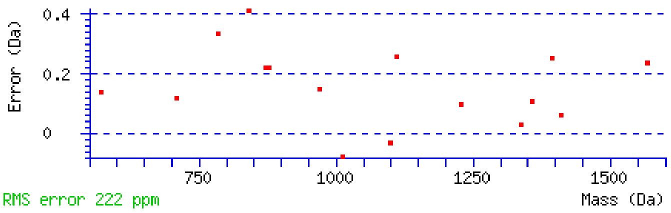
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

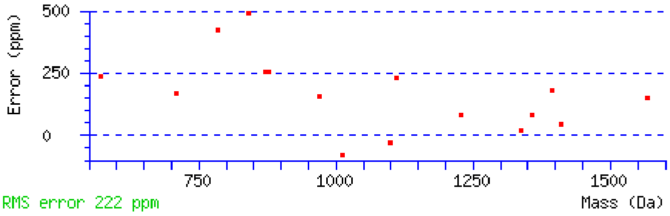


Monoisotopic mass of neutral peptide Mr(calc): 1979.0224
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 1.4e-005
Matches : 16/172 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			**N**							**18**
2	228.1343	114.5708	211.1077	106.0575			**I**	1865.9868	933.4971	1848.9603	924.9838	1847.9763	924.4918	**17**
3	299.1714	150.0893	282.1448	141.5761			**A**	1752.9028	876.9550	1735.8762	868.4417	1734.8922	867.9497	**16**
4	412.2554	206.6314	395.2289	198.1181			**I**	1681.8656	841.4365	1664.8391	832.9232	1663.8551	832.4312	**15**
5	469.2769	235.1421	452.2504	226.6288			**G**	***1568.7816***	784.8944	1551.7550	776.3812	1550.7710	775.8891	**14**
6	526.2984	263.6528	509.2718	255.1396			**G**	1511.7601	756.3837	1494.7336	747.8704	1493.7496	747.3784	**13**
7	625.3668	313.1870	608.3402	304.6738			**V**	1454.7387	727.8730	1437.7121	719.3597	1436.7281	718.8677	**12**
8	753.4254	377.2163	736.3988	368.7030			**Q**	***1355.6702***	678.3388	1338.6437	669.8255	1337.6597	669.3335	**11**
9	882.4680	441.7376	865.4414	433.2243	864.4574	432.7323	**E**	***1227.6117***	614.3095	1210.5851	605.7962	1209.6011	605.3042	**10**
10	**1011.5106**	506.2589	994.4840	497.7456	993.5000	497.2536	**E**	***1098.5691***	549.7882	1081.5425	541.2749	1080.5585	540.7829	**9**
11	**1110.5790**	555.7931	1093.5524	547.2798	1092.5684	546.7878	**V**	***969.5265***	485.2669	952.4999	476.7536			**8**
12	1273.6423	637.3248	1256.6157	628.8115	1255.6317	628.3195	**Y**	***870.4581***	435.7327	853.4315	427.2194			**7**
13	**1410.7012**	705.8542	1393.6747	697.3410	1392.6906	696.8490	**H**	***707.3947***	354.2010	690.3682	345.6877			**6**
14	1507.7540	754.3806	1490.7274	745.8673	1489.7434	745.3753	**P**	***570.3358***	285.6715	553.3093	277.1583			**5**
15	1621.7969	811.4021	1604.7703	802.8888	1603.7863	802.3968	**N**	473.2831	237.1452	456.2565	228.6319			**4**
16	1692.8340	846.9206	1675.8075	838.4074	1674.8234	837.9154	**A**	359.2401	180.1237	342.2136	171.6104			**3**
17	1805.9181	903.4627	1788.8915	894.9494	1787.9075	894.4574	**L**	288.2030	144.6051	271.1765	136.0919			**2**
18							**R**	175.1190	88.0631	158.0924	79.5498			**1**

AT3G26520.1





NCBI **BLAST** search of NIAIGGVQEEVYHPNALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.0	1979.0224	-0.0016	NIAIGGVQEEVYHPNALR

Mascot: http://www.matrixscience.com/

AT3G26618.1

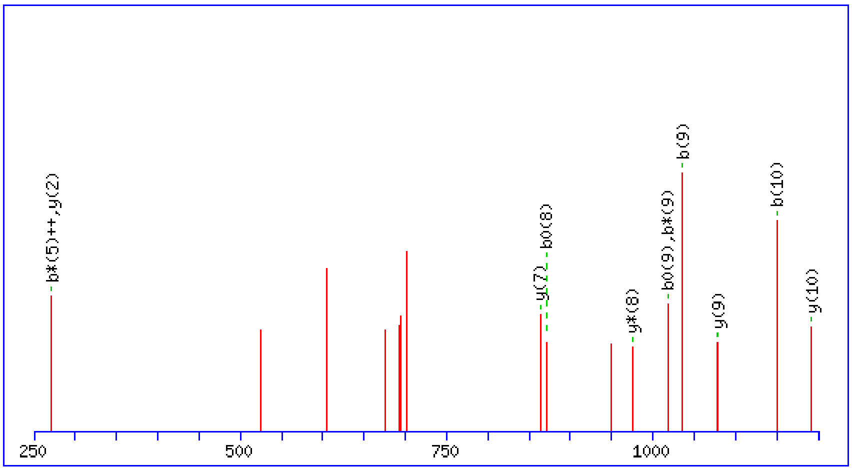
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TELSQSELFDPR**
Found in **AT3G26618.1** in **TAIR_Arabidopsis**, Symbols: ERF1-3 | ERF1-3 (EUKARYOTIC RELEASE FACTOR 1-3); translation release factor | chr3:9790091-9791398 FORWARD

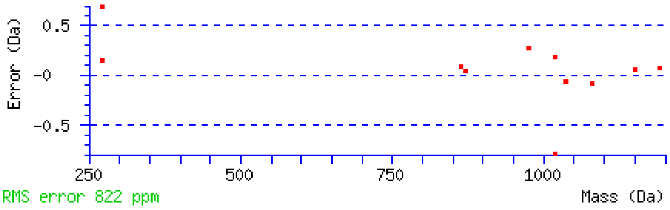
Match to Query 5459: 1420.681758 from(711.348155,2+) index(5679)
Title: Elution from: 52.751 to 52.751 scan no 7295 cid35.00 polarity:+
Data file D1d-2_1.mgf

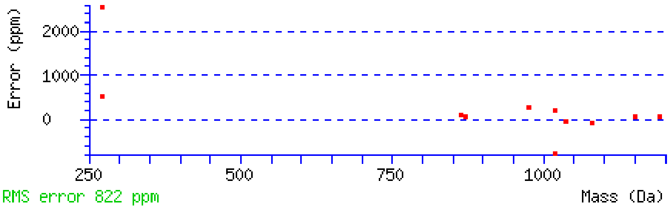
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1420.6834
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0046
Matches : 11/120 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	231.0975	116.0524			213.0870	107.0471	E	1320.6430	660.8251	1303.6165	652.3119	1302.6325	651.8199	11
3	344.1816	172.5944			326.1710	163.5892	L	***1191.6004***	596.3039	1174.5739	587.7906	1173.5899	587.2986	10
4	431.2136	216.1105			413.2031	207.1052	S	***1078.5164***	539.7618	1061.4898	531.2485	1060.5058	530.7565	9
5	559.2722	280.1397	542.2457	271.6265	541.2617	271.1345	Q	991.4843	496.2458	974.4578	487.7325	973.4738	487.2405	8
6	646.3042	323.6558	629.2777	315.1425	628.2937	314.6505	S	***863.4258***	432.2165	846.3992	423.7032	845.4152	423.2112	7
7	775.3468	388.1771	758.3203	379.6638	757.3363	379.1718	E	776.3937	388.7005	759.3672	380.1872	758.3832	379.6952	6
8	888.4309	444.7191	871.4044	436.2058	870.4203	435.7138	L	647.3511	324.1792	630.3246	315.6659	629.3406	315.1739	5
9	**1035.4993**	518.2533	1018.4728	509.7400	1017.4888	509.2480	F	534.2671	267.6372	517.2405	259.1239	516.2565	258.6319	4
10	**1150.5263**	575.7668	1133.4997	567.2535	1132.5157	566.7615	D	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	3
11	1247.5790	624.2932	1230.5525	615.7799	1229.5685	615.2879	P	***272.1717***	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TELSQSELFDPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G26618.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.0	1420.6834	-0.0017	TELSQSELFDPR
3.1	1420.6834	-0.0016	QYGKKPAPTESSE

Mascot: http://www.matrixscience.com/

AT3G26650.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDSTLGIFDADVKPSGETAISVDGK**
Found in **AT3G26650.1** in **TAIR_Arabidopsis**, Symbols: GAPA-1, GAPA | GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase | chr3:9796463-9798085 FORWARD

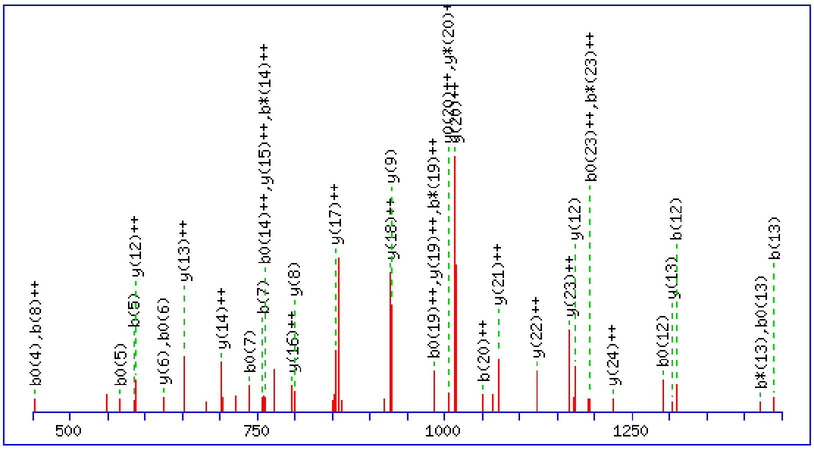
Match to Query 9867: 2611.181583 from(871.401137,3+) index(7807)
Title: Elution from: 69.773 to 69.773 scan no 10386 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1450 Da Full range

Label all possible matches ○ Label matches used for scoring ●

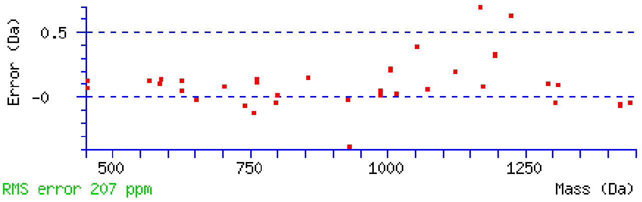
Show Y-axis ☐

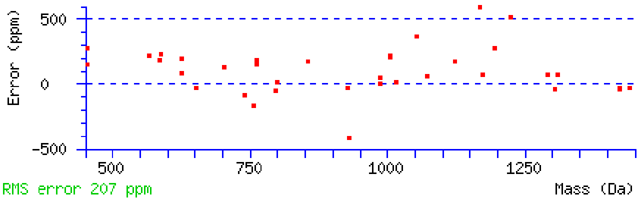


Monoisotopic mass of neutral peptide Mr(calc): 2611.1743
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 98 **Expect:** 1e-009
Matches : 39/258 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							25
2	281.0916	141.0494			263.0811	132.0442	D	2448.1213	1224.5643	2430.0977	1215.5525	2430.1107	1215.5590	24
3	369.1207	185.0640			351.1101	176.0587	S	2332.0973	1166.5523	2314.0737	1157.5405	2314.0868	1157.5470	23
4	471.1654	236.0863			453.1548	227.0811	T	2244.0683	1122.5378	2226.0447	1113.5260	2226.0577	1113.5325	22
5	**585.2465**	293.1269			567.2359	284.1216	L	2142.0235	1071.5154	2124.0000	1062.5036	2124.0130	1062.5101	21
6	643.2650	322.1361			625.2544	313.1309	G	2027.9424	1014.4749	2009.9189	1005.4631	2009.9319	1005.4696	20
7	**757.3461**	379.1767			739.3355	370.1714	I	1969.9239	985.4656	1951.9004	976.4538	1951.9134	976.4603	19
8	905.4115	453.2094			887.4010	444.2041	F	1855.8428	928.4251	1837.8193	919.4133	1837.8323	919.4198	18
9	1021.4355	511.2214			1003.4250	502.2161	D	1707.7774	854.3923	1689.7538	845.3805	1689.7668	845.3871	17
10	1093.4697	547.2385			1075.4591	538.2332	A	1591.7534	796.3803	1573.7298	787.3686	1573.7429	787.3751	16
11	1209.4936	605.2505			1191.4831	596.2452	D	1519.7193	760.3633	1501.6957	751.3515	1501.7087	751.3580	15
12	**1309.5591**	655.2832			1291.5485	646.2779	V	1403.6953	702.3513	1385.6717	693.3395	1385.6847	693.3460	14
13	**1439.6481**	720.3277	1421.6245	711.3159	1421.6376	711.3224	K	**1303.6298**	652.3186	1285.6063	643.3068	1285.6193	643.3133	13
14	1537.6979	769.3526	1519.6743	760.3408	1519.6874	760.3473	P	**1173.5408**	587.2740	1155.5172	578.2623	1155.5302	578.2688	12
15	1625.7270	813.3671	1607.7034	804.3553	1607.7164	804.3618	S	1075.4910	538.2491	1057.4674	529.2374	1057.4804	529.2439	11
16	1683.7455	842.3764	1665.7219	833.3646	1665.7349	833.3711	G	987.4620	494.2346	969.4384	485.2228	969.4514	485.2293	10
17	1813.7851	907.3962	1795.7615	898.3844	1795.7746	898.3909	E	**929.4435**	465.2254	911.4199	456.2136	911.4329	456.2201	9
18	1915.8298	958.4186	1897.8062	949.4068	1897.8193	949.4133	T	**799.4038**	400.2056	781.3802	391.1938	781.3933	391.2003	8
19	1987.8640	994.4356	1969.8404	985.4238	1969.8534	985.4303	A	697.3591	349.1832	679.3355	340.1714	679.3485	340.1779	7
20	2101.9451	1051.4762	2083.9215	1042.4644	2083.9345	1042.4709	I	**625.3250**	313.1661	607.3014	304.1543	607.3144	304.1608	6
21	2189.9741	1095.4907	2171.9506	1086.4789	2171.9636	1086.4854	S	511.2439	256.1256	493.2203	247.1138	493.2333	247.1203	5
22	2290.0396	1145.5234	2272.0160	1136.5116	2272.0290	1136.5181	V	423.2148	212.1110	405.1912	203.0992	405.2042	203.1058	4
23	2406.0636	1203.5354	2388.0400	1194.5236	2388.0530	1194.5301	D	323.1494	162.0783	305.1258	153.0665	305.1388	153.0730	3
24	2464.0821	1232.5447	2446.0585	1223.5329	2446.0715	1223.5394	G	207.1254	104.0663	189.1018	95.0545			2

25							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YDSTLGIFDADVKPSGETAISVDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
98.1	2611.1743	0.0072	YDSTLGIFDADVKPSGETAISVDGK
2.1	2611.1864	-0.0048	TTVPYGAWFHKSQVGGWAIEYGK
0.7	2611.1783	0.0033	QGLTREALGVFNLMMDSGVRPDR
0.0	2611.1887	-0.0071	TREDAVALALKAGLNMNCGDFLGK

Mascot: http://www.matrixscience.com/

AT3G26670.1

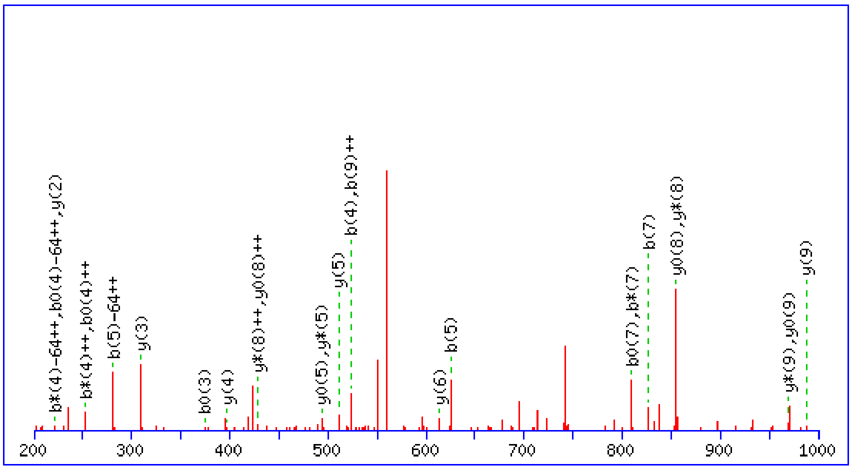
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLEKTISSKA**
Found in **AT3G26670.1** in **TAIR_Arabidopsis**, Symbols: | similar to permease-related [Arabidopsis thaliana] (TAIR:AT3G23870.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49131.1); contains InterPro domain Protein of unknown function DUF803 (InterPro:IPR008521) | chr3:9799473-

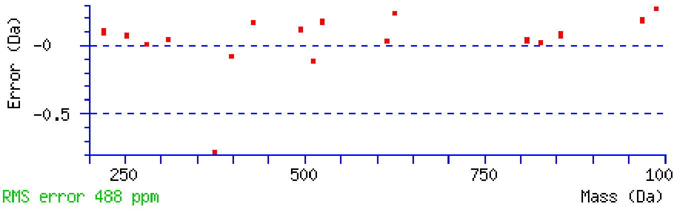
Match to Query 3605: 1134.557642 from(568.286097,2+) index(5331)
Title: Elution from: 47.696 to 47.696 scan no 6758 cid35.00 polarity:+
Data file D6h-3_2.mgf

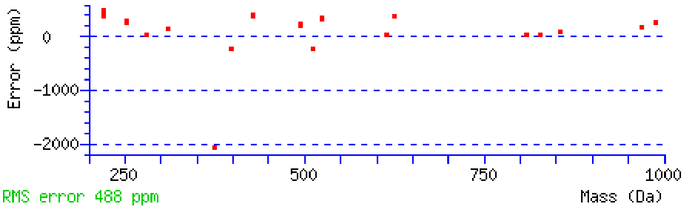
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1134.5599
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 32 **Expect:** 0.0062
Matches : 26/136 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							10
2	263.1208	132.0640					L	***987.5347***	494.2710	969.5111	485.2592	969.5242	485.2657	9
3	393.1604	197.0839			375.1499	188.0786	E	873.4536	437.2304	855.4300	428.2187	855.4431	428.2252	8
4	**523.2495**	262.1284	505.2259	253.1166	505.2389	253.1231	K	743.4140	372.2106	725.3904	363.1988	725.4034	363.2054	7
5	**625.2942**	313.1507	607.2706	304.1389	607.2836	304.1454	T	***613.3250***	307.1661	595.3014	298.1543	595.3144	298.1608	6
6	739.3753	370.1913	721.3517	361.1795	721.3647	361.1860	I	***511.2802***	256.1438	493.2567	247.1320	493.2697	247.1385	5
7	**827.4043**	414.2058	809.3808	405.1940	809.3938	405.2005	S	***397.1991***	199.1032	379.1756	190.0914	379.1886	190.0979	4
8	915.4334	458.2203	897.4098	449.2086	897.4228	449.2151	S	***309.1701***	155.0887	291.1465	146.0769	291.1595	146.0834	3
9	1045.5224	523.2649	1027.4989	514.2531	1027.5119	514.2596	K	***221.1410***	111.0741	203.1174	102.0624			2
10							A	91.0520	46.0296					1





NCBI **BLAST** search of MLEKTISSKA
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G26670.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.5	1134.5599	-0.0022	MLEKTISSKA
19.9	1134.5578	-0.0002	QRKAMNIMK
12.7	1134.5592	-0.0015	VQYGSPVSRK
10.2	1134.5565	0.0012	DITELYLTR
7.6	1134.5587	-0.0011	DVYKLDFPK
7.6	1134.5592	-0.0015	YIAAAAEQRK
7.5	1134.5565	0.0011	LYELSNVSAK
6.0	1134.5592	-0.0015	KVFDQISQR
3.1	1134.5544	0.0032	RTMLWLAGR
1.1	1134.5578	-0.0002	MATMLRLGAR

AT3G26830.1

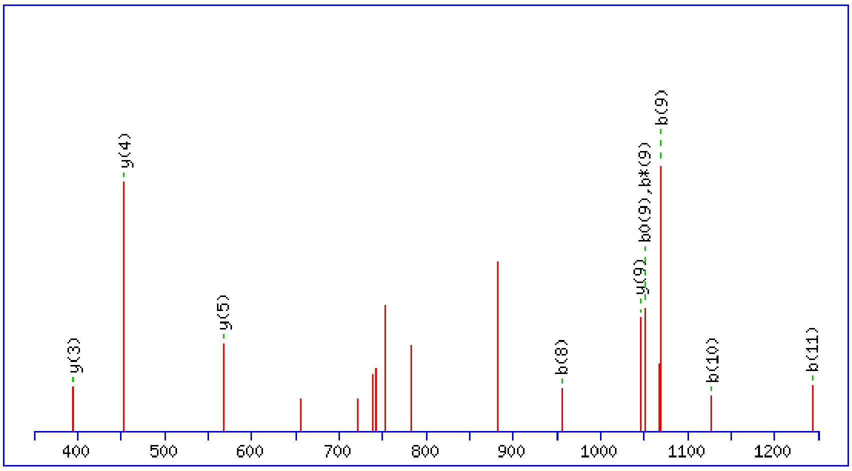
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQDEIRTTLGDKK**
Found in **AT3G26830.1** in **TAIR_Arabidopsis**, Symbols: CYP71B15, PAD3 | PAD3 (PHYTOALEXIN DEFICIENT 3); oxygen binding | chr3:9889227-9890797 FORWARD

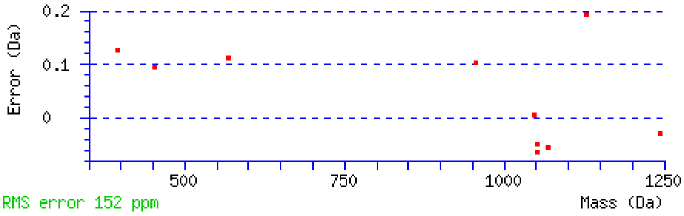
Match to Query 6291: 1520.752532 from(761.383542,2+) index(10590)
Title: Elution from: 107.779 to 107.779 scan no 15557 cid35.00 polarity:+
Data file D12h-1_3.mgf

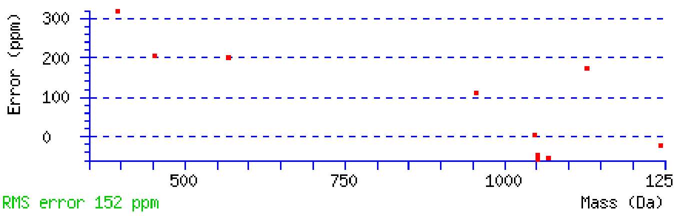
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1520.7536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0057
Matches : 10/134 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							13
2	231.1254	116.0663	213.1018	107.0545			Q	1421.6955	711.3514	1403.6719	702.3396	1403.6849	702.3461	12
3	347.1493	174.0783	329.1258	165.0665	329.1388	165.0730	D	1291.6429	646.3251	1273.6193	637.3133	1273.6323	637.3198	11
4	477.1890	239.0981	459.1654	230.0863	459.1784	230.0928	E	1175.6189	588.3131	1157.5953	579.3013	1157.6083	579.3078	10
5	591.2701	296.1387	573.2465	287.1269	573.2595	287.1334	I	***1045.5793***	523.2933	1027.5557	514.2815	1027.5687	514.2880	9
6	751.3593	376.1833	733.3357	367.1715	733.3488	367.1780	R	931.4982	466.2527	913.4746	457.2409	913.4876	457.2474	8
7	853.4040	427.2057	835.3805	418.1939	835.3935	418.2004	T	771.4089	386.2081	753.3853	377.1963	753.3983	377.2028	7
8	***955.4488***	478.2280	937.4252	469.2162	937.4382	469.2227	T	669.3642	335.1857	651.3406	326.1739	651.3536	326.1805	6
9	***1069.5299***	535.2686	1051.5063	526.2568	1051.5193	526.2633	L	***567.3195***	284.1634	549.2959	275.1516	549.3089	275.1581	5
10	***1127.5484***	564.2778	1109.5248	555.2660	1109.5378	555.2725	G	***453.2384***	227.1228	435.2148	218.1110	435.2278	218.1175	4
11	***1243.5723***	622.2898	1225.5487	613.2780	1225.5618	613.2845	D	***395.2199***	198.1136	377.1963	189.1018	377.2093	189.1083	3
12	1373.6614	687.3343	1355.6378	678.3225	1355.6508	678.3290	K	279.1959	140.1016	261.1723	131.0898			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VQDEIRTTLGDKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G26830.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.8	1520.7536	-0.0011	VQDEIRTTLGDKK
11.7	1520.7537	-0.0011	SGLDKIESDLAKAR
3.5	1520.7559	-0.0034	VVADQIARIFDEK
0.6	1520.7519	0.0007	IDLSLKDCGLLMK
0.3	1520.7512	0.0014	LRMDQLLNLGWK

AT3G27160.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KKDEEEDNWEMPGGDVPS**
Found in **AT3G27160.1** in **TAIR_Arabidopsis**, Symbols: GHS1 | GHS1 (GLUCOSE HYPERSENSITIVE 1); structural constituent of ribosome | chr3:10018768-10020091 FORWARD

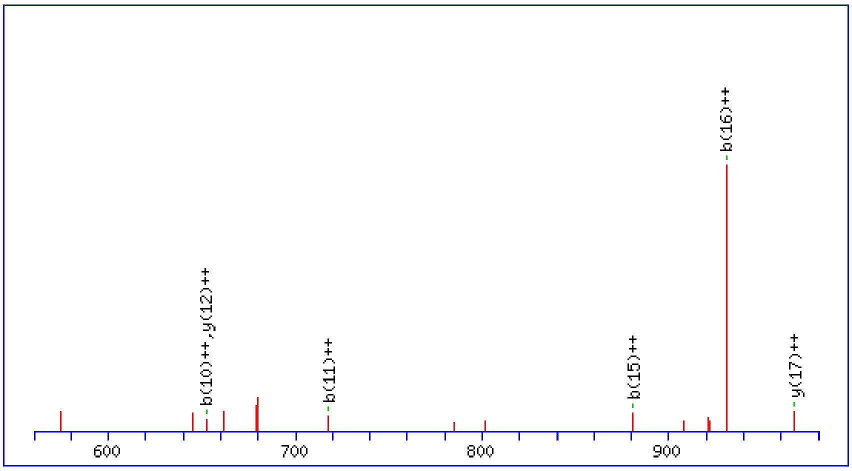
Match to Query 9029: 2060.862903 from(687.961577,3+) index(4257)
Title: Elution from: 43.052 to 43.052 scan no 5490 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 560 to 980 Da Full range

Label all possible matches ○ Label matches used for scoring ●

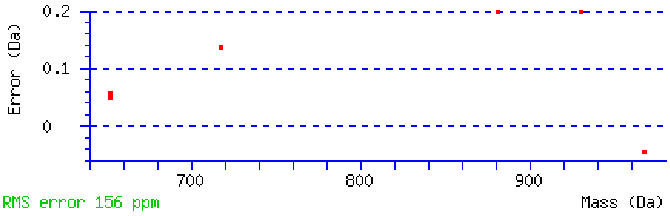
Show Y-axis ☐

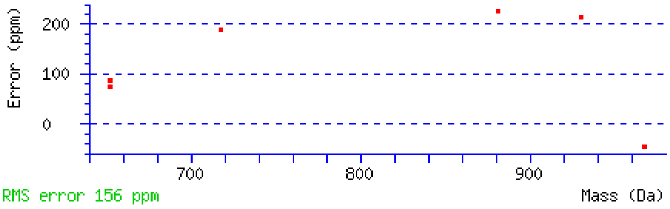


Monoisotopic mass of neutral peptide Mr(calc): 2060.8633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 0.032
Matches : 6/180 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							18
2	257.1972	129.1022	240.1707	120.5890			K	1933.7756	967.3915	1916.7491	958.8782	1915.7651	958.3862	17
3	372.2241	186.6157	355.1976	178.1024	354.2136	177.6104	D	1805.6807	903.3440	1788.6541	894.8307	1787.6701	894.3387	16
4	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	E	1690.6537	845.8305	1673.6272	837.3172	1672.6432	836.8252	15
5	630.3093	315.6583	613.2828	307.1450	612.2988	306.6530	E	1561.6111	781.3092	1544.5846	772.7959	1543.6006	772.3039	14
6	759.3519	380.1796	742.3254	371.6663	741.3414	371.1743	E	1432.5685	716.7879	1415.5420	708.2746	1414.5580	707.7826	13
7	874.3789	437.6931	857.3523	429.1798	856.3683	428.6878	D	1303.5259	652.2666	1286.4994	643.7533	1285.5154	643.2613	12
8	988.4218	494.7145	971.3952	486.2013	970.4112	485.7093	N	1188.4990	594.7531	1171.4725	586.2399	1170.4884	585.7479	11
9	1174.5011	587.7542	1157.4746	579.2409	1156.4905	578.7489	W	1074.4561	537.7317			1056.4455	528.7264	10
10	1303.5437	***652.2755***	1286.5172	643.7622	1285.5331	643.2702	E	888.3768	444.6920			870.3662	435.6867	9
11	1434.5842	***717.7957***	1417.5576	709.2825	1416.5736	708.7904	M	759.3342	380.1707			741.3236	371.1654	8
12	1531.6369	766.3221	1514.6104	757.8088	1513.6264	757.3168	P	628.2937	314.6505			610.2831	305.6452	7
13	1588.6584	794.8328	1571.6319	786.3196	1570.6478	785.8276	G	531.2409	266.1241			513.2304	257.1188	6
14	1645.6799	823.3436	1628.6533	814.8303	1627.6693	814.3383	G	474.2195	237.6134			456.2089	228.6081	5
15	1760.7068	***880.8570***	1743.6803	872.3438	1742.6963	871.8518	D	417.1980	209.1026			399.1874	200.0974	4
16	1859.7752	***930.3913***	1842.7487	921.8780	1841.7647	921.3860	V	302.1710	151.5892			284.1605	142.5839	3
17	1956.8280	978.9176	1939.8014	970.4044	1938.8174	969.9124	P	203.1026	102.0550			185.0921	93.0497	2
18							S	106.0499	53.5286			88.0393	44.5233	1

AT3G27160.1





NCBI **BLAST** search of KKDEEEDNWEMPGGDVPS
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.0	2060.8633	-0.0004	KKDEEEDNWEMPGGDVPS

Mascot: http://www.matrixscience.com/

AT3G27280.1

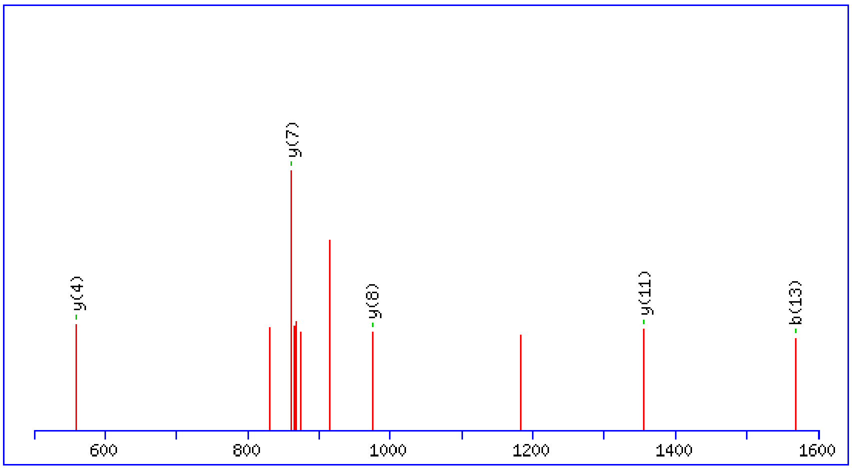
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPYIFQTLGLEYDEK**
Found in **AT3G27280.1** in **TAIR_Arabidopsis**, Symbols: ATPHB4 | ATPHB4 (PROHIBITIN 4) | chr3:10078141-10079288 FORWARD

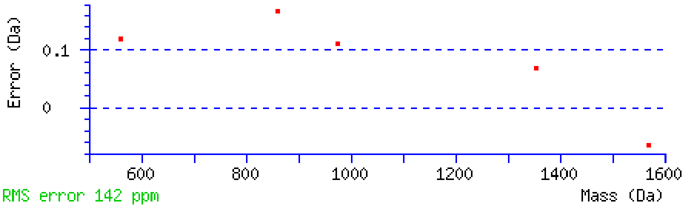
Match to Query 9125: 1844.878070 from(923.446311,2+) index(10793)
Title: Elution from: 101.936 to 101.936 scan no 15264 cid35.00 polarity:+
Data file C7-2_1.mgf

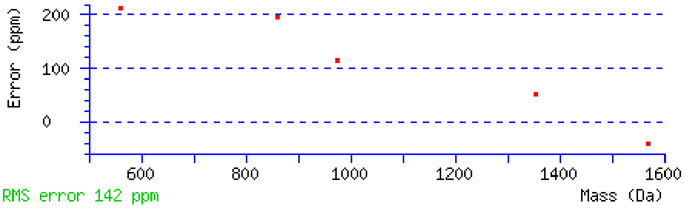
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1844.8790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.034
Matches : 5/144 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							15
2	213.1382	107.0727					P	1731.8052	866.4063	1713.7817	857.3945	1713.7947	857.4010	14
3	377.1985	189.1029					Y	1633.7554	817.3814	1615.7319	808.3696	1615.7449	808.3761	13
4	491.2796	246.1435					I	1469.6951	735.3512	1451.6715	726.3394	1451.6845	726.3459	12
5	639.3451	320.1762					F	***1355.6140***	678.3106	1337.5904	669.2988	1337.6034	669.3053	11
6	769.3977	385.2025	751.3741	376.1907			Q	1207.5485	604.2779	1189.5249	595.2661	1189.5380	595.2726	10
7	871.4424	436.2249	853.4189	427.2131	853.4319	427.2196	T	1077.4959	539.2516	1059.4723	530.2398	1059.4853	530.2463	9
8	985.5235	493.2654	967.5000	484.2536	967.5130	484.2601	L	***975.4512***	488.2292	957.4276	479.2174	957.4406	479.2239	8
9	1043.5420	522.2747	1025.5185	513.2629	1025.5315	513.2694	G	***861.3701***	431.1887	843.3465	422.1769	843.3595	422.1834	7
10	1157.6231	579.3152	1139.5996	570.3034	1139.6126	570.3099	L	803.3516	402.1794	785.3280	393.1676	785.3410	393.1741	6
11	1287.6628	644.3350	1269.6392	635.3232	1269.6522	635.3297	E	689.2705	345.1389	671.2469	336.1271	671.2599	336.1336	5
12	1451.7231	726.3652	1433.6996	717.3534	1433.7126	717.3599	Y	***559.2308***	280.1191	541.2073	271.1073	541.2203	271.1138	4
13	1567.7471	784.3772	1549.7235	775.3654	1549.7365	775.3719	D	395.1705	198.0889	377.1469	189.0771	377.1599	189.0836	3
14	1697.7867	849.3970	1679.7632	840.3852	1679.7762	840.3917	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LPYIFQTLGLEYDEK

AT3G27280.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.4	1844.8790	-0.0010	LPYIFQTLGLEYDEK
12.7	1844.8806	-0.0026	KMDGQTIAISSLSTLSR
2.9	1844.8777	0.0004	DIKTAFWLLGLMEMK
2.9	1844.8759	0.0022	MNTSVRAVLSSMKAPSK
1.5	1844.8786	-0.0005	LMIEQSCRLSRITGR

AT3G27610.1

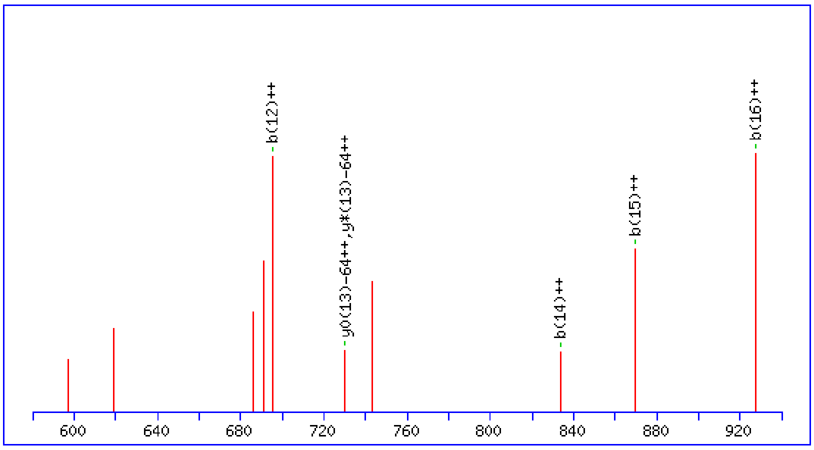
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPNQHCSQSMANEMALLAYNRALK**
Found in **AT3G27610.1** in **TAIR_Arabidopsis**, Symbols: | similar to nucleotidyltransferase [Arabidopsis thaliana] (TAIR:AT2G01220.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO42196.1); contains domain SSF52374 (SSF52374) | chr3:10226966-10229389 REVERSE

Match to Query 10713: 2813.199024 from(704.307032,4+) index(6830)
Title: Elution from: 61.060 to 61.060 scan no 8867 cid35.00 polarity:+
Data file 0-1_2.mgf

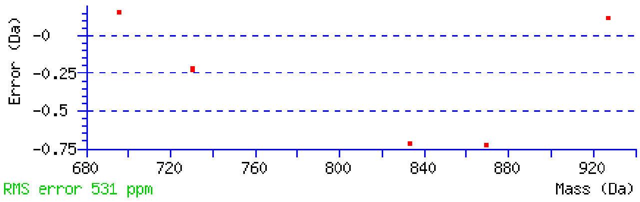
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 580 to 940 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

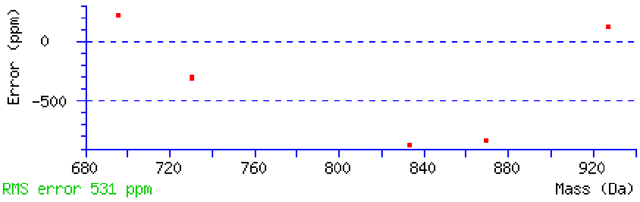


Monoisotopic mass of neutral peptide Mr(calc): 2813.1980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.037
Matches : 6/398 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							24
2	199.1225	100.0649					P	2714.1398	1357.5736	2696.1162	1348.5618	2696.1293	1348.5683	23
3	315.1595	158.0834	297.1359	149.0716			N	2616.0900	1308.5487	2598.0664	1299.5369	2598.0795	1299.5434	22
4	445.2122	223.1097	427.1886	214.0979			Q	2500.0530	1250.5302	2482.0294	1241.5184	2482.0425	1241.5249	21
5	585.2622	293.1347	567.2386	284.1229			H	2370.0004	1185.5038	2351.9768	1176.4920	2351.9898	1176.4985	20
6	747.2869	374.1471	729.2633	365.1353			C	2229.9504	1115.4788	2211.9268	1106.4670	2211.9398	1106.4735	19
7	835.3160	418.1616	817.2924	409.1498	817.3054	409.1563	S	2067.9256	1034.4665	2049.9021	1025.4547	2049.9151	1025.4612	18
8	965.3686	483.1879	947.3450	474.1762	947.3580	474.1827	Q	1979.8966	990.4519	1961.8730	981.4401	1961.8860	981.4466	17
9	1053.3977	527.2025	1035.3741	518.1907	1035.3871	518.1972	S	1849.8439	925.4256	1831.8204	916.4138	1831.8334	916.4203	16
10	1201.4301	601.2187	1183.4065	592.2069	1183.4195	592.2134	M	1761.8149	881.4111	1743.7913	872.3993	1743.8043	872.4058	15
11	1273.4643	637.2358	1255.4407	628.2240	1255.4537	628.2305	A	1613.7824	807.3949	1595.7589	798.3831	1595.7719	798.3896	14
12	1389.5013	***695.2543***	1371.4777	686.2425	1371.4907	686.2490	N	1541.7483	771.3778	1523.7247	762.3660	1523.7377	762.3725	13
13	1519.5409	760.2741	1501.5173	751.2623	1501.5303	751.2688	E	1425.7113	713.3593	1407.6877	704.3475	1407.7007	704.3540	12
14	1667.5733	***834.2903***	1649.5497	825.2785	1649.5628	825.2850	M	1295.6717	648.3395	1277.6481	639.3277			11
15	1739.6075	***870.3074***	1721.5839	861.2956	1721.5969	861.3021	A	1147.6392	574.3233	1129.6156	565.3115			10
16	1853.6886	***927.3479***	1835.6650	918.3361	1835.6780	918.3426	L	1075.6051	538.3062	1057.5815	529.2944			9
17	1967.7697	984.3885	1949.7461	975.3767	1949.7591	975.3832	L	961.5240	481.2656	943.5004	472.2538			8
18	2039.8038	1020.4055	2021.7802	1011.3938	2021.7933	1011.4003	A	847.4429	424.2251	829.4193	415.2133			7
19	2203.8642	1102.4357	2185.8406	1093.4239	2185.8536	1093.4304	Y	775.4087	388.2080	757.3852	379.1962			6
20	2319.9012	1160.4542	2301.8776	1151.4424	2301.8906	1151.4489	N	611.3484	306.1778	593.3248	297.1660			5
21	2479.9904	1240.4989	2461.9668	1231.4871	2461.9799	1231.4936	R	495.3114	248.1593	477.2878	239.1475			4
22	2552.0246	1276.5159	2534.0010	1267.5041	2534.0140	1267.5106	A	335.2221	168.1147	317.1985	159.1029			3

23	2666.1057	1333.5565	2648.0821	1324.5447	2648.0951	1324.5512	**L**	263.1880	132.0976	245.1644	123.0858			2
24							**K**	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VPNQHCSQSMANEMALLAYNRALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	2813.1980	0.0010	VPNQHCSQSMANEMALLAYNRALK
9.6	2813.1960	0.0031	IGIAHSPAWFEAHDLADSQDGASIDR
7.1	2813.2054	-0.0064	CIGVVKMYIPDGPWFCPECTINK
4.2	2813.2005	-0.0015	LDNVSAQEEMLRNQSNNVICASASK
4.2	2813.1915	0.0075	VTDTEMFLLSSMYFSFPRGEGGPGK
4.2	2813.1919	0.0071	KCILGDNVYMKSGHTFEHSSDEVK
0.6	2813.2023	-0.0033	TLSKYCQDMLPDGSTSPASPNAIWK
0.0	2813.2050	-0.0059	MYPCGYVAQVTNLSPQATEKDVHR

AT3G27740.1

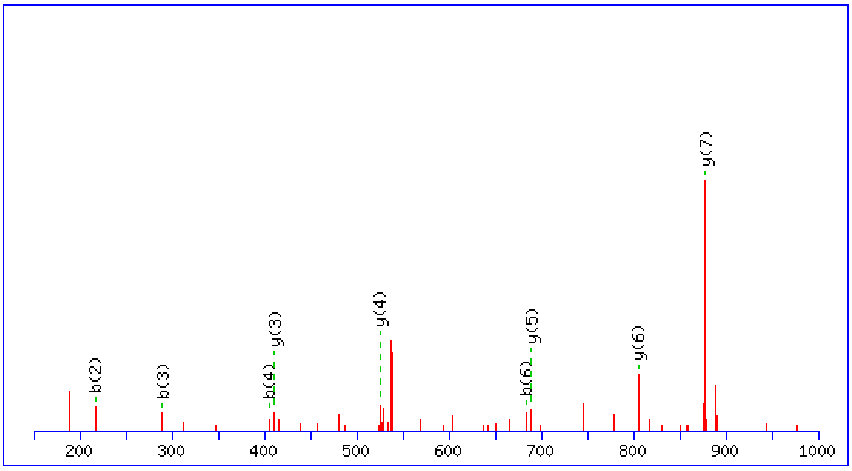
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLADYLTER**
Found in **AT3G27740.1** in **TAIR_Arabidopsis**, Symbols: CARA | CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing) | chr3:10282707-10285029 REVERSE

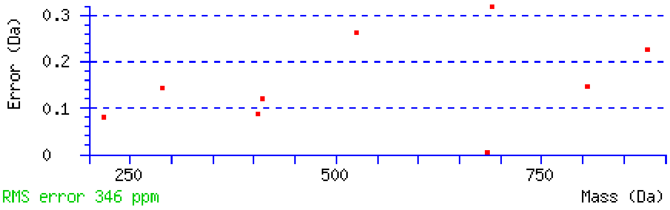
Match to Query 2990: 1092.510048 from(547.262300,2+) index(5940)
Title: Elution from: 55.665 to 55.665 scan no 7697 cid35.00 polarity:+
Data file D12h-2_1.mgf

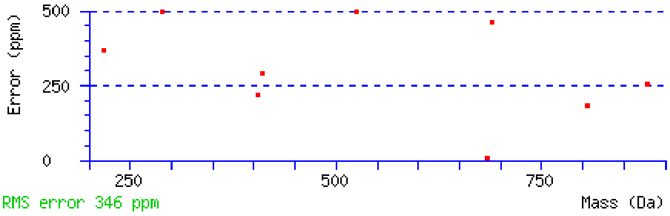
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1092.5095
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.022
Matches : 9/78 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							9
2	**217.1331**	109.0702	199.1225	100.0649	L	991.4721	496.2397	973.4485	487.2279	973.4616	487.2344	8
3	**289.1672**	145.0873	271.1567	136.0820	A	***877.3910***	439.1991	859.3674	430.1874	859.3805	430.1939	7
4	**405.1912**	203.0992	387.1807	194.0940	D	***805.3569***	403.1821	787.3333	394.1703	787.3463	394.1768	6
5	569.2516	285.1294	551.2410	276.1241	Y	***689.3329***	345.1701	671.3093	336.1583	671.3223	336.1648	5
6	**683.3327**	342.1700	665.3221	333.1647	L	***525.2725***	263.1399	507.2489	254.1281	507.2620	254.1346	4
7	785.3774	393.1923	767.3668	384.1871	T	***411.1914***	206.0994	393.1678	197.0876	393.1809	197.0941	3
8	915.4170	458.2121	897.4065	449.2069	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TLADYLTER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G27740.1

27.1	1092.5095	0.0005	TLADYLTER
8.7	1092.5096	0.0005	TLPIDEEHK
3.3	1092.5082	0.0019	TLMKKDCGK
3.2	1092.5096	0.0005	GDFSIQISSK
1.4	1092.5122	-0.0021	IGGGFGGKETR
1.4	1092.5122	-0.0021	LGGGFGGKETR
0.5	1092.5122	-0.0022	VDVYNRQGK

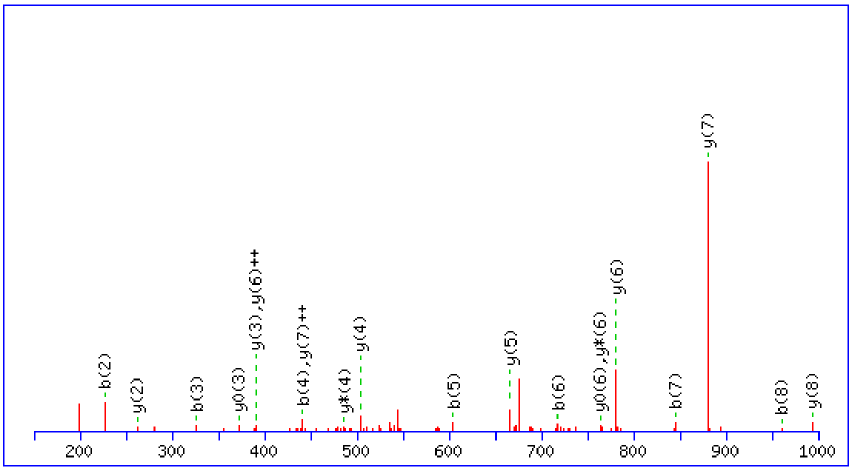
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILVDYLQDK**
Found in **AT3G27830.1** in **TAIR_Arabidopsis**, Symbols: RPL12, RPL12-A | RPL12-A (RIBOSOMAL PROTEIN L12-A); structural constituent of ribosome | chr3:10319813-10320388 FORWARD

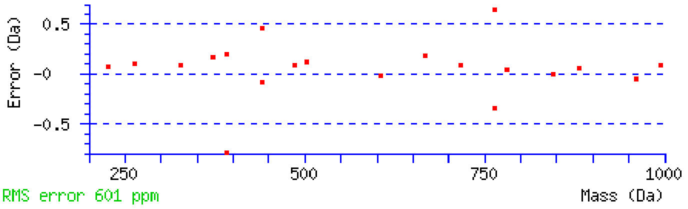
Match to Query 3591: 1105.599298 from(553.806925,2+) index(5868)
Title: Elution from: 51.821 to 51.821 scan no 7370 cid35.00 polarity:+
Data file C7-3_1.mgf

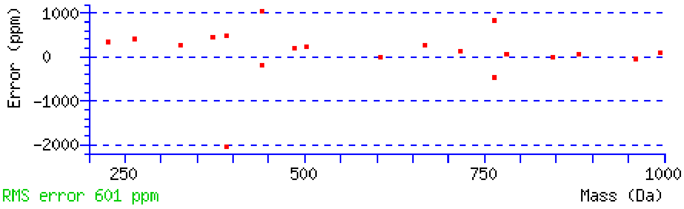
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1105.6019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 5e-007
Matches : 20/76 fragment ions using 23 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							9
2	***227.1754***	114.0913					L	***993.5251***	497.2662	976.4986	488.7529	975.5146	488.2609	8
3	***326.2438***	163.6255					V	***880.4411***	440.7242	863.4145	432.2109	862.4305	431.7189	7
4	***441.2708***	221.1390			423.2602	212.1337	D	***781.3727***	391.1900	764.3461	382.6767	763.3621	382.1847	6
5	***604.3341***	302.6707			586.3235	293.6654	Y	***666.3457***	333.6765	649.3192	325.1632	648.3352	324.6712	5
6	***717.4182***	359.2127			699.4076	350.2074	L	***503.2824***	252.1448	486.2558	243.6316	485.2718	243.1396	4
7	***845.4767***	423.2420	828.4502	414.7287	827.4662	414.2367	Q	***390.1983***	195.6028	373.1718	187.0895	372.1878	186.5975	3
8	***960.5037***	480.7555	943.4771	472.2422	942.4931	471.7502	D	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ILVDYLQDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G27830.1

69.0	1105.6019	-0.0026	ILVDYLQDK
10.5	1105.5992	0.0001	FNQLVRSSR
4.8	1105.6019	-0.0026	LFEIETQVK

AT3G27850.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGSEISSLTLEEAR**
Found in **AT3G27850.1** in **TAIR_Arabidopsis**, Symbols: RPL12-C | RPL12-C (RIBOSOMAL PROTEIN L12-C); structural constituent of ribosome | chr3:10326142-10326705 FORWARD

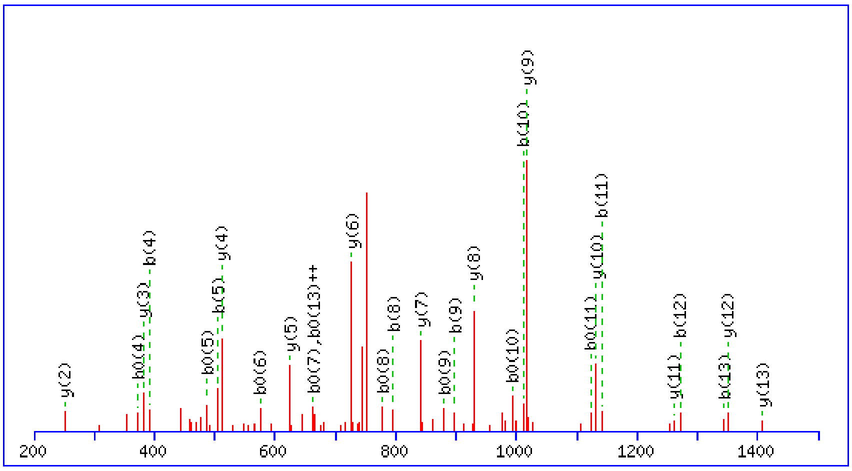
Match to Query 6064: 1520.727206 from(761.370879,2+) index(5577)
Title: Elution from: 52.879 to 52.879 scan no 7232 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

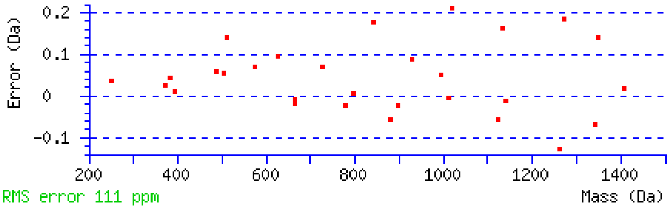
Label all possible matches ○ Label matches used for scoring ●

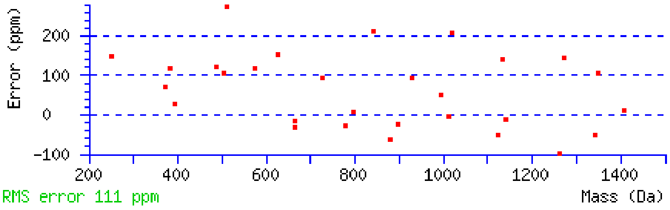
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1520.7276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 119 **Expect:** 1.3e-011
Matches : 29/122 fragment ions using 39 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478			I							14
2	173.1069	87.0571			G	***1407.6538***	704.3305	1389.6302	695.3188	1389.6433	695.3253	13
3	261.1359	131.0716	243.1254	122.0663	S	***1349.6353***	675.3213	1331.6117	666.3095	1331.6248	666.3160	12
4	**391.1756**	196.0914	373.1650	187.0861	E	***1261.6063***	631.3068	1243.5827	622.2950	1243.5957	622.3015	11
5	**505.2567**	253.1320	487.2461	244.1267	I	***1131.5666***	566.2870	1113.5430	557.2752	1113.5561	557.2817	10
6	593.2857	297.1465	575.2752	288.1412	S	***1017.4855***	509.2464	999.4619	500.2346	999.4750	500.2411	9
7	681.3148	341.1610	663.3042	332.1558	S	***929.4565***	465.2319	911.4329	456.2201	911.4459	456.2266	8
8	**795.3959**	398.2016	777.3853	389.1963	L	***841.4274***	421.2173	823.4038	412.2056	823.4168	412.2121	7
9	**897.4406**	449.2239	879.4300	440.2187	T	***727.3463***	364.1768	709.3227	355.1650	709.3357	355.1715	6
10	**1011.5217**	506.2645	993.5111	497.2592	L	***625.3016***	313.1544	607.2780	304.1426	607.2910	304.1492	5
11	**1141.5613**	571.2843	1123.5508	562.2790	E	***511.2205***	256.1139	493.1969	247.1021	493.2099	247.1086	4
12	**1271.6010**	636.3041	1253.5904	627.2988	E	***381.1809***	191.0941	363.1573	182.0823	363.1703	182.0888	3
13	**1343.6351**	672.3212	1325.6245	663.3159	A	***251.1412***	126.0743	233.1177	117.0625			2
14					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IGSEISSLTLEEAR

AT3G27850.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
118.7	1520.7276	-0.0004	IGSEISSLTLEEAR
21.2	1520.7303	-0.0031	AVEAKETAAEKAQR
18.2	1520.7252	0.0020	EAWLSSINLAICK
14.6	1520.7240	0.0032	FTHLSPVWYDLK
13.8	1520.7303	-0.0031	LAANDSLGKEKEAR
7.1	1520.7249	0.0023	RGFATHPRSIAER
4.3	1520.7303	-0.0031	GLSDLAGVGDNTVRK
3.4	1520.7303	-0.0031	SDAINRELVSLER
3.2	1520.7303	-0.0031	ETVKENGLQKNGGK
1.9	1520.7229	0.0043	EKSLPDKLSMEAR

AT3G27870.1

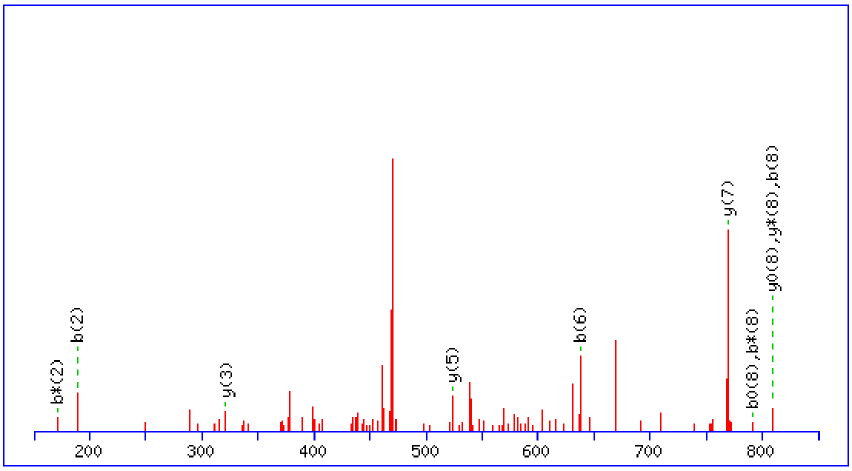
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGDKEAVAK**
Found in **AT3G27870.1** in **TAIR_Arabidopsis**, Symbols: | haloacid dehalogenase-like hydrolase family protein | chr3:10332187-10336525 FORWARD

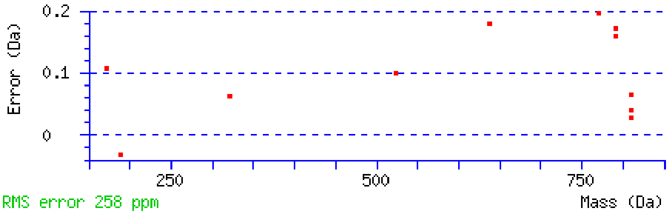
Match to Query 2136: 956.456790 from(479.235671,2+) index(3024)
Title: Elution from: 30.340 to 30.340 scan no 3762 cid35.00 polarity:+
Data file D12h-1_2.mgf

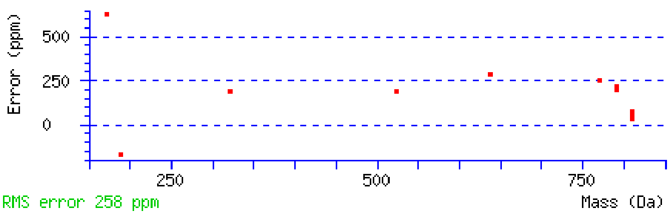
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 956.4571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.048
Matches : 11/84 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							9
2	***189.0784***	95.0428	171.0548	86.0311			G	827.4118	414.2095	809.3882	405.1977	809.4012	405.2042	8
3	305.1024	153.0548	287.0788	144.0430	287.0918	144.0496	D	***769.3933***	385.2003	751.3697	376.1885	751.3827	376.1950	7
4	435.1914	218.0994	417.1678	209.0876	417.1809	209.0941	K	653.3693	327.1883	635.3457	318.1765	635.3587	318.1830	6
5	565.2311	283.1192	547.2075	274.1074	547.2205	274.1139	E	***523.2802***	262.1438	505.2567	253.1320	505.2697	253.1385	5
6	***637.2652***	319.1362	619.2416	310.1245	619.2546	310.1310	A	393.2406	197.1239	375.2170	188.1122			4
7	737.3307	369.1690	719.3071	360.1572	719.3201	360.1637	V	***321.2065***	161.1069	303.1829	152.0951			3
8	***809.3648***	405.1860	791.3412	396.1742	791.3542	396.1808	A	221.1410	111.0741	203.1174	102.0624			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QGDKEAVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G27870.1

23.8	956.4571	-0.0003	QGDKEAVAK
13.3	956.4594	-0.0026	WLNEKEK
10.7	956.4571	-0.0003	GENALKDAK
9.0	956.4593	-0.0025	VWDAATGVK
7.9	956.4594	-0.0026	FHSSLLDK
7.5	956.4545	0.0023	ESTLEELK
3.5	956.4571	-0.0003	SLQGEGQVK
3.5	956.4593	-0.0025	TVHDFTVK
2.4	956.4571	-0.0003	EVVKNNDK
1.9	956.4571	-0.0003	ADEALKGNK

AT3G28540.1

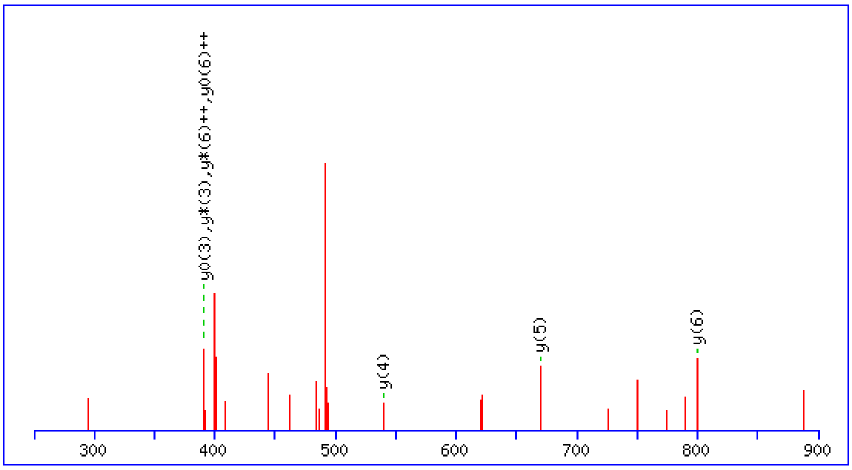
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLEEEKEK**
Found in **AT3G28540.1** in **TAIR_Arabidopsis**, Symbols: | AAA-type ATPase family protein | chr3:10695681-10697213 FORWARD

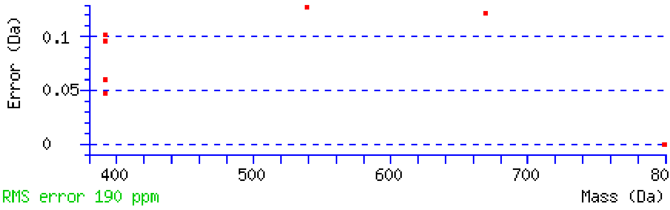
Match to Query 2383: 1000.456448 from(501.235500,2+) index(713)
Title: Elution from: 13.284 to 13.284 scan no 1054 cid35.00 polarity:+
Data file C7-1_3.mgf

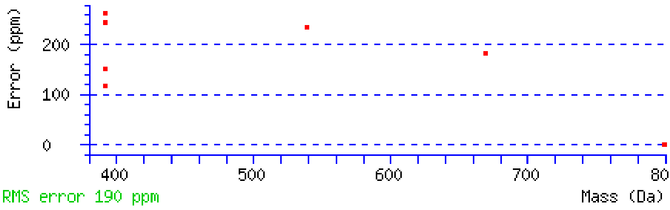
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1000.4573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.031
Matches : 7/72 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							8
2	203.1174	102.0624			185.1069	93.0571	L	913.4355	457.2214	895.4119	448.2096	895.4250	448.2161	7
3	333.1571	167.0822			315.1465	158.0769	E	***799.3544***	400.1808	781.3308	391.1691	781.3439	391.1756	6
4	463.1967	232.1020			445.1861	223.0967	E	***669.3148***	335.1610	651.2912	326.1492	651.3042	326.1558	5
5	593.2363	297.1218			575.2258	288.1165	E	***539.2752***	270.1412	521.2516	261.1294	521.2646	261.1359	4
6	723.3254	362.1663	705.3018	353.1545	705.3148	353.1610	K	409.2355	205.1214	391.2120	196.1096	391.2250	196.1161	3
7	853.3650	427.1861	835.3414	418.1743	835.3544	418.1808	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SLEEEKEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.1	1000.4573	-0.0009	SLEEEKEK
3.9	1000.4552	0.0012	LSLSSHMGR

AT3G28540.1

3.4	1000.4552	0.0012	SICQNRPL
0.4	1000.4552	0.0012	LKDNNMPR
0.3	1000.4573	-0.0008	LEEDTEKK

AT3G28570.1

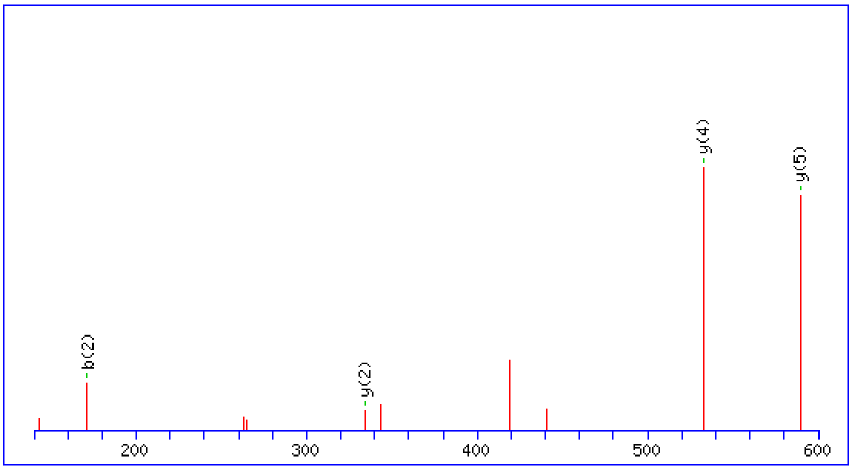
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGKAWK**
Found in **AT3G28570.1** in **TAIR_Arabidopsis**, Symbols: | AAA-type ATPase family protein | chr3:10711771-10713126 FORWARD

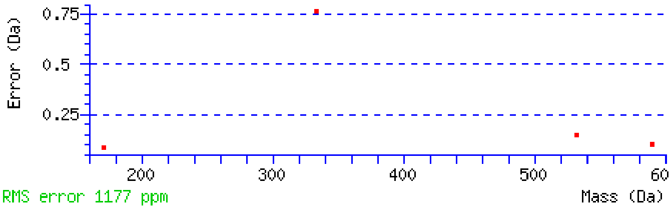
Match to Query 673: 701.422430 from(351.718491,2+) index(4820)
Title: Elution from: 43.696 to 43.696 scan no 6005 cid35.00 polarity:+
Data file C7-3_1.mgf

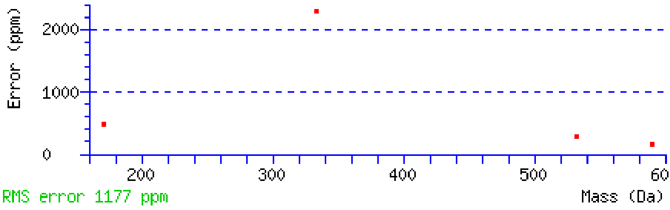
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 701.4224
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.013
Matches : 4/36 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			I					6
2	171.1128	86.0600			G	***589.3457***	295.1765	572.3191	286.6632	5
3	299.2078	150.1075	282.1812	141.5942	K	***532.3242***	266.6657	515.2976	258.1525	4
4	370.2449	185.6261	353.2183	177.1128	A	404.2292	202.6183	387.2027	194.1050	3
5	556.3242	278.6657	539.2976	270.1525	W	***333.1921***	167.0997	316.1656	158.5864	2
6					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of IGKAWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.5	701.4224	0.0000	IGKAWK
11.3	701.4224	-0.0000	LLGFPR
7.5	701.4224	0.0000	IKQWK
7.5	701.4224	0.0000	IQKWK

AT3G28570.1

7.5	701.4224	0.0000	LKQWK
7.5	701.4224	0.0000	LQKWK

AT3G28710.1

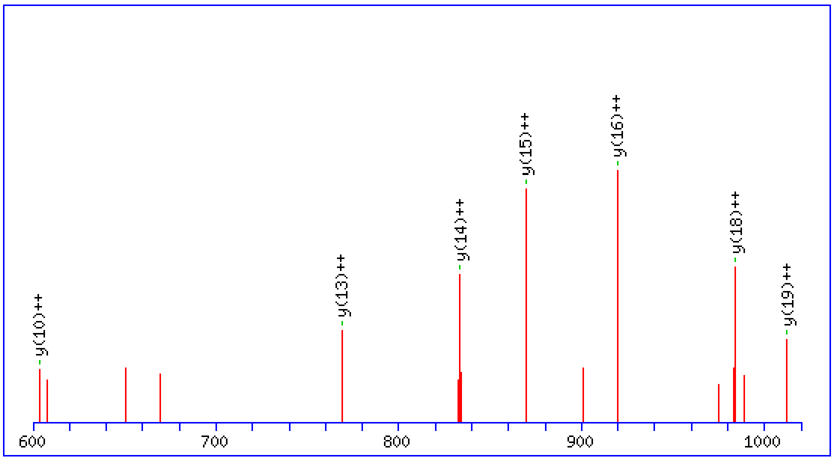
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGGATAEIMSDLLAFEADRR**
Found in **AT3G28710.1** in **TAIR_Arabidopsis**, Symbols: | H+-transporting two-sector ATPase, putative | chr3:10774381-10776831 REVERSE

Match to Query 10104: 2135.067897 from(712.696575,3+) index(10950)
Title: Elution from: 104.808 to 104.808 scan no 15597 cid35.00 polarity:+
Data file C7-2_1.mgf

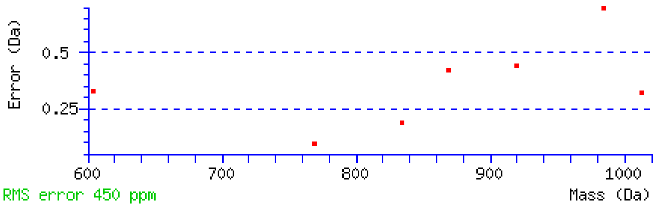
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1020 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

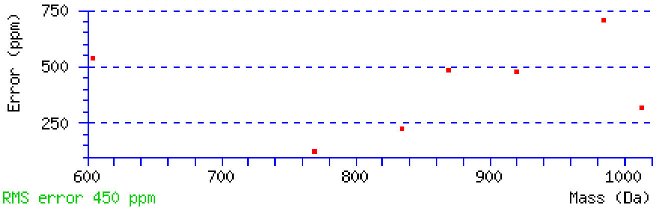


Monoisotopic mass of neutral peptide Mr(calc): 2135.0681
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 4.3e-006
Matches : 7/180 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							20
2	171.1128	86.0600					G	2022.9913	1011.9993	2005.9648	1003.4860	2004.9808	1002.9940	19
3	228.1343	114.5708					G	1965.9699	983.4886	1948.9433	974.9753	1947.9593	974.4833	18
4	299.1714	150.0893					A	1908.9484	954.9778	1891.9218	946.4646	1890.9378	945.9725	17
5	400.2191	200.6132			382.2085	191.6079	T	1837.9113	919.4593	1820.8847	910.9460	1819.9007	910.4540	16
6	471.2562	236.1317			453.2456	227.1264	A	1736.8636	868.9354	1719.8370	860.4222	1718.8530	859.9302	15
7	600.2988	300.6530			582.2882	291.6477	E	1665.8265	833.4169	1648.7999	824.9036	1647.8159	824.4116	14
8	713.3828	357.1951			695.3723	348.1898	I	1536.7839	768.8956	1519.7573	760.3823	1518.7733	759.8903	13
9	844.4233	422.7153			826.4128	413.7100	M	1423.6998	712.3536	1406.6733	703.8403	1405.6893	703.3483	12
10	931.4553	466.2313			913.4448	457.2260	S	1292.6593	646.8333	1275.6328	638.3200	1274.6488	637.8280	11
11	1046.4823	523.7448			1028.4717	514.7395	D	1205.6273	603.3173	1188.6008	594.8040	1187.6167	594.3120	10
12	1159.5664	580.2868			1141.5558	571.2815	L	1090.6004	545.8038	1073.5738	537.2905	1072.5898	536.7985	9
13	1272.6504	636.8288			1254.6399	627.8236	L	977.5163	489.2618	960.4898	480.7485	959.5057	480.2565	8
14	1343.6875	672.3474			1325.6770	663.3421	A	864.4322	432.7198	847.4057	424.2065	846.4217	423.7145	7
15	1490.7559	745.8816			1472.7454	736.8763	F	793.3951	397.2012	776.3686	388.6879	775.3846	388.1959	6
16	1619.7985	810.4029			1601.7880	801.3976	E	646.3267	323.6670	629.3002	315.1537	628.3161	314.6617	5
17	1690.8357	845.9215			1672.8251	836.9162	A	517.2841	259.1457	500.2576	250.6324	499.2736	250.1404	4
18	1805.8626	903.4349			1787.8520	894.4297	D	446.2470	223.6271	429.2205	215.1139	428.2364	214.6219	3
19	1961.9637	981.4855	1944.9372	972.9722	1943.9531	972.4802	R	331.2201	166.1137	314.1935	157.6004			2
20							R	175.1190	88.0631	158.0924	79.5498			1

AT3G28710.1





NCBI **BLAST** search of LGGATAEIMSDLLAFEADRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.2	2135.0681	-0.0002	LGGATAEIMSDLLAFEADRR
3.9	2135.0656	0.0023	ARATHICLDCGFIYTLPK
1.9	2135.0694	-0.0015	IALGSARGLAYLHEDCHPR
1.9	2135.0714	-0.0035	IKGEMSQVRNVMIENIDK
1.5	2135.0681	-0.0002	VTPKLPTTEKNGMNSPSYR

Mascot: http://www.matrixscience.com/

AT3G29240.1

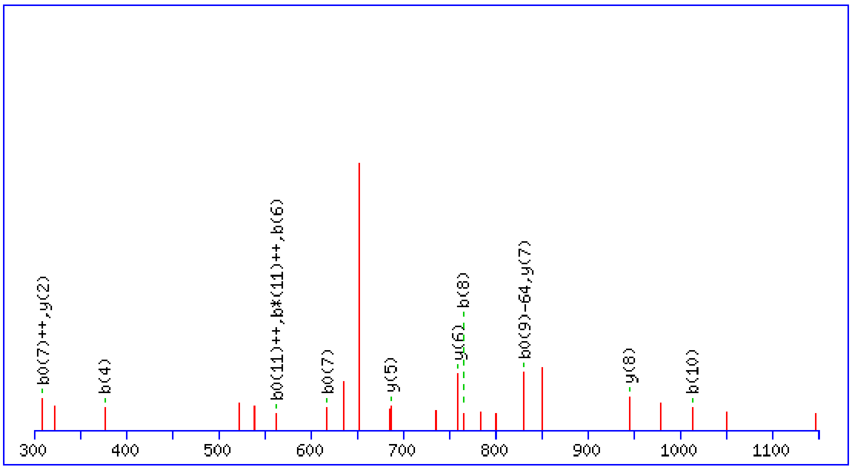
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESVGLAAEMVKR**
Found in **AT3G29240.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G33780.1); similar to hypothetical protein OsI_032014 [Oryza sativa (indica cultivar-group)] (GB:EAY78055.1); similar to Os10g0330400 [Oryza sativa (japonica cultivar-group)] (G

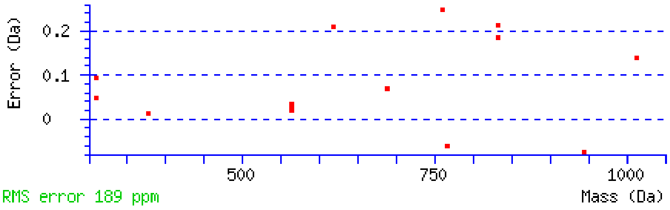
Match to Query 4758: 1320.629910 from(661.322231,2+) index(5366)
Title: Elution from: 47.705 to 47.705 scan no 6740 cid35.00 polarity:+
Data file 0-3_2.mgf

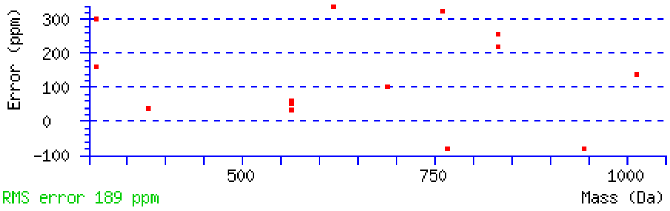
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.6284
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.033
Matches : 14/164 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							12
2	219.0760	110.0416			201.0654	101.0363	S	1191.5960	596.3017	1173.5725	587.2899	1173.5855	587.2964	11
3	319.1414	160.0743			301.1309	151.0691	V	1103.5670	552.2871	1085.5434	543.2753	1085.5564	543.2818	10
4	***377.1599***	189.0836			359.1494	180.0783	G	1003.5015	502.2544	985.4779	493.2426	985.4910	493.2491	9
5	491.2410	246.1241			473.2304	237.1189	L	***945.4830***	473.2452	927.4594	464.2334	927.4725	464.2399	8
6	***563.2752***	282.1412			545.2646	273.1359	A	***831.4019***	416.2046	813.3784	407.1928	813.3914	407.1993	7
7	635.3093	318.1583			617.2987	309.1530	A	***759.3678***	380.1875	741.3442	371.1757	741.3572	371.1822	6
8	***765.3489***	383.1781			747.3384	374.1728	E	***687.3336***	344.1705	669.3101	335.1587	669.3231	335.1652	5
9	913.3814	457.1943			895.3708	448.1890	M	557.2940	279.1506	539.2704	270.1389			4
10	***1013.4468***	507.2270			995.4363	498.2218	V	409.2616	205.1344	391.2380	196.1226			3
11	1143.5359	572.2716	1125.5123	563.2598	1125.5253	563.2663	K	***309.1961***	155.1017	291.1725	146.0899			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ESVGLAAEMVKR

AT3G29240.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	1320.6284	0.0015	ESVGLAAEMVKR
13.0	1320.6277	0.0022	RFSSVDPNPKR
7.4	1320.6284	0.0015	MEIEATTVQKR
7.4	1320.6284	0.0015	LEMKADSVLAGR
2.7	1320.6273	0.0027	FPESPVVSFAAR
2.2	1320.6277	0.0022	DGLSRGDKWLR
2.1	1320.6273	0.0027	ANLAFEPLFER
0.8	1320.6277	0.0022	QKNSFAAIPNGR
0.8	1320.6277	0.0022	WEDVTNVRRK
0.6	1320.6272	0.0027	EVWAEKFLER

AT3G29320.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FITDVASTINHDPEIGDLLK**
Found in **AT3G29320.1** in **TAIR_Arabidopsis**, Symbols: | glucan phosphorylase, putative | chr3:11254108-11258824 FORWARD

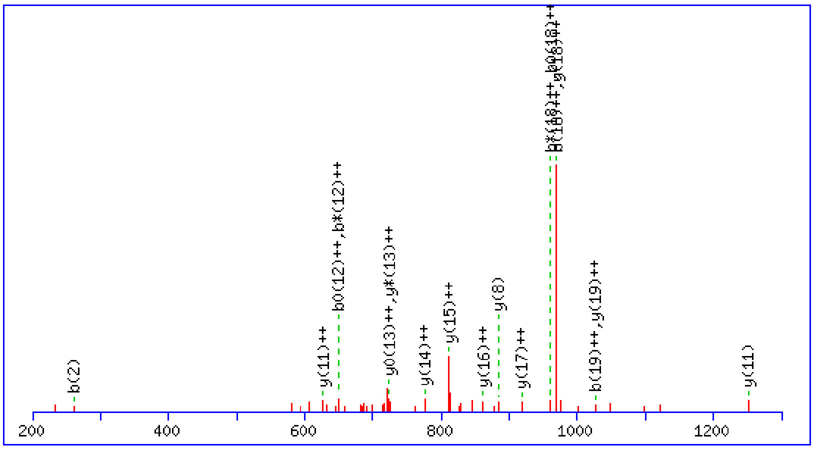
Match to Query 10008: 2197.125927 from(733.382585,3+) index(9658)
Title: Elution from: 89.206 to 89.206 scan no 13246 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

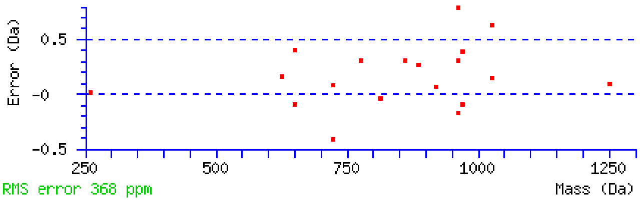
Show Y-axis ☐

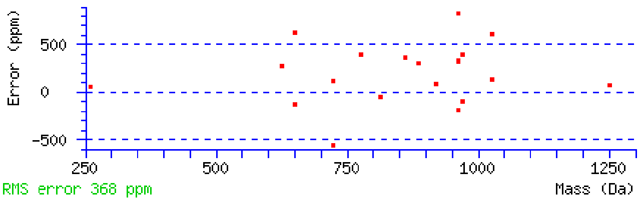


Monoisotopic mass of neutral peptide Mr(calc): 2197.1267
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0015
Matches : 20/200 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							20
2	261.1598	131.0835					I	2051.0655	1026.0364	2034.0390	1017.5231	2033.0550	1017.0311	19
3	362.2074	181.6074			344.1969	172.6021	T	1937.9815	969.4944	1920.9549	960.9811	1919.9709	960.4891	18
4	477.2344	239.1208			459.2238	230.1155	D	1836.9338	918.9705	1819.9072	910.4573	1818.9232	909.9652	17
5	576.3028	288.6550			558.2922	279.6498	V	1721.9068	861.4571	1704.8803	852.9438	1703.8963	852.4518	16
6	647.3399	324.1736			629.3293	315.1683	A	1622.8384	811.9229	1605.8119	803.4096	1604.8279	802.9176	15
7	734.3719	367.6896			716.3614	358.6843	S	1551.8013	776.4043	1534.7748	767.8910	1533.7907	767.3990	14
8	835.4196	418.2134			817.4090	409.2082	T	1464.7693	732.8883	1447.7427	724.3750	1446.7587	723.8830	13
9	948.5037	474.7555			930.4931	465.7502	I	1363.7216	682.3644	1346.6951	673.8512	1345.7110	673.3592	12
10	1062.5466	531.7769	1045.5201	523.2637	1044.5360	522.7717	N	**1250.6375**	625.8224	1233.6110	617.3091	1232.6270	616.8171	11
11	1199.6055	600.3064	1182.5790	591.7931	1181.5949	591.3011	H	1136.5946	568.8009	1119.5681	560.2877	1118.5840	559.7957	10
12	1314.6325	657.8199	1297.6059	649.3066	1296.6219	648.8146	D	999.5357	500.2715	982.5092	491.7582	981.5251	491.2662	9
13	1411.6852	706.3462	1394.6587	697.8330	1393.6747	697.3410	P	**884.5088**	442.7580	867.4822	434.2447	866.4982	433.7527	8
14	1540.7278	770.8675	1523.7013	762.3543	1522.7172	761.8623	E	787.4560	394.2316	770.4294	385.7184	769.4454	385.2264	7
15	1653.8119	827.4096	1636.7853	818.8963	1635.8013	818.4043	I	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
16	1710.8333	855.9203	1693.8068	847.4070	1692.8228	846.9150	G	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
17	1825.8603	913.4338	1808.8337	904.9205	1807.8497	904.4285	D	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
18	1938.9443	**969.9758**	1921.9178	961.4625	1920.9338	960.9705	L	373.2809	187.1441	356.2544	178.6308			3
19	2052.0284	**1026.5178**	2035.0019	1018.0046	2034.0178	1017.5126	L	260.1969	130.6021	243.1703	122.0888			2
20							K	147.1128	74.0600	130.0863	65.5468			1

AT3G29320.1





NCBI **BLAST** search of FITDVASTINHDPEIGDLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.5	2197.1267	-0.0007	FITDVASTINHDPEIGDLLK
8.4	2197.1267	-0.0007	LLDFSSNQLSGSIPSGFSTLK
8.3	2197.1202	0.0058	GWSASTTGTIDGKKGLVMFGGK
3.8	2197.1300	-0.0041	ILLCGELVEVEKHDSDTLK
2.9	2197.1266	-0.0007	DHELEKGFEESKPIVEALK
2.4	2197.1313	-0.0054	GSAASGGKPIWMKHAEDAKIK
2.2	2197.1201	0.0058	FLTSELINGGEEMIYRAVR
1.5	2197.1235	0.0025	MVRISVLNDALKSMYNAEK
1.3	2197.1207	0.0052	FNIPFEYNAIAQKWESIK

Mascot: http://www.matrixscience.com/

AT3G29360.1

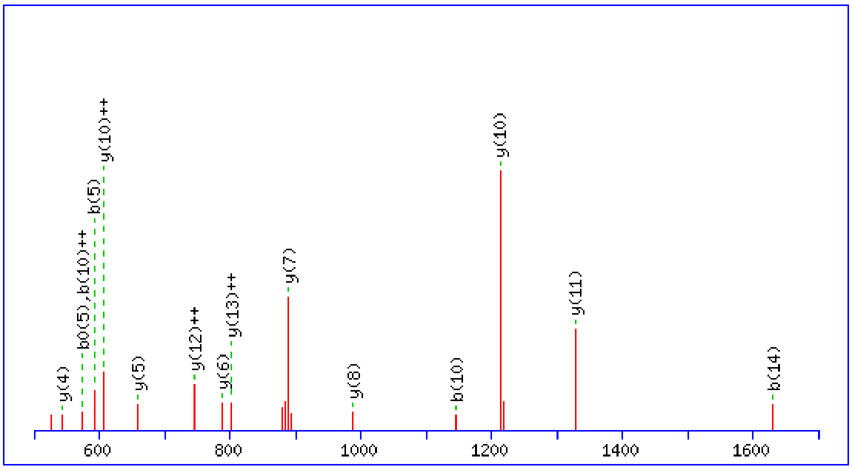
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSIYDPQVTEDQIQR**
Found in **AT3G29360.1** in **TAIR_Arabidopsis**, Symbols: | UDP-glucose 6-dehydrogenase, putative | chr3:11268612-11270054 REVERSE

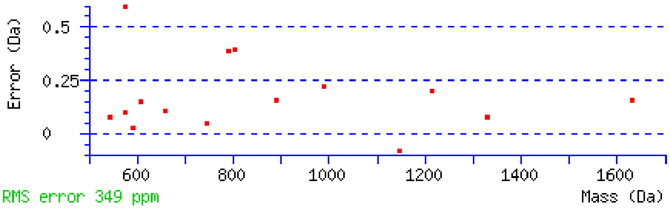
Match to Query 8753: 1803.901672 from(902.958112,2+) index(6376)
Title: Elution from: 56.617 to 56.617 scan no 8197 cid35.00 polarity:+
Data file D6h-3_1.mgf

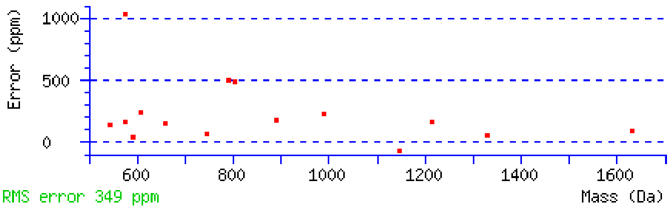
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1803.9003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 5.7e-005
Matches : 15/146 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							15
2	201.1234	101.0653			183.1128	92.0600	S	1691.8235	846.4154	1674.7970	837.9021	1673.8129	837.4101	14
3	314.2074	157.6074			296.1969	148.6021	I	1604.7915	802.8994	1587.7649	794.3861	1586.7809	793.8941	13
4	477.2708	239.1390			459.2602	230.1337	Y	1491.7074	746.3573	1474.6809	737.8441	1473.6969	737.3521	12
5	**592.2977**	296.6525			574.2871	287.6472	D	***1328.6441***	664.8257	1311.6175	656.3124	1310.6335	655.8204	11
6	689.3505	345.1789			671.3399	336.1736	P	***1213.6171***	607.3122	1196.5906	598.7989	1195.6066	598.3069	10
7	817.4090	409.2082	800.3825	400.6949	799.3985	400.2029	Q	1116.5644	558.7858	1099.5378	550.2726	1098.5538	549.7805	9
8	916.4775	458.7424	899.4509	450.2291	898.4669	449.7371	V	***988.5058***	494.7565	971.4793	486.2433	970.4952	485.7513	8
9	1017.5251	509.2662	1000.4986	500.7529	999.5146	500.2609	T	***889.4374***	445.2223	872.4108	436.7091	871.4268	436.2170	7
10	**1146.5677**	573.7875	1129.5412	565.2742	1128.5572	564.7822	E	***788.3897***	394.6985	771.3632	386.1852	770.3791	385.6932	6
11	1261.5947	631.3010	1244.5681	622.7877	1243.5841	622.2957	D	***659.3471***	330.1772	642.3206	321.6639	641.3365	321.1719	5
12	1389.6533	695.3303	1372.6267	686.8170	1371.6427	686.3250	Q	***544.3202***	272.6637	527.2936	264.1504			4
13	1502.7373	751.8723	1485.7108	743.3590	1484.7268	742.8670	I	416.2616	208.6344	399.2350	200.1212			3
14	**1630.7959**	815.9016	1613.7693	807.3883	1612.7853	806.8963	Q	303.1775	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LSIYDPQVTEDQIQR

AT3G29360.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.7	1803.9003	0.0014	LSIYDPQVTEDQIQR
6.0	1803.9043	-0.0026	LDFKSDPWPTISEAAK
2.1	1803.9036	-0.0020	SAASAASLPCTSGIISSPK

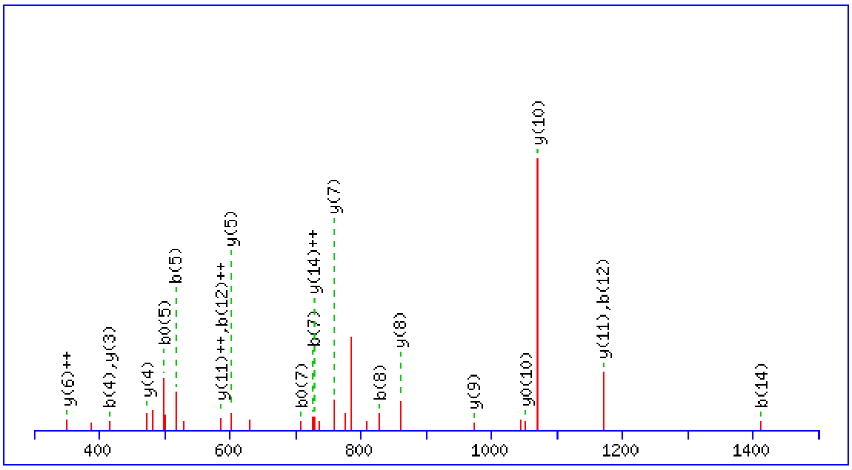
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGNITPLTGTQGQIR**
Found in **AT3G32980.1** in **TAIR_Arabidopsis**, Symbols: | peroxidase 32 (PER32) (P32) (PRXR3) | chr3:13530117-13533662 REVERSE

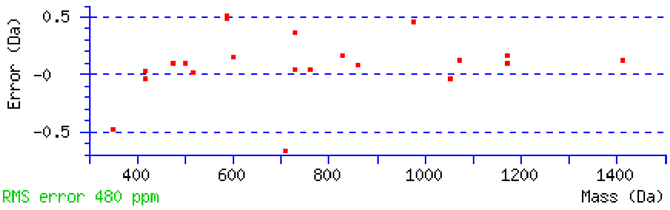
Match to Query 7022: 1585.825070 from(793.919811,2+) index(4493)
Title: Elution from: 43.520 to 43.520 scan no 5735 cid35.00 polarity:+
Data file D1d-2_1.mgf

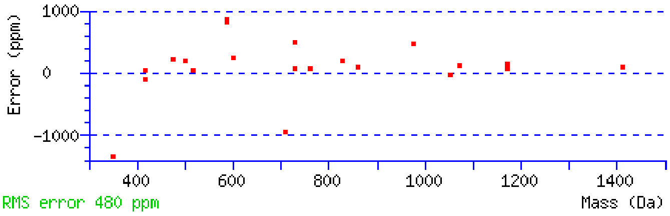
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1585.8246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 6.9e-006
Matches : 21/146 fragment ions using 28 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							15
2	189.0692	95.0383					G	1455.7914	728.3993	1438.7649	719.8861	1437.7809	719.3941	14
3	303.1122	152.0597	286.0856	143.5464			N	1398.7700	699.8886	1381.7434	691.3753	1380.7594	690.8833	13
4	**416.1962**	208.6017	399.1697	200.0885			I	1284.7270	642.8672	1267.7005	634.3539	1266.7165	633.8619	12
5	**517.2439**	259.1256	500.2173	250.6123	499.2333	250.1203	T	***1171.6430***	586.3251	1154.6164	577.8118	1153.6324	577.3198	11
6	614.2967	307.6520	597.2701	299.1387	596.2861	298.6467	P	***1070.5953***	535.8013	1053.5687	527.2880	1052.5847	526.7960	10
7	**727.3807**	364.1940	710.3542	355.6807	709.3702	355.1887	L	***973.5425***	487.2749	956.5160	478.7616	955.5320	478.2696	9
8	**828.4284**	414.7178	811.4019	406.2046	810.4178	405.7126	T	***860.4585***	430.7329	843.4319	422.2196	842.4479	421.7276	8
9	885.4499	443.2286	868.4233	434.7153	867.4393	434.2233	G	***759.4108***	380.2090	742.3842	371.6958	741.4002	371.2037	7
10	986.4975	493.7524	969.4710	485.2391	968.4870	484.7471	T	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	6
11	1114.5561	557.7817	1097.5296	549.2684	1096.5456	548.7764	Q	***601.3416***	301.1745	584.3151	292.6612			5
12	**1171.5776**	586.2924	1154.5510	577.7792	1153.5670	577.2871	G	***473.2831***	237.1452	456.2565	228.6319			4
13	1299.6362	650.3217	1282.6096	641.8084	1281.6256	641.3164	Q	***416.2616***	208.6344	399.2350	200.1212			3
14	**1412.7202**	706.8638	1395.6937	698.3505	1394.7097	697.8585	I	288.2030	144.6051	271.1765	136.0919			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MGNITPLTGTQGQIR

AT3G32980.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.9	1585.8246	0.0004	MGNITPLTGTQGQIR
0.5	1585.8246	0.0005	DGTLKQMVAKEPNR
0.1	1585.8253	-0.0002	FKKLYDDLNAGFR

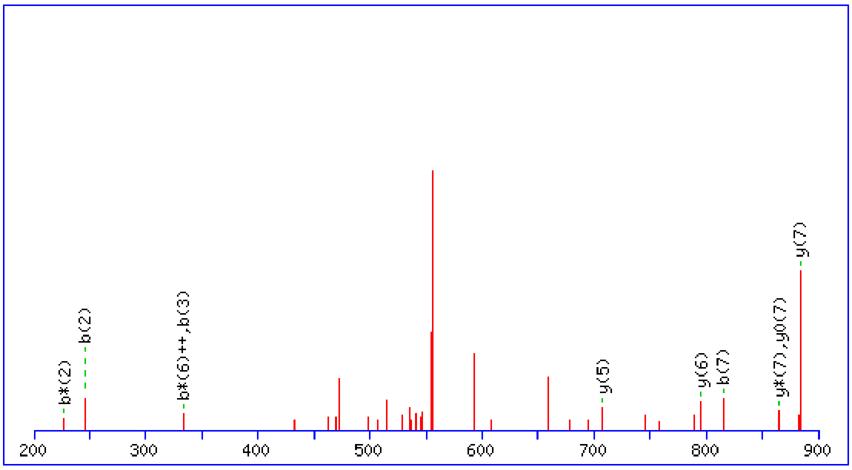
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLSSFDKYK**
Found in **AT3G42050.1** in **TAIR_Arabidopsis**, Symbols: | vacuolar ATP synthase subunit H family protein | chr3:14239832-14243214 REVERSE

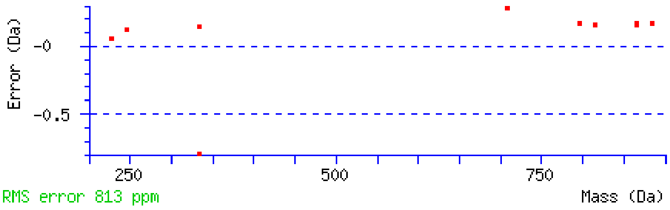
Match to Query 3796: 1126.569388 from(564.291970,2+) index(2520)
Title: Elution from: 27.439 to 27.439 scan no 3191 cid35.00 polarity:+
Data file C7-2_1.mgf

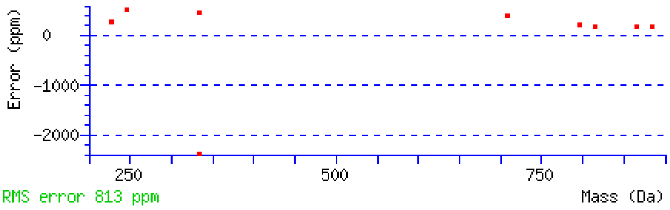
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1126.5667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.039
Matches : 10/86 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							9
2	***245.1774***	123.0923	227.1538	114.0805			L	997.4849	499.2461	979.4613	490.2343	979.4744	490.2408	8
3	***333.2065***	167.1069	315.1829	158.0951	315.1959	158.1016	S	***883.4038***	442.2056	865.3802	433.1938	865.3933	433.2003	7
4	421.2355	211.1214	403.2120	202.1096	403.2250	202.1161	S	***795.3748***	398.1910	777.3512	389.1792	777.3642	389.1857	6
5	569.3010	285.1541	551.2774	276.1423	551.2904	276.1488	F	***707.3457***	354.1765	689.3221	345.1647	689.3351	345.1712	5
6	685.3250	343.1661	667.3014	334.1543	667.3144	334.1608	D	559.2802	280.1438	541.2567	271.1320	541.2697	271.1385	4
7	***815.4140***	408.2106	797.3904	399.1988	797.4034	399.2054	K	443.2563	222.1318	425.2327	213.1200			3
8	979.4744	490.2408	961.4508	481.2290	961.4638	481.2355	Y	313.1672	157.0873	295.1437	148.0755			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KLSSFDKYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	1126.5667	0.0027	KLSSFDKYK

AT3G42050.1

2.8	1126.5694	0.0000	IKNPLDAWR
1.6	1126.5667	0.0027	AKYTAAYLSK
1.3	1126.5701	-0.0007	MASPIPVGVTK
0.1	1126.5671	0.0023	EGRAISIHTK

AT3G42060.1

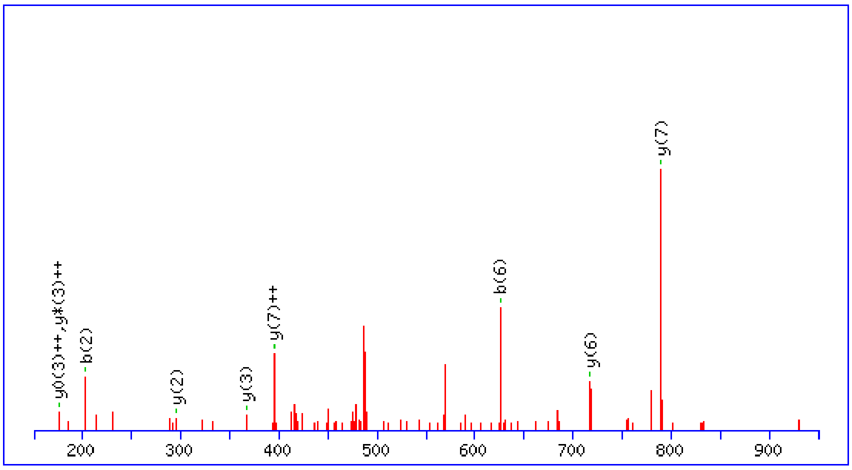
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLATSRADR**
Found in **AT3G42060.1** in **TAIR_Arabidopsis**, Symbols: | myosin heavy chain-related | chr3:14262586-14265255 REVERSE

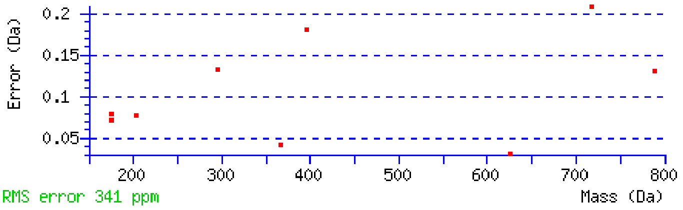
Match to Query 2359: 990.465388 from(496.239970,2+) index(4364)
Title: Elution from: 41.431 to 41.431 scan no 5527 cid35.00 polarity:+
Data file 0-3_1.mgf

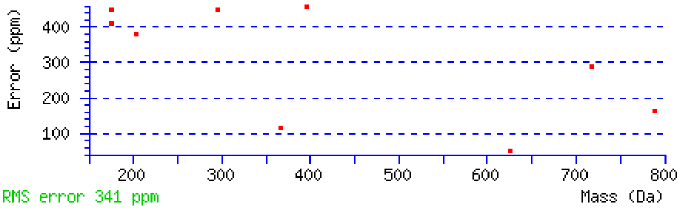
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 990.4653
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.035
Matches : 9/84 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							9
2	**203.1174**	102.0624			185.1069	93.0571	L	903.4435	452.2254	885.4199	443.2136	885.4329	443.2201	8
3	275.1516	138.0794			257.1410	129.0741	A	***789.3624***	395.1848	771.3388	386.1730	771.3518	386.1796	7
4	377.1963	189.1018			359.1857	180.0965	T	***717.3282***	359.1678	699.3047	350.1560	699.3177	350.1625	6
5	465.2254	233.1163			447.2148	224.1110	S	615.2835	308.1454	597.2599	299.1336	597.2730	299.1401	5
6	**625.3146**	313.1609	607.2910	304.1492	607.3040	304.1557	R	527.2545	264.1309	509.2309	255.1191	509.2439	255.1256	4
7	697.3488	349.1780	679.3252	340.1662	679.3382	340.1727	A	***367.1652***	184.0862	349.1416	175.0745	349.1547	175.0810	3
8	813.3727	407.1900	795.3492	398.1782	795.3622	398.1847	D	***295.1311***	148.0692	277.1075	139.0574	277.1205	139.0639	2
9							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SLATSRADR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	990.4653	0.0001	SLATSRADR

AT3G42060.1

10.0	990.4671	-0.0017	AEYPVFQK
5.9	990.4635	0.0019	LSVMIMNR
2.2	990.4635	0.0019	LSVMIMNR

AT3G43210.1

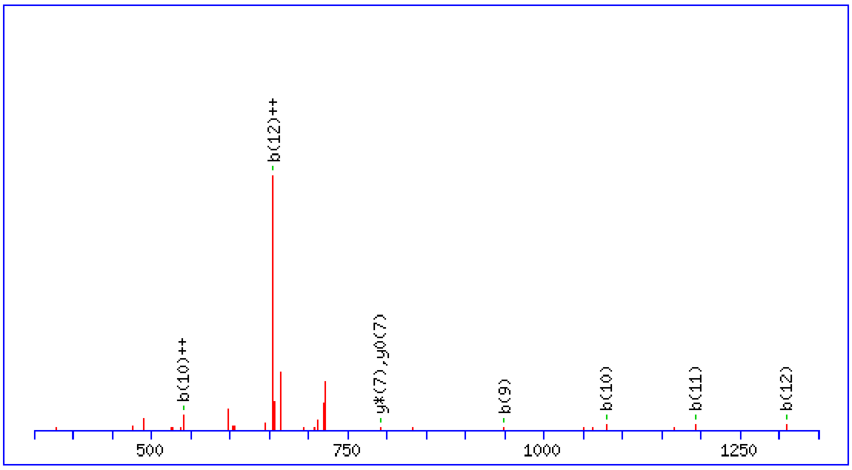
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGPPRTPLSKIDK**
Found in **AT3G43210.1** in **TAIR_Arabidopsis**, Symbols: TES | TES (TETRASPORE); microtubule motor | chr3:15202417-15207009 FORWARD

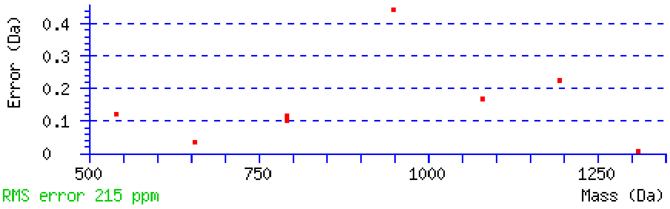
Match to Query 5810: 1456.743482 from(729.379017,2+) index(4674)
Title: Elution from: 45.657 to 45.657 scan no 6019 cid35.00 polarity:+
Data file D12h-2_1.mgf

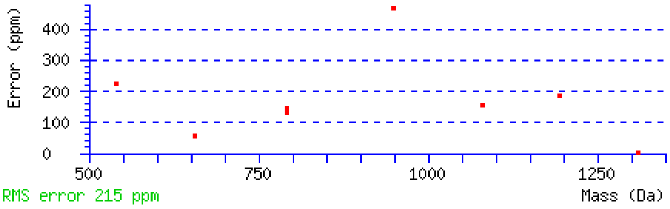
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1456.7433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.011
Matches : 8/124 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							13
2	191.0633	96.0353					G	1325.7130	663.3601	1307.6894	654.3483	1307.7024	654.3549	12
3	289.1131	145.0602					P	1267.6945	634.3509	1249.6709	625.3391	1249.6839	625.3456	11
4	387.1629	194.0851					P	1169.6447	585.3260	1151.6211	576.3142	1151.6341	576.3207	10
5	547.2521	274.1297	529.2286	265.1179			R	1071.5949	536.3011	1053.5713	527.2893	1053.5843	527.2958	9
6	649.2969	325.1521	631.2733	316.1403	631.2863	316.1468	T	911.5057	456.2565	893.4821	447.2447	893.4951	447.2512	8
7	747.3467	374.1770	729.3231	365.1652	729.3361	365.1717	P	809.4609	405.2341	791.4374	396.2223	791.4504	396.2288	7
8	861.4278	431.2175	843.4042	422.2057	843.4172	422.2122	L	711.4111	356.2092	693.3876	347.1974	693.4006	347.2039	6
9	***949.4568***	475.2320	931.4332	466.2203	931.4463	466.2268	S	597.3300	299.1687	579.3065	290.1569	579.3195	290.1634	5
10	***1079.5459***	**540.2766**	1061.5223	531.2648	1061.5353	531.2713	K	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	4
11	***1193.6270***	597.3171	1175.6034	588.3053	1175.6164	588.3118	I	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	***1309.6509***	**655.3291**	1291.6273	646.3173	1291.6404	646.3238	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MGPPRTPLSKIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G43210.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.5	1456.7433	0.0002	MGPPRTPLSKIDK
15.2	1456.7432	0.0002	ILHGEMQKLKDK
15.1	1456.7455	-0.0020	EKIIHWMKVEK
10.9	1456.7426	0.0009	KLHLFSSSHRPK
8.5	1456.7399	0.0036	FLLEKVESYRR
4.5	1456.7403	0.0032	KRHVALEINGGNK
4.1	1456.7399	0.0036	YEPGKQVHGLALK
3.9	1456.7399	0.0036	NNGPSPPPPPPLKK
3.9	1456.7455	-0.0020	KFLDILNMYRK
3.5	1456.7406	0.0029	VDPLGEKAMIELK

AT3G44100.1

Mascot Search Results

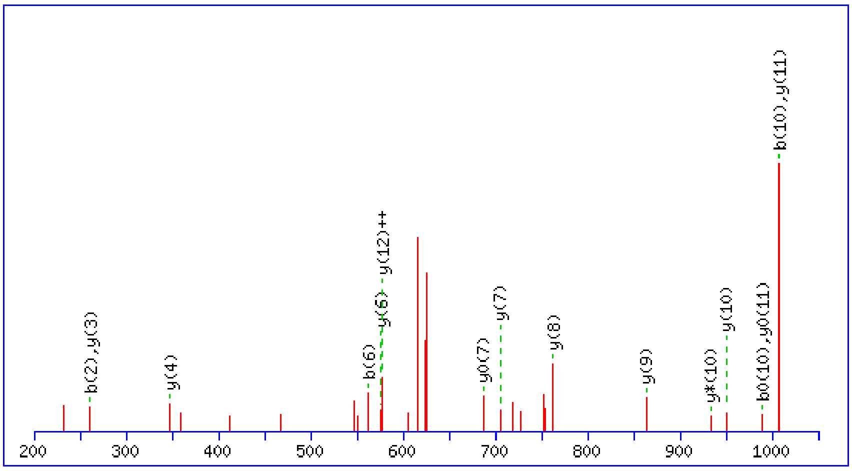
Peptide View

MS/MS Fragmentation of **IFGSTGEDISGGK**
Found in **AT3G44100.1** in **TAIR_Arabidopsis**, Symbols: | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein | chr3:15877149-15878260 REVERSE

Match to Query 4890: 1266.607944 from(634.311248,2+) index(3346)
Title: Elution from: 32.378 to 32.378 scan no 4134 cid35.00 polarity:+
Data file D6h-1_1.mgf

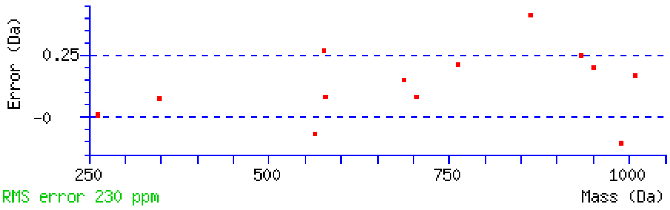
Click mouse within plot area to zoom in by factor of two about that point

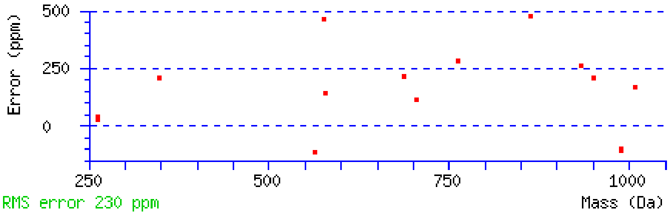
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1266.6092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 1.7e-005
Matches : 16/108 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							13
2	**261.1598**	131.0835			F	1154.5324	577.7698	1137.5059	569.2566	1136.5218	568.7646	12
3	318.1812	159.5942			G	***1007.4640***	504.2356	990.4374	495.7224	989.4534	495.2304	11
4	405.2132	203.1103	387.2027	194.1050	S	***950.4425***	475.7249	933.4160	467.2116	932.4320	466.7196	10
5	506.2609	253.6341	488.2504	244.6288	T	***863.4105***	432.2089	846.3840	423.6956	845.3999	423.2036	9
6	**563.2824**	282.1448	545.2718	273.1396	G	***762.3628***	381.6851	745.3363	373.1718	744.3523	372.6798	8
7	692.3250	346.6661	674.3144	337.6608	E	***705.3414***	353.1743	688.3148	344.6610	687.3308	344.1690	7
8	807.3519	404.1796	789.3414	395.1743	D	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	6
9	920.4360	460.7216	902.4254	451.7164	I	461.2718	231.1395	444.2453	222.6263	443.2613	222.1343	5
10	**1007.4680**	504.2376	989.4575	495.2324	S	***348.1878***	174.5975	331.1612	166.0842	330.1772	165.5922	4
11	1064.4895	532.7484	1046.4789	523.7431	G	***261.1557***	131.0815	244.1292	122.5682			3
12	1121.5109	561.2591	1103.5004	552.2538	G	204.1343	102.5708	187.1077	94.0575			2
13					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IFGSTGEDISGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G44100.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.9	1266.6092	-0.0013	IFGSTGEDISGGK

Mascot: http://www.matrixscience.com/

AT3G44200.1

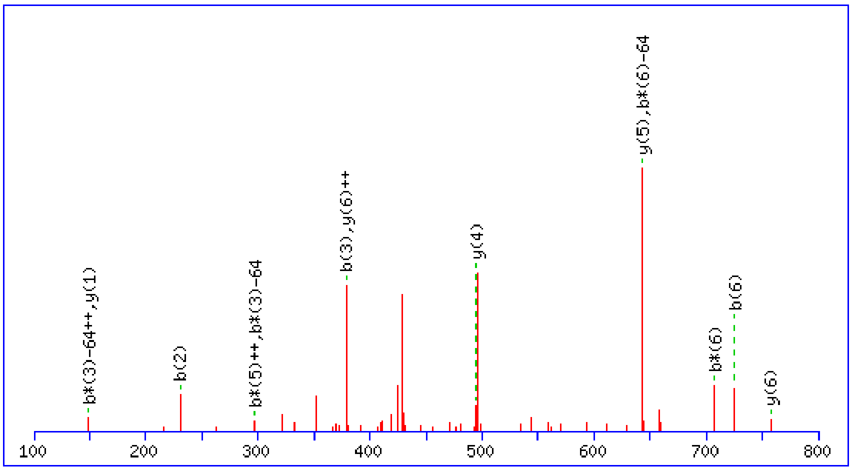
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIMMVLK**
Found in **AT3G44200.1** in **TAIR_Arabidopsis**, Symbols: ATNEK6, NEK6, IBO1 | ATNEK6/IBO1/NEK6 (NIMA (NEVER IN MITOSIS, GENE A)-RELATED 6); kinase | chr3:15917775-15922352 FORWARD

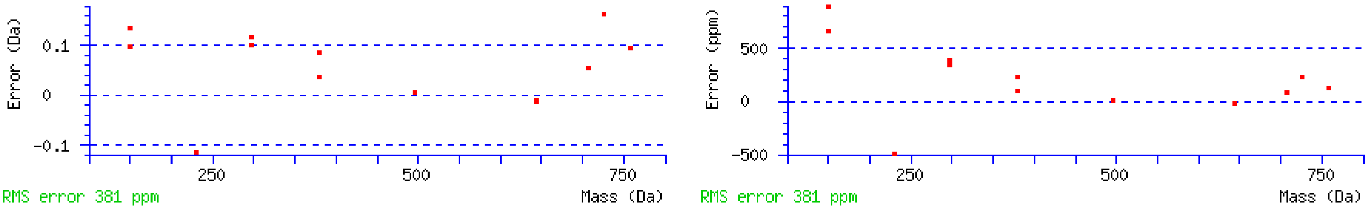
Match to Query 1431: 872.432698 from(437.223625,2+) index(4078)
Title: Elution from: 38.105 to 38.105 scan no 5137 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 872.4342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 34 **Expect:** 0.0017
Matches : 13/72 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	117.0443	59.0258	99.0207	50.0140	N					7
2	**231.1254**	116.0663	213.1018	107.0545	I	***757.4045***	379.2059	739.3809	370.1941	6
3	**379.1578**	190.0825	361.1342	181.0707	M	***643.3234***	322.1653	625.2998	313.1535	5
4	511.1953	256.1013	493.1717	247.0895	M	***495.2909***	248.1491	477.2674	239.1373	4
5	611.2608	306.1340	593.2372	297.1222	V	363.2534	182.1303	345.2298	173.1186	3
6	**725.3419**	363.1746	707.3183	354.1628	L	263.1880	132.0976	245.1644	123.0858	2
7					K	***149.1069***	75.0571	131.0833	66.0453	1



NCBI **BLAST** search of NIMMVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
34.2	872.4342	-0.0015	NIMMVLK	Oxidation M3 97.88%

AT3G44200.1

27.8	872.4308	0.0019	MQVVPFK	
17.5	872.4342	-0.0015	NIMMVLK	Oxidation M4 2.12%
15.4	872.4313	0.0014	NLCLGRK	
12.9	872.4333	-0.0006	ETSSLSLK	
9.8	872.4313	0.0014	AMGRAINK	
8.5	872.4333	-0.0006	ESTISSLK	
5.7	872.4306	0.0021	FHRRNK	
5.1	872.4313	0.0014	NMKPKSR	
4.5	872.4308	0.0019	MALIWSK	

AT3G44300.1

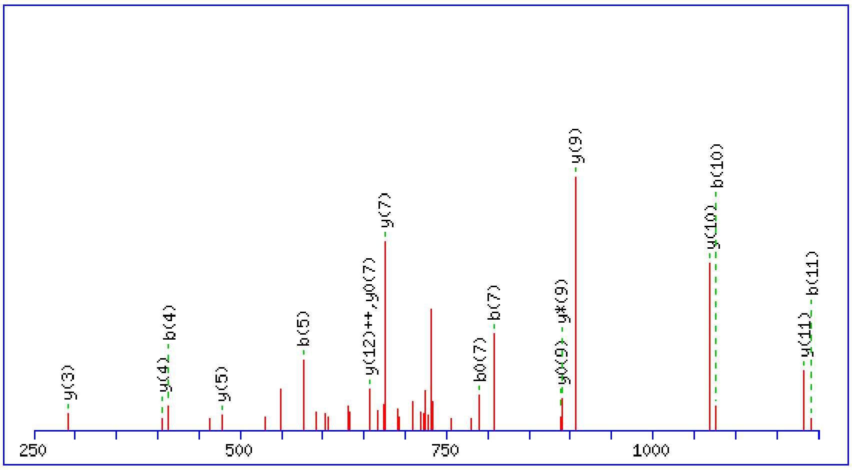
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GIELYCAPTADGSK**
Found in **AT3G44300.1** in **TAIR_Arabidopsis**, Symbols: NIT2 | NIT2 (NITRILASE 2) | chr3:15994338-15996159 FORWARD

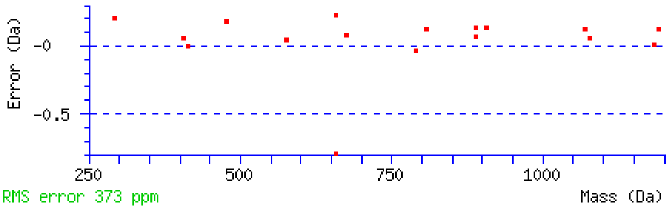
Match to Query 6014: 1480.685212 from(741.349882,2+) index(4228)
Title: Elution from: 38.260 to 38.260 scan no 5284 cid35.00 polarity:+
Data file C7-2_3.mgf

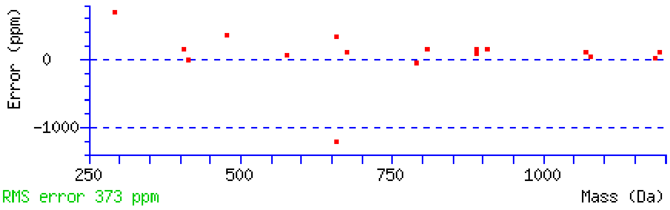
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1480.6868
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 1.4e-006
Matches : 17/124 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							14
2	171.1128	86.0600			I	1424.6726	712.8399	1407.6461	704.3267	1406.6620	703.8347	13
3	300.1554	150.5813	282.1448	141.5761	E	1311.5885	656.2979	1294.5620	647.7846	1293.5780	647.2926	12
4	**413.2395**	207.1234	395.2289	198.1181	L	***1182.5460***	591.7766	1165.5194	583.2633	1164.5354	582.7713	11
5	**576.3028**	288.6550	558.2922	279.6498	Y	***1069.4619***	535.2346	1052.4353	526.7213	1051.4513	526.2293	10
6	736.3334	368.6704	718.3229	359.6651	C	***906.3986***	453.7029	889.3720	445.1896	888.3880	444.6976	9
7	**807.3706**	404.1889	789.3600	395.1836	A	746.3679	373.6876	729.3414	365.1743	728.3573	364.6823	8
8	904.4233	452.7153	886.4128	443.7100	P	***675.3308***	338.1690	658.3042	329.6558	657.3202	329.1638	7
9	1005.4710	503.2391	987.4604	494.2339	T	578.2780	289.6427	561.2515	281.1294	560.2675	280.6374	6
10	**1076.5081**	538.7577	1058.4975	529.7524	A	***477.2304***	239.1188	460.2038	230.6055	459.2198	230.1135	5
11	**1191.5351**	596.2712	1173.5245	587.2659	D	***406.1932***	203.6003	389.1667	195.0870	388.1827	194.5950	4
12	1248.5565	624.7819	1230.5460	615.7766	G	***291.1663***	146.0868	274.1397	137.5735	273.1557	137.0815	3
13	1335.5885	668.2979	1317.5780	659.2926	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GIELYCAPTADGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G44300.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.0	1480.6868	-0.0016	GIELYCAPTADGSK
8.8	1480.6834	0.0018	EEFGDTNLVGWSK
0.4	1480.6875	-0.0022	RNMVQNMLSSNR

AT3G44310.1

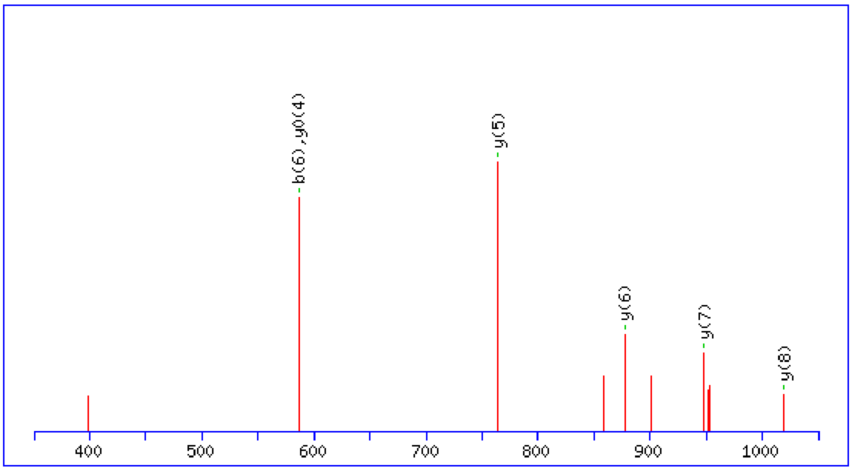
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGAAICWENR**
Found in **AT3G44310.1** in **TAIR_Arabidopsis**, Symbols: NIT1, ATNIT1, NITI | ATNIT1/NIT1/NITI (NITRILASE 1); nitrilase | chr3:15997888-15999828 FORWARD

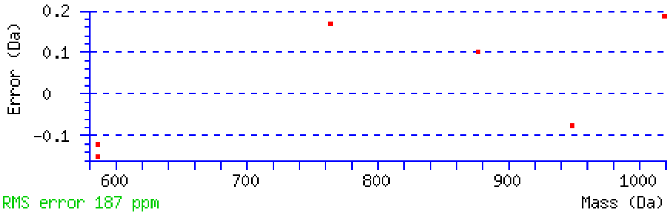
Match to Query 4103: 1188.568620 from(595.291586,2+) index(4617)
Title: Elution from: 43.671 to 43.671 scan no 5831 cid35.00 polarity:+
Data file D6h-2_1.mgf

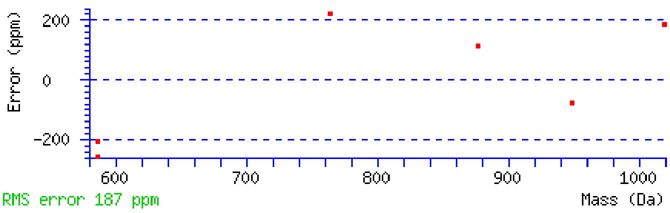
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1188.5710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.00088
Matches : 6/74 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							10
2	171.1128	86.0600					G	1076.4942	538.7507	1059.4676	530.2375	1058.4836	529.7455	9
3	242.1499	121.5786					A	***1019.4727***	510.2400	1002.4462	501.7267	1001.4622	501.2347	8
4	313.1870	157.0972					A	***948.4356***	474.7214	931.4091	466.2082	930.4250	465.7162	7
5	426.2711	213.6392					I	***877.3985***	439.2029	860.3719	430.6896	859.3879	430.1976	6
6	586.3017	293.6545					C	***764.3144***	382.6609	747.2879	374.1476	746.3039	373.6556	5
7	772.3811	386.6942					W	604.2838	302.6455	587.2572	294.1323	586.2732	293.6402	4
8	901.4237	451.2155			883.4131	442.2102	E	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
9	1015.4666	508.2369	998.4400	499.7237	997.4560	499.2316	N	289.1619	145.0846	272.1353	136.5713			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LGAAICWENR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G44310.1

Score	Mr(calc)	Delta	Sequence
33.6	1188.5710	-0.0023	IGAAICWENR
33.6	1188.5710	-0.0023	LGAAICWENR

Mascot: http://www.matrixscience.com/

AT3G44320.1

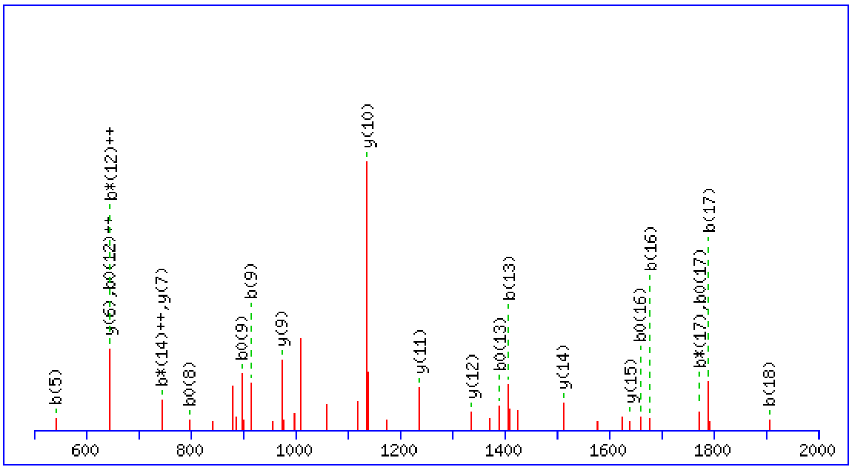
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTIVQSSTVYNDTPATLDK**
Found in **AT3G44320.1** in **TAIR_Arabidopsis**, Symbols: NIT3 | NIT3 (NITRILASE 3) | chr3:16004406-16006480 FORWARD

Match to Query 9497: 2051.045490 from(1026.530021,2+) index(5432)
Title: Elution from: 48.408 to 48.408 scan no 6855 cid35.00 polarity:+
Data file C7-1_2.mgf

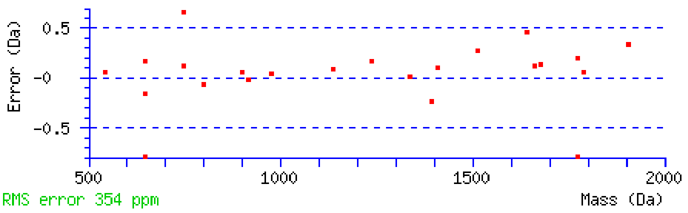
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

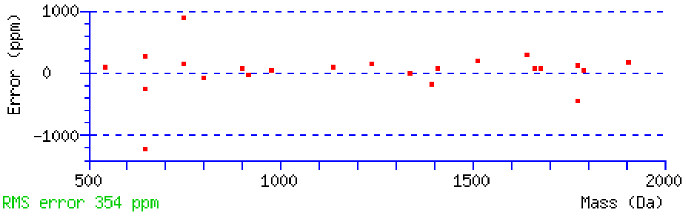


Monoisotopic mass of neutral peptide Mr(calc): 2051.0423
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.4e-007
Matches : 23/204 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							19
2	201.1234	101.0653			183.1128	92.0600	T	1952.9811	976.9942	1935.9546	968.4809	1934.9706	967.9889	18
3	314.2074	157.6074			296.1969	148.6021	I	1851.9335	926.4704	1834.9069	917.9571	1833.9229	917.4651	17
4	413.2758	207.1416			395.2653	198.1363	V	1738.8494	869.9283	1721.8228	861.4151	1720.8388	860.9230	16
5	***541.3344***	271.1709	524.3079	262.6576	523.3239	262.1656	Q	***1639.7810***	820.3941	1622.7544	811.8809	1621.7704	811.3888	15
6	628.3665	314.6869	611.3399	306.1736	610.3559	305.6816	S	***1511.7224***	756.3648	1494.6958	747.8516	1493.7118	747.3596	14
7	715.3985	358.2029	698.3719	349.6896	697.3879	349.1976	S	1424.6904	712.8488	1407.6638	704.3355	1406.6798	703.8435	13
8	816.4462	408.7267	799.4196	400.2134	798.4356	399.7214	T	***1337.6583***	669.3328	1320.6318	660.8195	1319.6478	660.3275	12
9	***915.5146***	458.2609	898.4880	449.7477	897.5040	449.2556	V	***1236.6107***	618.8090	1219.5841	610.2957	1218.6001	609.8037	11
10	1078.5779	539.7926	1061.5514	531.2793	1060.5673	530.7873	Y	***1137.5422***	569.2748	1120.5157	560.7615	1119.5317	560.2695	10
11	1192.6208	596.8141	1175.5943	588.3008	1174.6103	587.8088	N	***974.4789***	487.7431	957.4524	479.2298	956.4684	478.7378	9
12	1307.6478	654.3275	1290.6212	645.8143	1289.6372	645.3222	D	860.4360	430.7216	843.4094	422.2084	842.4254	421.7164	8
13	***1408.6955***	704.8514	1391.6689	696.3381	1390.6849	695.8461	T	***745.4090***	373.2082	728.3825	364.6949	727.3985	364.2029	7
14	1505.7482	753.3777	1488.7217	744.8645	1487.7377	744.3725	P	***644.3614***	322.6843	627.3348	314.1710	626.3508	313.6790	6
15	1576.7853	788.8963	1559.7588	780.3830	1558.7748	779.8910	A	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
16	***1677.8330***	839.4201	1660.8065	830.9069	1659.8224	830.4149	T	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
17	***1790.9171***	895.9622	1773.8905	887.4489	1772.9065	886.9569	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
18	***1905.9440***	953.4756	1888.9175	944.9624	1887.9335	944.4704	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT3G44320.1





NCBI **BLAST** search of VTIVQSSTVYNDTPATLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.5	2051.0423	0.0032	VTIVQSSTVYNDTPATIDK
74.5	2051.0423	0.0032	VTIVQSSTVYNDTPATLDK
2.8	2051.0470	-0.0015	SKIGDTGLLDHSLKHMDGK

Mascot: http://www.matrixscience.com/

AT3G44540.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QKLKELQK**
Found in **AT3G44540.1** in **TAIR_Arabidopsis**, Symbols: | oxidoreductase, acting on the CH-CH group of donors | chr3:16135066-16138756 FORWARD

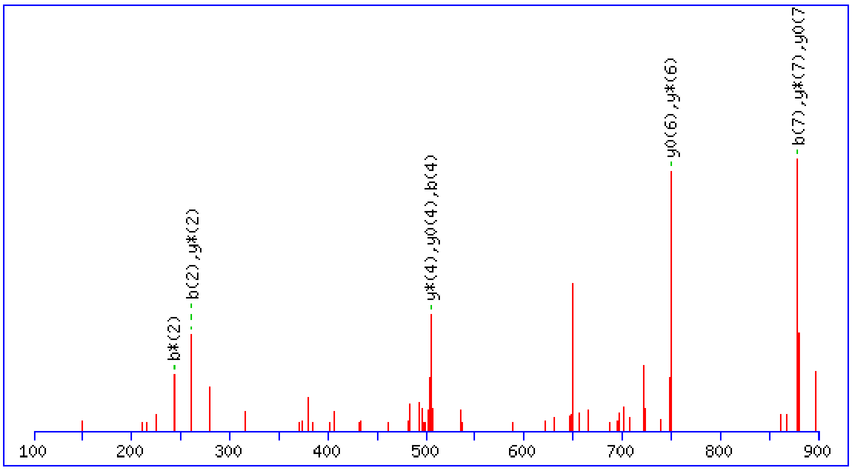
Match to Query 2884: 1026.585778 from(514.300165,2+) index(1589)
Title: Elution from: 21.562 to 21.562 scan no 2153 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 900 Da Full range

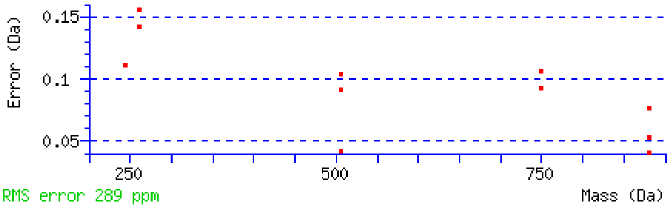
Label all possible matches ○ Label matches used for scoring ●

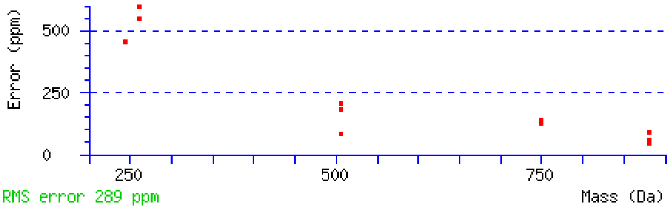
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1026.5848
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.019
Matches : 12/70 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							8
2	***261.1490***	131.0781	243.1254	122.0663			K	897.5394	449.2733	879.5158	440.2616	879.5288	440.2681	7
3	375.2301	188.1187	357.2065	179.1069			L	767.4504	384.2288	749.4268	375.2170	749.4398	375.2235	6
4	***505.3191***	253.1632	487.2955	244.1514			K	653.3693	327.1883	635.3457	318.1765	635.3587	318.1830	5
5	635.3587	318.1830	617.3351	309.1712	617.3482	309.1777	E	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	4
6	***749.4398***	375.2235	731.4162	366.2118	731.4293	366.2183	L	393.2406	197.1239	375.2170	188.1122			3
7	***879.4925***	440.2499	861.4689	431.2381	861.4819	431.2446	Q	279.1595	140.0834	261.1359	131.0716			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QKLKELQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.1	1026.5848	0.0010	QKLKELQK

AT3G44540.1

20.1	1026.5848	0.0010	RAVVTLVEK
17.5	1026.5848	0.0010	QTNGLLLKK
14.2	1026.5848	0.0010	KPTTSKPKK
13.7	1026.5848	0.0010	KEELVRLK
13.7	1026.5848	0.0010	QKLKQELK
13.7	1026.5848	0.0010	VASKKKPEK
12.3	1026.5848	0.0010	QLLISSVVR
11.2	1026.5848	0.0010	EVIRLKEK
11.2	1026.5870	-0.0012	LAKWKLEK

AT3G44710.1

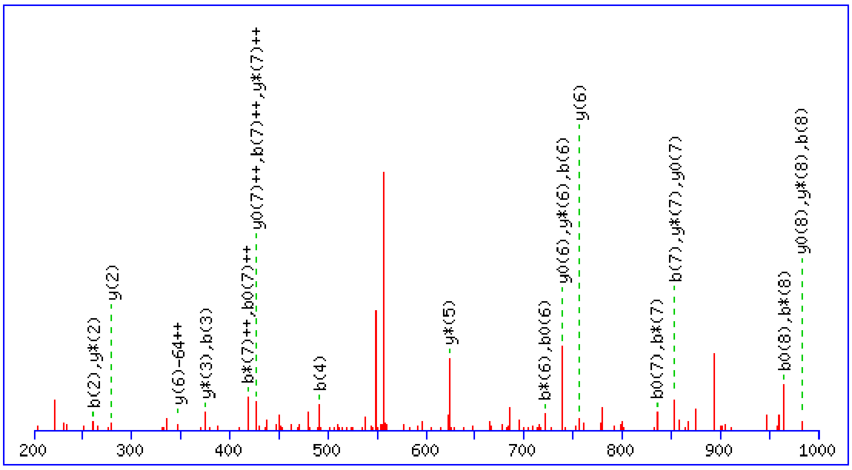
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QELDVMLKK**
Found in **AT3G44710.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G22540.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15956.1); contains InterPro domain Protein of unknown function DUF247, plant (InterPro:IPR004158) | chr3:16

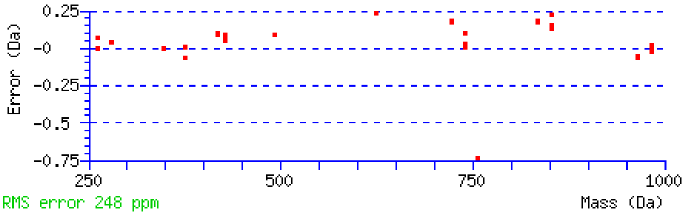
Match to Query 3913: 1130.567796 from(566.291174,2+) index(6502)
Title: Elution from: 56.618 to 56.618 scan no 8174 cid35.00 polarity:+
Data file D12h-1_1.mgf

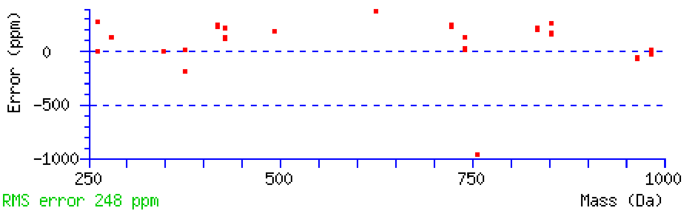
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1130.5650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.026
Matches : 29/128 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							9
2	***261.0996***	131.0534	243.0760	122.0416	243.0890	122.0481	E	1001.5196	501.2634	983.4960	492.2516	983.5090	492.2582	8
3	***375.1806***	188.0940	357.1571	179.0822	357.1701	179.0887	L	871.4800	436.2436	853.4564	427.2318	853.4694	427.2383	7
4	***491.2046***	246.1060	473.1810	237.0942	473.1941	237.1007	D	757.3989	379.2031	739.3753	370.1913	739.3883	370.1978	6
5	591.2701	296.1387	573.2465	287.1269	573.2595	287.1334	V	641.3749	321.1911	623.3513	312.1793			5
6	***739.3025***	370.1549	721.2789	361.1431	721.2919	361.1496	M	541.3094	271.1584	523.2859	262.1466			4
7	***853.3836***	427.1954	835.3600	418.1837	835.3730	418.1902	L	393.2770	197.1421	375.2534	188.1303			3
8	***983.4726***	492.2400	965.4491	483.2282	965.4621	483.2347	K	279.1959	140.1016	261.1723	131.0898			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QELDVMLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G44710.1

Score	Mr(calc)	Delta	Sequence
24.2	1130.5650	0.0028	QELDVMLKK
13.7	1130.5650	0.0028	MVALTTNLEK
13.2	1130.5650	0.0028	LESLQSLMAK
8.5	1130.5672	0.0006	KLFEVMPEK
7.7	1130.5676	0.0002	RLCLGEAVAK
7.4	1130.5676	0.0002	MGAQKKPAAAK
7.3	1130.5650	0.0028	GSLDIDMKLK
6.1	1130.5676	0.0002	AVGEMGKGLVR
3.2	1130.5699	-0.0021	LHLGYMLVR
2.9	1130.5665	0.0013	GFAAHFVAAVK

AT3G44850.1

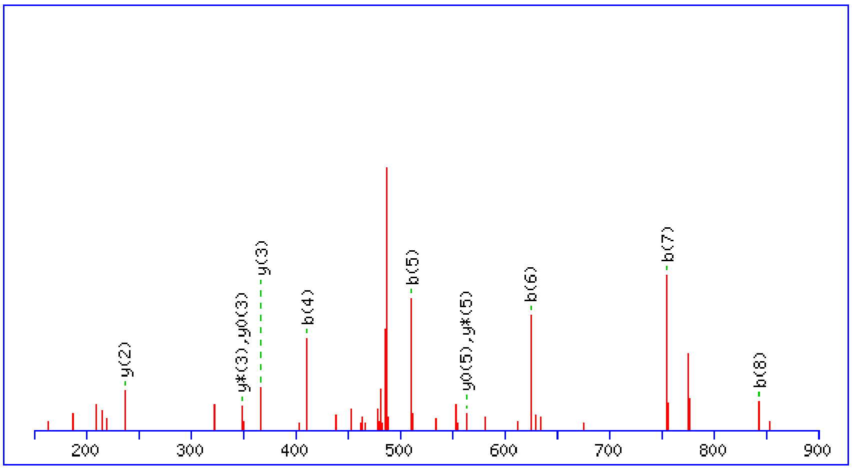
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of NGAYVIQSK
Found in **AT3G44850.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase-related | chr3:16385602-16387916 REVERSE

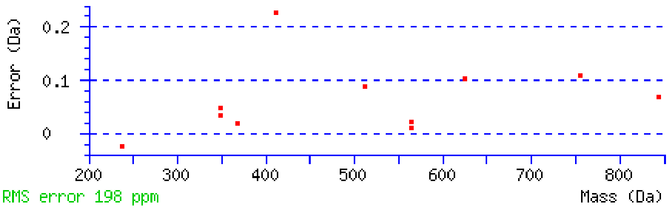
Match to Query 2343: 990.474938 from(496.244745,2+) index(1588)
Title: Elution from: 20.755 to 20.755 scan no 2117 cid35.00 polarity:+
Data file D12h-3_2.mgf

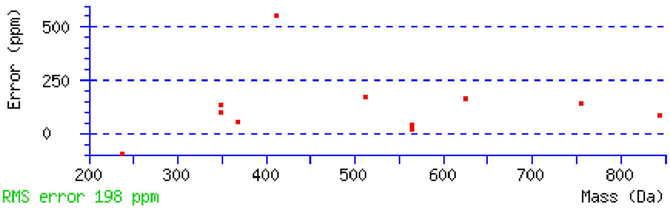
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 990.4779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0065
Matches : 11/80 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	175.0628	88.0350	157.0392	79.0232			G	875.4481	438.2277	857.4246	429.2159	857.4376	429.2224	8
3	247.0969	124.0521	229.0733	115.0403			A	817.4296	409.2185	799.4061	400.2067	799.4191	400.2132	7
4	***411.1573***	206.0823	393.1337	197.0705			Y	745.3955	373.2014	727.3719	364.1896	727.3849	364.1961	6
5	***511.2227***	256.1150	493.1992	247.1032			V	581.3351	291.1712	563.3115	282.1594	563.3246	282.1659	5
6	***625.3038***	313.1556	607.2802	304.1438			I	481.2697	241.1385	463.2461	232.1267	463.2591	232.1332	4
7	***755.3565***	378.1819	737.3329	369.1701			Q	**367.1886**	184.0979	349.1650	175.0861	349.1780	175.0926	3
8	***843.3855***	422.1964	825.3620	413.1846	825.3750	413.1911	S	**237.1359**	119.0716	219.1124	110.0598	219.1254	110.0663	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NGAYVIQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	990.4779	-0.0029	NGAYVIQSK

AT3G44850.1

23.4	990.4779	-0.0029	FSELGASLR
22.6	990.4779	-0.0029	GYAAPSAKSK
9.5	990.4779	-0.0029	YEAALERK
9.3	990.4779	-0.0029	KVNFEQSK
9.2	990.4752	-0.0003	ELYITESK
5.9	990.4779	-0.0029	NTALFQASK
3.4	990.4778	-0.0029	YAQELTVR
2.3	990.4778	-0.0029	KYDDLLGR
2.1	990.4778	-0.0029	YVDELGRK

AT3G44890.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQLMTPLLLK**
Found in **AT3G44890.1** in **TAIR_Arabidopsis**, Symbols: RP19, RPL9 | RPL9 (ribosomal protein L9); structural constituent of ribosome | chr3:16397490-16398948 FORWARD

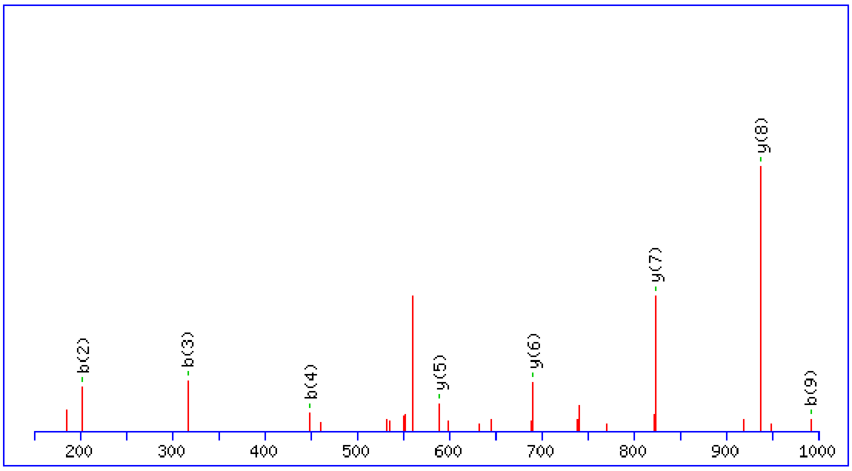
Match to Query 4011: 1138.640988 from(570.327770,2+) index(7733)
Title: Elution from: 67.183 to 67.183 scan no 10014 cid35.00 polarity:+
Data file D1d-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

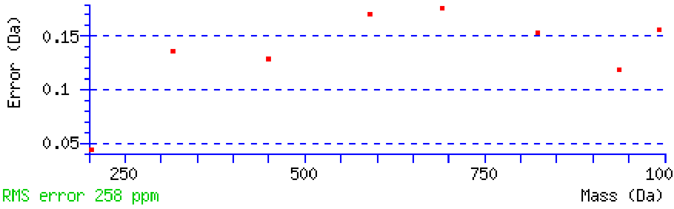
Label all possible matches ○ Label matches used for scoring ●

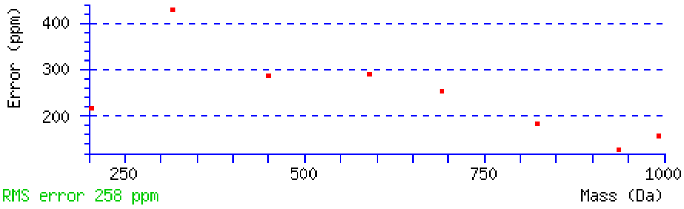
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1138.6428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 4e-005
Matches : 8/88 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							10
2	***203.0941***	102.0507	185.0705	93.0389			Q	1067.6159	534.3116	1049.5924	525.2998	1049.6054	525.3063	9
3	***317.1752***	159.0912	299.1516	150.0794			L	***937.5633***	469.2853	919.5397	460.2735	919.5527	460.2800	8
4	***449.2127***	225.1100	431.1891	216.0982			M	***823.4822***	412.2447	805.4586	403.2329	805.4716	403.2395	7
5	551.2574	276.1323	533.2338	267.1205	533.2468	267.1271	T	***691.4447***	346.2260	673.4211	337.2142	673.4341	337.2207	6
6	649.3072	325.1572	631.2836	316.1454	631.2966	316.1520	P	***589.4000***	295.2036	571.3764	286.1918			5
7	763.3883	382.1978	745.3647	373.1860	745.3777	373.1925	L	491.3502	246.1787	473.3266	237.1669			4
8	877.4694	439.2383	859.4458	430.2265	859.4588	430.2331	L	377.2691	189.1382	359.2455	180.1264			3
9	***991.5505***	496.2789	973.5269	487.2671	973.5399	487.2736	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AQLMTPLLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G44890.1

Score	Mr(calc)	Delta	Sequence
45.9	1138.6428	-0.0018	AQLMTPLLLK
9.5	1138.6394	0.0015	FTPLPKTPVK
2.5	1138.6399	0.0011	SLVIRHGTIK
1.1	1138.6394	0.0015	TIVALSWIPK

AT3G45030.1

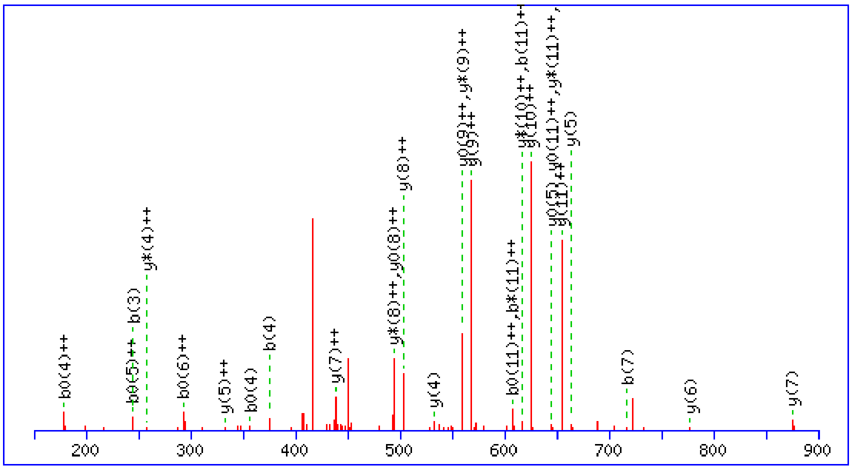
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLEEPLEQIHK**
Found in **AT3G45030.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S20 (RPS20A) | chr3:16482591-16483297 REVERSE

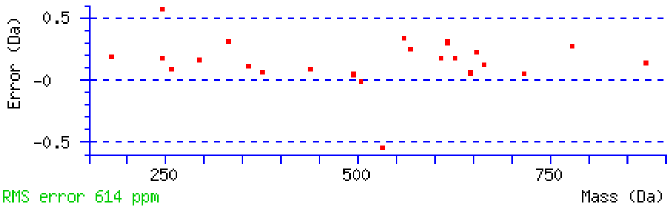
Match to Query 5701: 1378.667814 from(460.563214,3+) index(4320)
Title: Elution from: 39.575 to 39.575 scan no 5369 cid35.00 polarity:+
Data file D6h-1_1.mgf

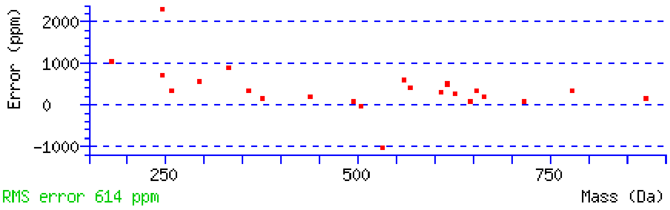
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1378.6669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.019
Matches : 31/102 fragment ions using 52 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244					A							12
2	131.0599	66.0336					G	1307.6400	654.3236	1289.6164	645.3119	1289.6295	645.3184	11
3	**245.1410**	123.0741					L	1249.6215	625.3144	1231.5979	616.3026	1231.6110	616.3091	10
4	**375.1807**	188.0940			357.1701	179.0887	E	1135.5404	568.2738	1117.5168	559.2621	1117.5299	559.2686	9
5	505.2203	253.1138			487.2097	244.1085	E	1005.5008	503.2540	987.4772	494.2422	987.4902	494.2488	8
6	603.2701	302.1387			585.2595	293.1334	P	***875.4612***	438.2342	857.4376	429.2224	857.4506	429.2289	7
7	**717.3512**	359.1792			699.3406	350.1739	L	***777.4114***	389.2093	759.3878	380.1975	759.4008	380.2040	6
8	847.3908	424.1990			829.3802	415.1938	E	***663.3303***	332.1688	645.3067	323.1570	645.3197	323.1635	5
9	977.4435	489.2254	959.4199	480.2136	959.4329	480.2201	Q	***533.2906***	267.1490	515.2671	258.1372			4
10	1091.5246	546.2659	1073.5010	537.2541	1073.5140	537.2606	I	403.2380	202.1226	385.2144	193.1108			3
11	1231.5746	616.2909	1213.5510	607.2791	1213.5640	607.2856	H	289.1569	145.0821	271.1333	136.0703			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AGLEEPLEQIHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G45030.1

Score	Mr(calc)	Delta	Sequence
27.3	1378.6669	0.0009	AGLEEPLEQIHK
11.8	1378.6669	0.0009	ELVQQIYSDIR
11.4	1378.6647	0.0032	ELISQSQNKSTK
10.6	1378.6702	-0.0024	QKLQTMETLQK
10.5	1378.6673	0.0005	GTDRKSVGAEALR
9.8	1378.6682	-0.0004	MHMKAISTRLR
9.8	1378.6682	-0.0004	MHMKAISTRLR
7.7	1378.6700	-0.0022	AIGRGQNSRELR
6.9	1378.6673	0.0005	SGPLAATTSAATRR
6.9	1378.6673	0.0005	QQLDDKTRSLR

AT3G45140.1

(MATRIX SCIENCE) Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYDYDVYNDVGDPDNDPELARPVIGGLTHPYPR**
Found in **AT3G45140.1** in **TAIR_Arabidopsis**, Symbols: ATLOX2, LOX2 | LOX2 (LIPOXYGENASE 2) | chr3:16536422-16540218 FORWARD

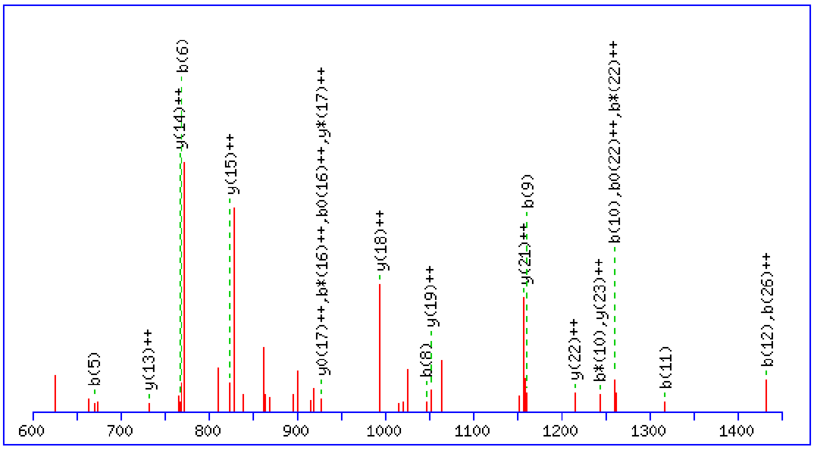
Match to Query 10915: 3744.767748 from(937.199213,4+) index(8846)
Title: Elution from: 78.558 to 78.558 scan no 11799 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 600 to 1450 Da Full range

Label all possible matches ○ Label matches used for scoring ●

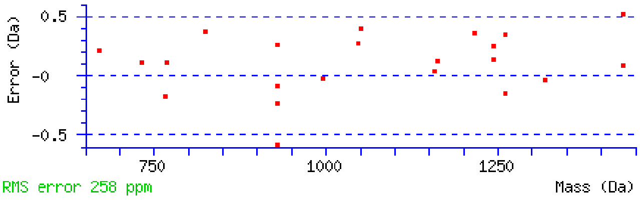
Show Y-axis ☐

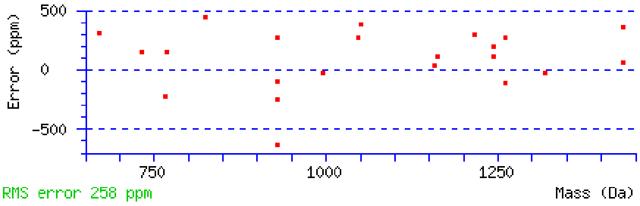


Monoisotopic mass of neutral peptide Mr(calc): 3744.7696
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0016
Matches : 23/356 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							33
2	277.1547	139.0810					Y	3632.6928	1816.8501	3615.6663	1808.3368	3614.6823	1807.8448	32
3	392.1816	196.5944			374.1710	187.5892	D	3469.6295	1735.3184	3452.6030	1726.8051	3451.6189	1726.3131	31
4	555.2449	278.1261			537.2344	269.1208	Y	3354.6026	1677.8049	3337.5760	1669.2916	3336.5920	1668.7996	30
5	***670.2719***	335.6396			652.2613	326.6343	D	3191.5392	1596.2733	3174.5127	1587.7600	3173.5287	1587.2680	29
6	***769.3403***	385.1738			751.3297	376.1685	V	3076.5123	1538.7598	3059.4857	1530.2465	3058.5017	1529.7545	28
7	932.4036	466.7055			914.3931	457.7002	Y	2977.4439	1489.2256	2960.4173	1480.7123	2959.4333	1480.2203	27
8	***1046.4466***	523.7269	1029.4200	515.2136	1028.4360	514.7216	N	2814.3805	1407.6939	2797.3540	1399.1806	2796.3700	1398.6886	26
9	***1161.4735***	581.2404	1144.4469	572.7271	1143.4629	572.2351	D	2700.3376	1350.6724	2683.3111	1342.1592	2682.3271	1341.6672	25
10	***1260.5419***	630.7746	1243.5154	622.2613	1242.5313	621.7693	V	2585.3107	1293.1590	2568.2841	1284.6457	2567.3001	1284.1537	24
11	***1317.5634***	659.2853	1300.5368	650.7721	1299.5528	650.2800	G	2486.2423	1243.6248	2469.2157	1235.1115	2468.2317	1234.6195	23
12	***1432.5903***	716.7988	1415.5638	708.2855	1414.5798	707.7935	D	2429.2208	1215.1140	2412.1943	1206.6008	2411.2102	1206.1088	22
13	1529.6431	765.3252	1512.6165	756.8119	1511.6325	756.3199	P	2314.1939	1157.6006	2297.1673	1149.0873	2296.1833	1148.5953	21
14	1644.6700	822.8387	1627.6435	814.3254	1626.6595	813.8334	D	2217.1411	1109.0742	2200.1145	1100.5609	2199.1305	1100.0689	20
15	1758.7130	879.8601	1741.6864	871.3468	1740.7024	870.8548	N	2102.1141	1051.5607	2085.0876	1043.0474	2084.1036	1042.5554	19
16	1873.7399	937.3736	1856.7133	928.8603	1855.7293	928.3683	D	1988.0712	994.5392	1971.0447	986.0260	1970.0607	985.5340	18
17	1970.7927	985.9000	1953.7661	977.3867	1952.7821	976.8947	P	1873.0443	937.0258	1856.0177	928.5125	1855.0337	928.0205	17
18	2099.8353	1050.4213	2082.8087	1041.9080	2081.8247	1041.4160	E	1775.9915	888.4994	1758.9650	879.9861	1757.9810	879.4941	16
19	2212.9193	1106.9633	2195.8928	1098.4500	2194.9088	1097.9580	L	1646.9489	823.9781	1629.9224	815.4648	1628.9384	814.9728	15
20	2283.9564	1142.4819	2266.9299	1133.9686	2265.9459	1133.4766	A	1533.8649	767.4361	1516.8383	758.9228	1515.8543	758.4308	14
21	2440.0575	1220.5324	2423.0310	1212.0191	2422.0470	1211.5271	R	1462.8277	731.9175	1445.8012	723.4042	1444.8172	722.9122	13
22	2537.1103	1269.0588	2520.0838	1260.5455	2519.0997	1260.0535	P	1306.7266	653.8670	1289.7001	645.3537	1288.7161	644.8617	12
23	2636.1787	1318.5930	2619.1522	1310.0797	2618.1682	1309.5877	V	1209.6739	605.3406	1192.6473	596.8273	1191.6633	596.3353	11
24	2749.2628	1375.1350	2732.2362	1366.6218	2731.2522	1366.1297	I	1110.6055	555.8064	1093.5789	547.2931	1092.5949	546.8011	10
25	2806.2842	1403.6458	2789.2577	1395.1325	2788.2737	1394.6405	G	997.5214	499.2643	980.4948	490.7511	979.5108	490.2591	9

26	2863.3057	1432.1565	2846.2792	1423.6432	2845.2951	1423.1512	**G**	940.4999	470.7536	923.4734	462.2403	922.4894	461.7483	**8**
27	2976.3898	1488.6985	2959.3632	1480.1853	2958.3792	1479.6932	**L**	883.4785	442.2429	866.4519	433.7296	865.4679	433.2376	**7**
28	3077.4375	1539.2224	3060.4109	1530.7091	3059.4269	1530.2171	**T**	770.3944	385.7008	753.3679	377.1876	752.3838	376.6956	**6**
29	3214.4964	1607.7518	3197.4698	1599.2385	3196.4858	1598.7465	**H**	669.3467	335.1770	652.3202	326.6637			**5**
30	3311.5491	1656.2782	3294.5226	1647.7649	3293.5386	1647.2729	**P**	532.2878	266.6475	515.2613	258.1343			**4**
31	3474.6125	1737.8099	3457.5859	1729.2966	3456.6019	1728.8046	**Y**	435.2350	218.1212	418.2085	209.6079			**3**
32	3571.6652	1786.3362	3554.6387	1777.8230	3553.6547	1777.3310	**P**	272.1717	136.5895	255.1452	128.0762			**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IYDYDVYNDVGDPDNDPELARPVIGGLTHPYPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.3	3744.7696	-0.0019	IYDYDVYNDVGDPDNDPELARPVIGGLTHPYPR
3.6	3744.7741	-0.0063	MLPIFGCTIMLNCCLAQLSTYSVHQAATMNRK
2.5	3744.7684	-0.0007	YMTDGMLLREILIDENLSQYSVIMLDEAHER

Mascot: http://www.matrixscience.com/

AT3G45310.1

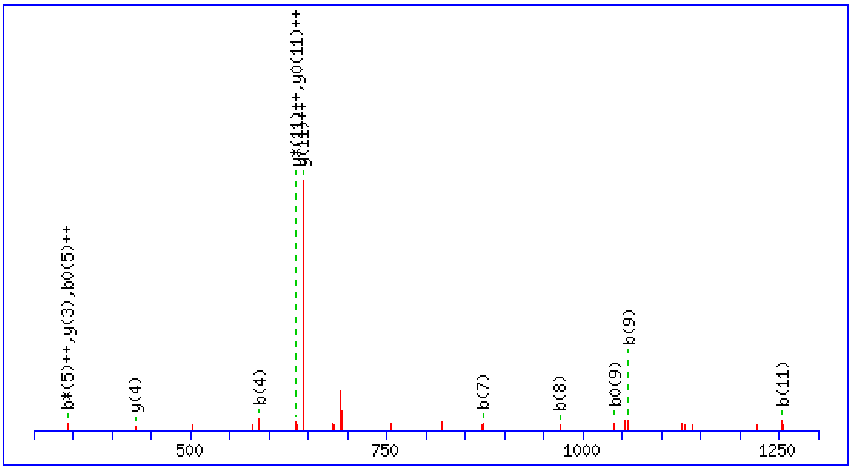
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWREDGIVSPVK**
Found in **AT3G45310.1** in **TAIR_Arabidopsis**, Symbols: | cysteine proteinase, putative | chr3:16639689-16641458 REVERSE

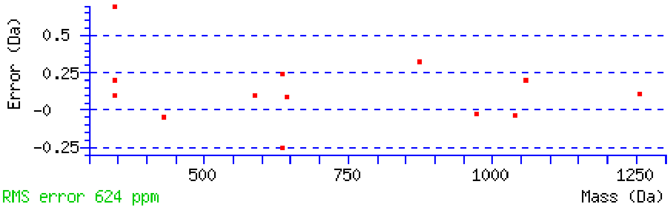
Match to Query 5546: 1399.709346 from(700.861949,2+) index(4946)
Title: Elution from: 43.635 to 43.635 scan no 6175 cid35.00 polarity:+
Data file D1d-3_2.mgf

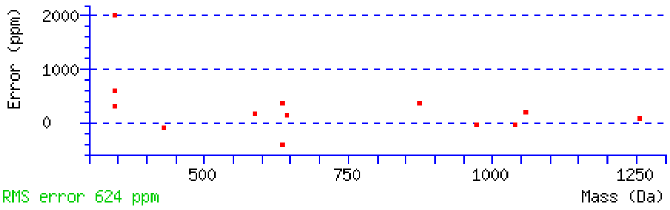
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1399.7096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.011
Matches : 13/122 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	302.1135	151.5604			284.1030	142.5551	W	1285.6899	643.3486	1268.6634	634.8353	1267.6793	634.3433	11
3	458.2146	229.6110	441.1881	221.0977	440.2041	220.6057	R	1099.6106	550.3089	1082.5841	541.7957	1081.6000	541.3037	10
4	***587.2572***	294.1323	570.2307	285.6190	569.2467	285.1270	E	943.5095	472.2584	926.4829	463.7451	925.4989	463.2531	9
5	702.2842	351.6457	685.2576	343.1325	684.2736	342.6404	D	814.4669	407.7371	797.4403	399.2238	796.4563	398.7318	8
6	759.3056	380.1565	742.2791	371.6432	741.2951	371.1512	G	699.4400	350.2236	682.4134	341.7103	681.4294	341.2183	7
7	***872.3897***	436.6985	855.3632	428.1852	854.3791	427.6932	I	642.4185	321.7129	625.3919	313.1996	624.4079	312.7076	6
8	***971.4581***	486.2327	954.4316	477.7194	953.4476	477.2274	V	529.3344	265.1709	512.3079	256.6576	511.3239	256.1656	5
9	***1058.4901***	529.7487	1041.4636	521.2354	1040.4796	520.7434	S	**430.2660**	215.6366	413.2395	207.1234	412.2554	206.6314	4
10	1155.5429	578.2751	1138.5164	569.7618	1137.5323	569.2698	P	**343.2340**	172.1206	326.2074	163.6074			3
11	***1254.6113***	627.8093	1237.5848	619.2960	1236.6008	618.8040	V	246.1812	123.5942	229.1547	115.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DWREDGIVSPVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G45310.1

Score	Mr(calc)	Delta	Sequence
27.4	1399.7096	-0.0002	DWREDGIVSPVK
6.7	1399.7129	-0.0036	DRPAIAMIADAEK
4.2	1399.7095	-0.0002	NPQASEKALWEK
3.4	1399.7055	0.0038	EGRVSPIQEETR
3.0	1399.7056	0.0038	NVSTTASAHSLQGK
2.8	1399.7096	-0.0002	DLRDDIFEHLK
2.7	1399.7055	0.0038	NNGSDLGDQKKPK
2.6	1399.7055	0.0038	NDNSKHTLEKSK
1.0	1399.7095	-0.0002	DKTHWEEKLSK

Mascot: http://www.matrixscience.com/

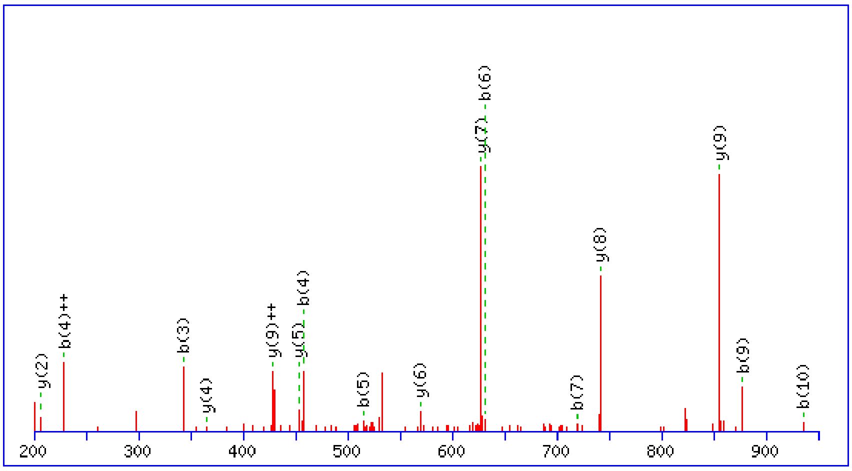
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLIGDSGVGK**
Found in **AT3G46060.1** in **TAIR_Arabidopsis**, Symbols: Ara-3, AtRABE1c, AtRab8A, ARA3 | ARA3; GTP binding | chr3:16928893-16930725 FORWARD

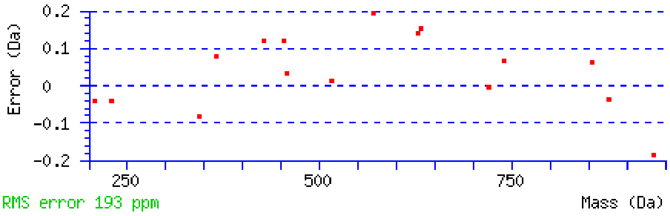
Match to Query 3154: 1082.597102 from(542.305827,2+) index(5794)
Title: Elution from: 51.687 to 51.687 scan no 7427 cid35.00 polarity:+
Data file D6h-3_2.mgf

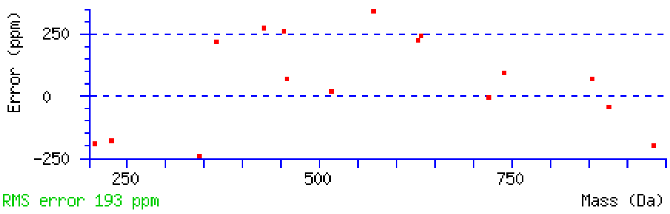
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1082.5980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 1.7e-005
Matches : 17/82 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							11
2	***229.1695***	115.0884			L	969.5242	485.2657	951.5006	476.2539	951.5136	476.2604	10
3	***343.2506***	172.1289			L	**855.4431**	428.2252	837.4195	419.2134	837.4325	419.2199	9
4	***457.3317***	229.1695			I	**741.3620**	371.1846	723.3384	362.1728	723.3514	362.1793	8
5	***515.3502***	258.1787			G	**627.2809**	314.1441	609.2573	305.1323	609.2703	305.1388	7
6	***631.3741***	316.1907	613.3636	307.1854	D	**569.2624**	285.1348	551.2388	276.1230	551.2518	276.1295	6
7	***719.4032***	360.2052	701.3926	351.2000	S	**453.2384**	227.1228	435.2148	218.1110	435.2278	218.1175	5
8	777.4217	389.2145	759.4111	380.2092	G	**365.2093**	183.1083	347.1857	174.0965			4
9	***877.4872***	439.2472	859.4766	430.2419	V	307.1908	154.0990	289.1672	145.0873			3
10	***935.5057***	468.2565	917.4951	459.2512	G	**207.1254**	104.0663	189.1018	95.0545			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LLLIGDSGVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G46060.1

Score	Mr(calc)	Delta	Sequence
53.4	1082.5980	-0.0009	IILLGDSGVGK
53.4	1082.5980	-0.0009	ILLIGDSGVGK
53.4	1082.5980	-0.0009	LLLIGDSGVGK
20.2	1082.5980	-0.0009	LILLDETVR
2.4	1082.5980	-0.0009	LGSLDPIKTK
1.9	1082.5980	-0.0009	ILKLVEDNK
0.8	1082.5980	-0.0009	ILALTATPGSK
0.8	1082.6002	-0.0031	ILFTEPPKK
0.8	1082.5980	-0.0009	LLAELGSIQK
0.8	1082.5980	-0.0009	LLDQVVEKK

Mascot: http://www.matrixscience.com/

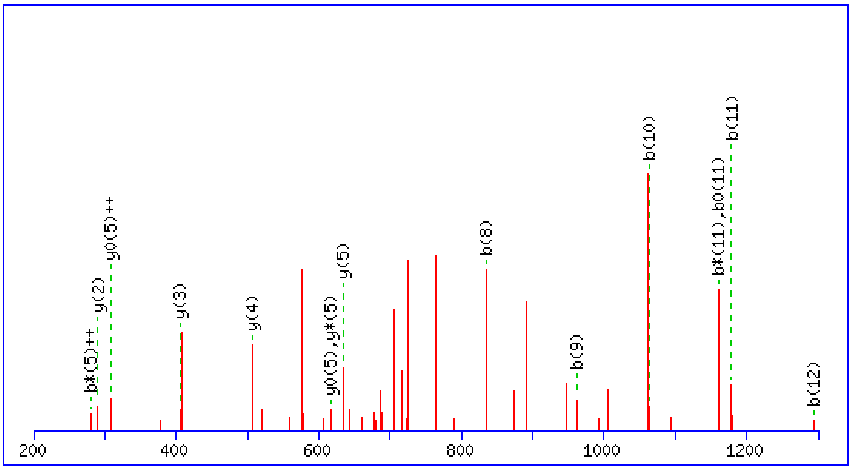
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLSMDASTQTDDR**
Found in **AT3G46110.1** in **TAIR_Arabidopsis**, Symbols: | signal transducer | chr3:16943229-16944573 FORWARD

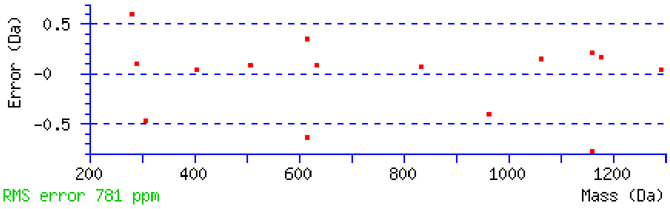
Match to Query 6120: 1466.666276 from(734.340414,2+) index(7547)
Title: Elution from: 65.485 to 65.485 scan no 9811 cid35.00 polarity:+
Data file D1d-3_2.mgf

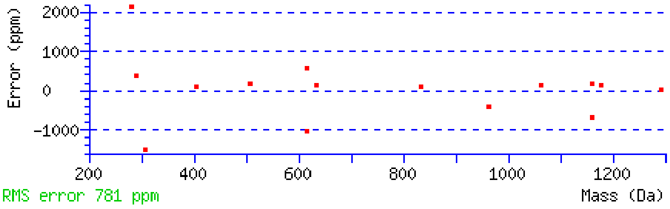
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1466.6671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.02
Matches : 15/138 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							13
2	242.1863	121.5968	225.1598	113.0835			L	1339.5794	670.2934	1322.5529	661.7801	1321.5689	661.2881	12
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	S	1226.4954	613.7513	1209.4688	605.2380	1208.4848	604.7460	11
4	460.2588	230.6330	443.2323	222.1198	442.2483	221.6278	M	1139.4633	570.2353	1122.4368	561.7220	1121.4528	561.2300	10
5	575.2858	288.1465	558.2592	279.6332	557.2752	279.1412	D	1008.4229	504.7151	991.3963	496.2018	990.4123	495.7098	9
6	646.3229	323.6651	629.2963	315.1518	628.3123	314.6598	A	893.3959	447.2016	876.3694	438.6883	875.3854	438.1963	8
7	733.3549	367.1811	716.3284	358.6678	715.3443	358.1758	S	822.3588	411.6830	805.3323	403.1698	804.3482	402.6778	7
8	***834.4026***	417.7049	817.3760	409.1917	816.3920	408.6996	T	735.3268	368.1670	718.3002	359.6538	717.3162	359.1617	6
9	***962.4612***	481.7342	945.4346	473.2209	944.4506	472.7289	Q	**634.2791**	317.6432	617.2525	309.1299	616.2685	308.6379	5
10	***1063.5088***	532.2581	1046.4823	523.7448	1045.4983	523.2528	T	**506.2205**	253.6139	489.1940	245.1006	488.2100	244.6086	4
11	***1178.5358***	589.7715	1161.5092	581.2583	1160.5252	580.7662	D	**405.1728**	203.0901	388.1463	194.5768	387.1623	194.0848	3
12	***1293.5627***	647.2850	1276.5362	638.7717	1275.5522	638.2797	D	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KLSMDASTQTDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G46110.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.1	1466.6671	-0.0008	KLSMDASTQTDDR
9.6	1466.6646	0.0017	LYNDCPKPSSMR

Mascot: http://www.matrixscience.com/

AT3G46430.1

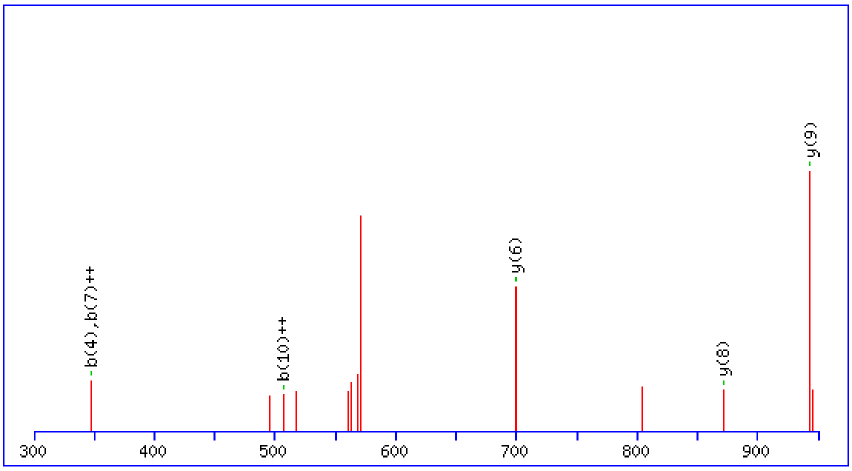
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTAGLTEEDAK**
Found in **AT3G46430.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G59613.1); similar to mitochondrial ATP synthase 6 KD subunit [Oryza sativa (japonica cultivar-group)] (GB:BAB21526.1) | chr3:17098672-17099482 FORWARD

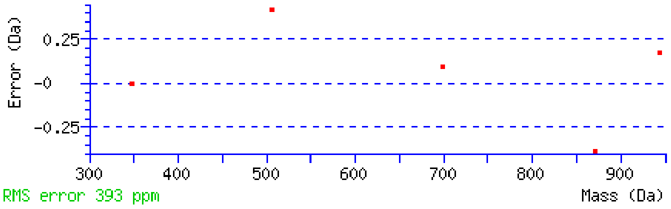
Match to Query 3467: 1158.540830 from(580.277691,2+) index(1419)
Title: Elution from: 22.439 to 22.439 scan no 2020 cid35.00 polarity:+
Data file D1d-1_1.mgf

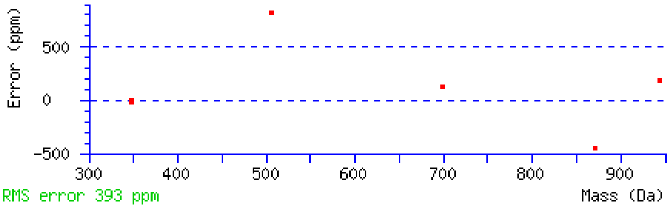
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1158.5412
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.017
Matches : 6/94 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*++	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							11
2	217.1331	109.0702	199.1225	100.0649	T	1045.4674	523.2374	1027.4438	514.2256	1027.4569	514.2321	10
3	289.1672	145.0873	271.1567	136.0820	A	***943.4227***	472.2150	925.3991	463.2032	925.4122	463.2097	9
4	347.1857	174.0965	329.1752	165.0912	G	***871.3886***	436.1979	853.3650	427.1861	853.3780	427.1926	8
5	461.2668	231.1371	443.2563	222.1318	L	813.3701	407.1887	795.3465	398.1769	795.3595	398.1834	7
6	563.3115	282.1594	545.3010	273.1541	T	***699.2890***	350.1481	681.2654	341.1363	681.2784	341.1428	6
7	693.3512	***347.1792***	675.3406	338.1739	E	597.2443	299.1258	579.2207	290.1140	579.2337	290.1205	5
8	823.3908	412.1990	805.3802	403.1938	E	467.2046	234.1060	449.1810	225.0942	449.1941	225.1007	4
9	939.4148	470.2110	921.4042	461.2057	D	337.1650	169.0861	319.1414	160.0743	319.1544	160.0809	3
10	1011.4489	***506.2281***	993.4384	497.2228	A	221.1410	111.0741	203.1174	102.0624			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LTAGLTEEDAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G46430.1

Score	Mr(calc)	Delta	Sequence
25.8	1158.5412	-0.0004	LTAGLTEEDAK
2.3	1158.5439	-0.0031	LSVQEQGQQK
2.3	1158.5421	-0.0013	QLTPMDLAMK
2.3	1158.5412	-0.0004	SLDEELEGKK
2.3	1158.5439	-0.0031	VGLEREAQDK
1.4	1158.5388	0.0021	MEWIQSLPK
1.4	1158.5439	-0.0031	NLNREELEK
0.8	1158.5380	0.0028	VAGNFHFAPGK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIAEVGAEIR**
Found in **AT3G46740.1** in **TAIR_Arabidopsis**, Symbols: TOC75-III | TOC75-III (translocon outer membrane complex 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter | chr3:17227089-17230281 REVERSE

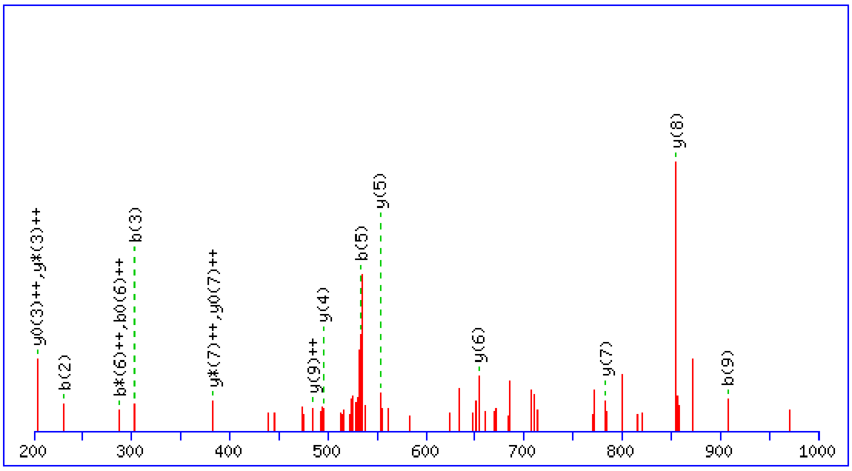
Match to Query 3130: 1084.528002 from(543.271277,2+) index(3459)
Title: Elution from: 33.331 to 33.331 scan no 4292 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1000 Da Full range

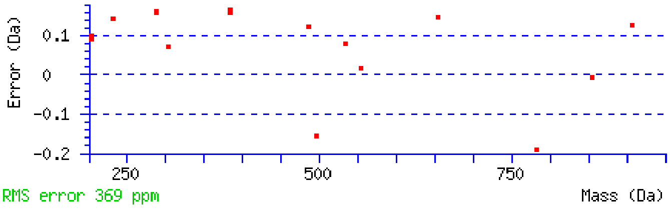
Label all possible matches ○ Label matches used for scoring ●

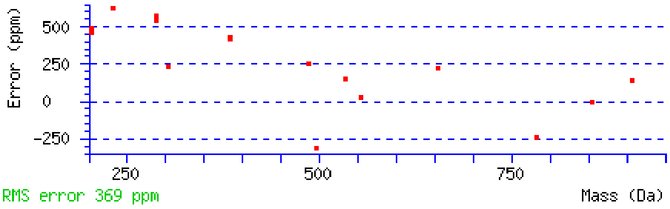
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1084.5305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.041
Matches : 16/98 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							10
2	***231.1254***	116.0663	213.1018	107.0545			I	969.5008	485.2540	951.4772	476.2422	951.4902	476.2488	9
3	***303.1595***	152.0834	285.1359	143.0716			A	***855.4197***	428.2135	837.3961	419.2017	837.4091	419.2082	8
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	E	***783.3855***	392.1964	765.3620	383.1846	765.3750	383.1911	7
5	***533.2646***	267.1359	515.2410	258.1241	515.2540	258.1307	V	***653.3459***	327.1766	635.3223	318.1648	635.3354	318.1713	6
6	591.2831	296.1452	573.2595	287.1334	573.2725	287.1399	G	***553.2805***	277.1439	535.2569	268.1321	535.2699	268.1386	5
7	663.3172	332.1623	645.2937	323.1505	645.3067	323.1570	A	***495.2620***	248.1346	477.2384	239.1228	477.2514	239.1293	4
8	793.3569	397.1821	775.3333	388.1703	775.3463	388.1768	E	423.2278	212.1175	405.2042	203.1058	405.2173	203.1123	3
9	***907.4380***	454.2226	889.4144	445.2108	889.4274	445.2173	I	293.1882	147.0977	275.1646	138.0859			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of NIAEVGAEIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G46740.1

Score	Mr(calc)	Delta	Sequence
21.6	1084.5305	-0.0025	NIAEVGAEIR
10.8	1084.5305	-0.0025	LGIIEDAANR
8.6	1084.5305	-0.0025	IDGKISGPER
8.3	1084.5305	-0.0025	INSIKEDPR
7.5	1084.5305	-0.0025	LVADGVVENR
6.7	1084.5257	0.0023	VQMQGVPVGR
6.6	1084.5278	0.0002	EVEAPTTSLK
4.1	1084.5305	-0.0025	LGGETKVDPR
3.7	1084.5305	-0.0025	LGEQLENLR

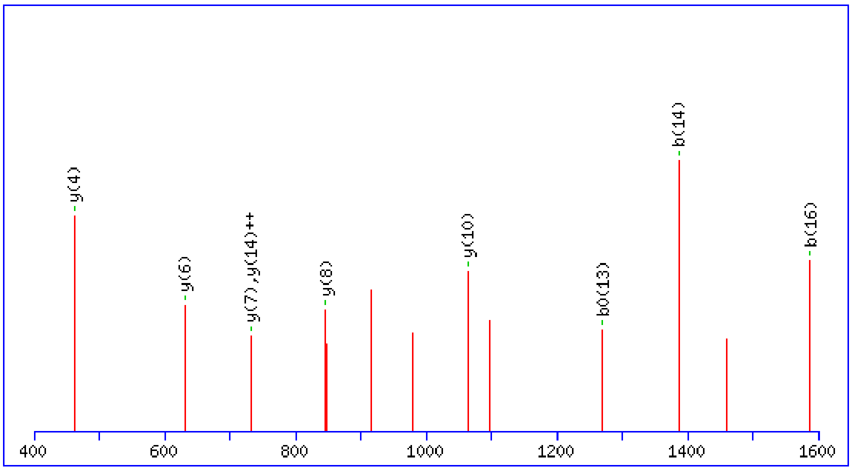
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IASLVADIFANTAVAENK**
Found in **AT3G46780.1** in **TAIR_Arabidopsis**, Symbols: PTAC16 | PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIVE18); binding / catalytic | chr3:17239751-17242006 FORWARD

Match to Query 8383: 1845.979234 from(923.996893,2+) index(9797)
Title: Elution from: 95.100 to 95.100 scan no 14023 cid35.00 polarity:+
Data file D1d-2_2.mgf

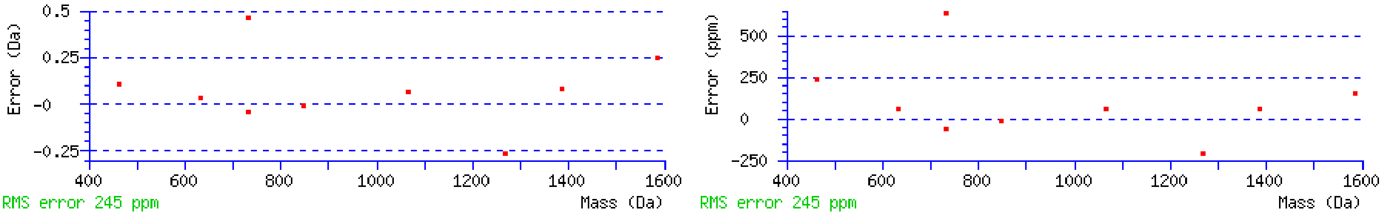
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1845.9836
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00038
Matches : 9/176 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							18
2	185.1285	93.0679					A	1733.9068	867.4571	1716.8803	858.9438	1715.8963	858.4518	17
3	272.1605	136.5839			254.1499	127.5786	S	1662.8697	831.9385	1645.8432	823.4252	1644.8592	822.9332	16
4	385.2445	193.1259			367.2340	184.1206	L	1575.8377	788.4225	1558.8112	779.9092	1557.8271	779.4172	15
5	484.3130	242.6601			466.3024	233.6548	V	1462.7536	731.8805	1445.7271	723.3672	1444.7431	722.8752	14
6	555.3501	278.1787			537.3395	269.1734	A	1363.6852	682.3462	1346.6587	673.8330	1345.6747	673.3410	13
7	670.3770	335.6921			652.3665	326.6869	D	1292.6481	646.8277	1275.6216	638.3144	1274.6375	637.8224	12
8	783.4611	392.2342			765.4505	383.2289	I	1177.6212	589.3142	1160.5946	580.8009	1159.6106	580.3089	11
9	930.5295	465.7684			912.5189	456.7631	F	***1064.5371***	532.7722	1047.5106	524.2589	1046.5265	523.7669	10
10	1001.5666	501.2869			983.5560	492.2817	A	917.4687	459.2380	900.4421	450.7247	899.4581	450.2327	9
11	1115.6095	558.3084	1098.5830	549.7951	1097.5990	549.3031	N	***846.4316***	423.7194	829.4050	415.2061	828.4210	414.7141	8
12	1216.6572	608.8322	1199.6307	600.3190	1198.6466	599.8270	T	***732.3886***	366.6980	715.3621	358.1847	714.3781	357.6927	7
13	1287.6943	644.3508	1270.6678	635.8375	1269.6838	635.3455	A	***631.3410***	316.1741	614.3144	307.6608	613.3304	307.1688	6
14	**1386.7627**	693.8850	1369.7362	685.3717	1368.7522	684.8797	V	560.3039	280.6556	543.2773	272.1423	542.2933	271.6503	5
15	1457.7999	729.4036	1440.7733	720.8903	1439.7893	720.3983	A	***461.2354***	231.1214	444.2089	222.6081	443.2249	222.1161	4
16	**1586.8424**	793.9249	1569.8159	785.4116	1568.8319	784.9196	E	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
17	1700.8854	850.9463	1683.8588	842.4331	1682.8748	841.9410	N	261.1557	131.0815	244.1292	122.5682			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT3G46780.1



NCBI **BLAST** search of IASLVADIFANTAVAENK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.2	1845.9836	-0.0044	IASLVADIFANTAVAENK
2.4	1845.9804	-0.0012	MEAEIAGLLKRMEVTR

Mascot: http://www.matrixscience.com/

AT3G46920.1

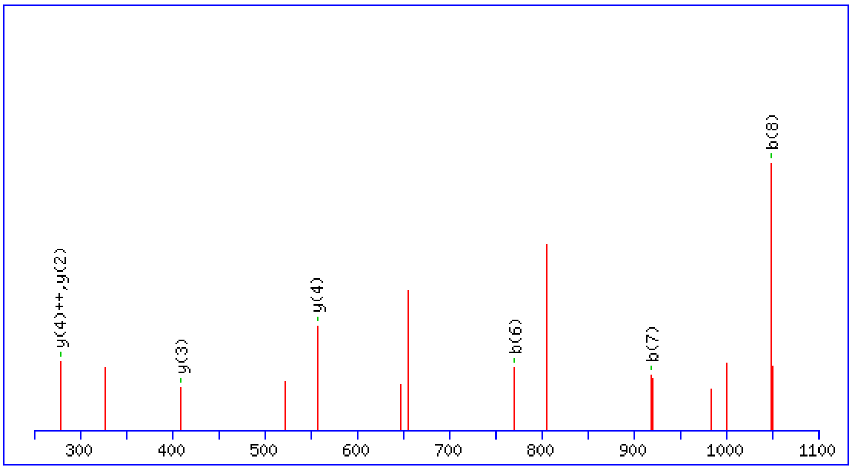
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVRFDEFEQK**
Found in **AT3G46920.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr3:17291415-17295842 REVERSE

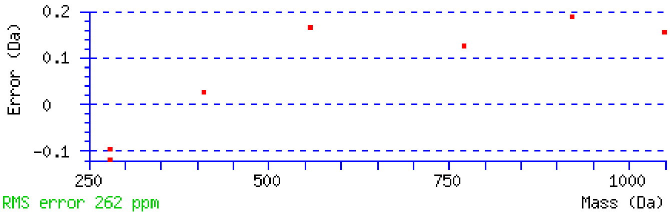
Match to Query 4503: 1326.576888 from(664.295720,2+) index(8655)
Title: Elution from: 77.796 to 77.796 scan no 11599 cid35.00 polarity:+
Data file D12h-2_3.mgf

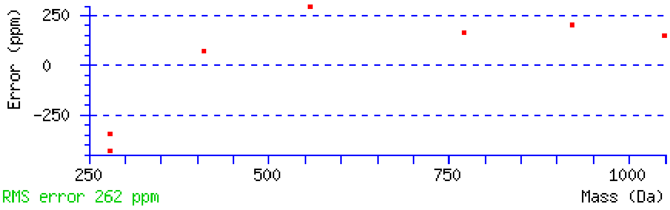
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1326.5780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.02
Matches : 7/96 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							10
2	217.1097	109.0585	199.0861	100.0467			V	1211.5484	606.2778	1193.5248	597.2660	1193.5378	597.2725	9
3	377.1990	189.1031	359.1754	180.0913			R	1111.4829	556.2451	1093.4593	547.2333	1093.4723	547.2398	8
4	525.2644	263.1358	507.2408	254.1241			F	951.3937	476.2005	933.3701	467.1887	933.3831	467.1952	7
5	641.2884	321.1478	623.2648	312.1360	623.2778	312.1426	D	803.3282	402.1677	785.3046	393.1559	785.3176	393.1625	6
6	***771.3280***	386.1677	753.3044	377.1559	753.3175	377.1624	E	687.3042	344.1558	669.2806	335.1440	669.2937	335.1505	5
7	***919.3935***	460.2004	901.3699	451.1886	901.3829	451.1951	F	***557.2646***	279.1359	539.2410	270.1241	539.2540	270.1307	4
8	***1049.4331***	525.2202	1031.4095	516.2084	1031.4225	516.2149	E	***409.1991***	205.1032	391.1756	196.0914	391.1886	196.0979	3
9	1179.4858	590.2465	1161.4622	581.2347	1161.4752	581.2412	Q	***279.1595***	140.0834	261.1359	131.0716			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NVRFDEFEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G46920.1

24.6	1326.5780	-0.0012	NVRFDEFEQK
21.8	1326.5808	-0.0039	EHNWPNKQQK
11.8	1326.5780	-0.0012	GTFVEFENNVR
11.8	1326.5754	0.0015	YKGFGEVEEEK
9.7	1326.5744	0.0025	MGTDTVMSGRVR
5.0	1326.5740	0.0029	MFPVVSSEVMR
1.9	1326.5733	0.0036	NCFSWNTIIR
1.9	1326.5774	-0.0005	MSGMLGLSAVMGK
1.5	1326.5758	0.0011	QSGSGDFSRLEK
0.9	1326.5763	0.0006	SSSSSRAPSRER

AT3G46970.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVNDVGDVVNSDPEVNEYLK**
Found in **AT3G46970.1** in **TAIR_Arabidopsis**, Symbols: ATPHS2, PHS2 | ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups | chr3:17312610-17317096 REVERSE

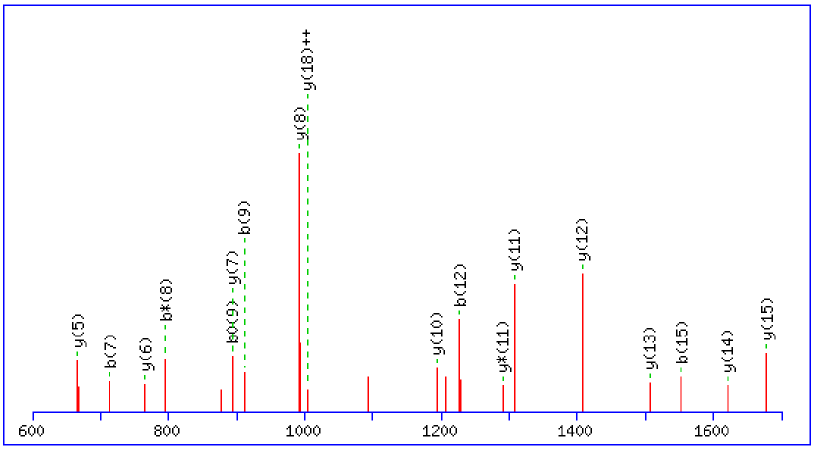
Match to Query 9521: 2217.078078 from(1109.546315,2+) index(7525)
Title: Elution from: 67.442 to 67.442 scan no 9927 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 600 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

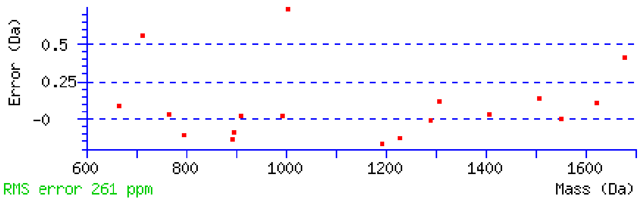
Show Y-axis ☐

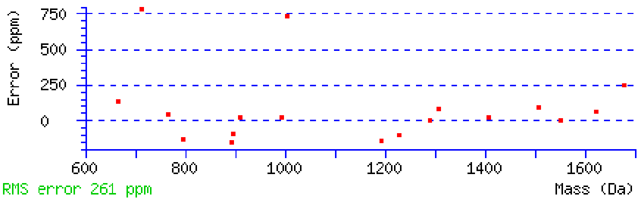


Monoisotopic mass of neutral peptide Mr(calc): 2217.0801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 3.3e-008
Matches : 20/212 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							20
2	213.1598	107.0835					V	2105.0033	1053.0053	2087.9768	1044.4920	2086.9928	1044.0000	19
3	327.2027	164.1050	310.1761	155.5917			N	2005.9349	1003.4711	1988.9084	994.9578	1987.9243	994.4658	18
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	D	1891.8920	946.4496	1874.8654	937.9364	1873.8814	937.4443	17
5	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	V	1776.8650	888.9362	1759.8385	880.4229	1758.8545	879.9309	16
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	G	***1677.7966***	839.4019	1660.7701	830.8887	1659.7861	830.3967	15
7	**713.3464**	357.1769	696.3199	348.6636	695.3359	348.1716	D	***1620.7752***	810.8912	1603.7486	802.3779	1602.7646	801.8859	14
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	V	***1505.7482***	753.3777	1488.7217	744.8645	1487.7376	744.3725	13
9	**911.4833**	456.2453	894.4567	447.7320	893.4727	447.2400	V	***1406.6798***	703.8435	1389.6533	695.3303	1388.6692	694.8383	12
10	1025.5262	513.2667	1008.4997	504.7535	1007.5156	504.2615	N	***1307.6114***	654.3093	1290.5848	645.7961	1289.6008	645.3040	11
11	1112.5582	556.7828	1095.5317	548.2695	1094.5477	547.7775	S	***1193.5685***	597.2879	1176.5419	588.7746	1175.5579	588.2826	10
12	**1227.5852**	614.2962	1210.5586	605.7829	1209.5746	605.2909	D	1106.5364	553.7719	1089.5099	545.2586	1088.5259	544.7666	9
13	1324.6379	662.8226	1307.6114	654.3093	1306.6274	653.8173	P	***991.5095***	496.2584	974.4829	487.7451	973.4989	487.2531	8
14	1453.6805	727.3439	1436.6540	718.8306	1435.6700	718.3386	E	***894.4567***	447.7320	877.4302	439.2187	876.4462	438.7267	7
15	**1552.7489**	776.8781	1535.7224	768.3648	1534.7384	767.8728	V	***765.4141***	383.2107	748.3876	374.6974	747.4036	374.2054	6
16	1666.7919	833.8996	1649.7653	825.3863	1648.7813	824.8943	N	***666.3457***	333.6765	649.3192	325.1632	648.3352	324.6712	5
17	1795.8345	898.4209	1778.8079	889.9076	1777.8239	889.4156	E	552.3028	276.6550	535.2762	268.1418	534.2922	267.6498	4
18	1958.8978	979.9525	1941.8712	971.4393	1940.8872	970.9473	Y	423.2602	212.1337	406.2336	203.6205			3
19	2071.9819	1036.4946	2054.9553	1027.9813	2053.9713	1027.4893	L	260.1969	130.6021	243.1703	122.0888			2
20							K	147.1128	74.0600	130.0863	65.5468			1

AT3G46970.1





NCBI **BLAST** search of LVNDVGDVVNSDPEVNEYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
80.3	2217.0801	-0.0020	LVNDVGDVVNSDPEVNEYLK

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQFYETNPLLK**
Found in **AT3G47070.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown [Populus trichocarpa] (GB:ABK95428.1) | chr3:17348190-17348492 REVERSE

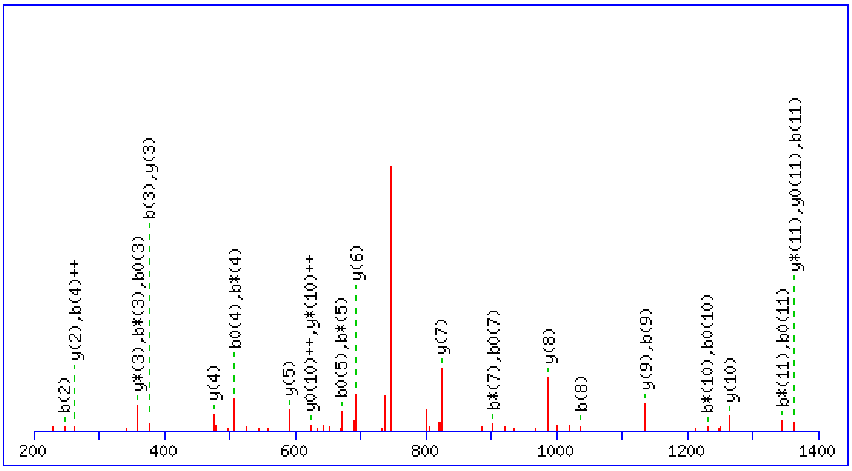
Match to Query 6489: 1510.686896 from(756.350724,2+) index(6494)
Title: Elution from: 57.611 to 57.611 scan no 8362 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

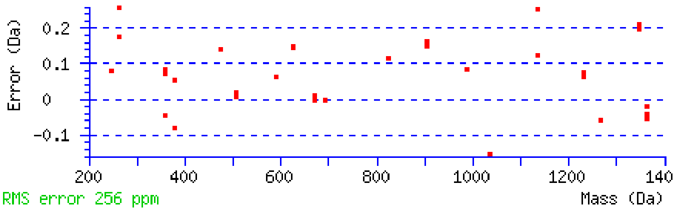
Label all possible matches ○ Label matches used for scoring ●

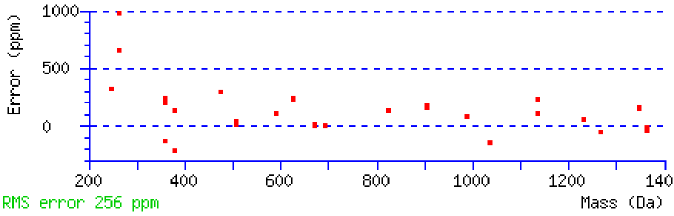
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1510.6880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 3.8e-008
Matches : 32/120 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							12
2	**247.0839**	124.0456	229.0603	115.0338	229.0733	115.0403	D	1381.6426	691.3250	1363.6191	682.3132	1363.6321	682.3197	11
3	**377.1365**	189.0719	359.1130	180.0601	359.1260	180.0666	Q	***1265.6187***	633.3130	1247.5951	624.3012	1247.6081	624.3077	10
4	525.2020	263.1046	507.1784	254.0928	507.1914	254.0994	F	***1135.5660***	568.2866	1117.5424	559.2749	1117.5555	559.2814	9
5	689.2624	345.1348	671.2388	336.1230	671.2518	336.1295	Y	***987.5006***	494.2539	969.4770	485.2421	969.4900	485.2486	8
6	819.3020	410.1546	801.2784	401.1428	801.2914	401.1494	E	***823.4402***	412.2237	805.4166	403.2120	805.4296	403.2185	7
7	921.3467	461.1770	903.3231	452.1652	903.3361	452.1717	T	***693.4006***	347.2039	675.3770	338.1921	675.3900	338.1986	6
8	**1037.3837**	519.1955	1019.3601	510.1837	1019.3731	510.1902	N	***591.3559***	296.1816	573.3323	287.1698			5
9	**1135.4335**	568.2204	1117.4099	559.2086	1117.4229	559.2151	P	***475.3189***	238.1631	457.2953	229.1513			4
10	1249.5146	625.2609	1231.4910	616.2491	1231.5040	616.2557	L	***377.2691***	189.1382	359.2455	180.1264			3
11	**1363.5957**	682.3015	1345.5721	673.2897	1345.5851	673.2962	L	***263.1880***	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QDQFYETNPLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G47070.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.4	1510.6880	-0.0011	QDQFYETNPLLK
12.6	1510.6840	0.0029	ALEGVIMMETFPK
9.5	1510.6857	0.0012	FDDERVTKEDLK
9.2	1510.6914	-0.0045	MQDYTLQKVEPK
4.8	1510.6914	-0.0045	KDFEMEGQILSAK
4.1	1510.6900	-0.0031	TCPGKQLAMTLMK
2.1	1510.6893	-0.0024	HLCVLHLNMNPK
2.0	1510.6893	-0.0024	MKLWGRNEVCAK
1.8	1510.6831	0.0038	YIKELTETDEEK
1.6	1510.6914	-0.0045	FAAEQASMSVDVIK

AT3G47110.1

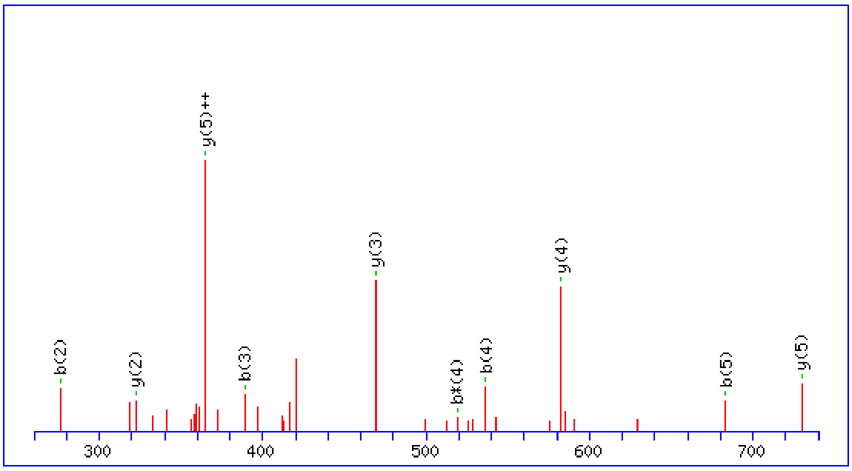
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QMIFFR**
Found in **AT3G47110.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr3:17358088-17361281 REVERSE

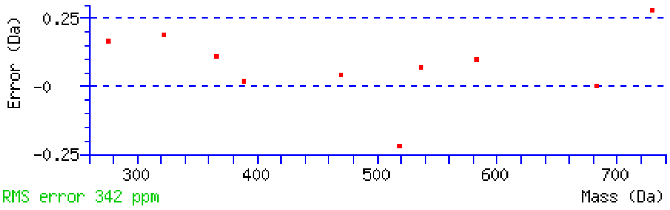
Match to Query 1292: 856.426878 from(429.220715,2+) index(4239)
Title: Elution from: 40.331 to 40.331 scan no 5398 cid35.00 polarity:+
Data file 0-1_2.mgf

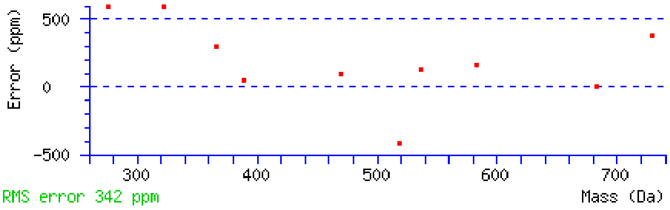
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 260 to 740 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 856.4265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.00075
Matches : 10/60 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.0659	65.0366	112.0393	56.5233	Q					6
2	***276.1013***	138.5543	259.0747	130.0410	M	***729.3752***	365.1913	712.3487	356.6780	5
3	***389.1853***	195.0963	372.1588	186.5830	I	***582.3398***	291.6736	565.3133	283.1603	4
4	***536.2537***	268.6305	519.2272	260.1172	F	***469.2558***	235.1315	452.2292	226.6183	3
5	***683.3221***	342.1647	666.2956	333.6514	F	***322.1874***	161.5973	305.1608	153.0840	2
6					R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of QMIFFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.6	856.4265	0.0003	QMIFFR
32.2	856.4265	0.0003	GAMIFFR

AT3G47110.1

10.8	856.4265	0.0003	QFFMIR
2.6	856.4290	-0.0022	KQPEVQE

Mascot: http://www.matrixscience.com/

AT3G47340.1

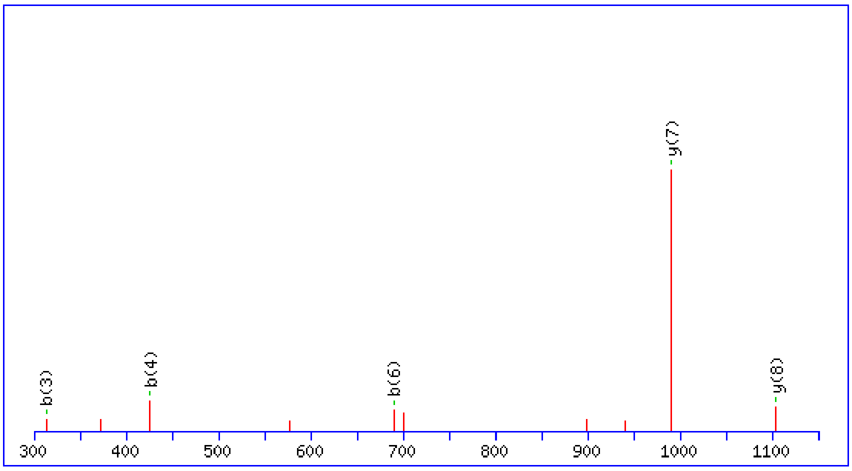
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IKALHKYDCLR**
Found in **AT3G47340.1** in **TAIR_Arabidopsis**, Symbols: DIN6, AT-ASN1, ASN1 | ASN1 (DARK INDUCIBLE 6) | chr3:17449121-17452028 REVERSE

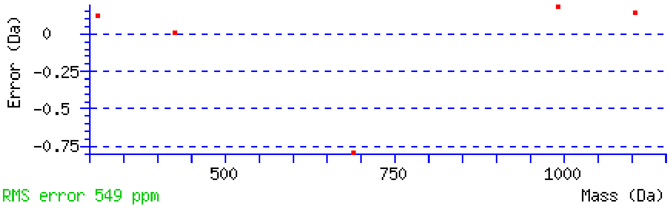
Match to Query 5812: 1415.771770 from(708.893161,2+) index(6509)
Title: Elution from: 57.423 to 57.423 scan no 8293 cid35.00 polarity:+
Data file 0-2_1.mgf

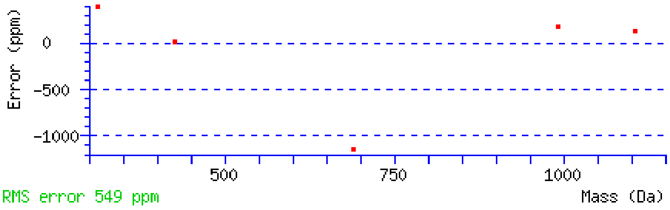
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1415.7707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.033
Matches : 5/98 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**I**							**11**
2	242.1863	121.5968	225.1598	113.0835			**K**	1303.6940	652.3506	1286.6674	643.8373	1285.6834	643.3453	**10**
3	***313.2234***	157.1153	296.1969	148.6021			**A**	1175.5990	588.3031	1158.5724	579.7899	1157.5884	579.2979	**9**
4	***426.3075***	213.6574	409.2809	205.1441			**L**	**1104.5619**	552.7846	1087.5353	544.2713	1086.5513	543.7793	**8**
5	563.3664	282.1868	546.3398	273.6736			**H**	**991.4778**	496.2425	974.4513	487.7293	973.4672	487.2373	**7**
6	***691.4614***	346.2343	674.4348	337.7210			**K**	854.4189	427.7131	837.3924	419.1998	836.4083	418.7078	**6**
7	854.5247	427.7660	837.4981	419.2527			**Y**	726.3239	363.6656	709.2974	355.1523	708.3134	354.6603	**5**
8	969.5516	485.2795	952.5251	476.7662	951.5411	476.2742	**D**	563.2606	282.1339	546.2341	273.6207	545.2500	273.1287	**4**
9	1129.5823	565.2948	1112.5557	556.7815	1111.5717	556.2895	**C**	448.2337	224.6205	431.2071	216.1072			**3**
10	1242.6663	621.8368	1225.6398	613.3235	1224.6558	612.8315	**L**	288.2030	144.6051	271.1765	136.0919			**2**
11							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IKALHKYDCLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G47340.1

Score	Mr(calc)	Delta	Sequence
20.1	1415.7707	0.0011	IKALHKYDCLR

AT3G47370.1

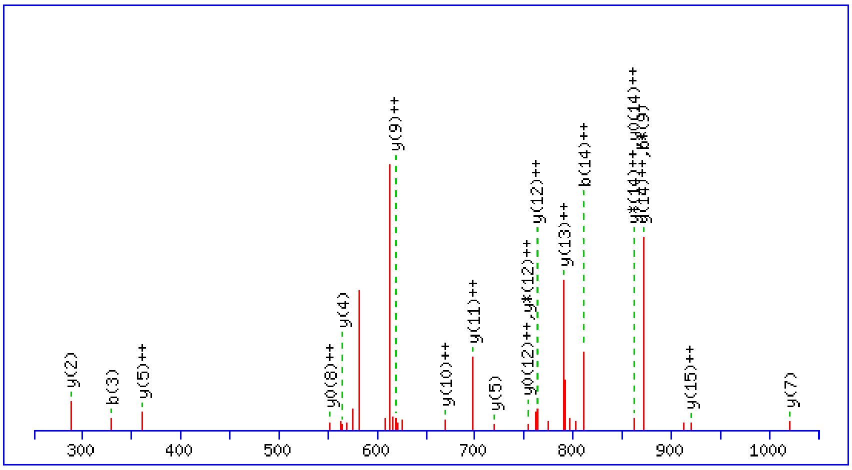
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APCGEGTNTWDRFELR**
Found in **AT3G47370.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S20 (RPS20B) | chr3:17464656-17465422 REVERSE

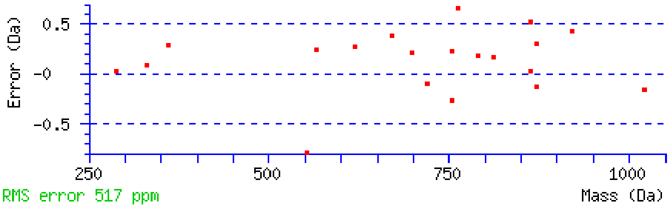
Match to Query 8639: 1907.857566 from(636.959798,3+) index(5515)
Title: Elution from: 50.560 to 50.560 scan no 7114 cid35.00 polarity:+
Data file D12h-2_3.mgf

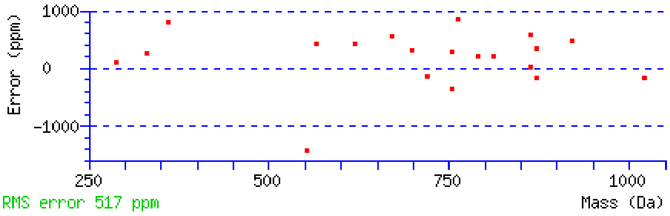
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1907.8584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 6.3e-005
Matches : 20/154 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							16
2	169.0972	85.0522					P	1837.8286	919.4179	1820.8021	910.9047	1819.8180	910.4127	15
3	329.1278	165.0675					C	1740.7758	870.8916	1723.7493	862.3783	1722.7653	861.8863	14
4	386.1493	193.5783					G	1580.7452	790.8762	1563.7186	782.3630	1562.7346	781.8710	13
5	515.1919	258.0996			497.1813	249.0943	E	1523.7237	762.3655	1506.6972	753.8522	1505.7132	753.3602	12
6	572.2133	286.6103			554.2028	277.6050	G	1394.6811	697.8442	1377.6546	689.3309	1376.6706	688.8389	11
7	673.2610	337.1341			655.2504	328.1289	T	1337.6597	669.3335	1320.6331	660.8202	1319.6491	660.3282	10
8	787.3039	394.1556	770.2774	385.6423	769.2934	385.1503	N	1236.6120	618.8096	1219.5854	610.2964	1218.6014	609.8044	9
9	888.3516	444.6794	871.3251	436.1662	870.3410	435.6742	T	1122.5691	561.7882	1105.5425	553.2749	1104.5585	552.7829	8
10	1074.4309	537.7191	1057.4044	529.2058	1056.4204	528.7138	W	***1021.5214***	511.2643	1004.4948	502.7511	1003.5108	502.2591	7
11	1189.4579	595.2326	1172.4313	586.7193	1171.4473	586.2273	D	835.4421	418.2247	818.4155	409.7114	817.4315	409.2194	6
12	1345.5590	673.2831	1328.5324	664.7699	1327.5484	664.2778	R	***720.4151***	360.7112	703.3886	352.1979	702.4046	351.7059	5
13	1492.6274	746.8173	1475.6008	738.3041	1474.6168	737.8121	F	***564.3140***	282.6606	547.2875	274.1474	546.3035	273.6554	4
14	1621.6700	811.3386	1604.6434	802.8254	1603.6594	802.3333	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
15	1734.7540	867.8807	1717.7275	859.3674	1716.7435	858.8754	L	***288.2030***	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1





AT3G47370.1

NCBI **BLAST** search of APCGEGTNTWDRFELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.9	1907.8584	-0.0009	APCGEGTNTWDRFELR

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WFVQAELVNGR**
Found in **AT3G47470.1** in **TAIR_Arabidopsis**, Symbols: CAB4, LHCA4 | LHCA4 (Photosystem I light harvesting complex gene 4); chlorophyll binding | chr3:17504607-17505758 REVERSE

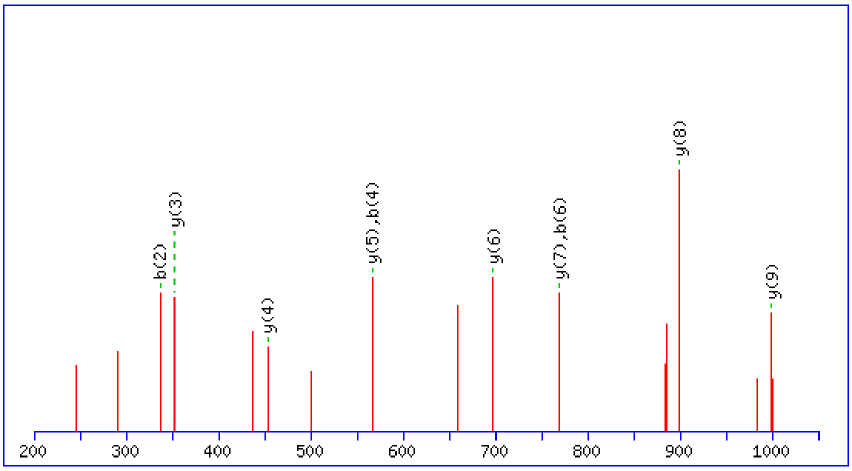
Match to Query 5030: 1334.632842 from(668.323697,2+) index(7258)
Title: Elution from: 64.889 to 64.889 scan no 9426 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

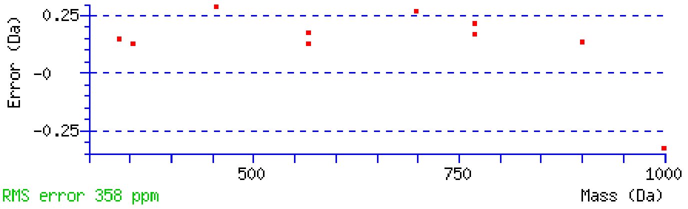
Label all possible matches ○ Label matches used for scoring ●

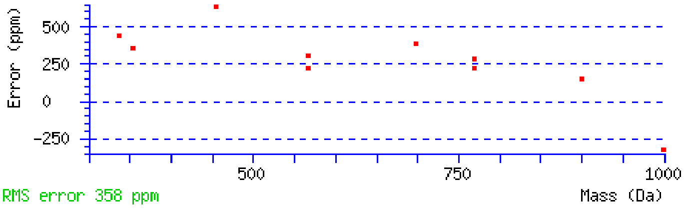
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1334.6325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 6.6e-007
Matches : 10/94 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440					W							11
2	**337.1461**	169.0767					F	1147.5665	574.2869	1129.5429	565.2751	1129.5559	565.2816	10
3	437.2116	219.1094					V	***999.5010***	500.2541	981.4774	491.2424	981.4904	491.2489	9
4	**567.2642**	284.1357	549.2406	275.1239			Q	***899.4356***	450.2214	881.4120	441.2096	881.4250	441.2161	8
5	639.2984	320.1528	621.2748	311.1410			A	***769.3829***	385.1951	751.3593	376.1833	751.3723	376.1898	7
6	**769.3380**	385.1726	751.3144	376.1608	751.3274	376.1673	E	***697.3488***	349.1780	679.3252	340.1662	679.3382	340.1727	6
7	883.4191	442.2132	865.3955	433.2014	865.4085	433.2079	L	***567.3091***	284.1582	549.2856	275.1464			5
8	983.4845	492.2459	965.4609	483.2341	965.4740	483.2406	V	***453.2280***	227.1177	435.2045	218.1059			4
9	1099.5215	550.2644	1081.4979	541.2526	1081.5110	541.2591	N	***353.1626***	177.0849	335.1390	168.0731			3
10	1157.5400	579.2737	1139.5164	570.2619	1139.5295	570.2684	G	237.1256	119.0664	219.1020	110.0546			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of WFVQAELVNGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G47470.1

Score	Mr(calc)	Delta	Sequence
71.9	1334.6325	0.0003	WFVQAELVNGR
26.6	1334.6310	0.0018	CALSVKTIDDAK
11.5	1334.6310	0.0018	MGKVSPKDLDSK
2.7	1334.6310	0.0018	VCDADISTKLAK
2.6	1334.6337	-0.0008	MAARETGALQAAK
1.0	1334.6337	-0.0009	ARISSDPLMVGR
0.7	1334.6337	-0.0009	RAIEENCLGKK
0.5	1334.6337	-0.0009	RRDSLDPSMIK
0.2	1334.6337	-0.0008	CNGADLLTRVAK

AT3G47520.1

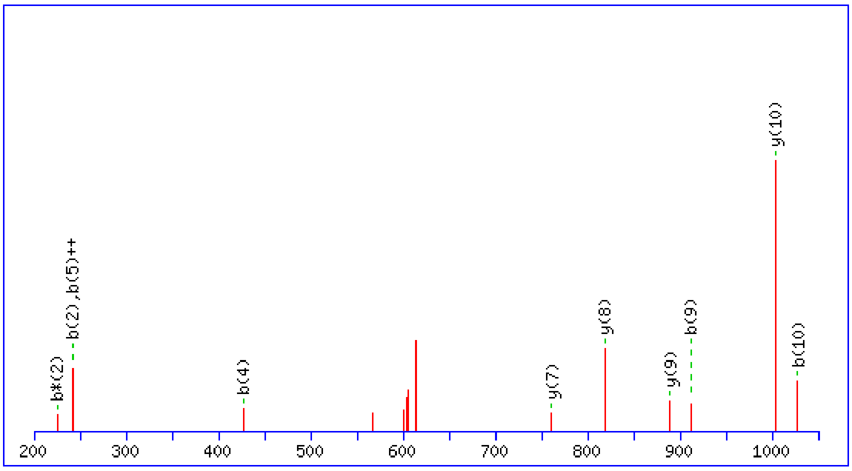
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQNAGTEVVDAK**
Found in **AT3G47520.1** in **TAIR_Arabidopsis**, Symbols: MDH | MDH (MALATE DEHYDROGENASE); malate dehydrogenase | chr3:17524642-17525853 FORWARD

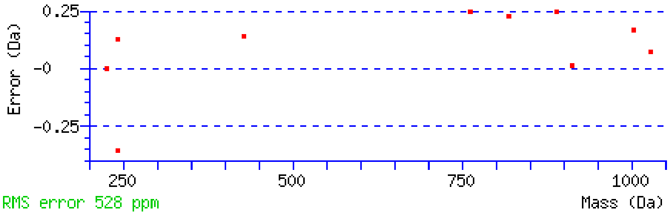
Match to Query 4691: 1243.640252 from(622.827402,2+) index(1390)
Title: Elution from: 19.316 to 19.316 scan no 1898 cid35.00 polarity:+
Data file D6h-1_1.mgf

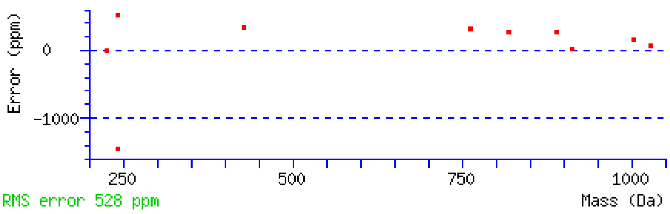
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1243.6408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 4e-005
Matches : 10/116 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							12
2	***242.1499***	121.5786	225.1234	113.0653			Q	1131.5640	566.2857	1114.5375	557.7724	1113.5535	557.2804	11
3	356.1928	178.6001	339.1663	170.0868			N	***1003.5055***	502.2564	986.4789	493.7431	985.4949	493.2511	10
4	***427.2300***	214.1186	410.2034	205.6053			A	***889.4625***	445.2349	872.4360	436.7216	871.4520	436.2296	9
5	484.2514	242.6293	467.2249	234.1161			G	***818.4254***	409.7164	801.3989	401.2031	800.4149	400.7111	8
6	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	T	***761.4040***	381.2056	744.3774	372.6923	743.3934	372.2003	7
7	714.3417	357.6745	697.3151	349.1612	696.3311	348.6692	E	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
8	813.4101	407.2087	796.3836	398.6954	795.3995	398.2034	V	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
9	***912.4785***	456.7429	895.4520	448.2296	894.4680	447.7376	V	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
10	***1027.5055***	514.2564	1010.4789	505.7431	1009.4949	505.2511	D	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
11	1098.5426	549.7749	1081.5160	541.2617	1080.5320	540.7696	A	218.1499	109.5786	201.1234	101.0653			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IQNAGTEVVDAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G47520.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.3	1243.6408	-0.0006	IQNAGTEVVDAK
14.7	1243.6408	-0.0006	IQNGGTEVVEAK
13.1	1243.6383	0.0019	KLNKCYGFSK
11.6	1243.6408	-0.0006	IQELETQLDR
4.2	1243.6383	0.0020	QLKNWMAPEK
0.7	1243.6408	-0.0006	QELITAPTESR
0.7	1243.6422	-0.0019	VVHFNRTDTR
0.1	1243.6383	0.0019	FHPSMNLSIAK

AT3G47650.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGGVNLIDHFNGQFK**
Found in **AT3G47650.1** in **TAIR_Arabidopsis**, Symbols: | bundle-sheath defective protein 2 family / bsd2 family | chr3:17580561-17581247 FORWARD

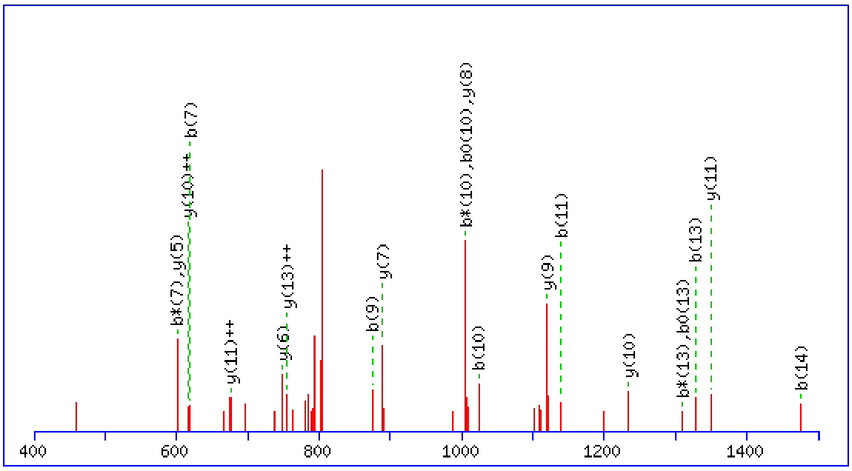
Match to Query 6772: 1622.732652 from(812.373602,2+) index(5850)
Title: Elution from: 54.405 to 54.405 scan no 7626 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1500 Da Full range

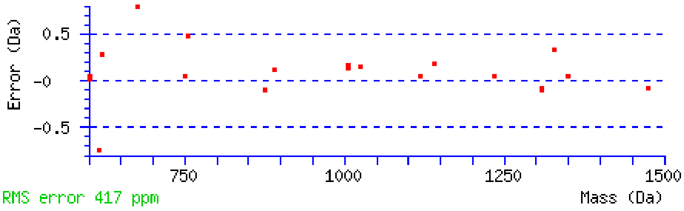
Label all possible matches ○ Label matches used for scoring ●

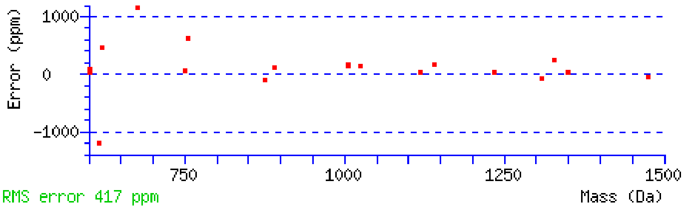
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1622.7327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 2.6e-006
Matches : 21/132 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							15
2	117.0443	59.0258					G	1565.7216	783.3644	1547.6980	774.3526	1547.7110	774.3591	14
3	175.0628	88.0350					G	1507.7031	754.3552	1489.6795	745.3434	1489.6925	745.3499	13
4	275.1282	138.0677					V	1449.6846	725.3459	1431.6610	716.3341	1431.6740	716.3406	12
5	391.1652	196.0862	373.1416	187.0745			N	***1349.6191***	675.3132	1331.5955	666.3014	1331.6085	666.3079	11
6	505.2463	253.1268	487.2227	244.1150			L	***1233.5821***	617.2947	1215.5585	608.2829	1215.5715	608.2894	10
7	***619.3274***	310.1673	601.3038	301.1556			I	***1119.5010***	560.2541	1101.4774	551.2424	1101.4904	551.2489	9
8	735.3514	368.1793	717.3278	359.1675	717.3408	359.1741	D	***1005.4199***	503.2136	987.3963	494.2018	987.4093	494.2083	8
9	***875.4014***	438.2043	857.3778	429.1926	857.3908	429.1991	H	***889.3959***	445.2016	871.3723	436.1898			7
10	***1023.4669***	512.2371	1005.4433	503.2253	1005.4563	503.2318	F	***749.3459***	375.1766	731.3223	366.1648			6
11	***1139.5039***	570.2556	1121.4803	561.2438	1121.4933	561.2503	N	***601.2805***	301.1439	583.2569	292.1321			5
12	1197.5224	599.2648	1179.4988	590.2530	1179.5118	590.2595	G	485.2435	243.1254	467.2199	234.1136			4
13	***1327.5750***	664.2911	1309.5514	655.2793	1309.5644	655.2859	Q	427.2250	214.1161	409.2014	205.1043			3
14	***1475.6405***	738.3239	1457.6169	729.3121	1457.6299	729.3186	F	297.1723	149.0898	279.1487	140.0780			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT3G47650.1

NCBI **BLAST** search of GGGVNLIDHFNGQFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.0	1622.7327	-0.0001	GGGVNLIDHFNGQFK
9.5	1622.7314	0.0013	MNKFRGLFVGNMR
9.3	1622.7278	0.0048	ARATIPGALFDDDDK
8.3	1622.7305	0.0021	HSKVREDDLYSPR
3.6	1622.7361	-0.0035	YKVGDMGVKHAEPR
2.8	1622.7280	0.0046	LCHSIYQWRNPK
0.8	1622.7361	-0.0035	NEIPKEGFTRHMK
0.6	1622.7339	-0.0013	LRSHVGSDKIDCSK

AT3G47800.1

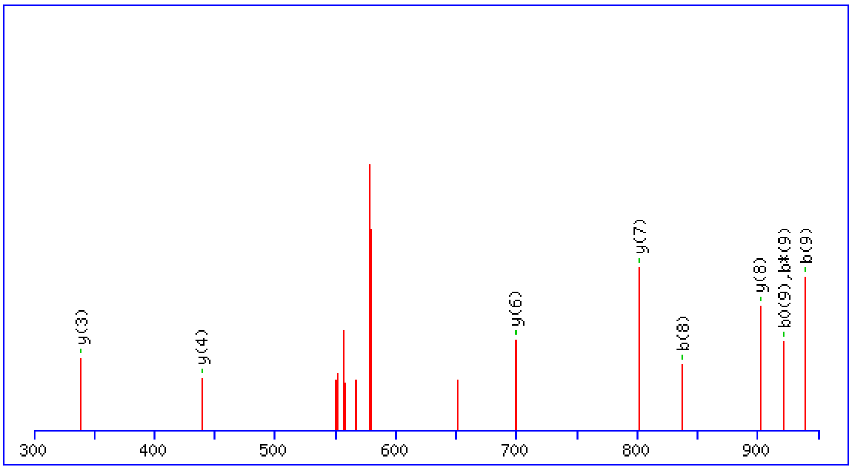
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAVVTEQVTGR**
Found in **AT3G47800.1** in **TAIR_Arabidopsis**, Symbols: | aldose 1-epimerase family protein | chr3:17645956-17647983 FORWARD

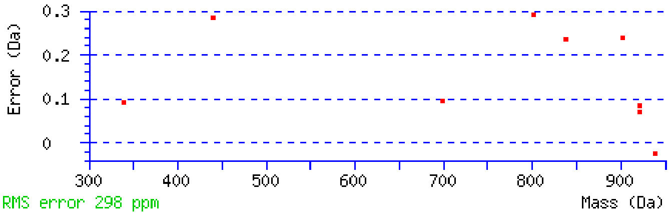
Match to Query 3555: 1174.576486 from(588.295519,2+) index(1203)
Title: Elution from: 21.026 to 21.026 scan no 1782 cid35.00 polarity:+
Data file D1d-1_1.mgf

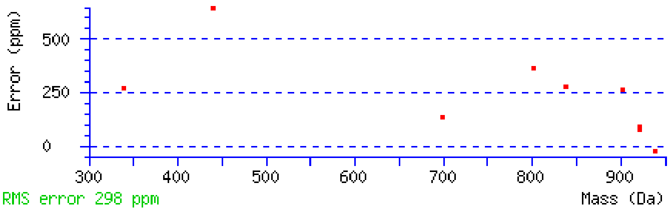
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1174.5752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00032
Matches : 9/104 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							11
2	175.0861	88.0467			157.0756	79.0414	A	1073.5378	537.2725	1055.5142	528.2607	1055.5272	528.2672	10
3	275.1516	138.0794			257.1410	129.0741	V	1001.5036	501.2555	983.4801	492.2437	983.4931	492.2502	9
4	375.2170	188.1122			357.2065	179.1069	V	***901.4382***	451.2227	883.4146	442.2109	883.4276	442.2175	8
5	477.2617	239.1345			459.2512	230.1292	T	***801.3727***	401.1900	783.3492	392.1782	783.3622	392.1847	7
6	607.3014	304.1543			589.2908	295.1490	E	***699.3280***	350.1677	681.3044	341.1559	681.3175	341.1624	6
7	737.3540	369.1807	719.3304	360.1689	719.3435	360.1754	Q	569.2884	285.1478	551.2648	276.1360	551.2778	276.1426	5
8	**837.4195**	419.2134	819.3959	410.2016	819.4089	410.2081	V	***439.2358***	220.1215	421.2122	211.1097	421.2252	211.1162	4
9	**939.4642**	470.2357	921.4406	461.2239	921.4536	461.2304	T	***339.1703***	170.0888	321.1467	161.0770	321.1597	161.0835	3
10	997.4827	499.2450	979.4591	490.2332	979.4721	490.2397	G	237.1256	119.0664	219.1020	110.0546			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TAVVTEQVTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G47800.1

Score	Mr(calc)	Delta	Sequence
45.8	1174.5752	0.0013	TAVVTEQVTGR
14.7	1174.5752	0.0013	VSLATEKQER
12.2	1174.5752	0.0013	GITDTGLASIGR
10.9	1174.5775	-0.0010	VYTAAHITASK
2.8	1174.5775	-0.0010	GFAVPKEAQSK
2.7	1174.5779	-0.0014	NSEIGNLVRR
2.5	1174.5752	0.0013	EIAGTERKEK
2.3	1174.5782	-0.0017	LVLTMEDLSK
2.1	1174.5779	-0.0014	IEERAQGRAK
2.1	1174.5752	0.0013	KIKNGGETDAK

AT3G48000.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGLAAGVFTK**
Found in **AT3G48000.1** in **TAIR_Arabidopsis**, Symbols: ALDH2, ALDH2B4 | ALDH2B4 (ALDEHYDE DEHYDROGENASE 2); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD) | chr3:17728067-17730828 REVERSE

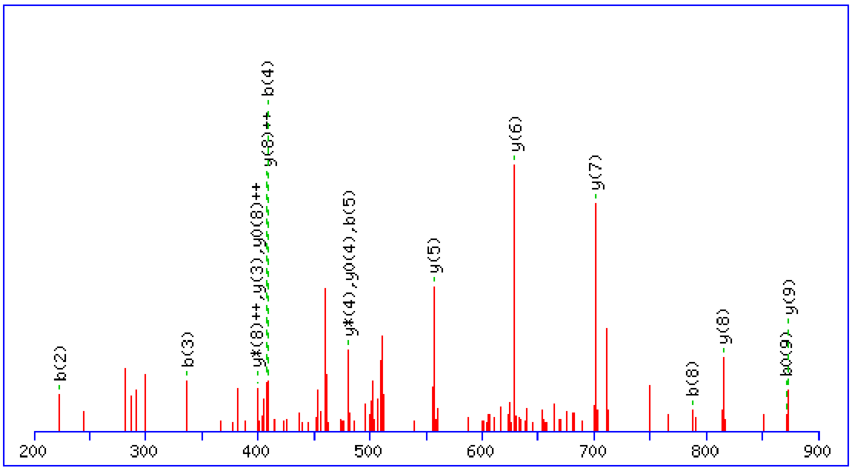
Match to Query 2718: 1036.522064 from(519.268308,2+) index(5104)
Title: Elution from: 45.935 to 45.935 scan no 6466 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

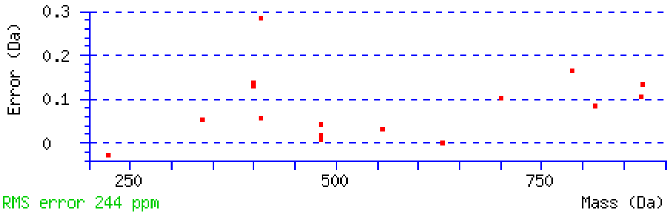
Label all possible matches ○ Label matches used for scoring ●

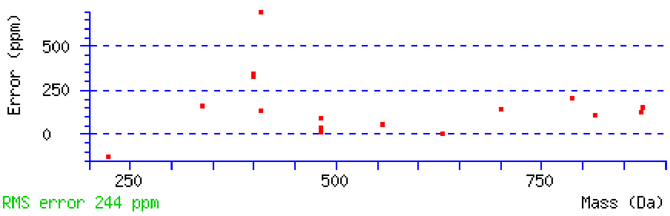
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1036.5219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00058
Matches : 17/72 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	165.0676	83.0375			**Y**							**10**
2	***223.0861***	112.0467			**G**	***873.4689***	437.2381	855.4453	428.2263	855.4583	428.2328	**9**
3	***337.1672***	169.0873			**L**	***815.4504***	408.2288	797.4268	399.2170	797.4398	399.2235	**8**
4	***409.2014***	205.1043			**A**	***701.3693***	351.1883	683.3457	342.1765	683.3587	342.1830	**7**
5	***481.2355***	241.1214			**A**	***629.3351***	315.1712	611.3115	306.1594	611.3246	306.1659	**6**
6	539.2540	270.1307			**G**	***557.3010***	279.1541	539.2774	270.1423	539.2904	270.1488	**5**
7	639.3195	320.1634			**V**	499.2825	250.1449	481.2589	241.1331	481.2719	241.1396	**4**
8	***787.3849***	394.1961			**F**	***399.2170***	200.1122	381.1935	191.1004	381.2065	191.1069	**3**
9	889.4296	445.2185	871.4191	436.2132	**T**	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	**2**
10					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of YGLAAGVFTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G48000.1

Score	Mr(calc)	Delta	Sequence
40.1	1036.5219	0.0001	YGLAAGVFTK
21.8	1036.5224	-0.0003	YLKARDTR
1.7	1036.5242	-0.0021	WFAYLLSK
1.5	1036.5231	-0.0010	TTVSSMKKK

AT3G48050.1

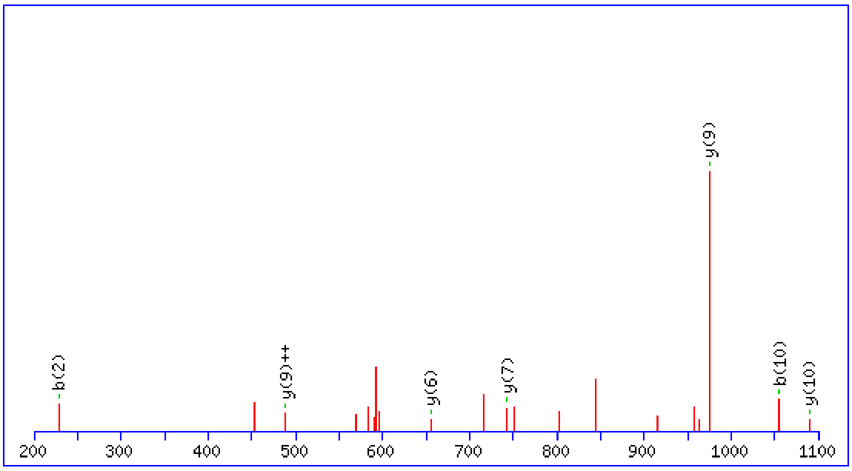
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILNDSDSGELK**
Found in **AT3G48050.1** in **TAIR_Arabidopsis**, Symbols: | bromo-adjacent homology (BAH) domain-containing protein | chr3:17745255-17750397 REVERSE

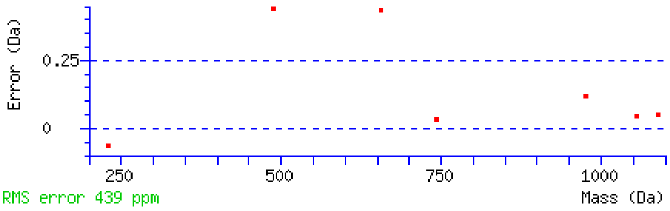
Match to Query 4286: 1202.547392 from(602.280972,2+) index(3086)
Title: Elution from: 29.661 to 29.661 scan no 3796 cid35.00 polarity:+
Data file D1d-3_2.mgf

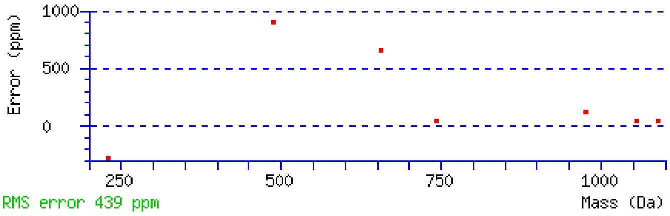
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1202.5441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.039
Matches : 7/106 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							11
2	**229.1695**	115.0884					L	***1089.4703***	545.2388	1071.4467	536.2270	1071.4597	536.2335	10
3	345.2065	173.1069	327.1829	164.0951			N	***975.3892***	488.1982	957.3656	479.1864	957.3786	479.1929	9
4	461.2304	231.1189	443.2069	222.1071	443.2199	222.1136	D	859.3522	430.1797	841.3286	421.1679	841.3416	421.1744	8
5	549.2595	275.1334	531.2359	266.1216	531.2489	266.1281	S	***743.3282***	372.1677	725.3046	363.1559	725.3176	363.1625	7
6	665.2835	333.1454	647.2599	324.1336	647.2729	324.1401	D	***655.2991***	328.1532	637.2756	319.1414	637.2886	319.1479	6
7	753.3126	377.1599	735.2890	368.1481	735.3020	368.1546	S	539.2752	270.1412	521.2516	261.1294	521.2646	261.1359	5
8	811.3311	406.1692	793.3075	397.1574	793.3205	397.1639	G	451.2461	226.1267	433.2225	217.1149	433.2355	217.1214	4
9	941.3707	471.1890	923.3471	462.1772	923.3601	462.1837	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
10	**1055.4518**	528.2295	1037.4282	519.2177	1037.4412	519.2242	L	263.1880	132.0976	245.1644	123.0858			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ILNDSDSGELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G48050.1

Score	Mr(calc)	Delta	Sequence
22.9	1202.5441	0.0033	ILNDSDSGELK
8.7	1202.5463	0.0011	EPDTTPFKEK
3.9	1202.5468	0.0006	DGLRSNPSDVK
2.6	1202.5441	0.0033	AVSEVEEKDGK
2.6	1202.5494	-0.0020	GTRRHETAEK
2.6	1202.5468	0.0006	NRILNEDEGK
2.5	1202.5463	0.0011	FDGETLDPLGK
0.9	1202.5476	-0.0002	YSVMRKTMR
0.7	1202.5468	0.0006	LEEENERLR

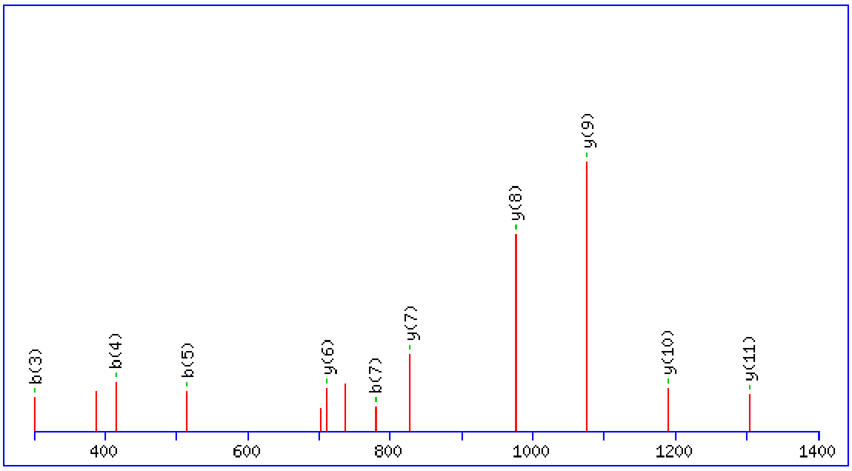
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPIIVFDDVDIDK**
Found in **AT3G48170.1** in **TAIR_Arabidopsis**, Symbols: ALDH10A9 | ALDH10A9 (Aldehyde dehydrogenase 10A9); 3-chloroallyl aldehyde dehydrogenase | chr3:17797275-17800903 REVERSE

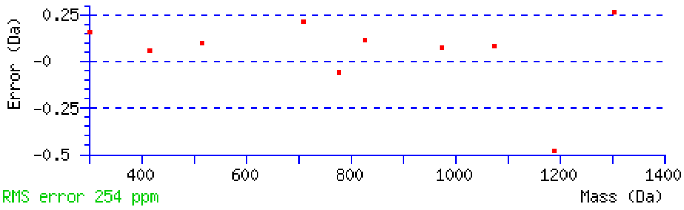
Match to Query 6105: 1488.715858 from(745.365205,2+) index(9010)
Title: Elution from: 80.597 to 80.597 scan no 12127 cid35.00 polarity:+
Data file 0-3_2.mgf

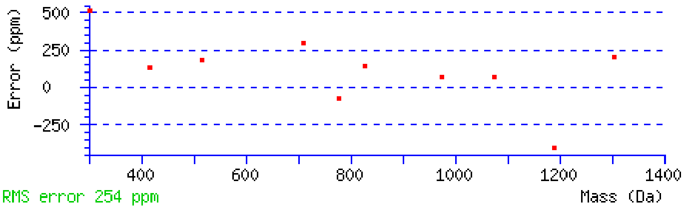
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1488.7140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 5.2e-005
Matches : 10/118 fragment ions using 14 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218	71.0258	36.0165	S							13
2	187.0861	94.0467	169.0756	85.0414	P	1401.6922	701.3498	1383.6686	692.3380	1383.6817	692.3445	12
3	**301.1672**	151.0873	283.1567	142.0820	I	***1303.6424***	652.3249	1285.6188	643.3131	1285.6319	643.3196	11
4	**415.2483**	208.1278	397.2378	199.1225	I	***1189.5613***	595.2843	1171.5377	586.2725	1171.5508	586.2790	10
5	**515.3138**	258.1605	497.3032	249.1552	V	***1075.4802***	538.2438	1057.4566	529.2320	1057.4697	529.2385	9
6	663.3792	332.1933	645.3687	323.1880	F	***975.4148***	488.2110	957.3912	479.1992	957.4042	479.2057	8
7	**779.4032**	390.2052	761.3926	381.2000	D	***827.3493***	414.1783	809.3257	405.1665	809.3388	405.1730	7
8	895.4272	448.2172	877.4166	439.2120	D	***711.3254***	356.1663	693.3018	347.1545	693.3148	347.1610	6
9	995.4926	498.2500	977.4821	489.2447	V	595.3014	298.1543	577.2778	289.1425	577.2908	289.1490	5
10	1111.5166	556.2619	1093.5061	547.2567	D	495.2359	248.1216	477.2123	239.1098	477.2254	239.1163	4
11	1225.5977	613.3025	1207.5872	604.2972	I	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	1341.6217	671.3145	1323.6111	662.3092	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SPIIVFDDVDIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G48170.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.3	1488.7140	0.0019	SPIIVFDDVDIDK
51.3	1488.7140	0.0019	SPLIVFDDVDLDK
12.9	1488.7201	-0.0042	VVEMGSHKELLSK
4.9	1488.7124	0.0035	LSRGISSRAMSFR
4.6	1488.7167	-0.0008	APELATEVSNWKK

AT3G48190.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVDMDLDLAEDTK**
Found in **AT3G48190.1** in **TAIR_Arabidopsis**, Symbols: ATATM, ATM | ATM (ATAXIA-TELANGIECTASIA MUTATED) | chr3:17808613-17834206 FORWARD

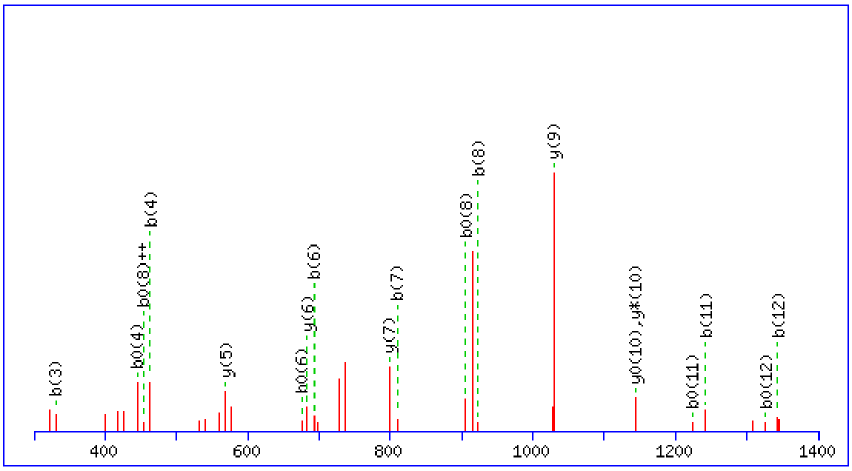
Match to Query 5799: 1490.656446 from(746.335499,2+) index(7132)
Title: Elution from: 64.325 to 64.325 scan no 9415 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1400 Da Full range

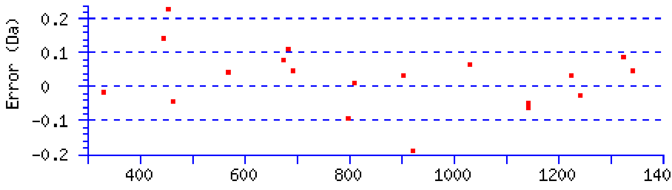
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

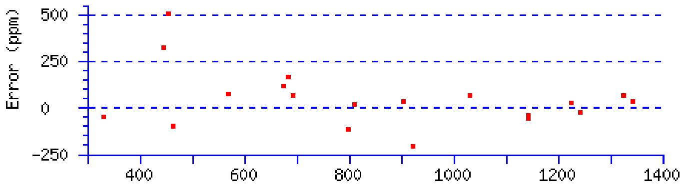


Monoisotopic mass of neutral peptide Mr(calc): 1490.6602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0013
Matches : 19/114 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			I							13
2	215.1538	108.0805			V	1377.5864	689.2969	1359.5629	680.2851	1359.5759	680.2916	12
3	***331.1778***	166.0925	313.1672	157.0873	D	1277.5210	639.2641	1259.4974	630.2523	1259.5104	630.2589	11
4	***463.2153***	232.1113	445.2048	223.1060	M	1161.4970	581.2521	1143.4734	572.2404	1143.4865	572.2469	10
5	579.2393	290.1233	561.2287	281.1180	D	**1029.4595**	515.2334	1011.4359	506.2216	1011.4489	506.2281	9
6	***693.3204***	347.1638	675.3098	338.1586	L	913.4355	457.2214	895.4119	448.2096	895.4250	448.2161	8
7	***809.3444***	405.1758	791.3338	396.1705	D	**799.3544**	400.1808	781.3308	391.1691	781.3439	391.1756	7
8	***923.4255***	462.2164	905.4149	453.2111	L	**683.3304**	342.1689	665.3069	333.1571	665.3199	333.1636	6
9	995.4596	498.2335	977.4491	489.2282	A	**569.2493**	285.1283	551.2258	276.1165	551.2388	276.1230	5
10	1125.4993	563.2533	1107.4887	554.2480	E	497.2152	249.1112	479.1916	240.0994	479.2046	240.1060	4
11	***1241.5232***	621.2653	1223.5127	612.2600	D	367.1756	184.0914	349.1520	175.0796	349.1650	175.0861	3
12	***1343.5679***	672.2876	1325.5574	663.2823	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
13					K	149.1069	75.0571	131.0833	66.0453			1



RMS error 160 ppm



RMS error 160 ppm

NCBI **BLAST** search of IVDMDLDLAEDTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G48190.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.8	1490.6602	-0.0038	IVDMDLDLAEDTK
7.7	1490.6600	-0.0035	NDDLGVARKDDPR
0.2	1490.6582	-0.0017	MTFATVKAMGTQR

AT3G48420.1

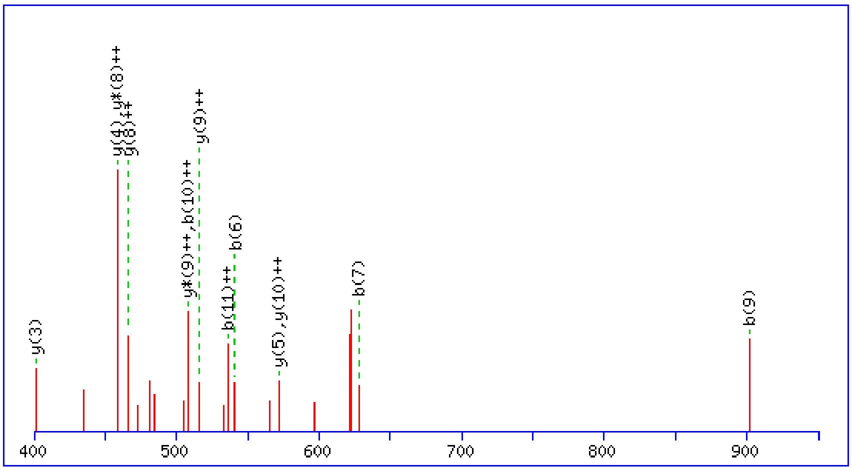
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVSAIVSCLLGPER**
Found in **AT3G48420.1** in **TAIR_Arabidopsis**, Symbols: | haloacid dehalogenase-like hydrolase family protein | chr3:17940728-17942536 FORWARD

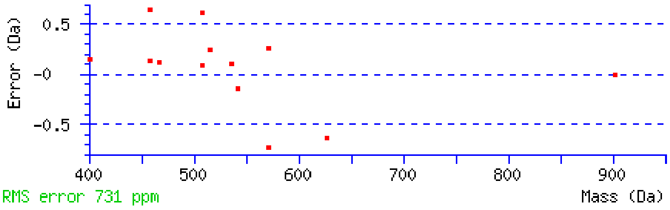
Match to Query 6168: 1470.789252 from(491.270360,3+) index(8606)
Title: Elution from: 75.480 to 75.480 scan no 11433 cid35.00 polarity:+
Data file D1d-3_2.mgf

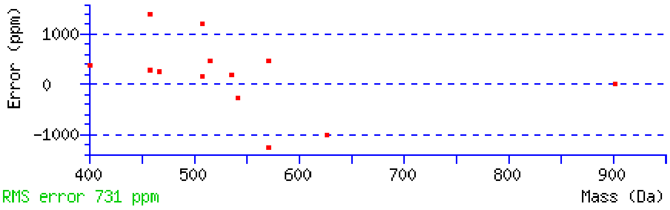
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1470.7864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.01
Matches : 13/124 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			A							14
2	171.1128	86.0600			V	1400.7566	700.8819	1383.7301	692.3687	1382.7460	691.8767	13
3	258.1448	129.5761	240.1343	120.5708	S	1301.6882	651.3477	1284.6616	642.8345	1283.6776	642.3425	12
4	329.1819	165.0946	311.1714	156.0893	A	1214.6562	607.8317	1197.6296	599.3184	1196.6456	598.8264	11
5	442.2660	221.6366	424.2554	212.6314	I	1143.6191	572.3132	1126.5925	563.7999	1125.6085	563.3079	10
6	***541.3344***	271.1709	523.3239	262.1656	V	1030.5350	515.7711	1013.5084	507.2579	1012.5244	506.7659	9
7	***628.3665***	314.6869	610.3559	305.6816	S	931.4666	466.2369	914.4400	457.7237	913.4560	457.2316	8
8	788.3971	394.7022	770.3865	385.6969	C	844.4346	422.7209	827.4080	414.2076	826.4240	413.7156	7
9	***901.4812***	451.2442	883.4706	442.2389	L	684.4039	342.7056	667.3774	334.1923	666.3933	333.7003	6
10	1014.5652	**507.7863**	996.5547	498.7810	L	***571.3198***	286.1636	554.2933	277.6503	553.3093	277.1583	5
11	1071.5867	**536.2970**	1053.5761	527.2917	G	***458.2358***	229.6215	441.2092	221.1083	440.2252	220.6162	4
12	1168.6395	584.8234	1150.6289	575.8181	P	***401.2143***	201.1108	384.1878	192.5975	383.2037	192.1055	3
13	1297.6821	649.3447	1279.6715	640.3394	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AVSAIVSCLLGPER

AT3G48420.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.1	1470.7864	0.0028	AVSAIVSCLLGPER
8.2	1470.7903	-0.0010	GGDIVKQLRNDTR
4.7	1470.7903	-0.0010	NDDIQRRLNSIK
3.5	1470.7871	0.0021	GGWLFKEPVDPVK
1.5	1470.7865	0.0028	VPSSSIPSLAVVCR
0.7	1470.7864	0.0028	DLIRKMLDPDQK
0.6	1470.7864	0.0028	LGATPKEMQDLIR
0.3	1470.7903	-0.0010	QAEERLERSVVR

AT3G48670.1

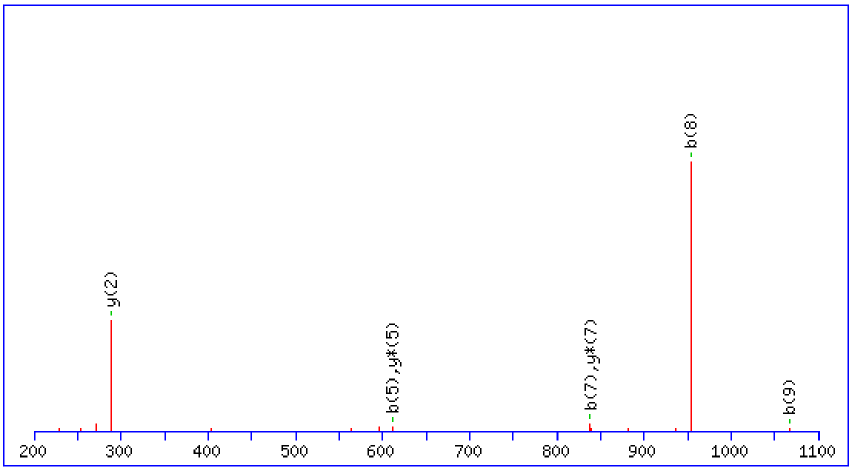
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQELLVQNLR**
Found in **AT3G48670.1** in **TAIR_Arabidopsis**, Symbols: | XH/XS domain-containing protein / XS zinc finger domain-containing protein | chr3:18042225-18044600 FORWARD

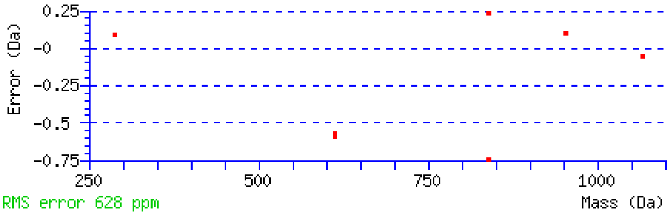
Match to Query 3864: 1239.728952 from(620.871752,2+) index(5715)
Title: Elution from: 52.163 to 52.163 scan no 7384 cid35.00 polarity:+
Data file D12h-2_3.mgf

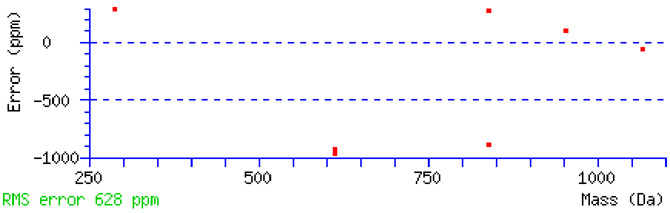
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1239.7299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0026
Matches : 7/90 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**10**
2	257.1608	129.0840	240.1343	120.5708			**Q**	1112.6422	556.8248	1095.6157	548.3115	1094.6317	547.8195	**9**
3	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	**E**	984.5837	492.7955	967.5571	484.2822	966.5731	483.7902	**8**
4	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	**L**	855.5411	428.2742	838.5145	419.7609			**7**
5	***612.3715***	306.6894	595.3450	298.1761	594.3610	297.6841	**L**	742.4570	371.7321	725.4304	363.2189			**6**
6	711.4400	356.2236	694.4134	347.7103	693.4294	347.2183	**V**	629.3729	315.1901	612.3464	306.6768			**5**
7	***839.4985***	420.2529	822.4720	411.7396	821.4880	411.2476	**Q**	530.3045	265.6559	513.2780	257.1426			**4**
8	***953.5415***	477.2744	936.5149	468.7611	935.5309	468.2691	**N**	402.2459	201.6266	385.2194	193.1133			**3**
9	***1066.6255***	533.8164	1049.5990	525.3031	1048.6150	524.8111	**L**	288.2030	144.6051	271.1765	136.0919			**2**
10							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of KQELLVQNLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G48670.1

Score	Mr(calc)	Delta	Sequence
28.6	1239.7299	-0.0009	KQELLVQNLR
26.3	1239.7299	-0.0009	ALAALRLEDLR
6.2	1239.7299	-0.0009	NGVALQKELIR
5.8	1239.7299	-0.0010	GNQQVILTVLR
2.1	1239.7299	-0.0010	NLVLKVPSSQR

Mascot: http://www.matrixscience.com/

AT3G48730.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLMPGGVNSPVR**
Found in **AT3G48730.1** in **TAIR_Arabidopsis**, Symbols: GSA2 | GSA2 (GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2); glutamate-1-semialdehyde 2,1-aminomutase | chr3:18060682-18062535 FORWARD

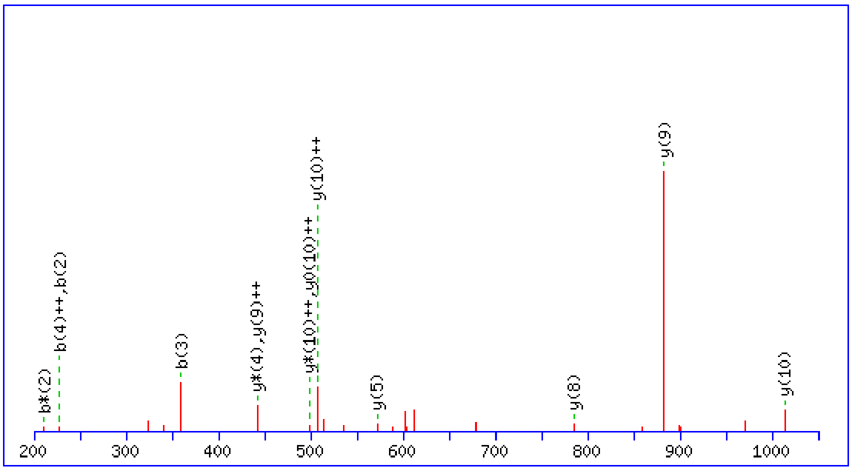
Match to Query 4628: 1239.635878 from(620.825215,2+) index(4236)
Title: Elution from: 39.477 to 39.477 scan no 5230 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1050 Da Full range

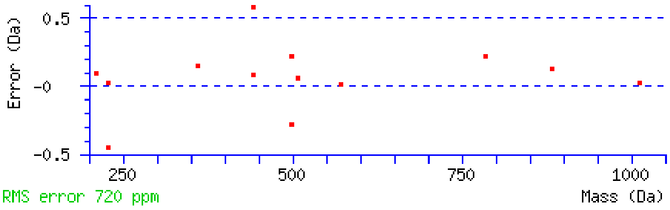
Label all possible matches ○ Label matches used for scoring ●

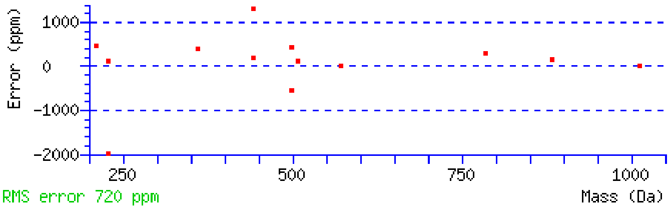
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1239.6394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.02
Matches : 13/110 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	**228.1343**	114.5708	211.1077	106.0575			L	1126.6037	563.8055	1109.5772	555.2922	1108.5932	554.8002	11
3	**359.1748**	180.0910	342.1482	171.5777			M	***1013.5197***	507.2635	996.4931	498.7502	995.5091	498.2582	10
4	456.2275	228.6174	439.2010	220.1041			P	***882.4792***	441.7432	865.4526	433.2300	864.4686	432.7380	9
5	513.2490	257.1281	496.2224	248.6149			G	***785.4264***	393.2169	768.3999	384.7036	767.4159	384.2116	8
6	570.2704	285.6389	553.2439	277.1256			G	728.4050	364.7061	711.3784	356.1928	710.3944	355.7008	7
7	669.3389	335.1731	652.3123	326.6598			V	671.3835	336.1954	654.3569	327.6821	653.3729	327.1901	6
8	783.3818	392.1945	766.3552	383.6813			N	***572.3151***	286.6612	555.2885	278.1479	554.3045	277.6559	5
9	870.4138	435.7105	853.3873	427.1973	852.4032	426.7053	S	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	4
10	967.4666	484.2369	950.4400	475.7237	949.4560	475.2316	P	371.2401	186.1237	354.2136	177.6104			3
11	1066.5350	533.7711	1049.5084	525.2579	1048.5244	524.7659	V	274.1874	137.5973	257.1608	129.0840			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of NLMPGGVNSPVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G48730.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.9	1239.6394	-0.0035	NLMPGGVNSPVR
7.4	1239.6394	-0.0035	LIGKLCTHNNA
7.2	1239.6360	-0.0001	RKDYDFGLAR

Mascot: http://www.matrixscience.com/

AT3G48770.1

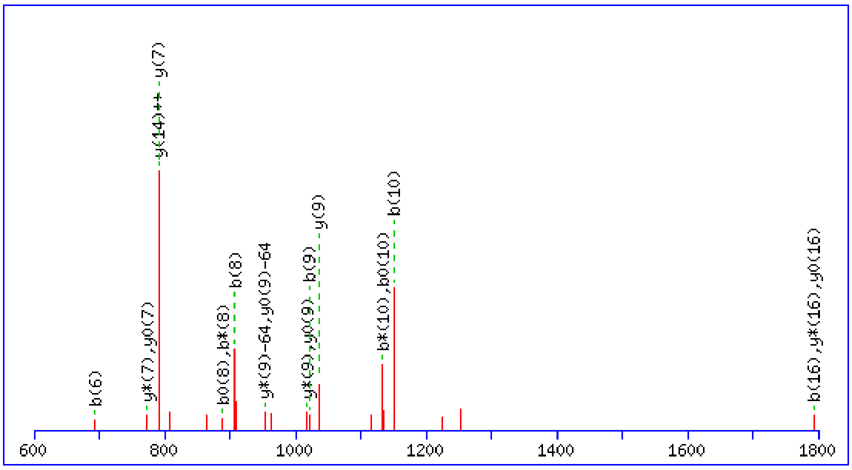
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETKTKPVIIETMTESAK**
Found in **AT3G48770.1** in **TAIR_Arabidopsis**, Symbols: | ATP binding / DNA binding | chr3:18090246-18097802 REVERSE

Match to Query 9066: 1940.948732 from(971.481642,2+) index(8341)
Title: Elution from: 74.102 to 74.102 scan no 11082 cid35.00 polarity:+
Data file 0-3_2.mgf

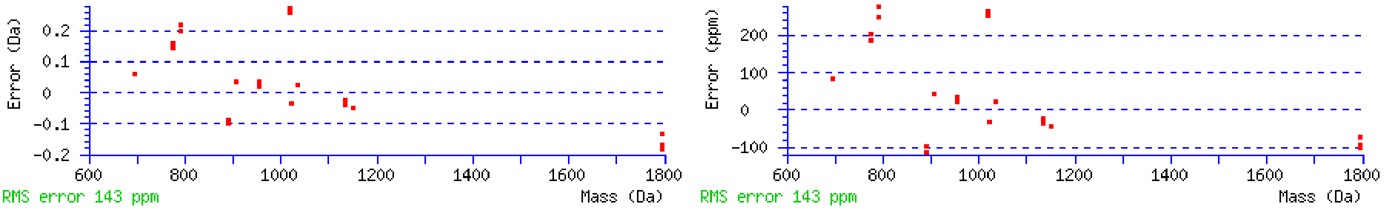
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1940.9485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.039
Matches : 20/280 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	**E**							**17**
2	233.0916	117.0494			215.0811	108.0442	**T**	1811.9161	906.4617	1793.8926	897.4499	1793.9056	897.4564	**16**
3	363.1806	182.0940	345.1571	173.0822	345.1701	173.0887	**K**	1709.8714	855.4394	1691.8478	846.4276	1691.8609	846.4341	**15**
4	465.2254	233.1163	447.2018	224.1045	447.2148	224.1110	**T**	1579.7824	790.3948	1561.7588	781.3830	1561.7718	781.3896	**14**
5	595.3144	298.1608	577.2908	289.1490	577.3038	289.1556	**K**	1477.7377	739.3725	1459.7141	730.3607	1459.7271	730.3672	**13**
6	***693.3642***	347.1857	675.3406	338.1739	675.3536	338.1805	**P**	1347.6486	674.3280	1329.6251	665.3162	1329.6381	665.3227	**12**
7	793.4296	397.2185	775.4061	388.2067	775.4191	388.2132	**V**	1249.5989	625.3031	1231.5753	616.2913	1231.5883	616.2978	**11**
8	***907.5107***	454.2590	889.4872	445.2472	889.5002	445.2537	**I**	1149.5334	575.2703	1131.5098	566.2585	1131.5228	566.2651	**10**
9	***1021.5918***	511.2996	1003.5683	502.2878	1003.5813	502.2943	**I**	**1035.4523**	518.2298	1017.4287	509.2180	1017.4417	509.2245	**9**
10	***1151.6315***	576.3194	1133.6079	567.3076	1133.6209	567.3141	**E**	921.3712	461.1892	903.3476	452.1774	903.3606	452.1840	**8**
11	1253.6762	627.3417	1235.6526	618.3299	1235.6656	618.3364	**T**	**791.3316**	396.1694	773.3080	387.1576	773.3210	387.1641	**7**
12	1401.7086	701.3579	1383.6850	692.3462	1383.6981	692.3527	**M**	689.2869	345.1471	671.2633	336.1353	671.2763	336.1418	**6**
13	1503.7533	752.3803	1485.7297	743.3685	1485.7428	743.3750	**T**	541.2544	271.1309	523.2308	262.1191	523.2439	262.1256	**5**
14	1633.7930	817.4001	1615.7694	808.3883	1615.7824	808.3948	**E**	439.2097	220.1085	421.1861	211.0967	421.1991	211.1032	**4**
15	1721.8220	861.4146	1703.7984	852.4029	1703.8115	852.4094	**S**	309.1701	155.0887	291.1465	146.0769	291.1595	146.0834	**3**
16	***1793.8562***	897.4317	1775.8326	888.4199	1775.8456	888.4264	**A**	221.1410	111.0741	203.1174	102.0624			**2**
17							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT3G48770.1



NCBI **BLAST** search of ETKTKPVIIETMTESAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.7	1940.9485	0.0002	ETKTKPVIIETMTESAK
8.6	1940.9431	0.0057	EILGICDNRLVLFNNK
4.4	1940.9478	0.0009	QKSEADFSSRAPELLLK
3.0	1940.9482	0.0005	LIGRNKPVDRSESTNTK
3.0	1940.9486	0.0001	VGIMGLHGMGGVGKTTLFK
2.0	1940.9512	-0.0024	ALSGSNIGVTIGIQNSMLK
2.0	1940.9430	0.0057	DMKQRHIASFLTTLEK
2.0	1940.9487	0.0001	RDPMGALGYAAMKPSLIK
1.2	1940.9504	-0.0017	AIVVDEPGVTRDRLYGR

Mascot: http://www.matrixscience.com/

AT3G48810.1

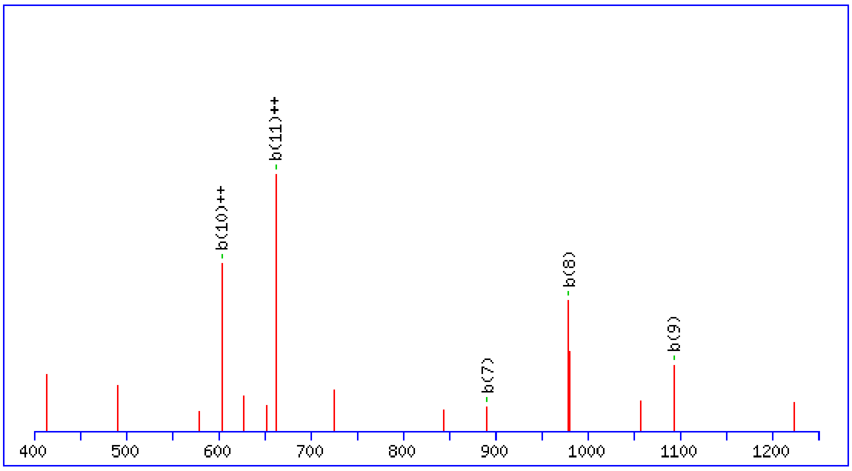
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MYLKEGCSLLLK**
Found in **AT3G48810.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:18108033-18110012 FORWARD

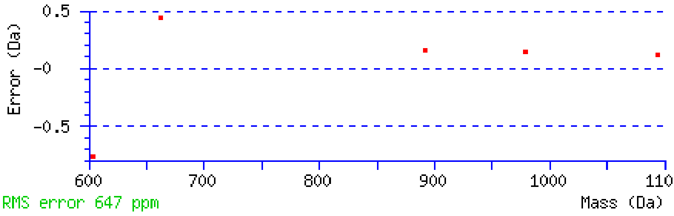
Match to Query 5994: 1468.720062 from(735.367307,2+) index(10455)
Title: Elution from: 100.393 to 100.393 scan no 14978 cid35.00 polarity:+
Data file D6h-1_2.mgf

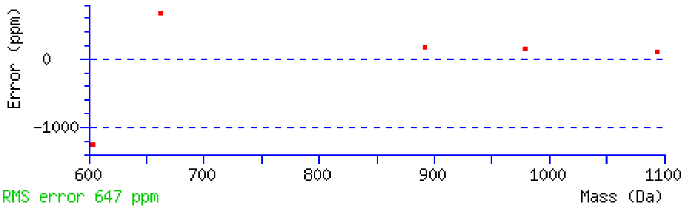
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.7228
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.034
Matches : 5/110 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					**M**							**12**
2	297.1052	149.0562					**Y**	1337.6926	669.3499	1319.6690	660.3381	1319.6820	660.3446	**11**
3	411.1863	206.0968					**L**	1173.6322	587.3197	1155.6086	578.3080	1155.6216	578.3145	**10**
4	541.2753	271.1413	523.2517	262.1295			**K**	1059.5511	530.2792	1041.5275	521.2674	1041.5405	521.2739	**9**
5	671.3149	336.1611	653.2913	327.1493	653.3044	327.1558	**E**	929.4621	465.2347	911.4385	456.2229	911.4515	456.2294	**8**
6	729.3334	365.1703	711.3098	356.1586	711.3229	356.1651	**G**	799.4225	400.2149	781.3989	391.2031	781.4119	391.2096	**7**
7	***891.3581***	446.1827	873.3346	437.1709	873.3476	437.1774	**C**	741.4040	371.2056	723.3804	362.1938	723.3934	362.2003	**6**
8	***979.3872***	490.1972	961.3636	481.1854	961.3766	481.1920	**S**	579.3792	290.1933	561.3556	281.1815	561.3687	281.1880	**5**
9	***1093.4683***	547.2378	1075.4447	538.2260	1075.4577	538.2325	**L**	491.3502	246.1787	473.3266	237.1669			**4**
10	1207.5494	***604.2783***	1189.5258	595.2665	1189.5388	595.2731	**L**	377.2691	189.1382	359.2455	180.1264			**3**
11	1321.6305	***661.3189***	1303.6069	652.3071	1303.6199	652.3136	**L**	263.1880	132.0976	245.1644	123.0858			**2**
12							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MYLKEGCSLLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G48810.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.0	1468.7228	-0.0028	MYLKEGCSLLLK
3.7	1468.7199	0.0002	DYCQRKINLLK
3.7	1468.7172	0.0029	LAKFGTSNMDLIK
3.7	1468.7199	0.0002	LTRFMVGANGQLK
3.4	1468.7194	0.0006	MQILFVGYGVEAK
3.3	1468.7228	-0.0027	VEQKMSLTLFMK
3.2	1468.7199	0.0002	FILMVNKQGQTR
3.1	1468.7194	0.0006	EAFVFLLCLTNK
3.1	1468.7187	0.0013	IFYRTYGHGPIK
3.1	1468.7228	-0.0028	KSVLSFMLECIK

Mascot: http://www.matrixscience.com/

AT3G48850.1

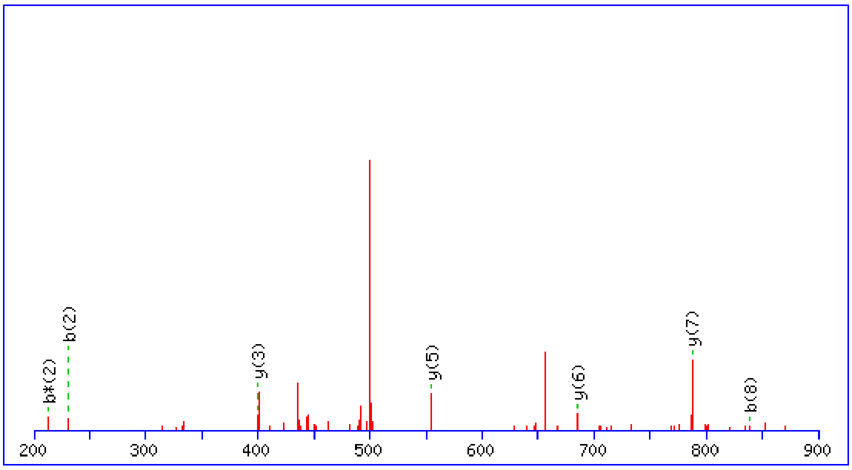
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQTQPGFAR**
Found in **AT3G48850.1** in **TAIR_Arabidopsis**, Symbols: | mitochondrial phosphate transporter, putative | chr3:18125744-18127405 REVERSE

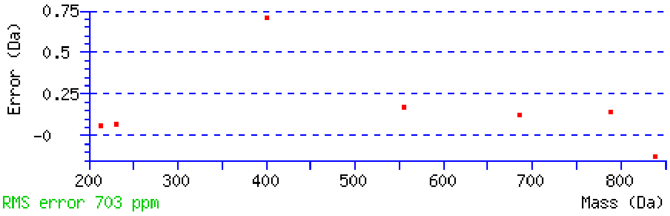
Match to Query 2663: 1016.482536 from(509.248544,2+) index(1024)
Title: Elution from: 13.961 to 13.961 scan no 1345 cid35.00 polarity:+
Data file D1d-3_3.mgf

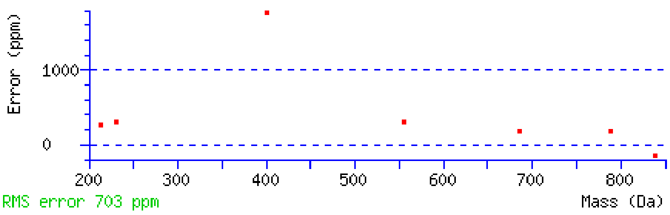
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1016.4831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.024
Matches : 7/78 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							9
2	**231.1254**	116.0663	213.1018	107.0545			Q	917.4250	459.2161	899.4014	450.2043	899.4144	450.2109	8
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	T	***787.3723***	394.1898	769.3488	385.1780	769.3618	385.1845	7
4	463.2227	232.1150	445.1991	223.1032	445.2122	223.1097	Q	***685.3276***	343.1675	667.3041	334.1557			6
5	561.2725	281.1399	543.2489	272.1281	543.2620	272.1346	P	***555.2750***	278.1411	537.2514	269.1293			5
6	619.2910	310.1492	601.2674	301.1374	601.2805	301.1439	G	457.2252	229.1162	439.2016	220.1044			4
7	767.3565	384.1819	749.3329	375.1701	749.3459	375.1766	F	***399.2067***	200.1070	381.1831	191.0952			3
8	**839.3906**	420.1990	821.3670	411.1872	821.3801	411.1937	A	251.1412	126.0743	233.1177	117.0625			2
9							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VQTQPGFAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	1016.4831	-0.0006	VQTQPGFAR

AT3G48850.1

10.6	1016.4805	0.0021	LDDDLFIR
9.3	1016.4839	-0.0013	SEIEIMLR
7.4	1016.4832	-0.0006	KAKEEGWR
7.3	1016.4836	-0.0010	VQGANQRAR
6.3	1016.4839	-0.0013	AKELAEMAK
5.6	1016.4809	0.0016	ARVEEDKR
2.7	1016.4836	-0.0010	VQANQRAGR
2.5	1016.4832	-0.0006	VENPFNKR
2.3	1016.4805	0.0021	LNGIDAFEK

Mascot: http://www.matrixscience.com/

AT3G48930.1

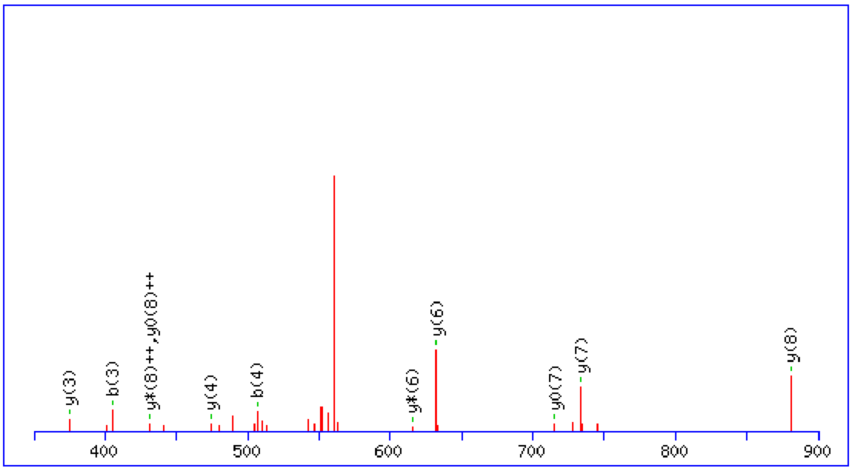
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CPFTGTVSIR**
Found in **AT3G48930.1** in **TAIR_Arabidopsis**, Symbols: EMB1080 | EMB1080 (EMBRYO DEFECTIVE 1080); structural constituent of ribosome | chr3:18152002-18153174 REVERSE

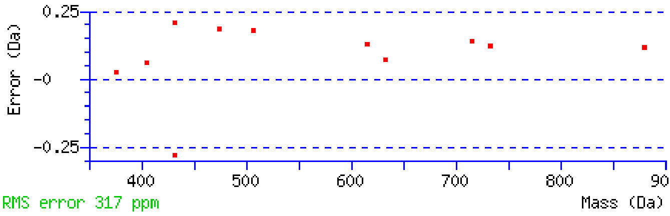
Match to Query 3672: 1136.561986 from(569.288269,2+) index(3874)
Title: Elution from: 36.466 to 36.466 scan no 4841 cid35.00 polarity:+
Data file 0-1_3.mgf

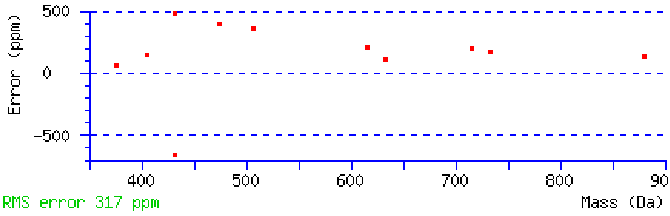
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1136.5649
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00077
Matches : 11/80 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.0379	81.0226			**C**							**10**
2	258.0907	129.5490			**P**	977.5415	489.2744	960.5149	480.7611	959.5309	480.2691	**9**
3	**405.1591**	203.0832			**F**	***880.4887***	440.7480	863.4621	432.2347	862.4781	431.7427	**8**
4	**506.2068**	253.6070	488.1962	244.6017	**T**	***733.4203***	367.2138	716.3937	358.7005	715.4097	358.2085	**7**
5	563.2282	282.1178	545.2177	273.1125	**G**	***632.3726***	316.6899	615.3461	308.1767	614.3620	307.6847	**6**
6	664.2759	332.6416	646.2654	323.6363	**T**	575.3511	288.1792	558.3246	279.6659	557.3406	279.1739	**5**
7	763.3443	382.1758	745.3338	373.1705	**V**	***474.3035***	237.6554	457.2769	229.1421	456.2929	228.6501	**4**
8	850.3764	425.6918	832.3658	416.6865	**S**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
9	963.4604	482.2339	945.4499	473.2286	**I**	288.2030	144.6051	271.1765	136.0919			**2**
10					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of CPFTGTVSIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G48930.1

Score	Mr(calc)	Delta	Sequence
38.0	1136.5649	-0.0029	CPFTGTVSIR
14.5	1136.5649	-0.0029	CFPTSIVTGR
0.6	1136.5648	-0.0028	LCDVVASFAR
0.6	1136.5614	0.0005	FINNPVDYR
0.6	1136.5648	-0.0028	VINDNCKFK
0.1	1136.5649	-0.0029	VFCEGIGVTR

AT3G49010.1

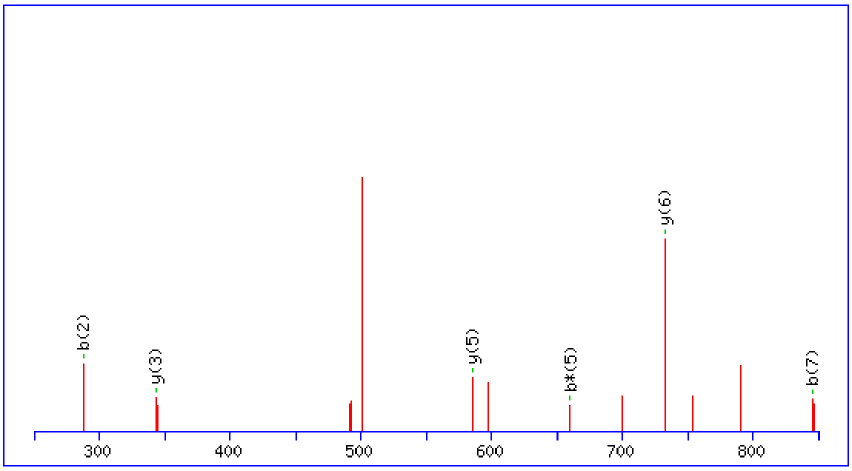
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWFNQPAR**
Found in **AT3G49010.1** in **TAIR_Arabidopsis**, Symbols: BBC1, RSU2 | ATBBC1 (breast basic conserved 1); structural constituent of ribosome | chr3:18177956-18179032 REVERSE

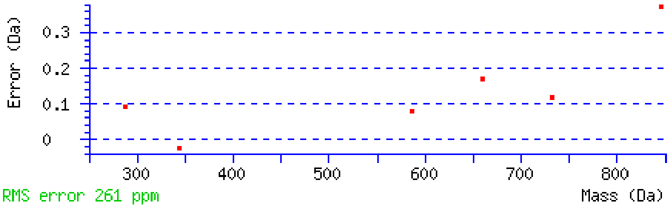
Match to Query 2816: 1018.497124 from(510.255838,2+) index(3503)
Title: Elution from: 32.632 to 32.632 scan no 4300 cid35.00 polarity:+
Data file D1d-3_2.mgf

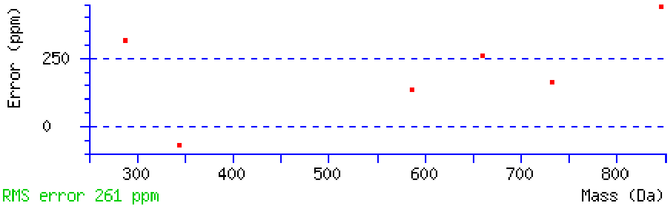
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1018.4985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.042
Matches : 6/64 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	102.0550	51.5311			84.0444	42.5258	T					8
2	***288.1343***	144.5708			270.1237	135.5655	W	918.4581	459.7327	901.4315	451.2194	7
3	435.2027	218.1050			417.1921	209.0997	F	***732.3787***	366.6930	715.3522	358.1797	6
4	549.2456	275.1264	532.2191	266.6132	531.2350	266.1212	N	***585.3103***	293.1588	568.2838	284.6455	5
5	677.3042	339.1557	660.2776	330.6425	659.2936	330.1504	Q	471.2674	236.1373	454.2409	227.6241	4
6	774.3570	387.6821	757.3304	379.1688	756.3464	378.6768	P	***343.2088***	172.1081	326.1823	163.5948	3
7	***845.3941***	423.2007	828.3675	414.6874	827.3835	414.1954	A	246.1561	123.5817	229.1295	115.0684	2
8							R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of TWFNQPAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.0	1018.4985	-0.0013	TWFNQPAR

AT3G49010.1

14.2	1018.4978	-0.0007	MNGGESRLR
3.9	1018.4978	-0.0007	MDNTNRLR
2.2	1018.4978	-0.0007	SRPCDKTR
1.2	1018.4978	-0.0007	TRAQQMER
1.1	1018.4978	-0.0007	CRALAGSER
1.1	1018.4978	-0.0007	MPSATRQGR
1.1	1018.4944	0.0027	YNGRAPGER
0.9	1018.4971	0.0000	TEDVEIWK

AT3G49120.1

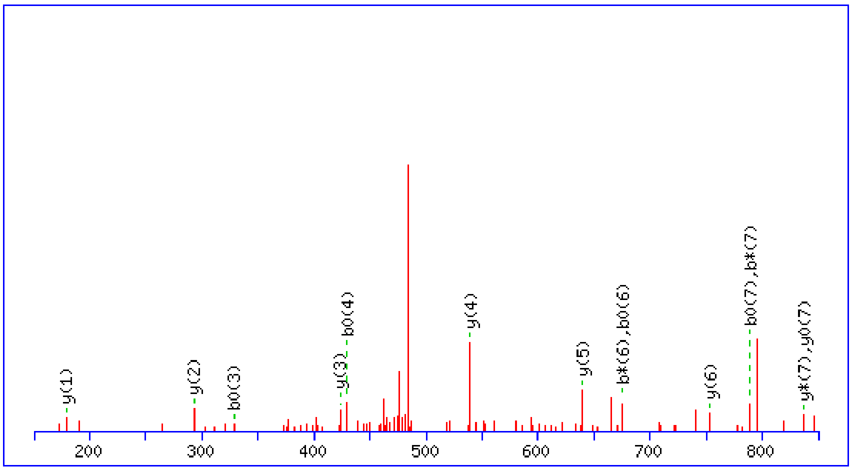
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETIVNELR**
Found in **AT3G49120.1** in **TAIR_Arabidopsis**, Symbols: ATPERX34, PERX34, PRXCB, ATPCB | ATPCB/ATPERX34/PERX34/PRXCB (PEROXIDASE 34); peroxidase | chr3:18218804-18221026 FORWARD

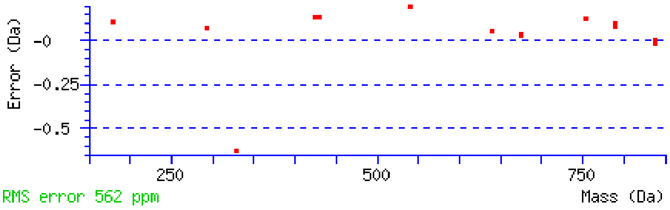
Match to Query 2262: 984.489442 from(493.251997,2+) index(3337)
Title: Elution from: 32.347 to 32.347 scan no 4143 cid35.00 polarity:+
Data file D6h-3_2.mgf

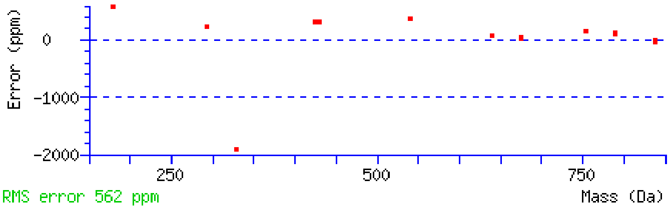
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.4884
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0033
Matches : 14/72 fragment ions using 21 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	131.0469	66.0271			113.0363	57.0218	**E**							8
2	233.0916	117.0494			215.0811	108.0442	**T**	855.4561	428.2317	837.4325	419.2199	837.4455	419.2264	7
3	347.1727	174.0900			329.1622	165.0847	**I**	***753.4114***	377.2093	735.3878	368.1975	735.4008	368.2040	6
4	447.2382	224.1227			429.2276	215.1174	**V**	***639.3303***	320.1688	621.3067	311.1570	621.3197	311.1635	5
5	563.2752	282.1412	545.2516	273.1294	545.2646	273.1359	**N**	***539.2648***	270.1360	521.2412	261.1243	521.2543	261.1308	4
6	693.3148	347.1610	675.2912	338.1492	675.3042	338.1558	**E**	***423.2278***	212.1175	405.2042	203.1058	405.2173	203.1123	3
7	807.3959	404.2016	789.3723	395.1898	789.3853	395.1963	**L**	***293.1882***	147.0977	275.1646	138.0859			2
8							**R**	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ETIVNELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.2	984.4884	0.0010	ETIVNELR

AT3G49120.1

23.0	984.4884	0.0010	IKEADELR
14.6	984.4884	0.0010	DDIIGATLR
13.9	984.4911	-0.0017	KHSSDKIR
12.4	984.4884	0.0010	SLLENELR
12.3	984.4884	0.0010	LELSDIAGR
9.4	984.4911	-0.0016	SKTQTHLR
9.2	984.4884	0.0010	ELENSLLR
8.2	984.4884	0.0010	SNDAGIVLGK
7.0	984.4884	0.0010	GNQTVLVDK

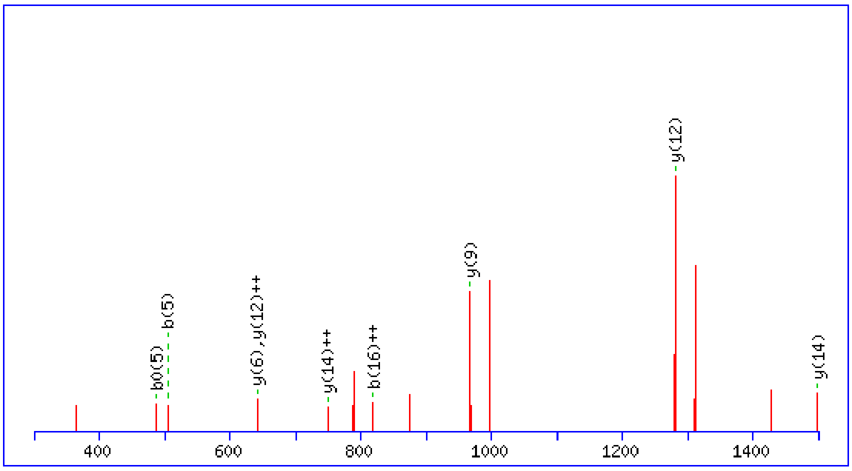
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLLTDPTLPLLTDSALK**
Found in **AT3G49560.1** in **TAIR_Arabidopsis**, Symbols: | mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr3:18381629-18382806 FORWARD

Match to Query 8640: 1784.949332 from(893.481942,2+) index(10528)
Title: Elution from: 99.363 to 99.363 scan no 14845 cid35.00 polarity:+
Data file 0-3_1.mgf

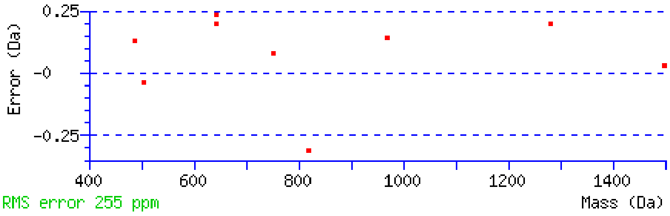
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

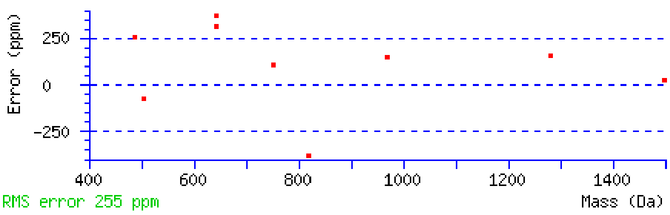


Monoisotopic mass of neutral peptide Mr(calc): 1784.9496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.017
Matches : 10/148 fragment ions using 14 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	59.0258	30.0165			G							17
2	173.1069	87.0571			L	1727.9384	864.4728	1709.9148	855.4610	1709.9278	855.4675	16
3	287.1880	144.0976			L	1613.8573	807.4323	1595.8337	798.4205	1595.8467	798.4270	15
4	389.2327	195.1200	371.2221	186.1147	T	***1499.7762***	750.3917	1481.7526	741.3799	1481.7656	741.3864	14
5	**505.2567**	253.1320	487.2461	244.1267	D	1397.7315	699.3694	1379.7079	690.3576	1379.7209	690.3641	13
6	603.3065	302.1569	585.2959	293.1516	P	***1281.7075***	641.3574	1263.6839	632.3456	1263.6969	632.3521	12
7	705.3512	353.1792	687.3406	344.1739	T	1183.6577	592.3325	1165.6341	583.3207	1165.6471	583.3272	11
8	**819.4323**	410.2198	801.4217	401.2145	L	1081.6130	541.3101	1063.5894	532.2983	1063.6024	532.3048	10
9	917.4821	459.2447	899.4715	450.2394	P	***967.5319***	484.2696	949.5083	475.2578	949.5213	475.2643	9
10	1031.5632	516.2852	1013.5526	507.2799	L	869.4821	435.2447	851.4585	426.2329	851.4715	426.2394	8
11	1145.6443	573.3258	1127.6337	564.3205	L	755.4010	378.2041	737.3774	369.1923	737.3904	369.1988	7
12	1247.6890	624.3481	1229.6784	615.3428	T	***641.3199***	321.1636	623.2963	312.1518	623.3093	312.1583	6
13	1363.7130	682.3601	1345.7024	673.3548	D	539.2752	270.1412	521.2516	261.1294	521.2646	261.1359	5
14	1451.7420	726.3747	1433.7315	717.3694	S	423.2512	212.1292	405.2276	203.1174	405.2406	203.1239	4
15	1523.7762	762.3917	1505.7656	753.3864	A	335.2221	168.1147	317.1985	159.1029			3
16	1637.8573	819.4323	1619.8467	810.4270	L	263.1880	132.0976	245.1644	123.0858			2
17					K	149.1069	75.0571	131.0833	66.0453			1

AT3G49560.1





NCBI **BLAST** search of GLLTDPTLPLLTDSALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.1	1784.9496	-0.0003	GLLTDPTLPLLTDSALK

Mascot: http://www.matrixscience.com/

AT3G49650.1

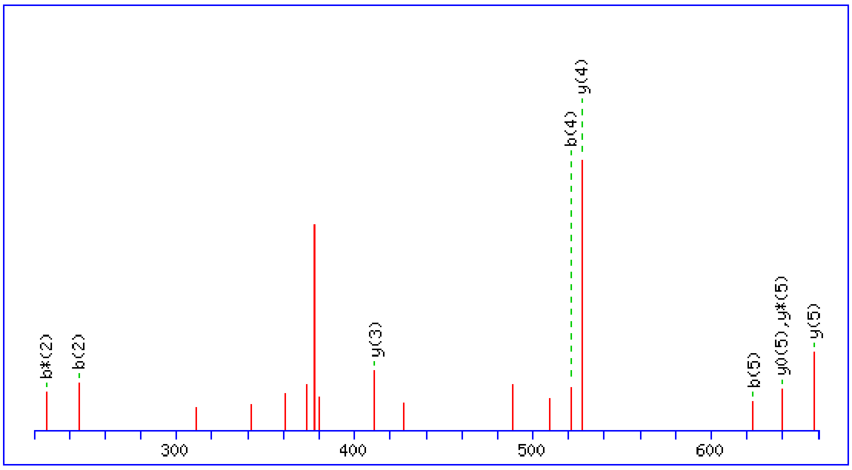
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQNRTK**
Found in **AT3G49650.1** in **TAIR_Arabidopsis**, Symbols: | kinesin motor protein-related | chr3:18416245-18420387 REVERSE

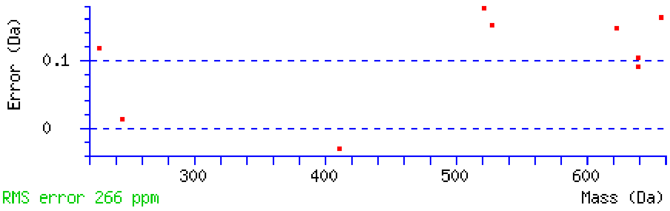
Match to Query 852: 770.405872 from(386.210212,2+) index(4039)
Title: Elution from: 37.205 to 37.205 scan no 4983 cid35.00 polarity:+
Data file C7-1_1.mgf

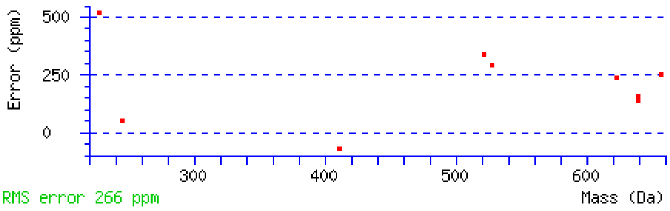
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.4043
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0039
Matches : 9/48 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							6
2	***245.1410***	123.0741	227.1174	114.0624			Q	***657.3305***	329.1689	639.3069	320.1571	639.3199	320.1636	5
3	361.1780	181.0926	343.1544	172.0809			N	***527.2778***	264.1426	509.2543	255.1308	509.2673	255.1373	4
4	***521.2673***	261.1373	503.2437	252.1255			R	***411.2408***	206.1241	393.2173	197.1123	393.2303	197.1188	3
5	***623.3120***	312.1596	605.2884	303.1478	605.3014	303.1543	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
6							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IQNRTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.0	770.4043	0.0016	IQNRTK
31.1	770.4072	-0.0014	LKDMLK
25.3	770.4039	0.0020	QIDFIK
25.3	770.4072	-0.0014	LKDLMK

AT3G49650.1

25.3	770.4039	0.0020	LQDLFK
19.5	770.4039	0.0020	LEFVQK
19.5	770.4072	-0.0014	LEMVKK
16.2	770.4072	-0.0014	KLMDIK
16.0	770.4039	0.0020	INEFLK
16.0	770.4072	-0.0014	LDKMLK

AT3G49910.1

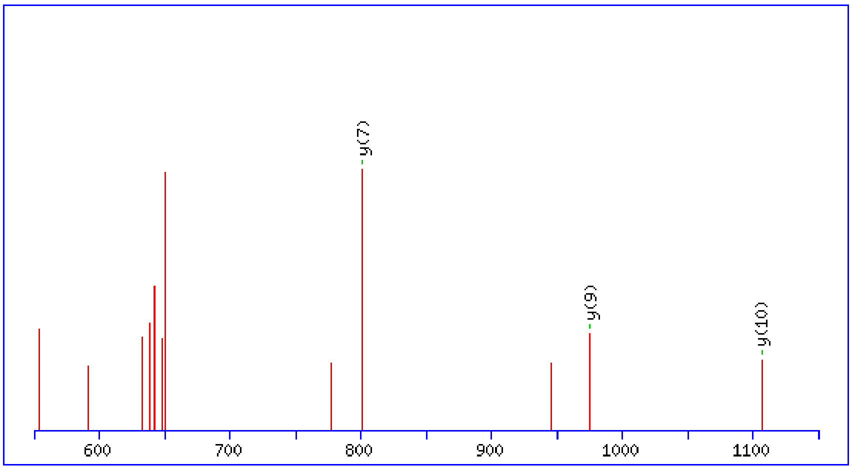
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIMSSPLSTDLR**
Found in **AT3G49910.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L26 (RPL26A) | chr3:18515296-18515736 FORWARD

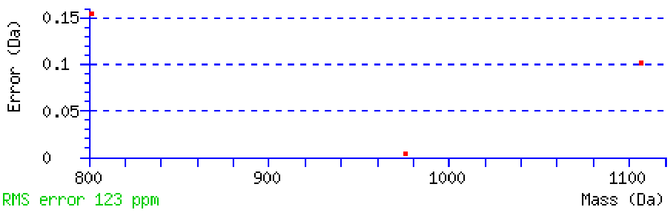
Match to Query 4329: 1317.698084 from(659.856318,2+) index(5496)
Title: Elution from: 52.848 to 52.848 scan no 7144 cid35.00 polarity:+
Data file D1d-1-2.mgf

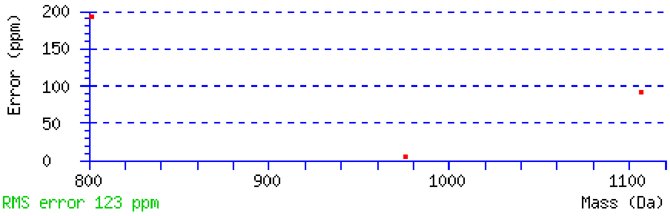
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1317.6962
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.043
Matches : 3/100 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							12
2	213.1598	107.0835			I	1219.6351	610.3212	1202.6085	601.8079	1201.6245	601.3159	11
3	344.2002	172.6038			M	***1106.5510***	553.7792	1089.5245	545.2659	1088.5405	544.7739	10
4	431.2323	216.1198	413.2217	207.1145	S	***975.5105***	488.2589	958.4840	479.7456	957.5000	479.2536	9
5	518.2643	259.6358	500.2537	250.6305	S	888.4785	444.7429	871.4520	436.2296	870.4680	435.7376	8
6	615.3171	308.1622	597.3065	299.1569	P	***801.4465***	401.2269	784.4199	392.7136	783.4359	392.2216	7
7	728.4011	364.7042	710.3906	355.6989	L	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
8	815.4332	408.2202	797.4226	399.2149	S	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
9	916.4808	458.7441	898.4703	449.7388	T	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
10	1031.5078	516.2575	1013.4972	507.2522	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
11	1144.5918	572.7996	1126.5813	563.7943	L	288.2030	144.6051	271.1765	136.0919			2
12					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VIMSSPLSTDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G49910.1

Score	Mr(calc)	Delta	Sequence
20.6	1317.6962	0.0019	VIMSSPLSTDLR
3.9	1317.7002	-0.0021	IVMWLEELASK
1.1	1317.6962	0.0019	VIGENGTKEMLK

Mascot: http://www.matrixscience.com/

AT3G50050.1

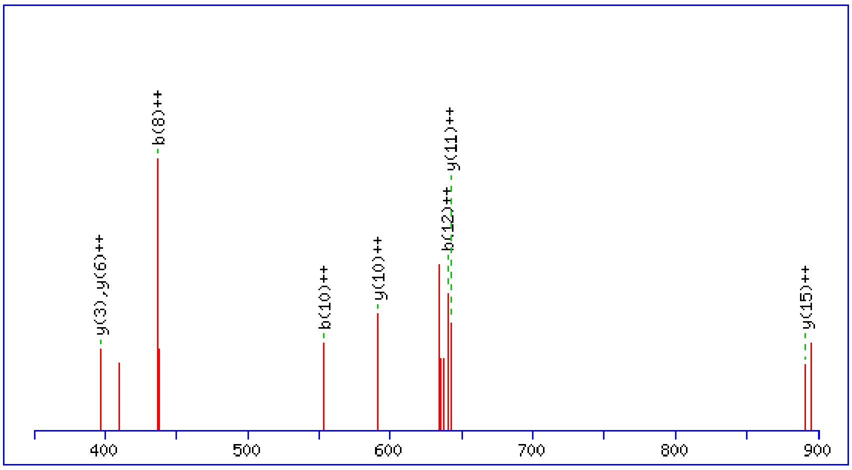
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVFGCETVETGDLYSQR**
Found in **AT3G50050.1** in **TAIR_Arabidopsis**, Symbols: | aspartyl protease family protein | chr3:18565121-18568098 REVERSE

Match to Query 8900: 1952.807337 from(651.943055,3+) index(6381)
Title: Elution from: 56.787 to 56.787 scan no 8188 cid35.00 polarity:+
Data file C7-1_3.mgf

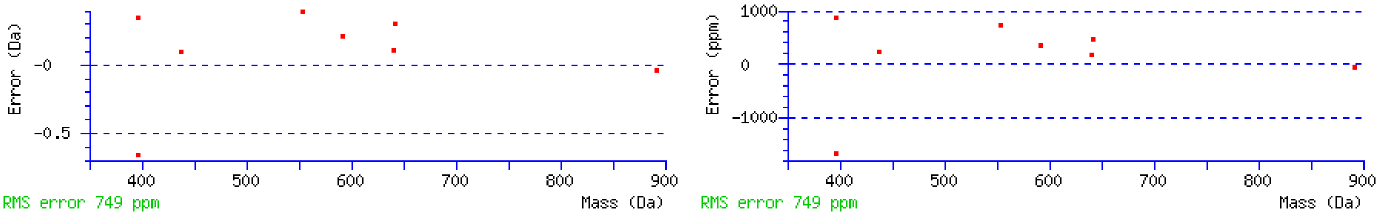
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1952.8078
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0025
Matches : 8/148 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							17
2	173.1069	87.0571					V	1881.7810	941.3941	1863.7574	932.3823	1863.7704	932.3888	16
3	321.1723	161.0898					F	1781.7155	891.3614	1763.6920	882.3496	1763.7050	882.3561	15
4	379.1908	190.0990					G	1633.6501	817.3287	1615.6265	808.3169	1615.6395	808.3234	14
5	541.2155	271.1114					C	1575.6316	788.3194	1557.6080	779.3076	1557.6210	779.3142	13
6	671.2552	336.1312			653.2446	327.1259	E	1413.6069	707.3071	1395.5833	698.2953	1395.5963	698.3018	12
7	773.2999	387.1536			755.2893	378.1483	T	1283.5672	642.2873	1265.5437	633.2755	1265.5567	633.2820	11
8	873.3653	***437.1863***			855.3548	428.1810	V	1181.5225	591.2649	1163.4989	582.2531	1163.5120	582.2596	10
9	1003.4050	502.2061			985.3944	493.2008	E	1081.4571	541.2322	1063.4335	532.2204	1063.4465	532.2269	9
10	1105.4497	***553.2285***			1087.4391	544.2232	T	951.4175	476.2124	933.3939	467.2006	933.4069	467.2071	8
11	1163.4682	582.2377			1145.4576	573.2324	G	849.3727	425.1900	831.3492	416.1782	831.3622	416.1847	7
12	1279.4921	***640.2497***			1261.4816	631.2444	D	791.3542	396.1808	773.3307	387.1690	773.3437	387.1755	6
13	1393.5732	697.2903			1375.5627	688.2850	L	675.3303	338.1688	657.3067	329.1570	657.3197	329.1635	5
14	1557.6336	779.3204			1539.6230	770.3152	Y	561.2492	281.1282	543.2256	272.1164	543.2386	272.1229	4
15	1645.6627	823.3350			1627.6521	814.3297	S	397.1888	199.0980	379.1652	190.0862	379.1782	190.0928	3
16	1775.7153	888.3613	1757.6917	879.3495	1757.7048	879.3560	Q	309.1597	155.0835	291.1362	146.0717			2
17							R	179.1071	90.0572	161.0835	81.0454			1

AT3G50050.1



NCBI **BLAST** search of AVFGCETVETGDLYSQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.1	1952.8078	-0.0005	AVFGCETVETGDLYSQR
0.7	1952.8109	-0.0035	TSLSRSSSSSSSNNNSPTK
0.6	1952.8061	0.0013	LQNVASSSGTGRSEMSSGR
0.0	1952.8065	0.0008	CGSISDARLVFDNMMAK
0.0	1952.8065	0.0008	CGSISDARLVFDNMMAK

Mascot: http://www.matrixscience.com/

AT3G50280.1

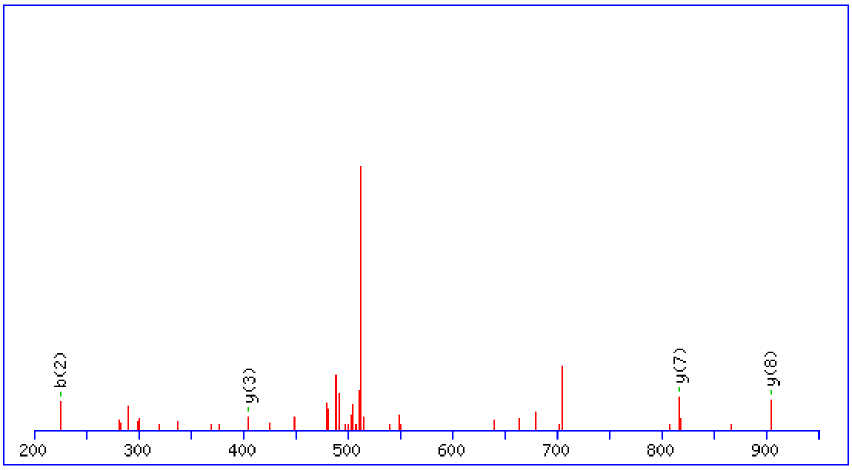
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HSGLNQEEK**
Found in **AT3G50280.1** in **TAIR_Arabidopsis**, Symbols: | transferase family protein | chr3:18648836-18650167 FORWARD

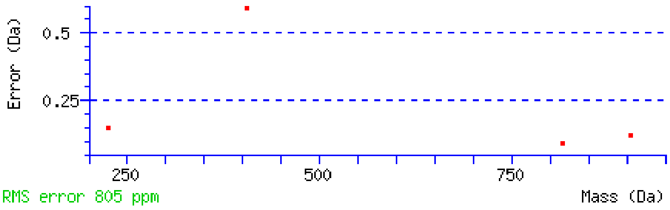
Match to Query 2837: 1040.490038 from(521.252295,2+) index(1286)
Title: Elution from: 20.367 to 20.367 scan no 1851 cid35.00 polarity:+
Data file D6h-2_1.mgf

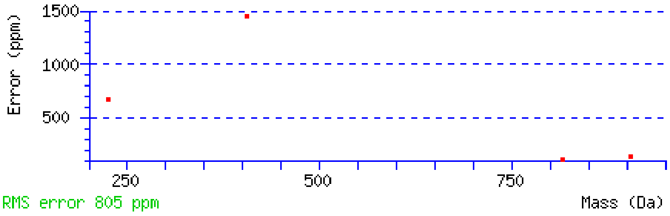
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1040.4887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 16 **Expect:** 0.04
Matches : 4/84 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							9
2	225.0982	113.0527			207.0877	104.0475	S	***904.4371***	452.7222	887.4105	444.2089	886.4265	443.7169	8
3	282.1197	141.5635			264.1091	132.5582	G	***817.4050***	409.2061	800.3785	400.6929	799.3945	400.2009	7
4	395.2037	198.1055			377.1932	189.1002	L	760.3836	380.6954	743.3570	372.1821	742.3730	371.6901	6
5	509.2467	255.1270	492.2201	246.6137	491.2361	246.1217	N	647.2995	324.1534	630.2729	315.6401	629.2889	315.1481	5
6	637.3052	319.1563	620.2787	310.6430	619.2947	310.1510	Q	533.2566	267.1319	516.2300	258.6186	515.2460	258.1266	4
7	766.3478	383.6776	749.3213	375.1643	748.3373	374.6723	E	***405.1980***	203.1026	388.1714	194.5894	387.1874	194.0974	3
8	895.3904	448.1989	878.3639	439.6856	877.3799	439.1936	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HSGLNQEEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.0	1040.4887	0.0014	HSGLNQEEK

AT3G50280.1

1.0	1040.4887	0.0014	SLHEGDEVR
0.4	1040.4896	0.0005	FMGCVKGAR

Mascot: http://www.matrixscience.com/

AT3G50370.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNMVSEK**
Found in **AT3G50370.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO71840.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81687.1) | chr3:18687418-18694926 REVERSE

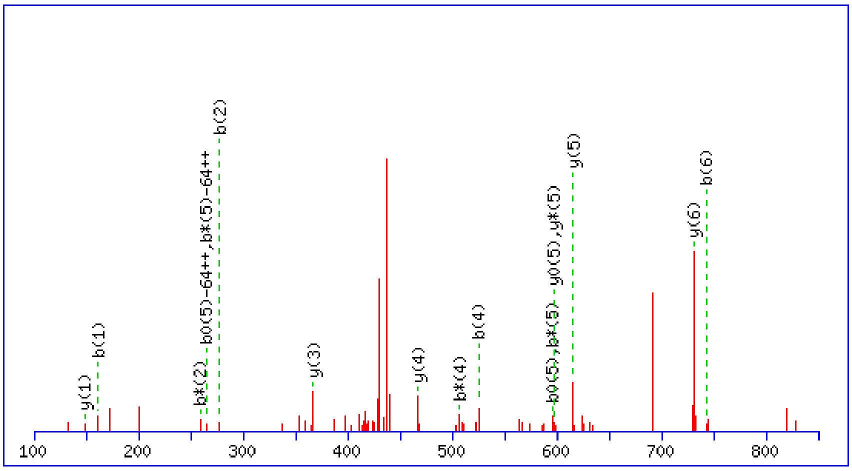
Match to Query 1504: 890.392142 from(446.203347,2+) index(751)
Title: Elution from: 12.222 to 12.222 scan no 1054 cid35.00 polarity:+
Data file D12h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 850 Da Full range

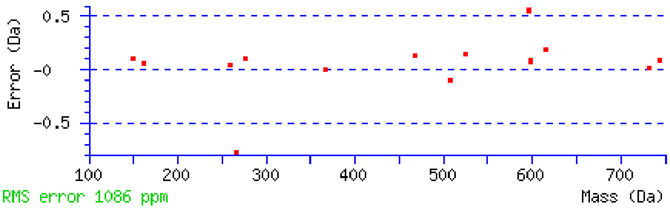
Label all possible matches ○ Label matches used for scoring ●

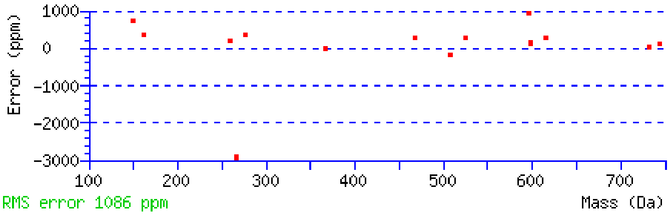
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 890.3924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.042
Matches : 17/94 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**161.0965**	81.0519	143.0729	72.0401			R							7
2	**277.1335**	139.0704	259.1099	130.0586			N	***731.3104***	366.1589	713.2869	357.1471	713.2999	357.1536	6
3	425.1660	213.0866	407.1424	204.0748			M	***615.2734***	308.1404	597.2499	299.1286	597.2629	299.1351	5
4	**525.2314**	263.1193	507.2078	254.1076			V	***467.2410***	234.1241	449.2174	225.1124	449.2304	225.1189	4
5	613.2605	307.1339	595.2369	298.1221	595.2499	298.1286	S	***367.1756***	184.0914	349.1520	175.0796	349.1650	175.0861	3
6	**743.3001**	372.1537	725.2765	363.1419	725.2895	363.1484	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
7							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RNMVSEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	890.3924	-0.0003	RNMVSEK

AT3G50370.1

12.2	890.3924	-0.0003	RNSEVMK
8.3	890.3895	0.0027	RDGRESR
8.3	890.3924	-0.0003	MDSLKNR
6.9	890.3947	-0.0025	KSMAWNK
5.7	890.3924	-0.0003	RQMTDTK
4.8	890.3924	-0.0003	RAMEASSK
4.3	890.3917	0.0004	ASRHYSR
4.1	890.3924	-0.0003	ATTMGVQR
3.7	890.3924	-0.0003	MKQNQSK

AT3G50610.1

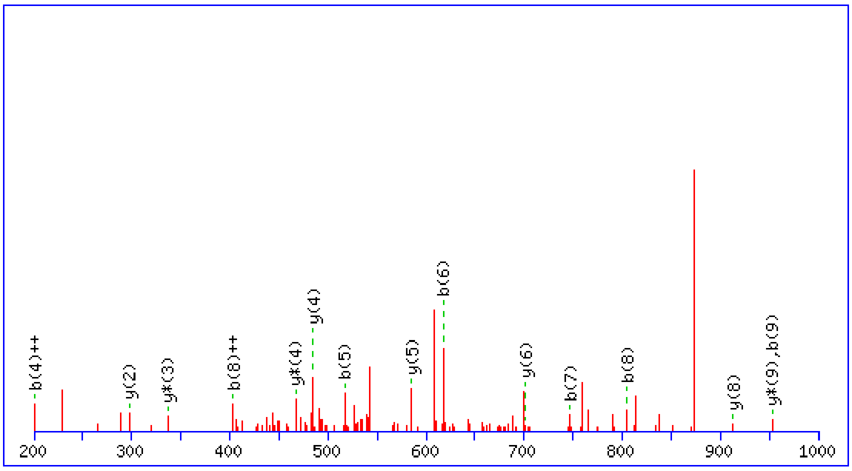
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHANVKGFK**
Found in **AT3G50610.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66816.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71825.1) | chr3:18790704-18791393 REVERSE

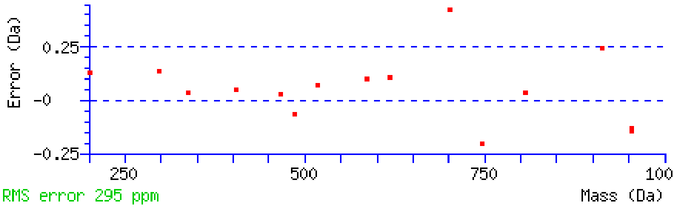
Match to Query 3272: 1100.566646 from(551.290599,2+) index(7493)
Title: Elution from: 66.816 to 66.816 scan no 9908 cid35.00 polarity:+
Data file C7-3_3.mgf

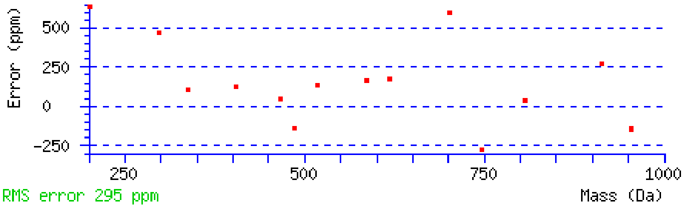
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1100.5667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.047
Matches : 15/72 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	131.0963	66.0518	113.0727	57.0400	K					10
2	189.1148	95.0610	171.0912	86.0492	G	971.4850	486.2461	953.4614	477.2343	9
3	329.1648	165.0861	311.1412	156.0743	H	***913.4665***	457.2369	895.4429	448.2251	8
4	401.1990	201.1031	383.1754	192.0913	A	773.4164	387.2119	755.3929	378.2001	7
5	***517.2360***	259.1216	499.2124	250.1098	N	***701.3823***	351.1948	683.3587	342.1830	6
6	***617.3014***	309.1543	599.2778	300.1426	V	***585.3453***	293.1763	567.3217	284.1645	5
7	***747.3905***	374.1989	729.3669	365.1871	K	***485.2799***	243.1436	467.2563	234.1318	4
8	***805.4090***	403.2081	787.3854	394.1963	G	355.1908	178.0990	337.1672	169.0873	3
9	***953.4744***	477.2408	935.4508	468.2290	F	***297.1723***	149.0898	279.1487	140.0780	2
10					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of KGHANVKGFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G50610.1

Score	Mr(calc)	Delta	Sequence
22.6	1100.5667	-0.0001	KGHANVKGFK
7.3	1100.5667	-0.0001	HGGLGGKFGKK
5.6	1100.5674	-0.0008	EVLVGMKAGGK
4.0	1100.5690	-0.0023	IAWRYLHK
3.1	1100.5696	-0.0030	IWVIMKGDK
1.1	1100.5640	0.0026	ILAVGEPAYR
0.2	1100.5648	0.0019	LLSMLEELK

AT3G50820.1

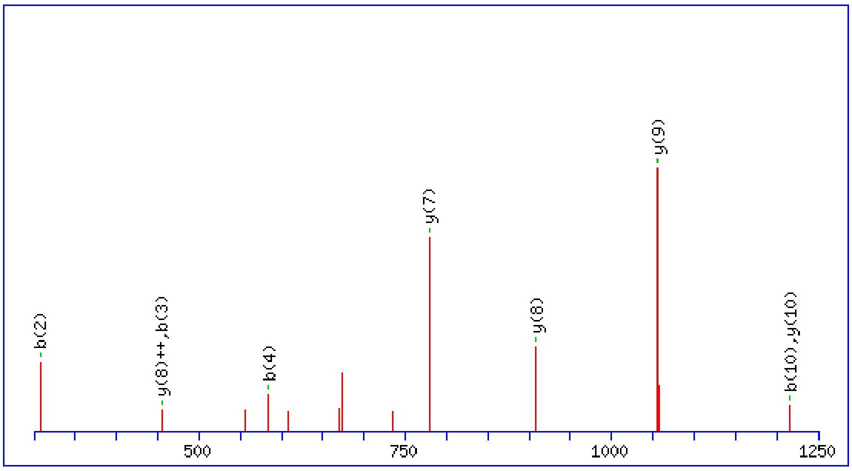
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FCFEPTSFTVK**
Found in **AT3G50820.1** in **TAIR_Arabidopsis**, Symbols: PSBO2, PSBO-2 | PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); oxygen evolving/ poly(U) binding | chr3:18901989-18903292 REVERSE

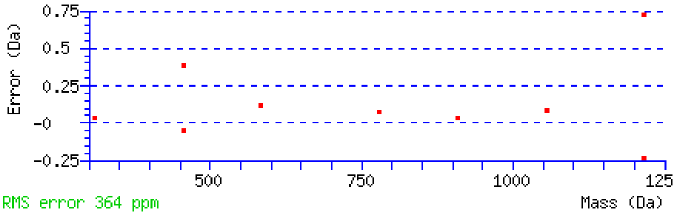
Match to Query 5235: 1361.630310 from(681.822431,2+) index(7849)
Title: Elution from: 70.064 to 70.064 scan no 10277 cid35.00 polarity:+
Data file 0-3_1.mgf

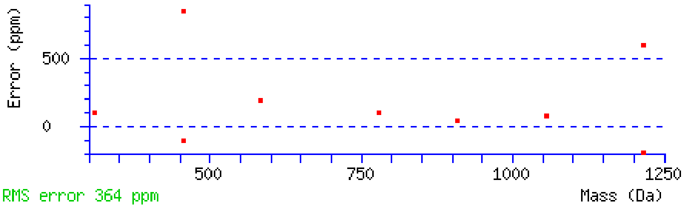
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1361.6326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 9.4e-005
Matches : 9/90 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			**F**							**11**
2	***308.1063***	154.5568			**C**	***1215.5714***	608.2894	1198.5449	599.7761	1197.5609	599.2841	**10**
3	***455.1748***	228.0910			**F**	***1055.5408***	528.2740	1038.5142	519.7608	1037.5302	519.2687	**9**
4	***584.2173***	292.6123	566.2068	283.6070	**E**	***908.4724***	454.7398	891.4458	446.2266	890.4618	445.7345	**8**
5	681.2701	341.1387	663.2595	332.1334	**P**	***779.4298***	390.2185	762.4032	381.7053	761.4192	381.2132	**7**
6	782.3178	391.6625	764.3072	382.6573	**T**	682.3770	341.6921	665.3505	333.1789	664.3665	332.6869	**6**
7	869.3498	435.1785	851.3393	426.1733	**S**	581.3293	291.1683	564.3028	282.6550	563.3188	282.1630	**5**
8	1016.4182	508.7128	998.4077	499.7075	**F**	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	**4**
9	1117.4659	559.2366	1099.4553	550.2313	**T**	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	**3**
10	***1216.5343***	608.7708	1198.5238	599.7655	**V**	246.1812	123.5942	229.1547	115.0810			**2**
11					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of FCFEPTSFTVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G50820.1

Score	Mr(calc)	Delta	Sequence
41.7	1361.6326	-0.0023	FCFEPTSFTVK

Mascot: http://www.matrixscience.com/

AT3G50840.1

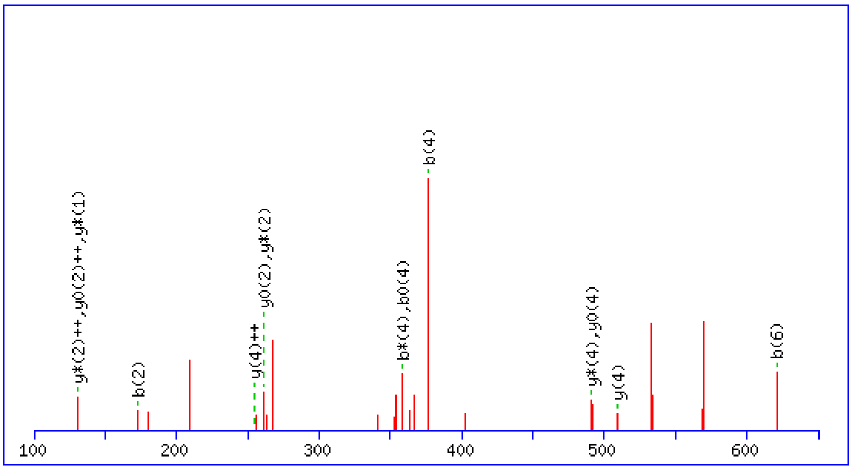
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGSNLEK**
Found in **AT3G50840.1** in **TAIR_Arabidopsis**, Symbols: | phototropic-responsive NPH3 family protein | chr3:18907334-18909355 REVERSE

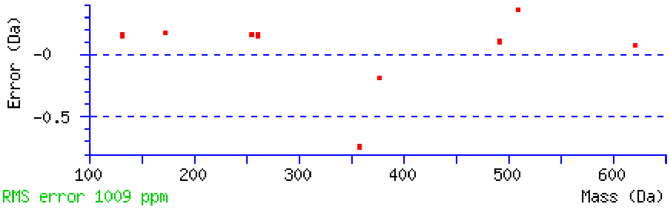
Match to Query 735: 768.386880 from(385.200716,2+) index(339)
Title: Elution from: 10.757 to 10.757 scan no 639 cid35.00 polarity:+
Data file D12h-2_1.mgf

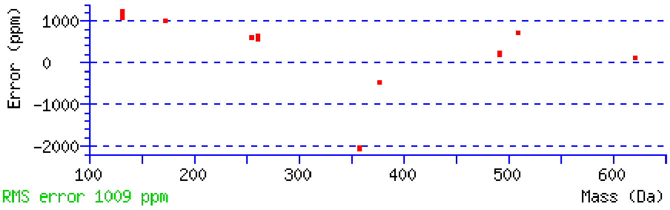
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 768.3860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.017
Matches : 17/60 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							7
2	***173.1069***	87.0571					G	655.3122	328.1597	637.2886	319.1479	637.3016	319.1544	6
3	***261.1359***	131.0716			243.1254	122.0663	S	597.2937	299.1505	579.2701	290.1387	579.2831	290.1452	5
4	***377.1729***	189.0901	359.1493	180.0783	359.1624	180.0848	N	509.2646	255.1359	491.2410	246.1241	491.2540	246.1307	4
5	***491.2540***	246.1307	473.2304	237.1189	473.2435	237.1254	L	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
6	***621.2937***	311.1505	603.2701	302.1387	603.2831	302.1452	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IGSNLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.6	768.3860	0.0009	IGSNLEK
21.9	768.3860	0.0009	EILNGSK
20.4	768.3860	0.0009	EKTAPKS

AT3G50840.1

17.6	768.3860	0.0009	EDQLKK
17.6	768.3860	0.0009	KDELQK
15.4	768.3860	0.0009	EELNKK
15.4	768.3860	0.0009	EKINEK
15.4	768.3860	0.0009	EKLNEK
15.4	768.3860	0.0009	EQVKEK
15.4	768.3860	0.0009	KQEVEK

AT3G51260.1

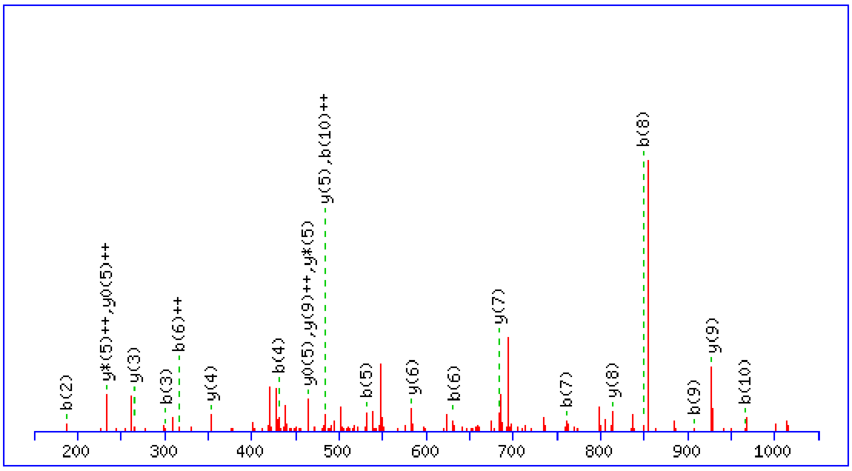
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLEVVESGGK**
Found in **AT3G51260.1** in **TAIR_Arabidopsis**, Symbols: PAD1 | PAD1 (20S PROTEASOME ALPHA SUBUNIT PAD1); peptidase | chr3:19042065-19043725 FORWARD

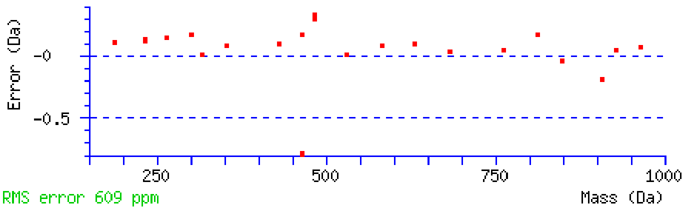
Match to Query 3468: 1112.569376 from(557.291964,2+) index(5171)
Title: Elution from: 46.699 to 46.699 scan no 6525 cid35.00 polarity:+
Data file D6h-3_1.mgf

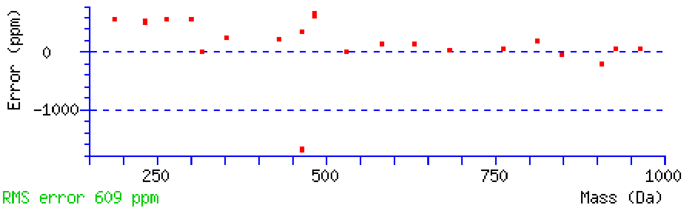
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1112.5721
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0026
Matches : 23/88 fragment ions using 74 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							11
2	*187.1225*	94.0649			L	1041.5453	521.2763	1023.5217	512.2645	1023.5347	512.2710	10
3	*301.2036*	151.1054			L	**927.4642**	464.2357	909.4406	455.2239	909.4536	455.2304	9
4	*431.2433*	216.1253	413.2327	207.1200	E	**813.3831**	407.1952	795.3595	398.1834	795.3725	398.1899	8
5	*531.3087*	266.1580	513.2981	257.1527	V	**683.3435**	342.1754	665.3199	333.1636	665.3329	333.1701	7
6	*631.3741*	316.1907	613.3636	307.1854	V	**583.2780**	292.1426	565.2544	283.1309	565.2674	283.1374	6
7	*761.4138*	381.2105	743.4032	372.2052	E	**483.2126**	242.1099	465.1890	233.0981	465.2020	233.1046	5
8	*849.4428*	425.2251	831.4323	416.2198	S	**353.1729**	177.0901	335.1494	168.0783	335.1624	168.0848	4
9	*907.4613*	454.2343	889.4508	445.2290	G	**265.1439**	133.0756	247.1203	124.0638			3
10	*965.4798*	483.2436	947.4693	474.2383	G	207.1254	104.0663	189.1018	95.0545			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ALLEVVESGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G51260.1

Score	Mr(calc)	Delta	Sequence
33.7	1112.5721	-0.0028	ALLEVVESGGK

AT3G51570.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GIFLNMNEMK**
Found in **AT3G51570.1** in **TAIR_Arabidopsis**, Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr3:19137337-19141435 FORWARD

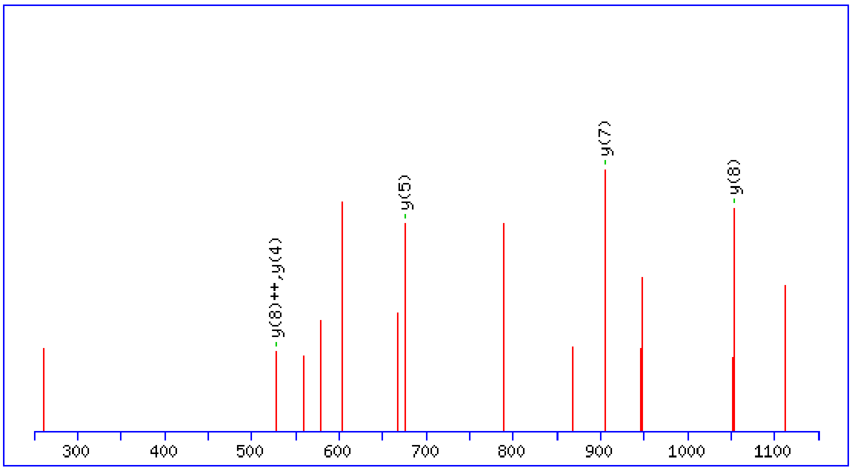
Match to Query 4055: 1224.532458 from(613.273505,2+) index(6290)
Title: Elution from: 56.039 to 56.039 scan no 8064 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1150 Da Full range

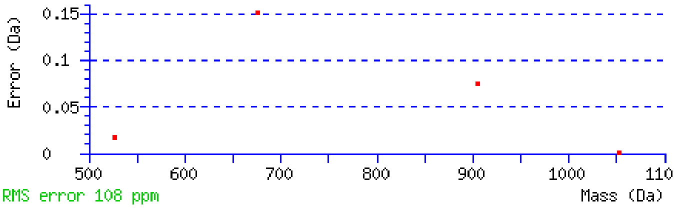
Label all possible matches ○ Label matches used for scoring ●

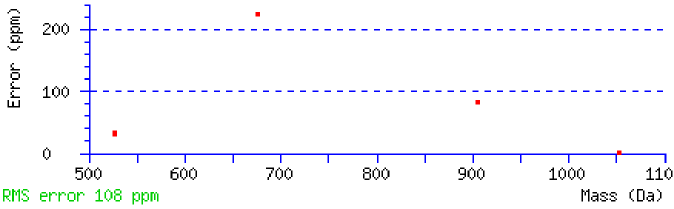
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1224.5293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.02
Matches : 5/132 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							10
2	173.1069	87.0571					I	1167.5181	584.2627	1149.4945	575.2509	1149.5075	575.2574	9
3	321.1723	161.0898					F	***1053.4370***	527.2221	1035.4134	518.2103	1035.4264	518.2169	8
4	435.2534	218.1303					L	***905.3716***	453.1894	887.3480	444.1776	887.3610	444.1841	7
5	551.2904	276.1488	533.2668	267.1371			N	791.2905	396.1489	773.2669	387.1371	773.2799	387.1436	6
6	699.3229	350.1651	681.2993	341.1533			M	***675.2535***	338.1304	657.2299	329.1186	657.2429	329.1251	5
7	815.3599	408.1836	797.3363	399.1718			N	***527.2210***	264.1141	509.1974	255.1024	509.2105	255.1089	4
8	945.3995	473.2034	927.3759	464.1916	927.3889	464.1981	E	411.1840	206.0956	393.1604	197.0839	393.1735	197.0904	3
9	1077.4370	539.2221	1059.4134	530.2103	1059.4264	530.2169	M	281.1444	141.0758	263.1208	132.0640			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GIFLNMNEMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G51570.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
24.6	1224.5293	0.0031	GIFLNMNEMK	Oxidation M6 92.24%
16.1	1224.5341	-0.0016	IGFSMISDAEK	
13.9	1224.5293	0.0031	GIFLNMNEMK	Oxidation M9 7.76%
1.8	1224.5289	0.0036	IGGSSNGSSSISR	
1.6	1224.5298	0.0027	SRGQLCVMNK	

AT3G51800.1

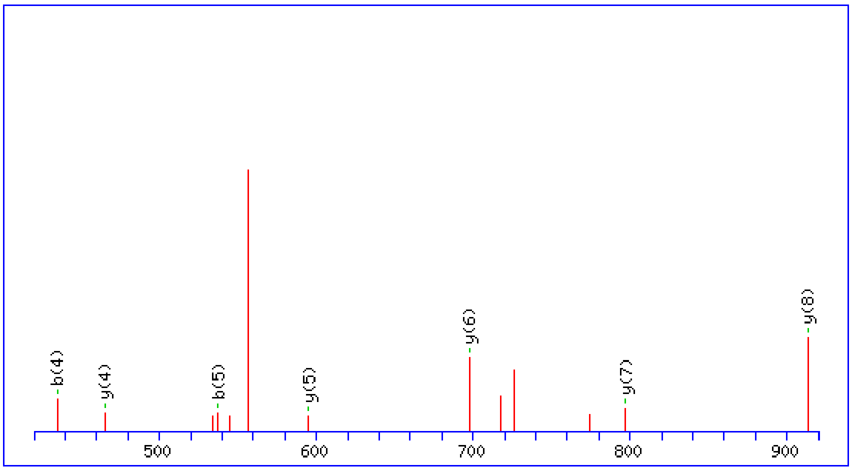
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTDVTEAIQK**
Found in **AT3G51800.1** in **TAIR_Arabidopsis**, Symbols: ATG2 | ATG2 (G2p-related protein); metalloexopeptidase | chr3:19222238-19224545 REVERSE

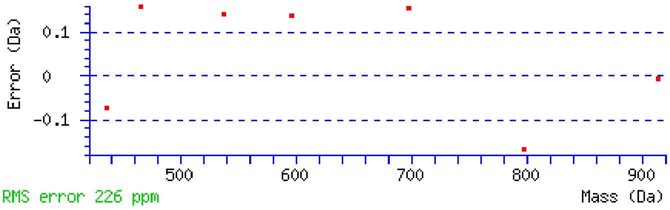
Match to Query 3493: 1130.521892 from(566.268222,2+) index(1457)
Title: Elution from: 19.471 to 19.471 scan no 1948 cid35.00 polarity:+
Data file D12h-1_3.mgf

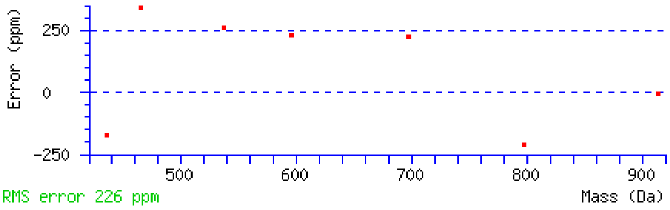
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 420 to 920 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1130.5229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0015
Matches : 7/98 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			**N**							**10**
2	219.0890	110.0481	201.0654	101.0363	201.0784	101.0428	**T**	1015.4933	508.2503	997.4697	499.2385	997.4827	499.2450	**9**
3	335.1130	168.0601	317.0894	159.0483	317.1024	159.0548	**D**	***913.4485***	457.2279	895.4250	448.2161	895.4380	448.2226	**8**
4	**435.1784**	218.0928	417.1548	209.0811	417.1678	209.0876	**V**	***797.4246***	399.2159	779.4010	390.2041	779.4140	390.2106	**7**
5	**537.2231**	269.1152	519.1995	260.1034	519.2126	260.1099	**T**	***697.3591***	349.1832	679.3355	340.1714	679.3485	340.1779	**6**
6	667.2628	334.1350	649.2392	325.1232	649.2522	325.1297	**E**	***595.3144***	298.1608	577.2908	289.1490	577.3038	289.1556	**5**
7	739.2969	370.1521	721.2733	361.1403	721.2863	361.1468	**A**	***465.2748***	233.1410	447.2512	224.1292			**4**
8	853.3780	427.1926	835.3544	418.1808	835.3674	418.1874	**I**	393.2406	197.1239	375.2170	188.1122			**3**
9	983.4306	492.2190	965.4071	483.2072	965.4201	483.2137	**Q**	279.1595	140.0834	261.1359	131.0716			**2**
10							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of NTDVTEAIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G51800.1

Score	Mr(calc)	Delta	Sequence
36.5	1130.5229	-0.0011	NTDVTEAIQK
10.7	1130.5229	-0.0011	TDDERELLK
10.4	1130.5230	-0.0011	SEDLEIEKR
2.8	1130.5230	-0.0011	DREEISEIK
2.4	1130.5236	-0.0017	NRQKLHCR
2.3	1130.5238	-0.0020	MAAANAPITMK

AT3G51840.1

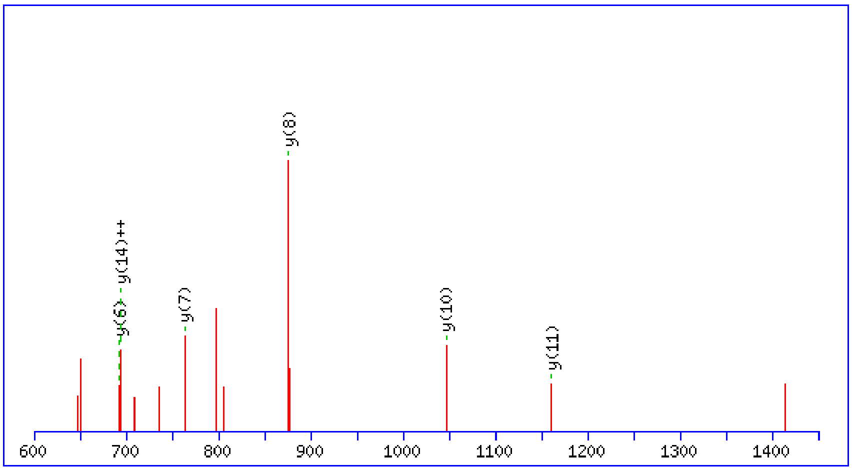
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLGGNGILADFLVAK**
Found in **AT3G51840.1** in **TAIR_Arabidopsis**, Symbols: ATSCX, ATG6, ACX4 | ACX4 (ACYL-COA OXIDASE 4); oxidoreductase | chr3:19236630-19239985 REVERSE

Match to Query 6995: 1628.915026 from(815.464789,2+) index(10456)
Title: Elution from: 105.819 to 105.819 scan no 15434 cid35.00 polarity:+
Data file D1d-2_2.mgf

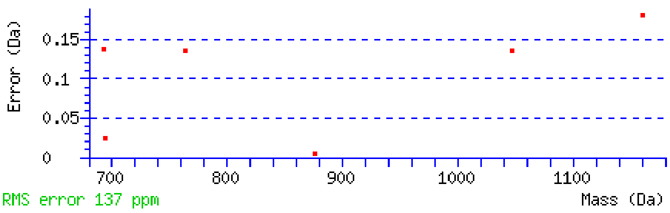
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

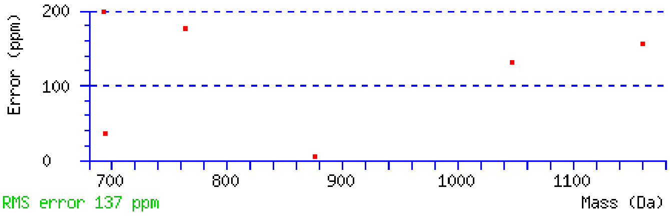


Monoisotopic mass of neutral peptide Mr(calc): 1628.9137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0037
Matches : 6/160 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	243.1339	122.0706			225.1234	113.0653	L	1500.8784	750.9429	1483.8519	742.4296	1482.8679	741.9376	15
3	356.2180	178.6126			338.2074	169.6074	L	1387.7944	694.4008	1370.7678	685.8876	1369.7838	685.3955	14
4	413.2395	207.1234			395.2289	198.1181	G	1274.7103	637.8588	1257.6838	629.3455	1256.6997	628.8535	13
5	470.2609	235.6341			452.2504	226.6288	G	1217.6889	609.3481	1200.6623	600.8348	1199.6783	600.3428	12
6	584.3039	292.6556	567.2773	284.1423	566.2933	283.6503	N	***1160.6674***	580.8373	1143.6408	572.3241	1142.6568	571.8320	11
7	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	G	***1046.6245***	523.8159	1029.5979	515.3026	1028.6139	514.8106	10
8	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	I	989.6030	495.3051	972.5764	486.7919	971.5924	486.2999	9
9	867.4934	434.2504	850.4669	425.7371	849.4829	425.2451	L	***876.5189***	438.7631	859.4924	430.2498	858.5084	429.7578	8
10	938.5306	469.7689	921.5040	461.2556	920.5200	460.7636	A	***763.4349***	382.2211	746.4083	373.7078	745.4243	373.2158	7
11	1053.5575	527.2824	1036.5310	518.7691	1035.5469	518.2771	D	***692.3978***	346.7025	675.3712	338.1892	674.3872	337.6972	6
12	1200.6259	600.8166	1183.5994	592.3033	1182.6154	591.8113	F	577.3708	289.1890	560.3443	280.6758			5
13	1313.7100	657.3586	1296.6834	648.8454	1295.6994	648.3533	L	430.3024	215.6548	413.2758	207.1416			4
14	1412.7784	706.8928	1395.7518	698.3796	1394.7678	697.8876	V	317.2183	159.1128	300.1918	150.5995			3
15	1483.8155	742.4114	1466.7890	733.8981	1465.8049	733.4061	A	218.1499	109.5786	201.1234	101.0653			2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT3G51840.1





NCBI **BLAST** search of ELLGGNGILADFLVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.3	1628.9137	0.0013	ELLGGNGILADFLVAK

Mascot: http://www.matrixscience.com/

AT3G52150.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYIGNIPR**
Found in **AT3G52150.1** in **TAIR_Arabidopsis**, Symbols: | RNA recognition motif (RRM)-containing protein | chr3:19353052-19354068 FORWARD

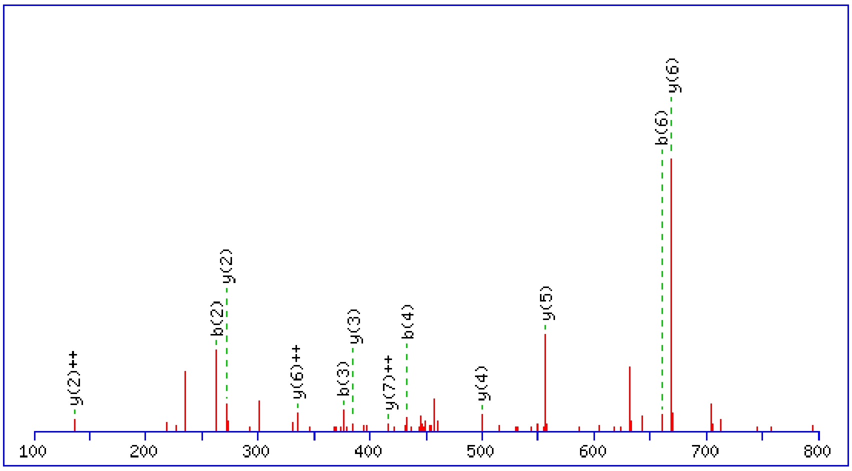
Match to Query 1836: 930.527690 from(466.271121,2+) index(3300)
Title: Elution from: 33.608 to 33.608 scan no 4128 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

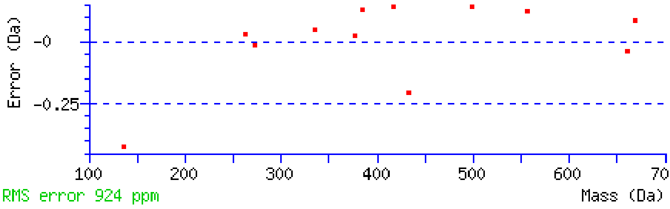
Label all possible matches ○ Label matches used for scoring ●

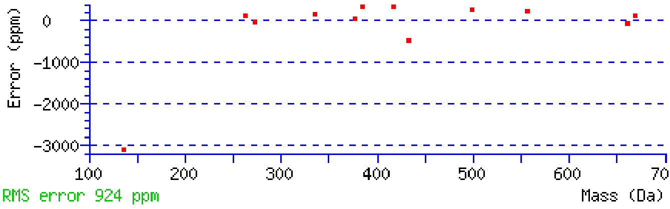
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 930.5287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.0055
Matches : 12/48 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	100.0757	50.5415			V					8
2	**263.1390**	132.0731			Y	832.4676	416.7374	815.4410	408.2241	7
3	**376.2231**	188.6152			I	***669.4042***	335.2058	652.3777	326.6925	6
4	**433.2445**	217.1259			G	***556.3202***	278.6637	539.2936	270.1504	5
5	547.2875	274.1474	530.2609	265.6341	N	***499.2987***	250.1530	482.2722	241.6397	4
6	**660.3715**	330.6894	643.3450	322.1761	I	***385.2558***	193.1315	368.2292	184.6183	3
7	757.4243	379.2158	740.3978	370.7025	P	***272.1717***	136.5895	255.1452	128.0762	2
8					R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of VYIGNIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	930.5287	-0.0010	VYIGNIPR

AT3G52150.1

Mascot: http://www.matrixscience.com/

AT3G52180.1

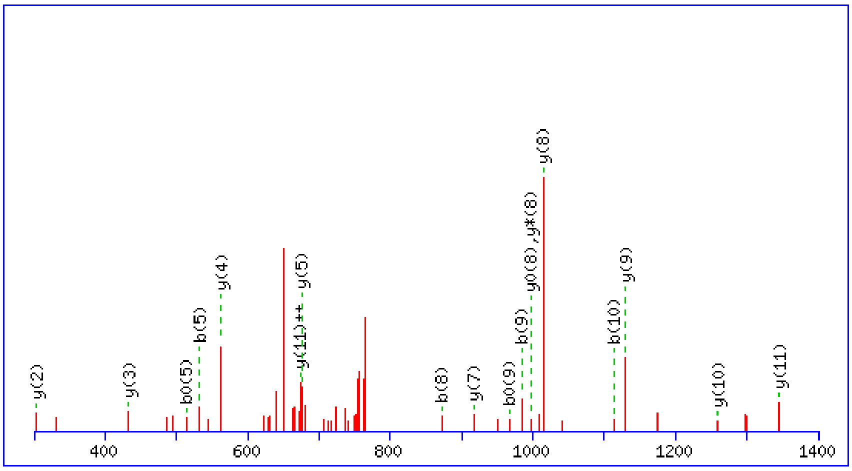
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSEDPELLEEER**
Found in **AT3G52180.1** in **TAIR_Arabidopsis**, Symbols: ATPTPKIS1, DSP4, SEX4 | ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase | chr3:19360862-19364437 REVERSE

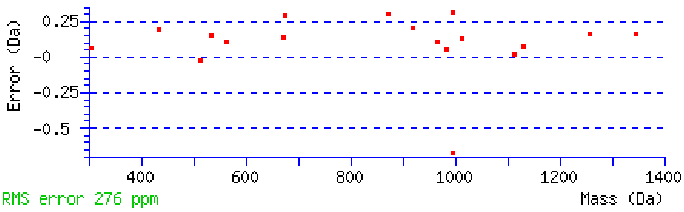
Match to Query 6479: 1544.720130 from(773.367341,2+) index(4177)
Title: Elution from: 42.145 to 42.145 scan no 5383 cid35.00 polarity:+
Data file D1d-1_1.mgf

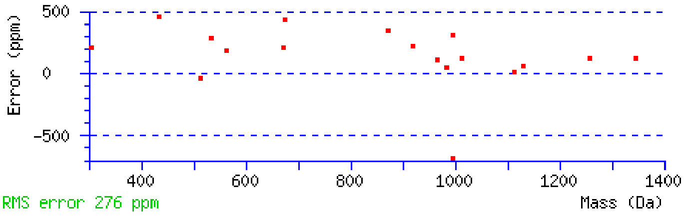
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1544.7206
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 2.1e-006
Matches : 18/116 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							13
2	201.1234	101.0653	183.1128	92.0600	S	1432.6438	716.8255	1415.6173	708.3123	1414.6332	707.8203	12
3	288.1554	144.5813	270.1448	135.5761	S	***1345.6118***	673.3095	1328.5852	664.7963	1327.6012	664.3042	11
4	417.1980	209.1026	399.1874	200.0973	E	***1258.5798***	629.7935	1241.5532	621.2802	1240.5692	620.7882	10
5	**532.2249**	266.6161	514.2144	257.6108	D	***1129.5372***	565.2722	1112.5106	556.7589	1111.5266	556.2669	9
6	629.2777	315.1425	611.2671	306.1372	P	***1014.5102***	507.7587	997.4837	499.2455	996.4997	498.7535	8
7	758.3203	379.6638	740.3097	370.6585	E	***917.4575***	459.2324	900.4309	450.7191	899.4469	450.2271	7
8	**871.4044**	436.2058	853.3938	427.2005	L	788.4149	394.7111	771.3883	386.1978	770.4043	385.7058	6
9	**984.4884**	492.7478	966.4779	483.7426	L	***675.3308***	338.1690	658.3042	329.6558	657.3202	329.1638	5
10	**1113.5310**	557.2691	1095.5204	548.2639	E	***562.2467***	281.6270	545.2202	273.1137	544.2362	272.6217	4
11	1242.5736	621.7904	1224.5630	612.7852	E	***433.2041***	217.1057	416.1776	208.5924	415.1936	208.1004	3
12	1371.6162	686.3117	1353.6056	677.3065	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
13					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LSSEDPELLEEER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G52180.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.0	1544.7206	-0.0004	LSSEDPELLEEER

Mascot: http://www.matrixscience.com/

AT3G52250.1

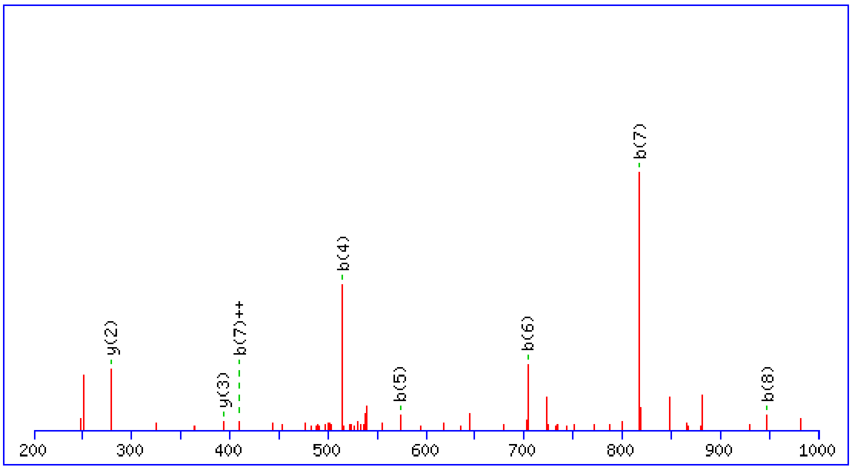
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDCFGKIKK**
Found in **AT3G52250.1** in **TAIR_Arabidopsis**, Symbols: | DNA binding / transcription factor | chr3:19387607-19394078 FORWARD

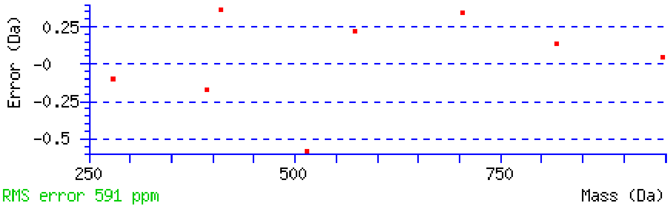
Match to Query 2986: 1094.521640 from(548.268096,2+) index(3502)
Title: Elution from: 36.018 to 36.018 scan no 4455 cid35.00 polarity:+
Data file D1d-2_1.mgf

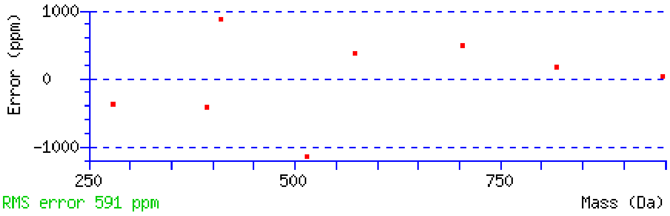
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1094.5205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.006
Matches : 8/72 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							9
2	205.0603	103.0338			187.0498	94.0285	D	1007.4987	504.2530	989.4751	495.2412	989.4881	495.2477	8
3	367.0850	184.0462			349.0745	175.0409	C	891.4747	446.2410	873.4511	437.2292			7
4	***515.1505***	258.0789			497.1399	249.0736	F	729.4500	365.2286	711.4264	356.2168			6
5	***573.1690***	287.0881			555.1584	278.0828	G	581.3845	291.1959	563.3610	282.1841			5
6	***703.2580***	352.1326	685.2344	343.1209	685.2475	343.1274	K	523.3660	262.1867	505.3425	253.1749			4
7	***817.3391***	409.1732	799.3155	400.1614	799.3285	400.1679	I	**393.2770**	197.1421	375.2534	188.1303			3
8	***947.4281***	474.2177	929.4046	465.2059	929.4176	465.2124	K	**279.1959**	140.1016	261.1723	131.0898			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SDCFGKIKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.1	1094.5205	0.0012	SDCFGKIKK

AT3G52250.1

18.2	1094.5205	0.0012	VIRMEYQK
16.1	1094.5205	0.0012	QFSAMNKLK
15.1	1094.5205	0.0012	MVASFEKVR
13.3	1094.5204	0.0012	FKVATGQGMK
12.4	1094.5205	0.0012	SFDCLKGKK
12.3	1094.5205	0.0012	LMKDAVYAR
11.1	1094.5205	0.0012	AVMRYVAEK
10.9	1094.5231	-0.0015	MKYNPRVR
7.7	1094.5205	0.0012	DMLRIYQK

AT3G52300.1

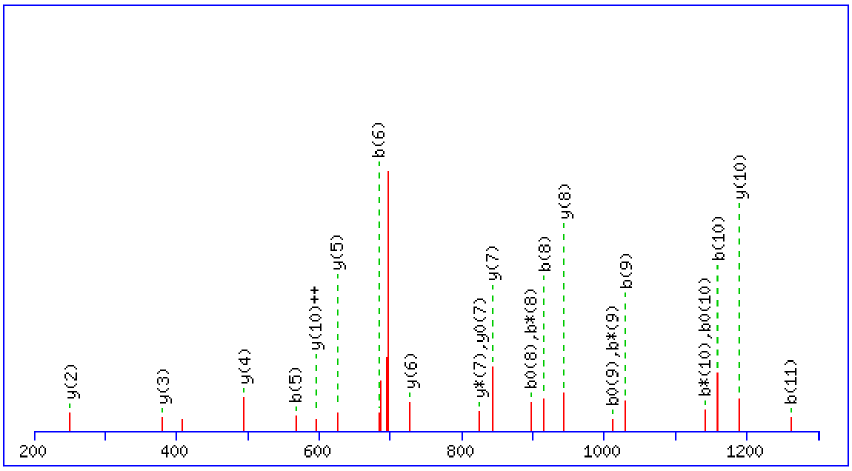
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFDEVNTQLQTK**
Found in **AT3G52300.1** in **TAIR_Arabidopsis**, Symbols: ATPQ | ATPQ (ATP SYNTHASE D CHAIN, MITOCHONDRIAL); hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transporting ATPase, rotational mechanism | chr3:19407667-19409097 FORWARD

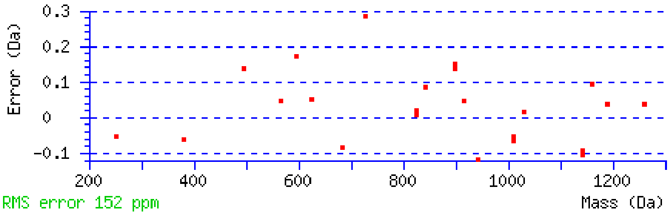
Match to Query 5403: 1408.637140 from(705.325846,2+) index(3474)
Title: Elution from: 32.414 to 32.414 scan no 4283 cid35.00 polarity:+
Data file C7-2_3.mgf

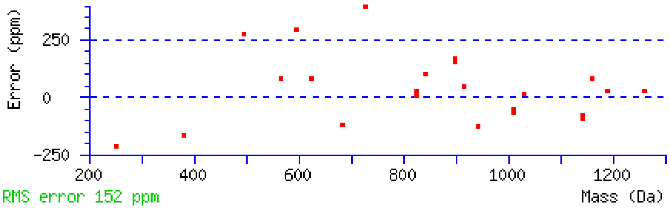
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1408.6410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 1.4e-007
Matches : 23/116 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							12
2	221.1069	111.0571					F	1337.6142	669.3107	1319.5906	660.2989	1319.6036	660.3055	11
3	337.1309	169.0691			319.1203	160.0638	D	***1189.5487***	595.2780	1171.5252	586.2662	1171.5382	586.2727	10
4	467.1705	234.0889			449.1599	225.0836	E	1073.5248	537.2660	1055.5012	528.2542	1055.5142	528.2607	9
5	**567.2359**	284.1216			549.2254	275.1163	V	***943.4851***	472.2462	925.4616	463.2344	925.4746	463.2409	8
6	**683.2729**	342.1401	665.2493	333.1283	665.2624	333.1348	N	***843.4197***	422.2135	825.3961	413.2017	825.4091	413.2082	7
7	785.3176	393.1625	767.2941	384.1507	767.3071	384.1572	T	***727.3827***	364.1950	709.3591	355.1832	709.3721	355.1897	6
8	**915.3703**	458.1888	897.3467	449.1770	897.3597	449.1835	Q	***625.3380***	313.1726	607.3144	304.1608	607.3274	304.1673	5
9	**1029.4514**	515.2293	1011.4278	506.2175	1011.4408	506.2240	L	***495.2853***	248.1463	477.2617	239.1345	477.2748	239.1410	4
10	**1159.5040**	580.2557	1141.4804	571.2439	1141.4935	571.2504	Q	***381.2042***	191.1058	363.1806	182.0940	363.1937	182.1005	3
11	**1261.5487**	631.2780	1243.5252	622.2662	1243.5382	622.2727	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AFDEVNTQLQTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G52300.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.1	1408.6410	-0.0039	AFDEVNTQLQTK
16.6	1408.6341	0.0031	MEEETRIKEAR
15.4	1408.6341	0.0031	MADKLEAKGGNGGK
14.5	1408.6411	-0.0039	YEDAADLLEKAR
14.5	1408.6385	-0.0014	DDFFKKPHMTK
10.4	1408.6412	-0.0041	RFPRGFPPECK
9.4	1408.6329	0.0042	FLDARNWDVEK
8.8	1408.6390	-0.0019	KNCVNRGLWDK
6.7	1408.6363	0.0008	KMTNSFDHVIGK
6.5	1408.6410	-0.0039	ETFADKLIDDAR

AT3G52380.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNFPEVPR**
Found in **AT3G52380.1** in **TAIR_Arabidopsis**, Symbols: PDE322, CP33 | CP33 (PIGMENT DEFECTIVE 322); RNA binding | chr3:19432597-19433833 FORWARD

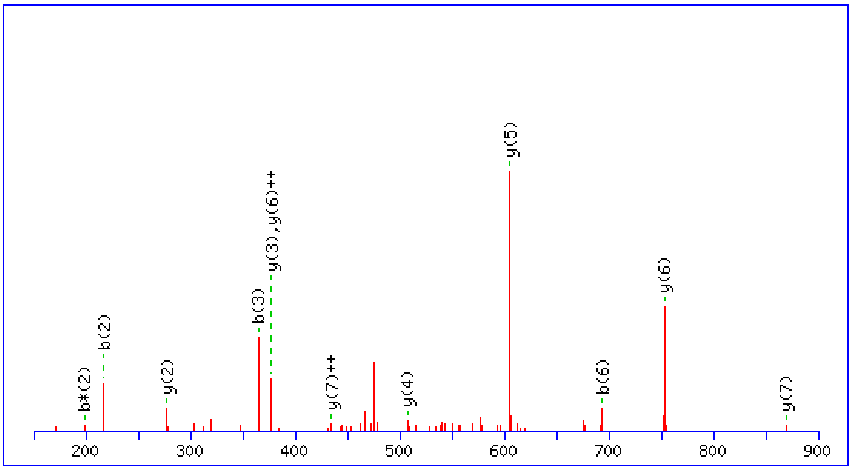
Match to Query 2173: 968.470414 from(485.242483,2+) index(4451)
Title: Elution from: 41.849 to 41.849 scan no 5656 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

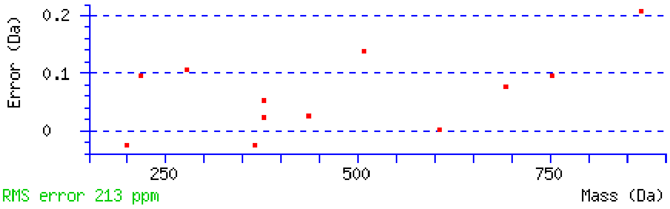
Label all possible matches ○ Label matches used for scoring ●

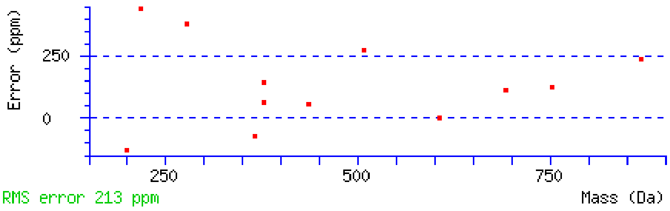
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.4724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 2.9e-005
Matches : 12/68 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							8
2	**217.1097**	109.0585	199.0861	100.0467			N	***869.4142***	435.2107	851.3906	426.1990	851.4036	426.2055	7
3	**365.1752**	183.0912	347.1516	174.0794			F	***753.3772***	377.1922	735.3536	368.1805	735.3667	368.1870	6
4	463.2250	232.1161	445.2014	223.1043			P	***605.3118***	303.1595	587.2882	294.1477	587.3012	294.1542	5
5	593.2646	297.1359	575.2410	288.1241	575.2540	288.1307	E	***507.2620***	254.1346	489.2384	245.1228	489.2514	245.1293	4
6	**693.3300**	347.1687	675.3065	338.1569	675.3195	338.1634	V	***377.2223***	189.1148	359.1988	180.1030			3
7	791.3798	396.1936	773.3563	387.1818	773.3693	387.1883	P	***277.1569***	139.0821	259.1333	130.0703			2
8							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VNFPEVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.6	968.4724	-0.0020	VNFPEVPR

AT3G52380.1

8.1	968.4701	0.0003	QIDGIASPR
4.4	968.4702	0.0003	SGENIIPAR
3.5	968.4701	0.0003	GSEAVGLAPR
3.4	968.4728	-0.0024	NRLSNPPR
1.8	968.4702	0.0003	SDRPPEKK

AT3G52720.1

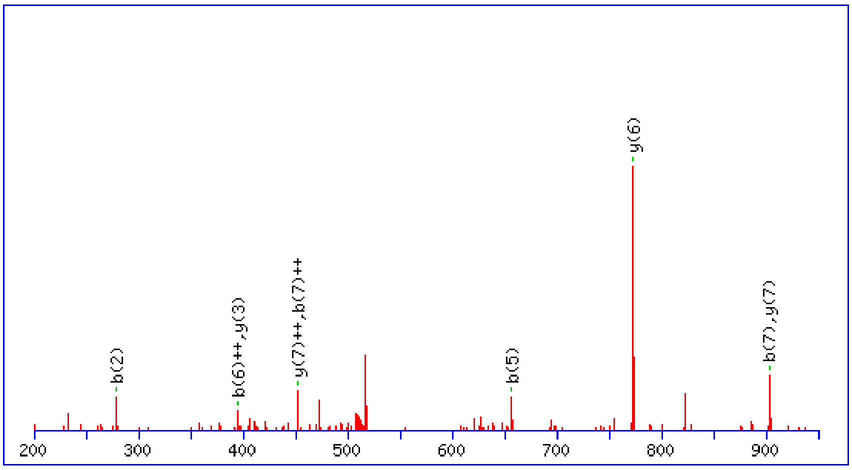
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKIMMMIK**
Found in **AT3G52720.1** in **TAIR_Arabidopsis**, Symbols: | carbonic anhydrase family protein | chr3:19549782-19552094 REVERSE

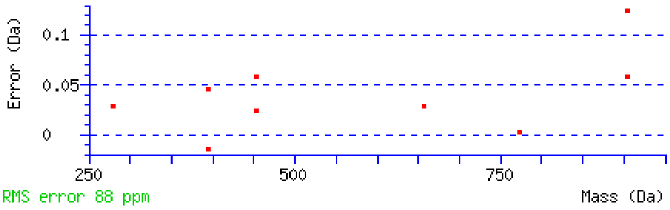
Match to Query 2717: 1050.497844 from(526.256198,2+) index(2188)
Title: Elution from: 23.549 to 23.549 scan no 2736 cid35.00 polarity:+
Data file D6h-3_3.mgf

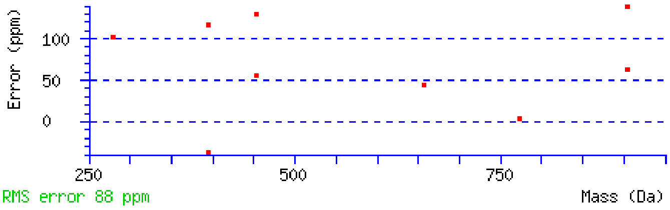
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1050.4958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.013
Matches : 9/80 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	149.0397	75.0235			M					8
2	***279.1287***	140.0680	261.1052	131.0562	K	***903.4707***	452.2390	885.4471	443.2272	7
3	393.2098	197.1086	375.1863	188.0968	I	***773.3816***	387.1945	755.3580	378.1827	6
4	525.2474	263.1273	507.2238	254.1155	M	659.3005	330.1539	641.2769	321.1421	5
5	***657.2849***	329.1461	639.2613	320.1343	M	527.2630	264.1351	509.2394	255.1234	4
6	789.3224	***395.1648***	771.2988	386.1530	M	***395.2255***	198.1164	377.2019	189.1046	3
7	***903.4035***	***452.2054***	885.3799	443.1936	I	263.1880	132.0976	245.1644	123.0858	2
8					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MKIMMMIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
25.0	1050.4958	0.0020	MKIMMMIK	Oxidation M1 76.27%

18.3	1050.4958	0.0020	MKIMMMIK	Oxidation M5 16.05%
13.5	1050.4958	0.0020	MKIMMMIK	Oxidation M4 5.37%
13.1	1050.4990	-0.0011	KFGSVSSEAK	
9.8	1050.4958	0.0020	MKIMMMIK	Oxidation M6 2.31%
9.5	1050.4990	-0.0011	QYKDTKEK	
5.2	1050.4990	-0.0011	KAGTYDEKK	
5.1	1050.4976	0.0002	ERLAMMKK	
4.6	1050.4990	-0.0011	DKSSTFVQK	
4.0	1050.4990	-0.0011	TEHPVISEK	

AT3G52880.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAEGGAAVEEYDYLPFFYSR**
Found in **AT3G52880.1** in **TAIR_Arabidopsis**, Symbols: ATMDAR1 | ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); monodehydroascorbate reductase (NADH) | chr3:19612455-19615344 REVERSE

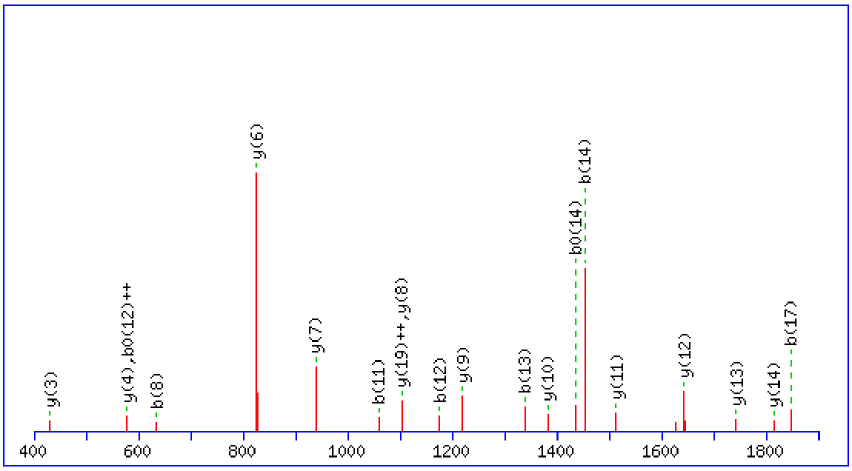
Match to Query 9759: 2276.954846 from(1139.484699,2+) index(9911)
Title: Elution from: 95.995 to 95.995 scan no 14103 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

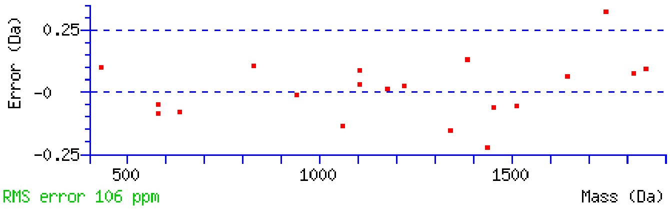
Show Y-axis ☐

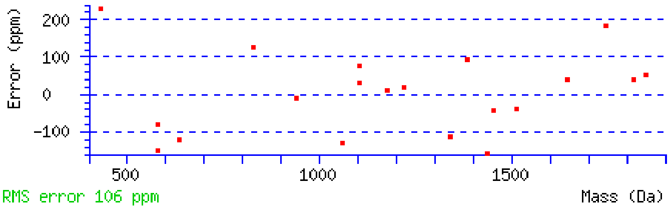


Monoisotopic mass of neutral peptide Mr(calc): 2276.9536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 2.8e-009
Matches : 20/184 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244			A							20
2	145.0756	73.0414			A	2205.9268	1103.4670	2187.9032	1094.4552	2187.9162	1094.4618	19
3	275.1152	138.0612	257.1046	129.0560	E	2133.8926	1067.4500	2115.8691	1058.4382	2115.8821	1058.4447	18
4	333.1337	167.0705	315.1231	158.0652	G	2003.8530	1002.4301	1985.8294	993.4184	1985.8425	993.4249	17
5	391.1522	196.0797	373.1416	187.0745	G	1945.8345	973.4209	1927.8109	964.4091	1927.8240	964.4156	16
6	463.1863	232.0968	445.1758	223.0915	A	1887.8160	944.4116	1869.7924	935.3999	1869.8055	935.4064	15
7	535.2205	268.1139	517.2099	259.1086	A	***1815.7819***	908.3946	1797.7583	899.3828	1797.7713	899.3893	14
8	**635.2859**	318.1466	617.2754	309.1413	V	***1743.7477***	872.3775	1725.7241	863.3657	1725.7372	863.3722	13
9	765.3256	383.1664	747.3150	374.1611	E	***1643.6823***	822.3448	1625.6587	813.3330	1625.6717	813.3395	12
10	895.3652	448.1862	877.3546	439.1810	E	***1513.6426***	757.3250	1495.6191	748.3132	1495.6321	748.3197	11
11	**1059.4256**	530.2164	1041.4150	521.2111	Y	***1383.6030***	692.3051	1365.5794	683.2934	1365.5925	683.2999	10
12	**1175.4495**	588.2284	1157.4390	579.2231	D	***1219.5427***	610.2750	1201.5191	601.2632	1201.5321	601.2697	9
13	**1339.5099**	670.2586	1321.4993	661.2533	Y	***1103.5187***	552.2630	1085.4951	543.2512	1085.5081	543.2577	8
14	**1453.5910**	727.2991	1435.5804	718.2939	L	***939.4583***	470.2328	921.4347	461.2210	921.4477	461.2275	7
15	1551.6408	776.3240	1533.6302	767.3188	P	***825.3772***	413.1922	807.3536	404.1805	807.3667	404.1870	6
16	1699.7063	850.3568	1681.6957	841.3515	F	727.3274	364.1673	709.3038	355.1556	709.3169	355.1621	5
17	**1847.7717**	924.3895	1829.7611	915.3842	F	***579.2620***	290.1346	561.2384	281.1228	561.2514	281.1293	4
18	2011.8321	1006.4197	1993.8215	997.4144	Y	***431.1965***	216.1019	413.1729	207.0901	413.1860	207.0966	3
19	2099.8611	1050.4342	2081.8506	1041.4289	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
20					R	179.1071	90.0572	161.0835	81.0454			1

AT3G52880.1





NCBI **BLAST** search of AAEGGAAVEEYDYLPFFYSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.4	2276.9536	0.0012	AAEGGAAVEEYDYLPFFYSR
15.4	2276.9505	0.0044	GLDRDRFVQNTLMDMYSR
0.4	2276.9512	0.0036	DCHLKKSCDDISDMSIALK

Mascot: http://www.matrixscience.com/

AT3G52930.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGENEPSEHSIHENAYGLAR**
Found in **AT3G52930.1** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr3:19638361-19639852 REVERSE

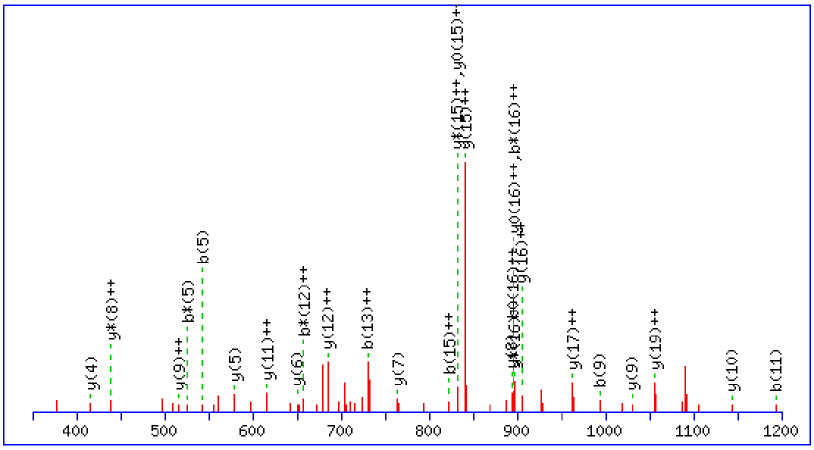
Match to Query 10071: 2222.033994 from(741.685274,3+) index(2739)
Title: Elution from: 30.627 to 30.627 scan no 3536 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1200 Da Full range

Label all possible matches ○ Label matches used for scoring ●

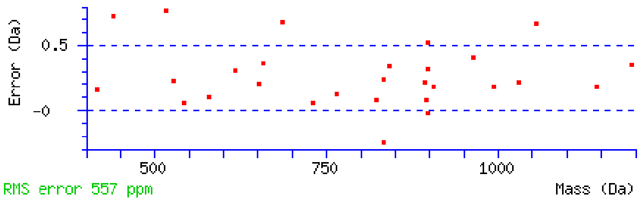
Show Y-axis ☐

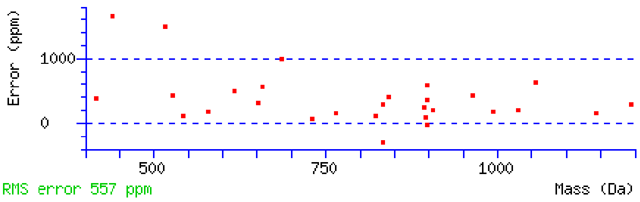


Monoisotopic mass of neutral peptide Mr(calc): 2222.0352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 9.9e-005
Matches : 28/204 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							20
2	171.1128	86.0600					G	2109.9584	1055.4829	2092.9319	1046.9696	2091.9479	1046.4776	19
3	300.1554	150.5813			282.1448	141.5761	E	2052.9370	1026.9721	2035.9104	1018.4588	2034.9264	1017.9668	18
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	N	1923.8944	962.4508	1906.8678	953.9376	1905.8838	953.4455	17
5	**543.2409**	272.1241	526.2144	263.6108	525.2304	263.1188	E	1809.8515	905.4294	1792.8249	896.9161	1791.8409	896.4241	16
6	640.2937	320.6505	623.2671	312.1372	622.2831	311.6452	P	1680.8089	840.9081	1663.7823	832.3948	1662.7983	831.9028	15
7	727.3257	364.1665	710.2992	355.6532	709.3151	355.1612	S	1583.7561	792.3817	1566.7295	783.8684	1565.7455	783.3764	14
8	856.3683	428.6878	839.3418	420.1745	838.3577	419.6825	E	1496.7241	748.8657	1479.6975	740.3524	1478.7135	739.8604	13
9	**993.4272**	497.2172	976.4007	488.7040	975.4166	488.2120	H	1367.6815	684.3444	1350.6549	675.8311	1349.6709	675.3391	12
10	1080.4592	540.7333	1063.4327	532.2200	1062.4487	531.7280	S	1230.6226	615.8149	1213.5960	607.3016	1212.6120	606.8096	11
11	**1193.5433**	597.2753	1176.5168	588.7620	1175.5327	588.2700	I	***1143.5905***	572.2989	1126.5640	563.7856	1125.5800	563.2936	10
12	1330.6022	665.8047	1313.5757	657.2915	1312.5917	656.7995	H	***1030.5065***	515.7569	1013.4799	507.2436	1012.4959	506.7516	9
13	1459.6448	730.3260	1442.6183	721.8128	1441.6342	721.3208	E	***893.4476***	447.2274	876.4210	438.7141	875.4370	438.2221	8
14	1573.6877	787.3475	1556.6612	778.8342	1555.6772	778.3422	N	***764.4050***	382.7061	747.3784	374.1928			7
15	1644.7249	822.8661	1627.6983	814.3528	1626.7143	813.8608	A	***650.3620***	325.6847	633.3355	317.1714			6
16	1807.7882	904.3977	1790.7616	895.8845	1789.7776	895.3924	Y	***579.3249***	290.1661	562.2984	281.6528			5
17	1864.8096	932.9085	1847.7831	924.3952	1846.7991	923.9032	G	***416.2616***	208.6344	399.2350	200.1212			4
18	1977.8937	989.4505	1960.8672	980.9372	1959.8831	980.4452	L	359.2401	180.1237	342.2136	171.6104			3
19	2048.9308	1024.9690	2031.9043	1016.4558	2030.9203	1015.9638	A	246.1561	123.5817	229.1295	115.0684			2
20							R	175.1190	88.0631	158.0924	79.5498			1

AT3G52930.1





NCBI **BLAST** search of IGENEPSEHSIHENAYGLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.2	2222.0352	-0.0012	IGENEPSEHSIHENAYGLAR
4.4	2222.0395	-0.0055	LLMGQPPDYSDGKCRLCGR
3.6	2222.0352	-0.0012	WDQINDHGTSHLSIIDSER
1.8	2222.0280	0.0060	NLNNGNINTSDMQNAKRMR
0.7	2222.0280	0.0060	ADVQKALQDYGYFEASFDR

Mascot: http://www.matrixscience.com/

AT3G52960.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGVELDLR**
Found in **AT3G52960.1** in **TAIR_Arabidopsis**, Symbols: | peroxiredoxin type 2, putative | chr3:19650677-19651381 FORWARD

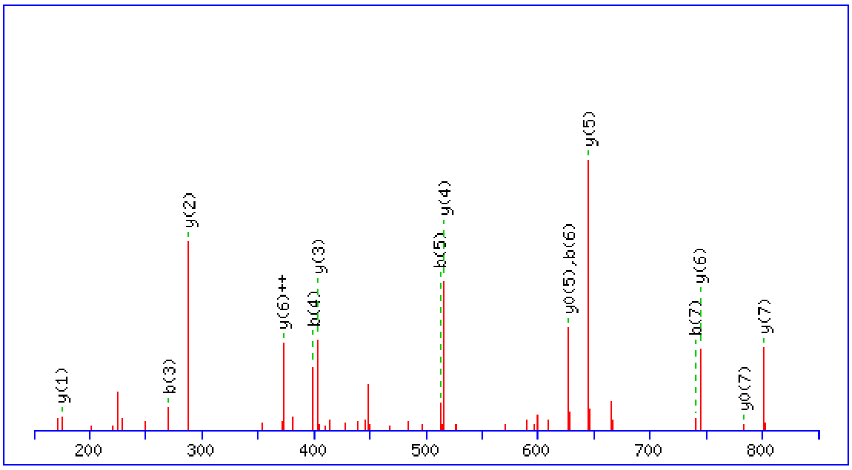
Match to Query 1382: 913.522792 from(457.768672,2+) index(5380)
Title: Elution from: 51.858 to 51.858 scan no 6980 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

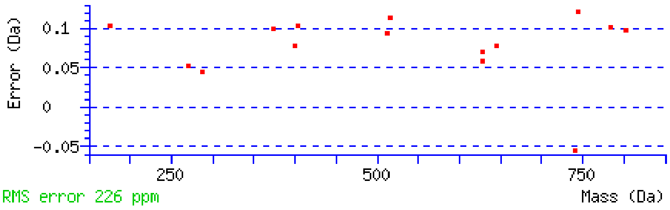
Label all possible matches ○ Label matches used for scoring ●

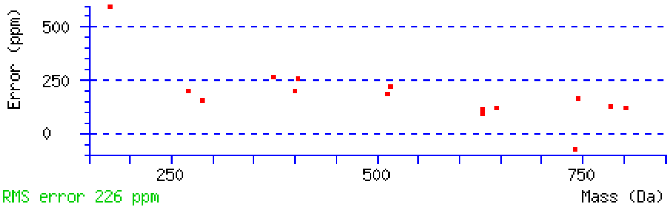
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 913.5233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 6.1e-006
Matches : 15/60 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							8
2	171.1128	86.0600			G	***801.4465***	401.2269	784.4199	392.7136	783.4359	392.2216	7
3	**270.1812**	135.5942			V	***744.4250***	372.7162	727.3985	364.2029	726.4145	363.7109	6
4	**399.2238**	200.1155	381.2132	191.1103	E	***645.3566***	323.1819	628.3301	314.6687	627.3461	314.1767	5
5	**512.3079**	256.6576	494.2973	247.6523	L	***516.3140***	258.6606	499.2875	250.1474	498.3035	249.6554	4
6	**627.3348**	314.1710	609.3243	305.1658	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
7	**740.4189**	370.7131	722.4083	361.7078	L	***288.2030***	144.6051	271.1765	136.0919			2
8					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LGVELDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.0	913.5233	-0.0005	LGVELDLR
15.6	913.5233	-0.0005	LLPTSDLR

14.2	913.5233	-0.0005	VAEVIVER
6.0	913.5233	-0.0005	IPSIESLR
1.9	913.5233	-0.0005	LVAEEVVR
1.4	913.5206	0.0022	RLAERNR
0.7	913.5233	-0.0005	STVPLLER

Mascot: http://www.matrixscience.com/

AT3G52990.1

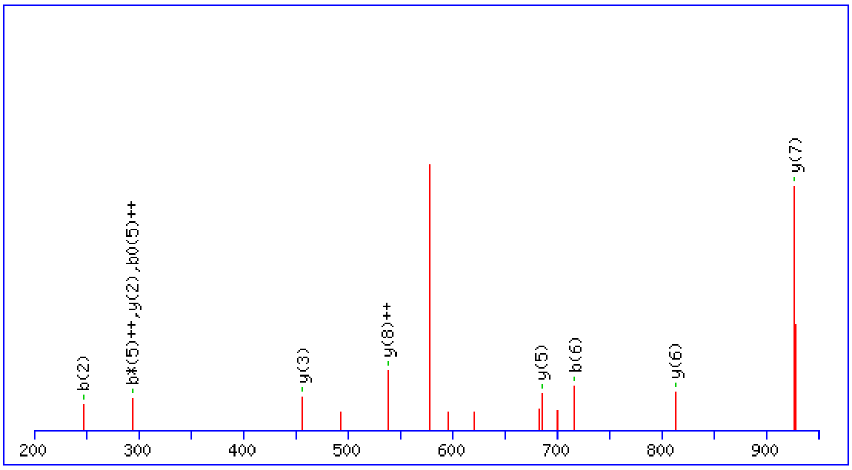
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFNQDLYFK**
Found in **AT3G52990.1** in **TAIR_Arabidopsis**, Symbols: | pyruvate kinase, putative | chr3:19660024-19663215 FORWARD

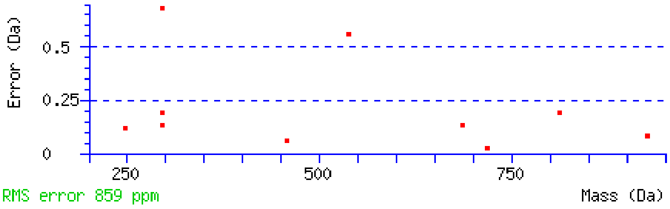
Match to Query 3668: 1172.586932 from(587.300742,2+) index(5660)
Title: Elution from: 52.609 to 52.609 scan no 7271 cid35.00 polarity:+
Data file D1d-2_1.mgf

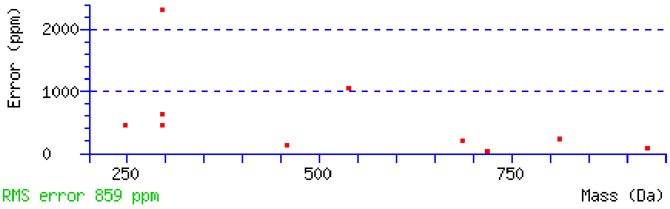
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1172.5866
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0004
Matches : 10/76 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							9
2	**247.1441**	124.0757					F	1074.5255	537.7664	1057.4989	529.2531	1056.5149	528.7611	8
3	361.1870	181.0972	344.1605	172.5839			N	***927.4571***	464.2322	910.4305	455.7189	909.4465	455.2269	7
4	489.2456	245.1264	472.2191	236.6132			Q	***813.4141***	407.2107	796.3876	398.6974	795.4036	398.2054	6
5	604.2726	302.6399	587.2460	294.1266	586.2620	293.6346	D	***685.3556***	343.1814	668.3290	334.6681	667.3450	334.1761	5
6	**717.3566**	359.1819	700.3301	350.6687	699.3461	350.1767	L	570.3286	285.6679	553.3021	277.1547			4
7	880.4199	440.7136	863.3934	432.2003	862.4094	431.7083	Y	***457.2445***	229.1259	440.2180	220.6126			3
8	1027.4884	514.2478	1010.4618	505.7345	1009.4778	505.2425	F	***294.1812***	147.5942	277.1547	139.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VFNQDLYFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.0	1172.5866	0.0003	VFNQDLYFK

AT3G52990.1

1.3	1172.5900	-0.0030	SPTVMKGYFK
0.8	1172.5900	-0.0030	FLQSMGLSFK

AT3G53020.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAWTAMYR**
Found in **AT3G53020.1** in **TAIR_Arabidopsis**, Symbols: RPL24B, RPL24, STV1 | STV1 (SHORT VALVE1); structural constituent of ribosome | chr3:19671727-19672890 REVERSE

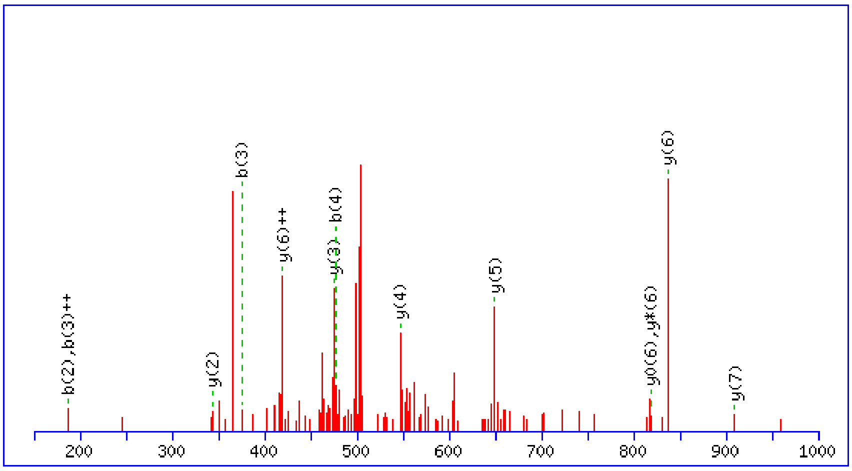
Match to Query 2636: 1022.463164 from(512.238858,2+) index(5481)
Title: Elution from: 49.348 to 49.348 scan no 6969 cid35.00 polarity:+
Data file D6h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

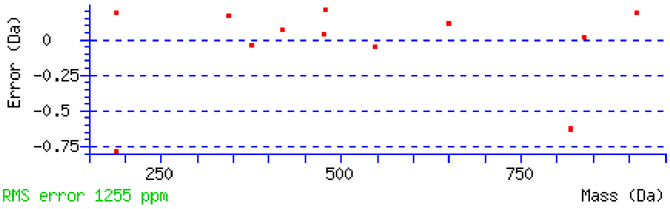
Label all possible matches ○ Label matches used for scoring ●

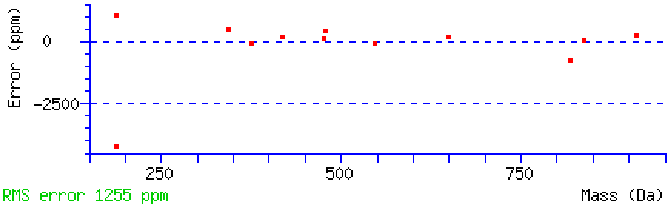
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1022.4652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.016
Matches : 13/56 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	**187.1225**	94.0649			A	***909.3914***	455.1993	891.3678	446.1875	891.3808	446.1940	7
3	**375.1959**	188.1016			W	***837.3572***	419.1822	819.3336	410.1705	819.3467	410.1770	6
4	**477.2406**	239.1239	459.2301	230.1187	T	***649.2838***	325.1456	631.2603	316.1338	631.2733	316.1403	5
5	549.2748	275.1410	531.2642	266.1357	A	***547.2391***	274.1232	529.2155	265.1114			4
6	681.3123	341.1598	663.3017	332.1545	M	***475.2050***	238.1061	457.1814	229.0943			3
7	845.3727	423.1900	827.3621	414.1847	Y	***343.1675***	172.0874	325.1439	163.0756			2
8					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LAWTAMYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.2	1022.4652	-0.0020	LAWTAMYR

AT3G53020.1

Mascot: http://www.matrixscience.com/

AT3G53260.1

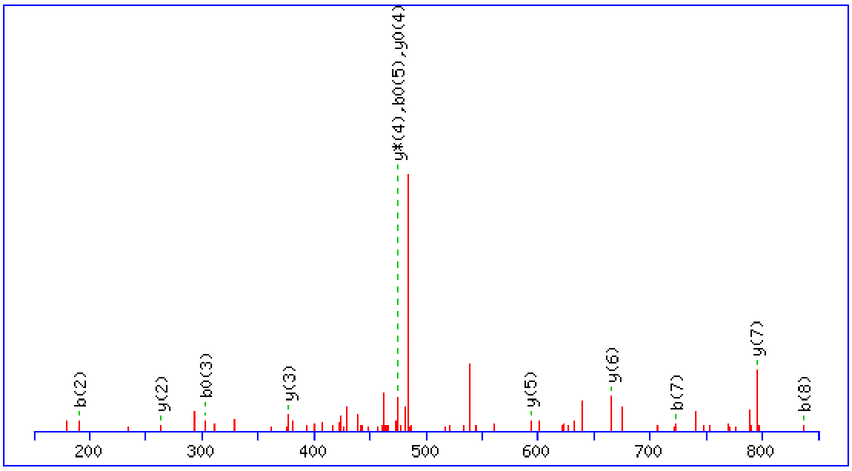
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSEAVDILK**
Found in **AT3G53260.1** in **TAIR_Arabidopsis**, Symbols: PAL2 | PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase | chr3:19755234-19757597 REVERSE

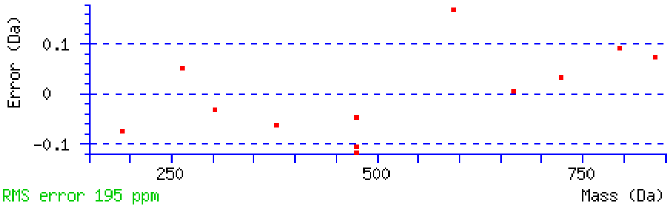
Match to Query 2405: 984.496794 from(493.255673,2+) index(3354)
Title: Elution from: 31.891 to 31.891 scan no 4144 cid35.00 polarity:+
Data file C7-3_2.mgf

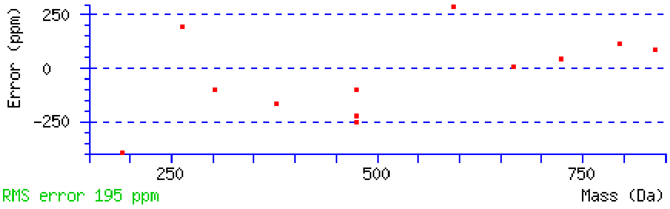
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.4988
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.03
Matches : 12/74 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							9
2	**191.0811**	96.0442	173.0705	87.0389	S	883.4613	442.2343	865.4378	433.2225	865.4508	433.2290	8
3	321.1207	161.0640	303.1101	152.0587	E	***795.4323***	398.2198	777.4087	389.2080	777.4217	389.2145	7
4	393.1548	197.0811	375.1443	188.0758	A	***665.3926***	333.2000	647.3691	324.1882	647.3821	324.1947	6
5	493.2203	247.1138	475.2097	238.1085	V	***593.3585***	297.1829	575.3349	288.1711	575.3479	288.1776	5
6	609.2443	305.1258	591.2337	296.1205	D	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
7	**723.3254**	362.1663	705.3148	353.1610	I	***377.2691***	189.1382	359.2455	180.1264			3
8	**837.4065**	419.2069	819.3959	410.2016	L	***263.1880***	132.0976	245.1644	123.0858			2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TSEAVDILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G53260.1

23.0	984.4988	-0.0020	TSEAVDILK
13.3	984.4996	-0.0029	QMIMPVIK
12.0	984.4988	-0.0020	KLEEVTEK
10.8	984.4940	0.0028	NIVDCLLK
10.2	984.4988	-0.0020	KTIDEELK
9.1	984.4940	0.0028	DVMLDLLR
9.1	984.4987	-0.0020	DVTATDILK
8.3	984.4988	-0.0020	DEEITKLK
7.0	984.4967	0.0001	LANPKCLR
5.3	984.4940	0.0028	LENVQMLK

AT3G53420.1

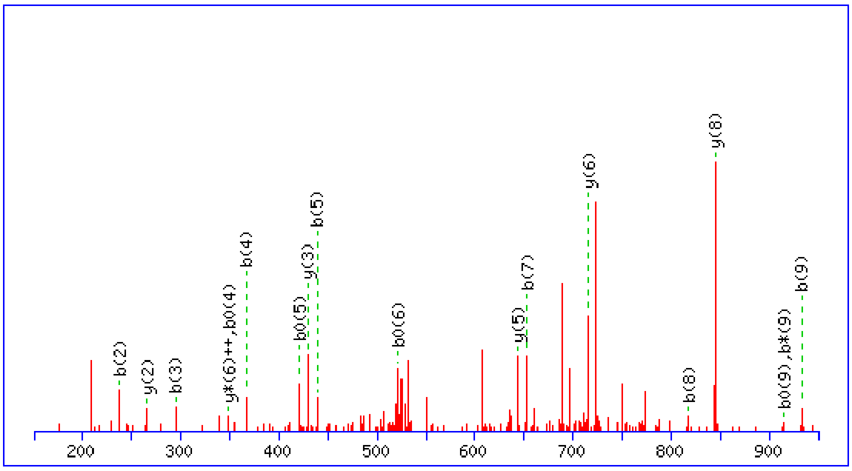
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFGAAVIYNK**
Found in **AT3G53420.1** in **TAIR_Arabidopsis**, Symbols: PIP2, PIP2;1, PIP2A | PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel | chr3:19814884-19816432 REVERSE

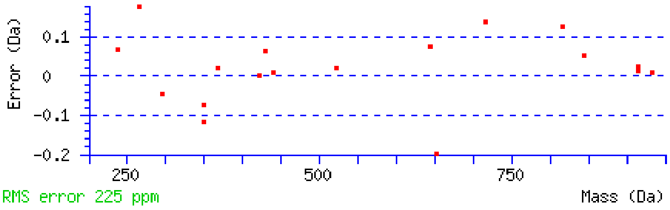
Match to Query 3131: 1080.521858 from(541.268205,2+) index(3738)
Title: Elution from: 35.390 to 35.390 scan no 4671 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

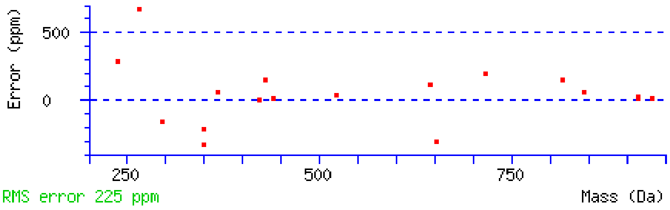


Monoisotopic mass of neutral peptide Mr(calc): 1080.5248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 4.6e-006
Matches : 18/74 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	89.0363	45.0218			71.0258	36.0165	S					10
2	***237.1018***	119.0545			219.0912	110.0492	F	993.5030	497.2552	975.4794	488.2434	9
3	***295.1203***	148.0638			277.1097	139.0585	G	**845.4376**	423.2224	827.4140	414.2106	8
4	***367.1544***	184.0809			349.1439	175.0756	A	787.4191	394.2132	769.3955	385.2014	7
5	***439.1886***	220.0979			421.1780	211.0926	A	**715.3849**	358.1961	697.3613	349.1843	6
6	539.2540	270.1307			521.2435	261.1254	V	**643.3508**	322.1790	625.3272	313.1672	5
7	***653.3351***	327.1712			635.3246	318.1659	I	543.2853	272.1463	525.2618	263.1345	4
8	***817.3955***	409.2014			799.3849	400.1961	Y	**429.2042**	215.1058	411.1807	206.0940	3
9	***933.4325***	467.2199	915.4089	458.2081	915.4219	458.2146	N	**265.1439**	133.0756	247.1203	124.0638	2
10							K	149.1069	75.0571	131.0833	66.0453	1



RMS error 225 ppm



RMS error 225 ppm

NCBI **BLAST** search of SFGAAVIYNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G53420.1

Score	Mr(calc)	Delta	Sequence
59.1	1080.5248	-0.0030	SFGAAVIYNK
8.0	1080.5199	0.0020	PEEDLVELK
1.8	1080.5248	-0.0030	FALGYEKNK

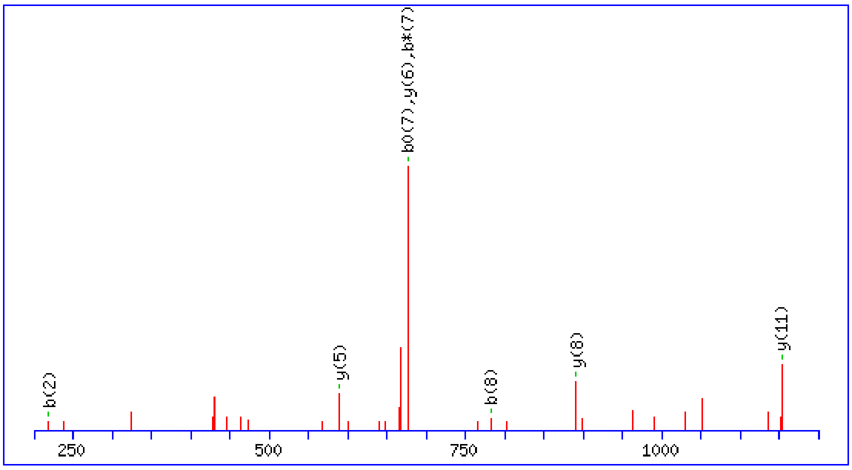
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSGNSVLSSCSTK**
Found in **AT3G53440.1** in **TAIR_Arabidopsis**, Symbols: | DNA binding | chr3:19821914-19823452 FORWARD

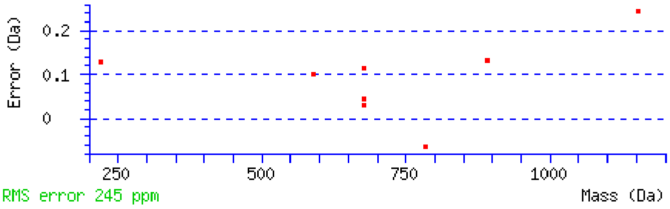
Match to Query 4693: 1370.604648 from(686.309600,2+) index(3639)
Title: Elution from: 38.383 to 38.383 scan no 4694 cid35.00 polarity:+
Data file D1d-1-2.mgf

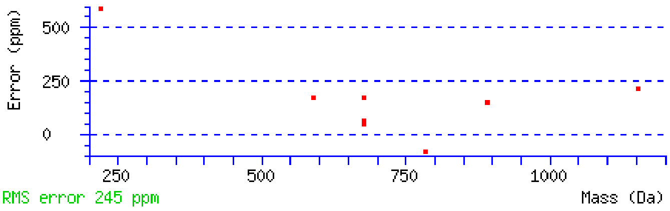
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1370.6054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.037
Matches : 8/140 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							13
2	**219.1254**	110.0663	201.1018	101.0545	201.1148	101.0610	S	1241.5237	621.2655	1223.5001	612.2537	1223.5131	612.2602	12
3	277.1439	139.0756	259.1203	130.0638	259.1333	130.0703	G	***1153.4946***	577.2509	1135.4710	568.2391	1135.4840	568.2457	11
4	393.1809	197.0941	375.1573	188.0823	375.1703	188.0888	N	1095.4761	548.2417	1077.4525	539.2299	1077.4655	539.2364	10
5	481.2099	241.1086	463.1863	232.0968	463.1994	232.1033	S	979.4391	490.2232	961.4155	481.2114	961.4285	481.2179	9
6	581.2754	291.1413	563.2518	282.1295	563.2648	282.1360	V	***891.4100***	446.2087	873.3865	437.1969	873.3995	437.2034	8
7	695.3565	348.1819	677.3329	339.1701	677.3459	339.1766	L	791.3446	396.1759	773.3210	387.1641	773.3340	387.1707	7
8	**783.3855**	392.1964	765.3620	383.1846	765.3750	383.1911	S	***677.2635***	339.1354	659.2399	330.1236	659.2529	330.1301	6
9	871.4146	436.2109	853.3910	427.1991	853.4040	427.2057	S	***589.2344***	295.1209	571.2108	286.1091	571.2239	286.1156	5
10	1033.4393	517.2233	1015.4157	508.2115	1015.4288	508.2180	C	501.2054	251.1063	483.1818	242.0945	483.1948	242.1010	4
11	1121.4684	561.2378	1103.4448	552.2260	1103.4578	552.2325	S	339.1806	170.0940	321.1571	161.0822	321.1701	161.0887	3
12	1223.5131	612.2602	1205.4895	603.2484	1205.5025	603.2549	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KSGNSVLSSCSTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G53440.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.8	1370.6054	-0.0008	KSGNSVLSSCSTK
4.0	1370.6016	0.0030	EKEEFISDFSK
0.8	1370.6047	-0.0001	ASNSNSAAAFGRAK

Mascot: http://www.matrixscience.com/

AT3G53460.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AINSLNGADLDGR**
Found in **AT3G53460.1** in **TAIR_Arabidopsis**, Symbols: CP29 | CP29 (chloroplast 29 kDa ribonucleoprotein); RNA binding / poly(U) binding | chr3:19830716-19832401 REVERSE

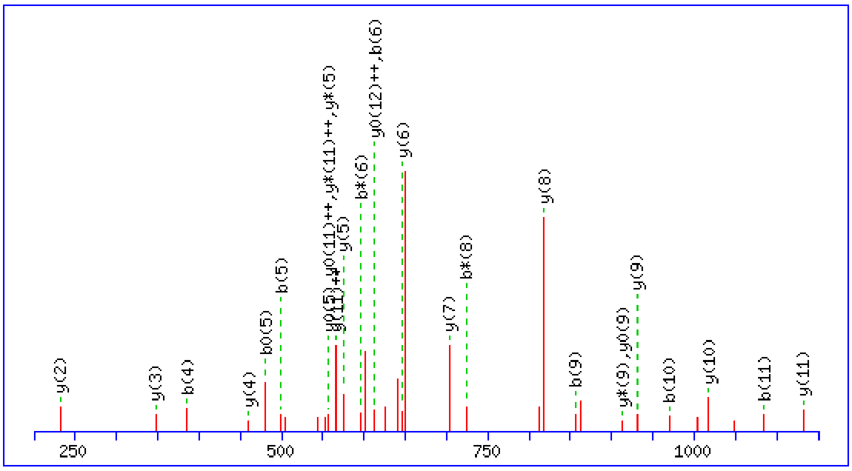
Match to Query 5231: 1314.650302 from(658.332427,2+) index(3645)
Title: Elution from: 34.407 to 34.407 scan no 4480 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1150 Da Full range

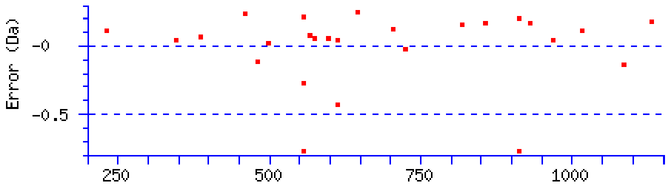
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

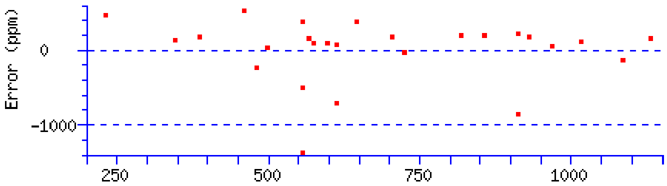


Monoisotopic mass of neutral peptide Mr(calc): 1314.6528
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 6e-009
Matches : 27/130 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							13
2	185.1285	93.0679					I	1244.6230	622.8151	1227.5964	614.3018	1226.6124	613.8098	12
3	299.1714	150.0893	282.1448	141.5761			N	***1131.5389***	566.2731	1114.5123	557.7598	1113.5283	557.2678	11
4	**386.2034**	193.6053	369.1769	185.0921	368.1928	184.6001	S	***1017.4960***	509.2516	1000.4694	500.7383	999.4854	500.2463	10
5	**499.2875**	250.1474	482.2609	241.6341	481.2769	241.1421	L	***930.4639***	465.7356	913.4374	457.2223	912.4534	456.7303	9
6	**613.3304**	307.1688	596.3039	298.6556	595.3198	298.1636	N	***817.3799***	409.1936	800.3533	400.6803	799.3693	400.1883	8
7	670.3519	335.6796	653.3253	327.1663	652.3413	326.6743	G	***703.3369***	352.1721	686.3104	343.6588	685.3264	343.1668	7
8	741.3890	371.1981	724.3624	362.6849	723.3784	362.1928	A	***646.3155***	323.6614	629.2889	315.1481	628.3049	314.6561	6
9	**856.4159**	428.7116	839.3894	420.1983	838.4054	419.7063	D	***575.2784***	288.1428	558.2518	279.6295	557.2678	279.1375	5
10	**969.5000**	485.2536	952.4734	476.7404	951.4894	476.2483	L	***460.2514***	230.6293	443.2249	222.1161	442.2409	221.6241	4
11	**1084.5269**	542.7671	1067.5004	534.2538	1066.5164	533.7618	D	***347.1674***	174.0873	330.1408	165.5740	329.1568	165.0820	3
12	1141.5484	571.2778	1124.5218	562.7646	1123.5378	562.2726	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 417 ppm



RMS error 417 ppm

NCBI **BLAST** search of AINSLNGADLDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G53460.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
87.0	1314.6528	-0.0025	AINSLNGADLDGR
0.5	1314.6528	-0.0025	SPQNLSNSALER

AT3G53540.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQLQLLK**
Found in **AT3G53540.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G28760.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G28760.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO18092.1); contains domain PHOSPHATIDY

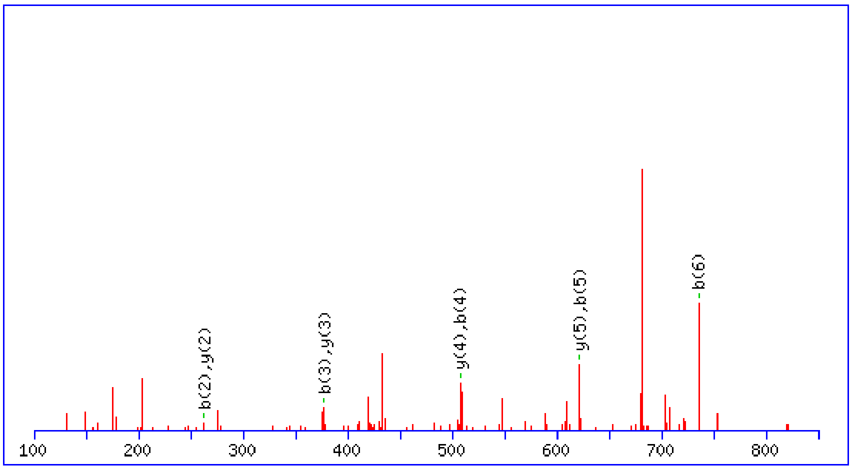
Match to Query 1541: 882.488004 from(442.251278,2+) index(1954)
Title: Elution from: 22.339 to 22.339 scan no 2500 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 850 Da Full range

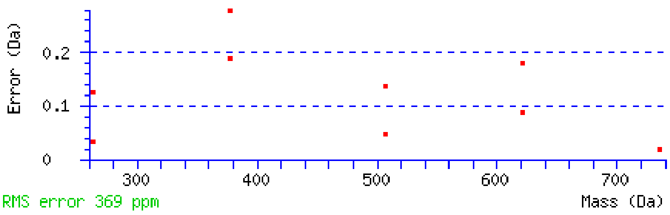
Label all possible matches ○ Label matches used for scoring ●

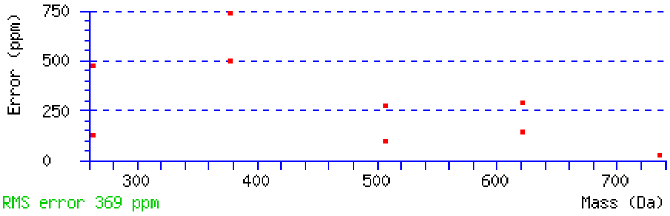
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 882.4857
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0055
Matches : 9/46 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	133.0448	67.0260			M					7
2	***263.0974***	132.0524	245.0739	123.0406	Q	751.4555	376.2314	733.4319	367.2196	6
3	***377.1785***	189.0929	359.1550	180.0811	L	**621.4028**	311.2050	603.3792	302.1933	5
4	***507.2312***	254.1192	489.2076	245.1074	Q	**507.3217**	254.1645	489.2981	245.1527	4
5	***621.3123***	311.1598	603.2887	302.1480	L	**377.2691**	189.1382	359.2455	180.1264	3
6	***735.3934***	368.2003	717.3698	359.1885	L	**263.1880**	132.0976	245.1644	123.0858	2
7					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MQLQLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.6	882.4857	0.0023	MQLQLLK

AT3G53540.1

21.2	882.4857	0.0023	KMLPEKK
17.5	882.4857	0.0023	KALGLPMK
13.5	882.4857	0.0023	QQLLMIK
12.2	882.4857	0.0023	MAKLVAPK
8.8	882.4904	-0.0024	ELTTLGIK
6.6	882.4857	0.0023	MEKPKLK
6.3	882.4904	-0.0024	ETVSVVLK
6.3	882.4854	0.0026	KRGRPPR
6.2	882.4879	0.0001	MLWLALK

AT3G53740.1

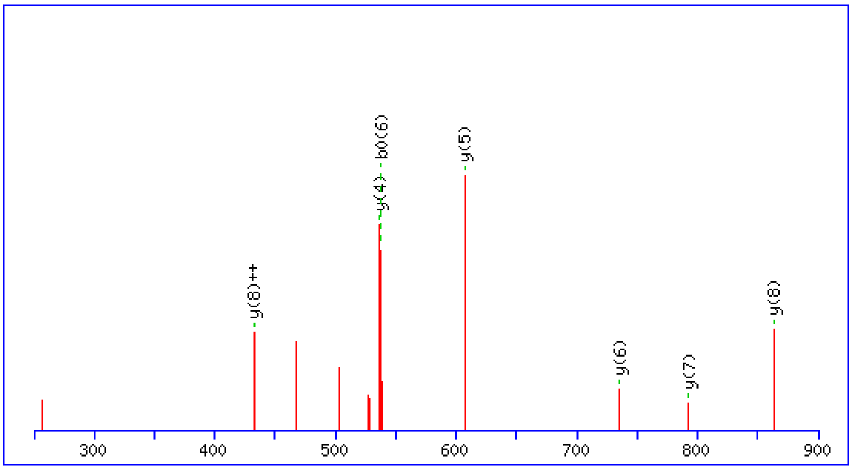
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVAGQAPYEK**
Found in **AT3G53740.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L36 (RPL36B) | chr3:19924899-19925791 REVERSE

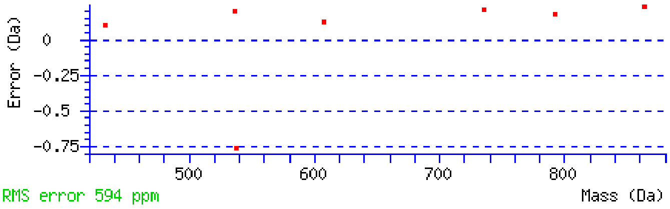
Match to Query 3475: 1090.529992 from(546.272272,2+) index(557)
Title: Elution from: 11.210 to 11.210 scan no 860 cid35.00 polarity:+
Data file C7-2_1.mgf

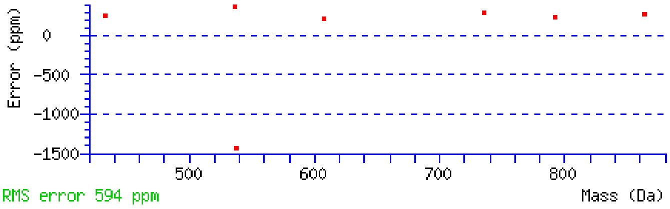
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1090.5295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00033
Matches : 7/98 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	229.1183	115.0628			211.1077	106.0575	V	962.4942	481.7507	945.4676	473.2375	944.4836	472.7454	9
3	300.1554	150.5813			282.1448	141.5761	A	***863.4258***	432.2165	846.3992	423.7032	845.4152	423.2112	8
4	357.1769	179.0921			339.1663	170.0868	G	***792.3886***	396.6980	775.3621	388.1847	774.3781	387.6927	7
5	485.2354	243.1214	468.2089	234.6081	467.2249	234.1161	Q	***735.3672***	368.1872	718.3406	359.6740	717.3566	359.1819	6
6	556.2726	278.6399	539.2460	270.1266	538.2620	269.6346	A	***607.3086***	304.1579	590.2821	295.6447	589.2980	295.1527	5
7	653.3253	327.1663	636.2988	318.6530	635.3148	318.1610	P	***536.2715***	268.6394	519.2449	260.1261	518.2609	259.6341	4
8	816.3886	408.6980	799.3621	400.1847	798.3781	399.6927	Y	439.2187	220.1130	422.1922	211.5997	421.2082	211.1077	3
9	945.4312	473.2193	928.4047	464.7060	927.4207	464.2140	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EVAGQAPYEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G53740.1

42.2	1090.5295	0.0005	EVAGQAPYEK
15.6	1090.5328	-0.0028	DQIQAMELK
4.5	1090.5295	0.0005	LDATANDFPK
3.7	1090.5329	-0.0029	LNTIIDCDK
2.0	1090.5295	0.0005	SAEPISSSWK

AT3G53870.1

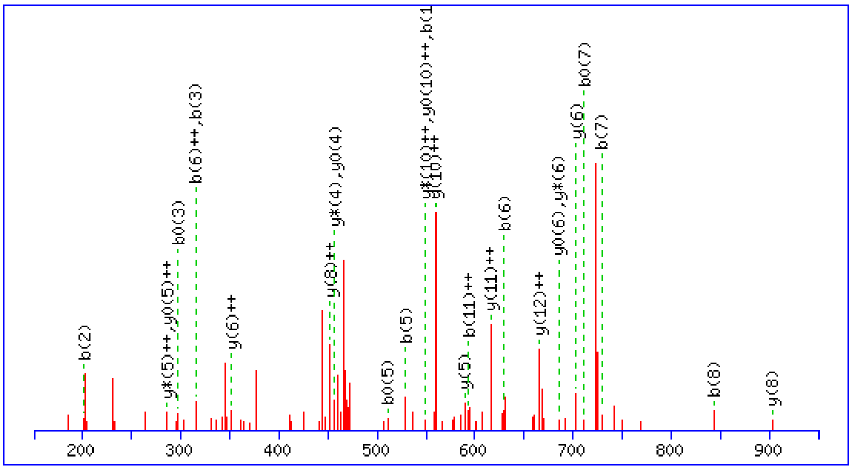
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPLPDVVIIHSPK**
Found in **AT3G53870.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S3 (RPS3B) | chr3:19962525-19963760 FORWARD

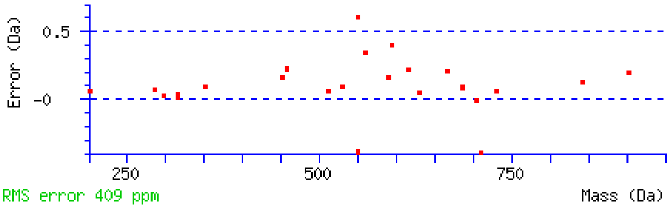
Match to Query 5579: 1430.770083 from(477.930637,3+) index(5688)
Title: Elution from: 51.661 to 51.661 scan no 7197 cid35.00 polarity:+
Data file D6h-2_2.mgf

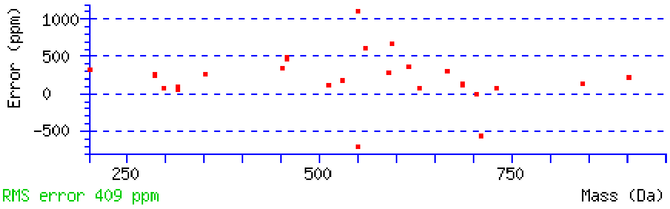
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1430.7710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.032
Matches : 28/116 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							13
2	***201.1018***	101.0545	183.0912	92.0492	P	1329.7335	665.3704	1311.7099	656.3586	1311.7230	656.3651	12
3	***315.1829***	158.0951	297.1723	149.0898	L	1231.6837	616.3455	1213.6601	607.3337	1213.6732	607.3402	11
4	413.2327	207.1200	395.2221	198.1147	P	1117.6026	559.3050	1099.5790	550.2932	1099.5921	550.2997	10
5	***529.2567***	265.1320	511.2461	256.1267	D	1019.5528	510.2801	1001.5292	501.2683	1001.5423	501.2748	9
6	***629.3221***	***315.1647***	611.3115	306.1594	V	**903.5288**	452.2681	885.5053	443.2563	885.5183	443.2628	8
7	***729.3876***	365.1974	711.3770	356.1921	V	803.4634	402.2353	785.4398	393.2235	785.4528	393.2301	7
8	***843.4687***	422.2380	825.4581	413.2327	I	**703.3980**	352.2026	685.3744	343.1908	685.3874	343.1973	6
9	957.5498	479.2785	939.5392	470.2732	I	**589.3169**	295.1621	571.2933	286.1503	571.3063	286.1568	5
10	1097.5998	***549.3035***	1079.5892	540.2982	H	475.2358	238.1215	457.2122	229.1097	457.2252	229.1162	4
11	1185.6288	***593.3181***	1167.6183	584.3128	S	335.1857	168.0965	317.1622	159.0847	317.1752	159.0912	3
12	1283.6786	642.3430	1265.6681	633.3377	P	247.1567	124.0820	229.1331	115.0702			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TPLPDVVIIHSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G53870.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.5	1430.7710	-0.0009	TPLPDVVIIHSPK
4.7	1430.7714	-0.0013	VKLGVIVNNVSNR
2.0	1430.7709	-0.0009	VVLSLTGVKEGWK
0.7	1430.7736	-0.0035	VVKQILWVNGTR

AT3G54050.1

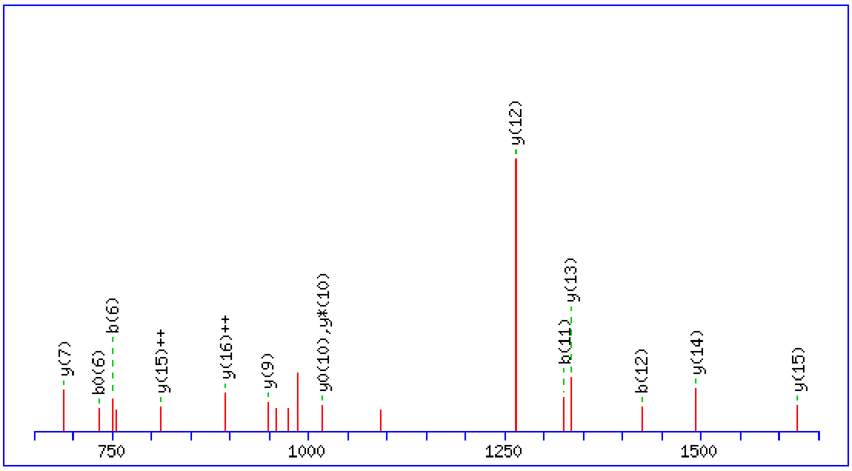
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLYECAPMSFIVEQAGGK**
Found in **AT3G54050.1** in **TAIR_Arabidopsis**, Symbols: | fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative | chr3:20027929-20029505 FORWARD

Match to Query 8890: 2011.974722 from(1006.994637,2+) index(9241)
Title: Elution from: 88.674 to 88.674 scan no 12958 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

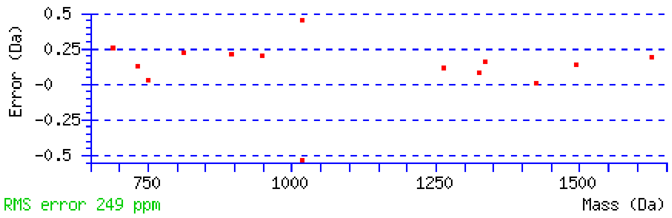


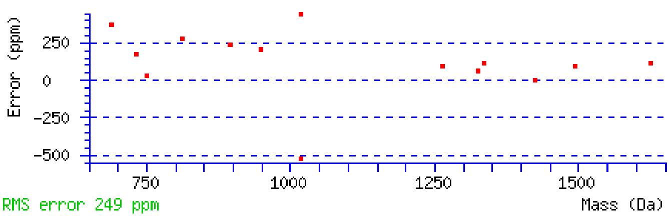
`**Monoisotopic mass of neutral peptide Mr(calc):** 2011.9747`

Monoisotopic mass of neutral peptide Mr(calc): 2011.9747
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 5.9e-005
Matches : 14/162 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							18
2	227.1754	114.0913					L	1899.8979	950.4526	1882.8714	941.9393	1881.8874	941.4473	17
3	390.2387	195.6230					Y	1786.8139	893.9106	1769.7873	885.3973	1768.8033	884.9053	16
4	519.2813	260.1443			501.2708	251.1390	E	***1623.7505***	812.3789	1606.7240	803.8656	1605.7400	803.3736	15
5	679.3120	340.1596			661.3014	331.1543	C	***1494.7079***	747.8576	1477.6814	739.3443	1476.6974	738.8523	14
6	**750.3491**	375.6782			732.3385	366.6729	A	***1334.6773***	667.8423	1317.6508	659.3290	1316.6667	658.8370	13
7	847.4019	424.2046			829.3913	415.1993	P	***1263.6402***	632.3237	1246.6136	623.8105	1245.6296	623.3184	12
8	978.4423	489.7248			960.4318	480.7195	M	1166.5874	583.7973	1149.5609	575.2841	1148.5769	574.7921	11
9	1065.4744	533.2408			1047.4638	524.2355	S	1035.5469	518.2771	1018.5204	509.7638	1017.5364	509.2718	10
10	1212.5428	606.7750			1194.5322	597.7697	F	***948.5149***	474.7611	931.4884	466.2478	930.5043	465.7558	9
11	**1325.6268**	663.3171			1307.6163	654.3118	I	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	8
12	**1424.6953**	712.8513			1406.6847	703.8460	V	***688.3624***	344.6849	671.3359	336.1716	670.3519	335.6796	7
13	1553.7379	777.3726			1535.7273	768.3673	E	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	6
14	1681.7964	841.4019	1664.7699	832.8886	1663.7859	832.3966	Q	460.2514	230.6293	443.2249	222.1161			5
15	1752.8335	876.9204	1735.8070	868.4071	1734.8230	867.9151	A	332.1928	166.6001	315.1663	158.0868			4
16	1809.8550	905.4311	1792.8285	896.9179	1791.8444	896.4259	G	261.1557	131.0815	244.1292	122.5682			3
17	1866.8765	933.9419	1849.8499	925.4286	1848.8659	924.9366	G	204.1343	102.5708	187.1077	94.0575			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT3G54050.1





NCBI **BLAST** search of LLYECAPMSFIVEQAGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.9	2011.9747	0.0000	LLYECAPMSFIVEQAGGK

Mascot: http://www.matrixscience.com/

AT3G54110.1

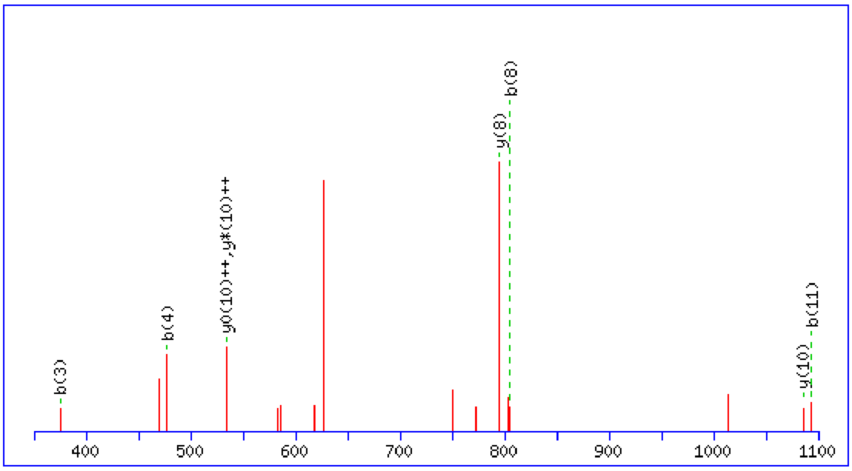
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALWTGLGPNVAR**
Found in **AT3G54110.1** in **TAIR_Arabidopsis**, Symbols: UCP, PUMP1, ATUCP1, UCP1, ATPUMP1 | ATPUMP1; binding / oxidative phosphorylation uncoupler | chr3:20049868-20051974 FORWARD

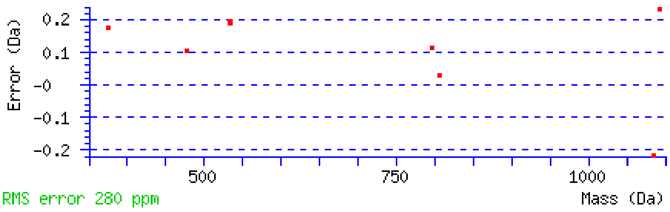
Match to Query 4797: 1270.636624 from(636.325588,2+) index(4424)
Title: Elution from: 41.034 to 41.034 scan no 5521 cid35.00 polarity:+
Data file C7-2_1.mgf

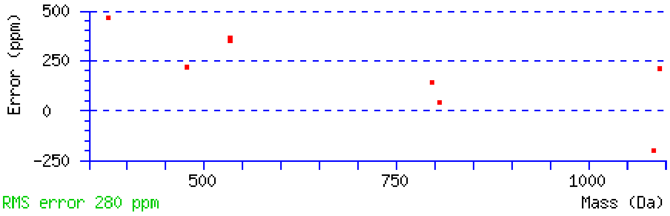
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1270.6376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.034
Matches : 8/94 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					**A**							**12**
2	187.1225	94.0649					**L**	1199.6108	600.3090	1181.5872	591.2972	1181.6002	591.3037	**11**
3	***375.1959***	188.1016					**W**	**1085.5297**	543.2685	1067.5061	534.2567	1067.5191	534.2632	**10**
4	***477.2406***	239.1239			459.2301	230.1187	**T**	897.4563	449.2318	879.4327	440.2200	879.4457	440.2265	**9**
5	535.2591	268.1332			517.2486	259.1279	**G**	**795.4116**	398.2094	777.3880	389.1976			**8**
6	649.3402	325.1737			631.3297	316.1685	**L**	737.3931	369.2002	719.3695	360.1884			**7**
7	707.3587	354.1830			689.3482	345.1777	**G**	623.3120	312.1596	605.2884	303.1478			**6**
8	***805.4085***	403.2079			787.3980	394.2026	**P**	565.2935	283.1504	547.2699	274.1386			**5**
9	921.4455	461.2264	903.4219	452.2146	903.4349	452.2211	**N**	467.2437	234.1255	449.2201	225.1137			**4**
10	1021.5110	511.2591	1003.4874	502.2473	1003.5004	502.2538	**V**	351.2067	176.1070	333.1831	167.0952			**3**
11	***1093.5451***	547.2762	1075.5215	538.2644	1075.5345	538.2709	**A**	251.1412	126.0743	233.1177	117.0625			**2**
12							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of ALWTGLGPNVAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G54110.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.0	1270.6376	-0.0010	ALWTGLGPNVAR
8.2	1270.6384	-0.0017	IADIGPNIIMGK
1.7	1270.6384	-0.0017	HLVIESMALTK
1.6	1270.6354	0.0012	AIKVHERGDTK
0.2	1270.6354	0.0012	TTSVPHISQKR

AT3G54160.1

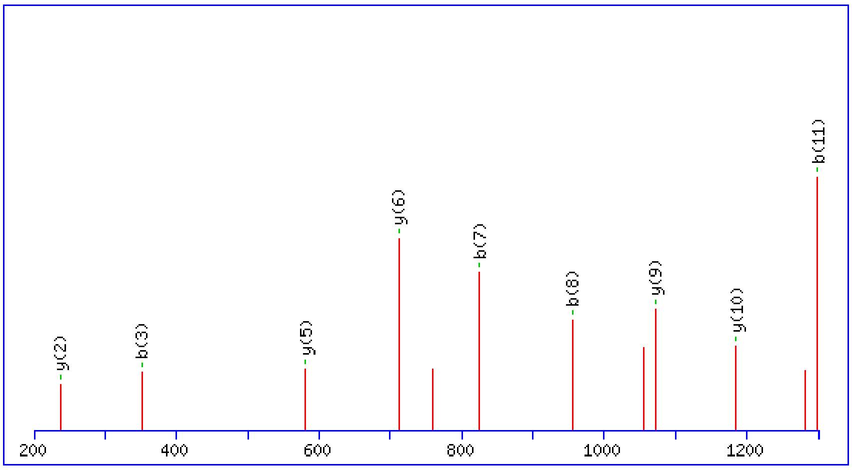
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSEIVRVQEIVSK**
Found in **AT3G54160.1** in **TAIR_Arabidopsis**, Symbols: | syntaxin-related family protein | chr3:20064446-20066005 FORWARD

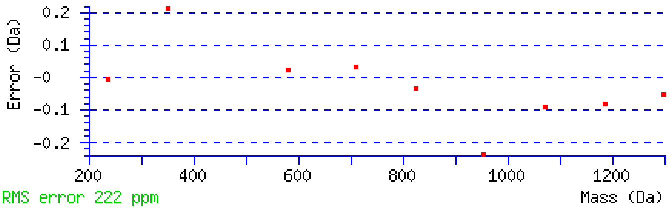
Match to Query 6727: 1534.774800 from(768.394676,2+) index(10217)
Title: Elution from: 94.622 to 94.622 scan no 14313 cid35.00 polarity:+
Data file D1d-3_2.mgf

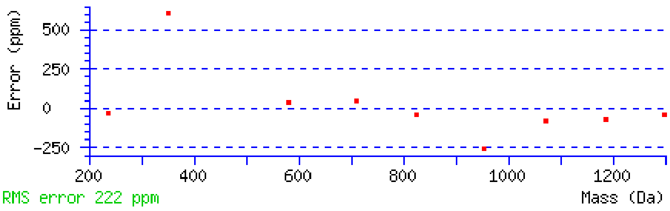
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1534.7749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00011
Matches : 9/130 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							13
2	221.0739	111.0406			203.0633	102.0353	S	1403.7447	702.3760	1385.7211	693.3642	1385.7341	693.3707	12
3	***351.1135***	176.0604			333.1029	167.0551	E	1315.7156	658.3615	1297.6921	649.3497	1297.7051	649.3562	11
4	465.1946	233.1009			447.1840	224.0956	I	***1185.6760***	593.3416	1167.6524	584.3298	1167.6654	584.3364	10
5	565.2600	283.1337			547.2495	274.1284	V	***1071.5949***	536.3011	1053.5713	527.2893	1053.5843	527.2958	9
6	725.3493	363.1783	707.3257	354.1665	707.3387	354.1730	R	971.5295	486.2684	953.5059	477.2566	953.5189	477.2631	8
7	***825.4147***	413.2110	807.3912	404.1992	807.4042	404.2057	V	811.4402	406.2237	793.4166	397.2120	793.4296	397.2185	7
8	***955.4674***	478.2373	937.4438	469.2255	937.4568	469.2320	Q	***711.3748***	356.1910	693.3512	347.1792	693.3642	347.1857	6
9	1085.5070	543.2571	1067.4834	534.2454	1067.4964	534.2519	E	***581.3221***	291.1647	563.2985	282.1529	563.3115	282.1594	5
10	1199.5881	600.2977	1181.5645	591.2859	1181.5775	591.2924	I	451.2825	226.1449	433.2589	217.1331	433.2719	217.1396	4
11	***1299.6536***	650.3304	1281.6300	641.3186	1281.6430	641.3251	V	337.2014	169.1043	319.1778	160.0925	319.1908	160.0990	3
12	1387.6826	694.3449	1369.6590	685.3332	1369.6721	685.3397	S	***237.1359***	119.0716	219.1124	110.0598	219.1254	110.0663	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MSEIVRVQEIVSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G54160.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.6	1534.7749	-0.0001	MSEIVRVQEIVSK
12.0	1534.7720	0.0028	QQRSIRLGNLSLE
11.9	1534.7776	-0.0028	VQLQCPTGRKISK
7.5	1534.7749	-0.0001	LVKAADSVQVCLSK
5.7	1534.7749	-0.0001	LELNMVSLDRISK
4.2	1534.7749	-0.0001	EKACVALQALSLSK
4.0	1534.7772	-0.0024	NTYPLLMLVNGGVK
0.6	1534.7716	0.0032	LFSEEHVVKSSKK

AT3G54210.1

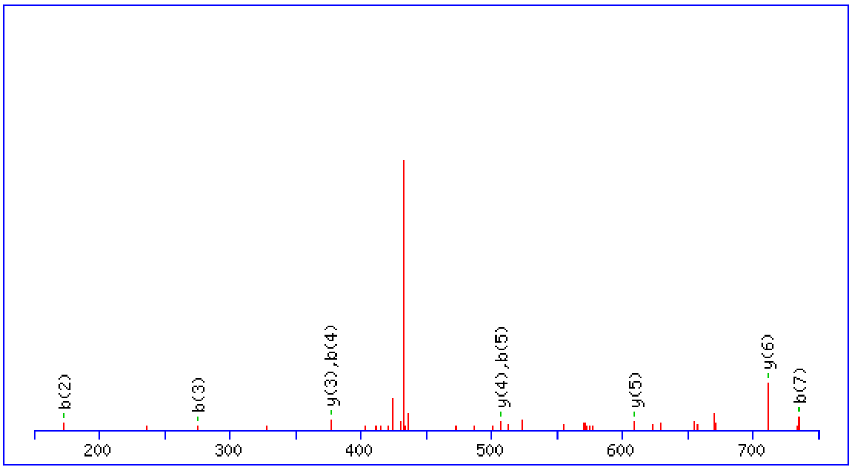
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLTTQLLK**
Found in **AT3G54210.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L17 family protein | chr3:20078650-20079363 REVERSE

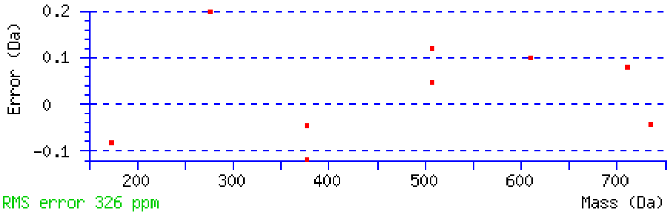
Match to Query 1459: 882.501900 from(442.258226,2+) index(3680)
Title: Elution from: 34.926 to 34.926 scan no 4591 cid35.00 polarity:+
Data file D6h-3_2.mgf

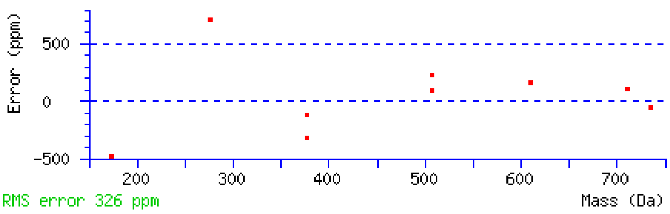
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 882.5034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0057
Matches : 9/64 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							8
2	***173.1069***	87.0571					L	825.4922	413.2498	807.4687	404.2380	807.4817	404.2445	7
3	***275.1516***	138.0794			257.1410	129.0741	T	**711.4111**	356.2092	693.3876	347.1974	693.4006	347.2039	6
4	***377.1963***	189.1018			359.1857	180.0965	T	**609.3664**	305.1869	591.3428	296.1751	591.3559	296.1816	5
5	***507.2489***	254.1281	489.2254	245.1163	489.2384	245.1228	Q	**507.3217**	254.1645	489.2981	245.1527			4
6	621.3300	311.1687	603.3065	302.1569	603.3195	302.1634	L	**377.2691**	189.1382	359.2455	180.1264			3
7	***735.4111***	368.2092	717.3876	359.1974	717.4006	359.2039	L	263.1880	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GLTTQLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.4	882.5034	-0.0015	GLTTQLLK
17.8	882.5035	-0.0016	KAATEILK

AT3G54210.1

11.4	882.5035	-0.0016	LGVEKLSK
8.7	882.5034	-0.0015	GTVDKIIK
3.4	882.5035	-0.0016	GLDIKSLK
3.4	882.5034	-0.0015	GLVKEVTK
2.9	882.5035	-0.0016	LLLGSVGSK
2.9	882.5035	-0.0016	AATSGLLIK
2.8	882.5035	-0.0016	LDKASVIK
2.8	882.5035	-0.0016	ATIQSLLK

AT3G54400.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLIDVPNSR**
Found in **AT3G54400.1** in **TAIR_Arabidopsis**, Symbols: | aspartyl protease family protein | chr3:20151269-20153577 REVERSE

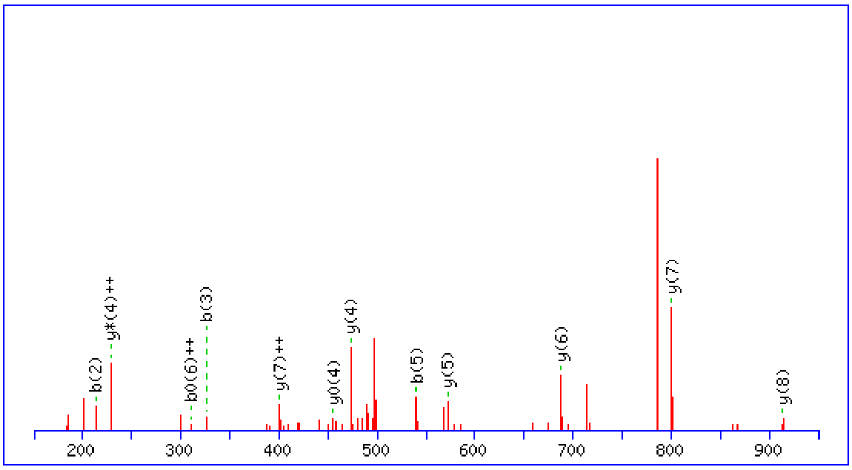
Match to Query 2532: 1011.571278 from(506.792915,2+) index(3545)
Title: Elution from: 34.147 to 34.147 scan no 4416 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

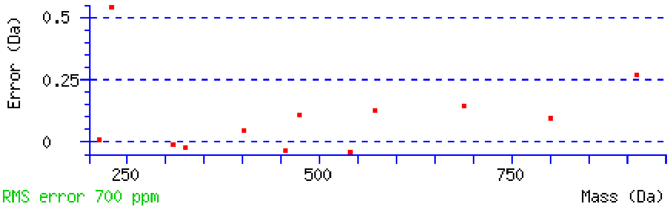
Label all possible matches ○ Label matches used for scoring ●

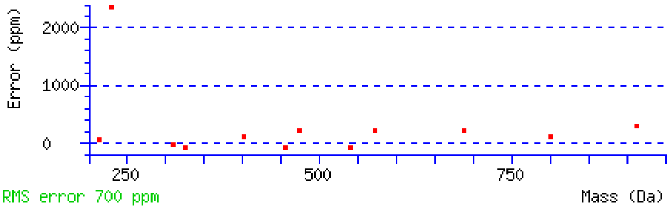
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1011.5713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.014
Matches : 12/76 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							9
2	**213.1598**	107.0835					L	***913.5102***	457.2587	896.4836	448.7454	895.4996	448.2534	8
3	**326.2438**	163.6255					I	***800.4261***	400.7167	783.3995	392.2034	782.4155	391.7114	7
4	441.2708	221.1390			423.2602	212.1337	D	***687.3420***	344.1747	670.3155	335.6614	669.3315	335.1694	6
5	**540.3392**	270.6732			522.3286	261.6679	V	***572.3151***	286.6612	555.2885	278.1479	554.3045	277.6559	5
6	637.3919	319.1996			619.3814	310.1943	P	***473.2467***	237.1270	456.2201	228.6137	455.2361	228.1217	4
7	751.4349	376.2211	734.4083	367.7078	733.4243	367.2158	N	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	3
8	838.4669	419.7371	821.4403	411.2238	820.4563	410.7318	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VLIDVPNSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.6	1011.5713	-0.0000	VLIDVPNSR

AT3G54400.1

Mascot: http://www.matrixscience.com/

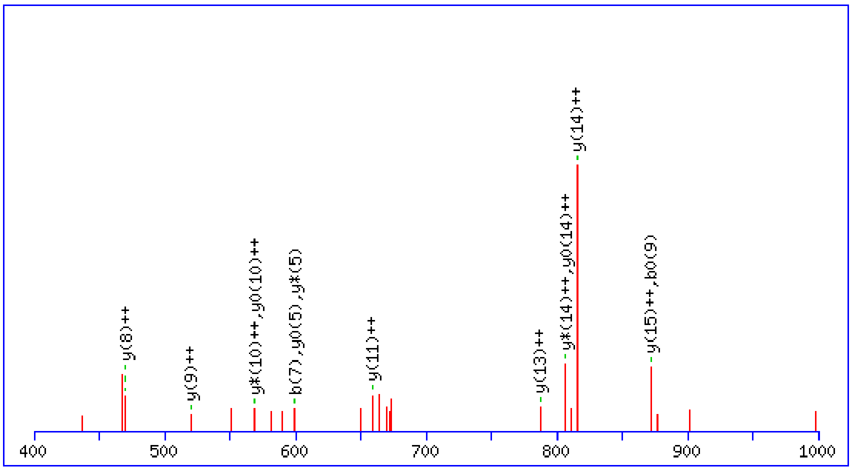
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGDALGQQYNTPHSVITER**
Found in **AT3G54470.1** in **TAIR_Arabidopsis**, Symbols: | uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS) | chr3:20179263-20181223 REVERSE

Match to Query 9376: 2041.983501 from(681.668443,3+) index(3660)
Title: Elution from: 33.812 to 33.812 scan no 4502 cid35.00 polarity:+
Data file D1d-3_2.mgf

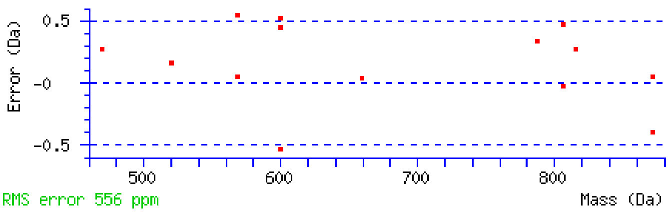
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

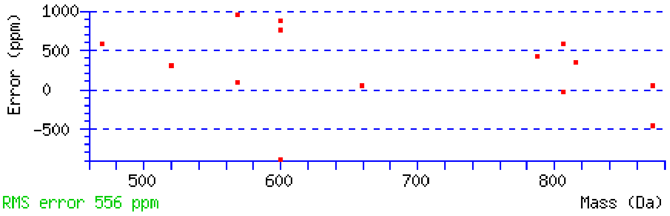


Monoisotopic mass of neutral peptide Mr(calc): 2041.9817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.011
Matches : 14/198 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							19
2	115.0502	58.0287					G	1985.9675	993.4874	1968.9410	984.9741	1967.9570	984.4821	18
3	230.0771	115.5422			212.0666	106.5369	D	1928.9461	964.9767	1911.9195	956.4634	1910.9355	955.9714	17
4	301.1143	151.0608			283.1037	142.0555	A	1813.9191	907.4632	1796.8926	898.9499	1795.9086	898.4579	16
5	414.1983	207.6028			396.1878	198.5975	L	1742.8820	871.9447	1725.8555	863.4314	1724.8715	862.9394	15
6	471.2198	236.1135			453.2092	227.1083	G	1629.7980	815.4026	1612.7714	806.8893	1611.7874	806.3973	14
7	599.2784	300.1428	582.2518	291.6295	581.2678	291.1375	Q	1572.7765	786.8919	1555.7499	778.3786	1554.7659	777.8866	13
8	727.3369	364.1721	710.3104	355.6588	709.3264	355.1668	Q	1444.7179	722.8626	1427.6914	714.3493	1426.7074	713.8573	12
9	890.4003	445.7038	873.3737	437.1905	872.3897	436.6985	Y	1316.6593	658.8333	1299.6328	650.3200	1298.6488	649.8280	11
10	1004.4432	502.7252	987.4167	494.2120	986.4326	493.7200	N	1153.5960	577.3016	1136.5695	568.7884	1135.5854	568.2964	10
11	1105.4909	553.2491	1088.4643	544.7358	1087.4803	544.2438	T	1039.5531	520.2802	1022.5265	511.7669	1021.5425	511.2749	9
12	1202.5436	601.7755	1185.5171	593.2622	1184.5331	592.7702	P	938.5054	469.7563	921.4789	461.2431	920.4948	460.7511	8
13	1339.6026	670.3049	1322.5760	661.7916	1321.5920	661.2996	H	841.4526	421.2300	824.4261	412.7167	823.4421	412.2247	7
14	1426.6346	713.8209	1409.6080	705.3077	1408.6240	704.8156	S	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
15	1525.7030	763.3551	1508.6764	754.8419	1507.6924	754.3499	V	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
16	1638.7871	819.8972	1621.7605	811.3839	1620.7765	810.8919	I	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
17	1739.8347	870.4210	1722.8082	861.9077	1721.8242	861.4157	T	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
18	1868.8773	934.9423	1851.8508	926.4290	1850.8668	925.9370	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT3G54470.1





NCBI **BLAST** search of GGDALGQQYNTPHSVITER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	2041.9817	0.0018	GGDALGQQYNTPHSVITER
0.8	2041.9886	-0.0051	VDEAMKTMCLFEGALVTK

Mascot: http://www.matrixscience.com/

AT3G54640.1

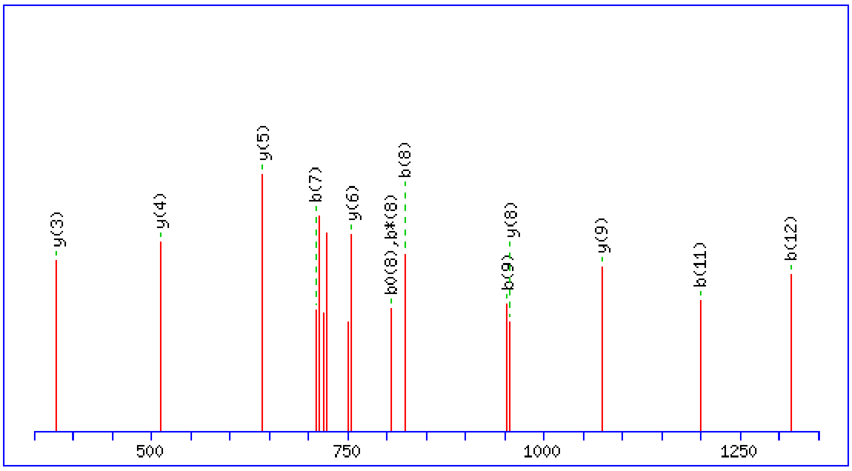
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTNLDSILEMLDK**
Found in **AT3G54640.1** in **TAIR_Arabidopsis**, Symbols: TRP3, TSA1 | TSA1 (TRYPTOPHAN SYNTHASE ALPHA CHAIN); tryptophan synthase | chr3:20234309-20236281 REVERSE

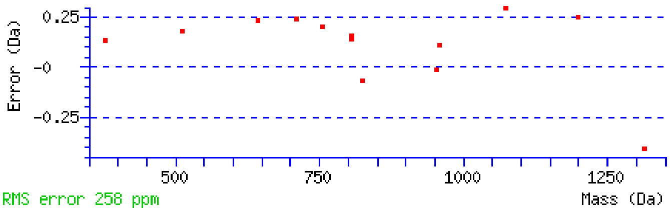
Match to Query 6392: 1462.679608 from(732.347080,2+) index(11042)
Title: Elution from: 104.047 to 104.047 scan no 15653 cid35.00 polarity:+
Data file D6h-1_1.mgf

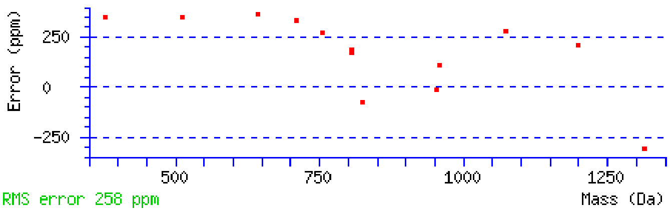
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1462.6784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 9.7e-007
Matches : 13/136 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							13
2	161.0705	81.0389			143.0599	72.0336	T	1405.6671	703.3372	1387.6436	694.3254	1387.6566	694.3319	12
3	277.1075	139.0574	259.0839	130.0456	259.0969	130.0521	N	1303.6224	652.3149	1285.5988	643.3031	1285.6119	643.3096	11
4	391.1886	196.0979	373.1650	187.0861	373.1780	187.0926	L	1187.5854	594.2964	1169.5619	585.2846	1169.5749	585.2911	10
5	507.2126	254.1099	489.1890	245.0981	489.2020	245.1046	D	***1073.5043***	537.2558	1055.4808	528.2440	1055.4938	528.2505	9
6	595.2416	298.1245	577.2180	289.1127	577.2311	289.1192	S	***957.4804***	479.2438	939.4568	470.2320	939.4698	470.2385	8
7	***709.3227***	355.1650	691.2991	346.1532	691.3122	346.1597	I	869.4513	435.2293	851.4277	426.2175	851.4407	426.2240	7
8	***823.4038***	412.2055	805.3802	403.1938	805.3933	403.2003	L	***755.3702***	378.1887	737.3466	369.1769	737.3596	369.1835	6
9	***953.4435***	477.2254	935.4199	468.2136	935.4329	468.2201	E	***641.2891***	321.1482	623.2655	312.1364	623.2785	312.1429	5
10	1085.4810	543.2441	1067.4574	534.2323	1067.4704	534.2388	M	***511.2495***	256.1284	493.2259	247.1166	493.2389	247.1231	4
11	***1199.5621***	600.2847	1181.5385	591.2729	1181.5515	591.2794	L	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	***1315.5860***	658.2967	1297.5625	649.2849	1297.5755	649.2914	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GTNLDSILEMLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G54640.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.8	1462.6784	0.0012	GTNLDSILEMLDK
30.3	1462.6754	0.0042	QREIAAAAKEDDK
20.7	1462.6777	0.0019	NNYLEAPKNSAPK
15.7	1462.6833	-0.0037	EQWLSQVAMINK
11.3	1462.6776	0.0020	ALRDQLDSWVDK
10.6	1462.6810	-0.0014	SPRTPQGSILMDK
9.8	1462.6810	-0.0014	EKTQMPVAREEK
8.9	1462.6810	-0.0014	TRDGIGLMDINPK
6.4	1462.6810	-0.0014	MAQSSENVLPTLR
5.8	1462.6781	0.0015	SNGPVLRSQSPSGR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLGAAIIYNK**
Found in **AT3G54820.1** in **TAIR_Arabidopsis**, Symbols: PIP2D, PIP2;5 | PIP2;5/PIP2D (plasma membrane intrinsic protein 2;5); water channel | chr3:20313095-20314716 FORWARD

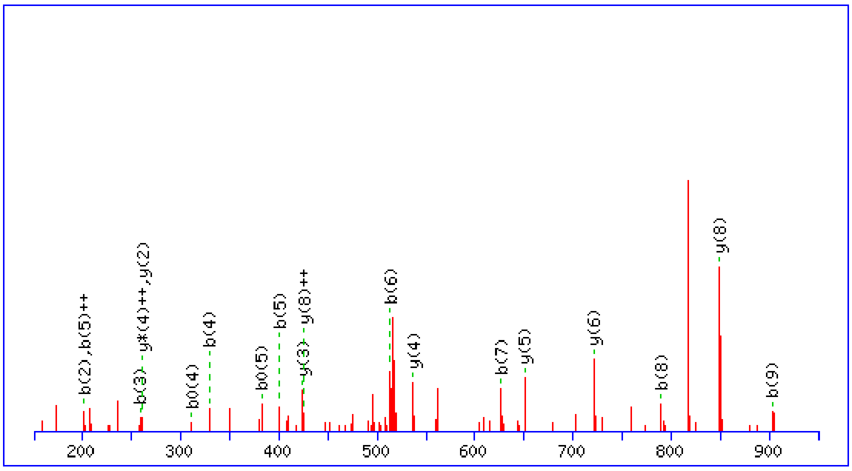
Match to Query 2902: 1048.589226 from(525.301889,2+) index(3910)
Title: Elution from: 37.975 to 37.975 scan no 4931 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

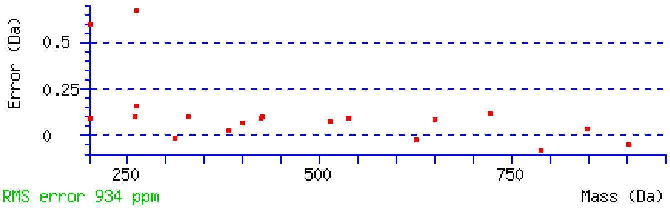
Label all possible matches ○ Label matches used for scoring ●

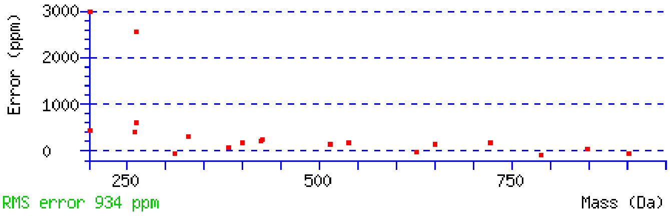
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1048.5917
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 8.4e-005
Matches : 19/74 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**					**10**
2	***201.1234***	101.0653			183.1128	92.0600	**L**	962.5669	481.7871	945.5404	473.2738	**9**
3	***258.1448***	129.5761			240.1343	120.5708	**G**	**849.4829**	425.2451	832.4563	416.7318	**8**
4	***329.1819***	165.0946			311.1714	156.0893	**A**	792.4614	396.7343	775.4349	388.2211	**7**
5	***400.2191***	200.6132			382.2085	191.6079	**A**	**721.4243**	361.2158	704.3978	352.7025	**6**
6	***513.3031***	257.1552			495.2926	248.1499	**I**	**650.3872**	325.6972	633.3606	317.1840	**5**
7	***626.3872***	313.6972			608.3766	304.6919	**I**	**537.3031**	269.1552	520.2766	260.6419	**4**
8	***789.4505***	395.2289			771.4400	386.2236	**Y**	**424.2191**	212.6132	407.1925	204.0999	**3**
9	***903.4934***	452.2504	886.4669	443.7371	885.4829	443.2451	**N**	**261.1557**	131.0815	244.1292	122.5682	**2**
10							**K**	147.1128	74.0600	130.0863	65.5468	**1**





NCBI **BLAST** search of SLGAAIIYNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G54820.1

Score	Mr(calc)	Delta	Sequence
48.3	1048.5917	-0.0024	SLGAAIIYNK
0.6	1048.5917	-0.0024	AKISDFGLAK

Mascot: http://www.matrixscience.com/

AT3G54890.1

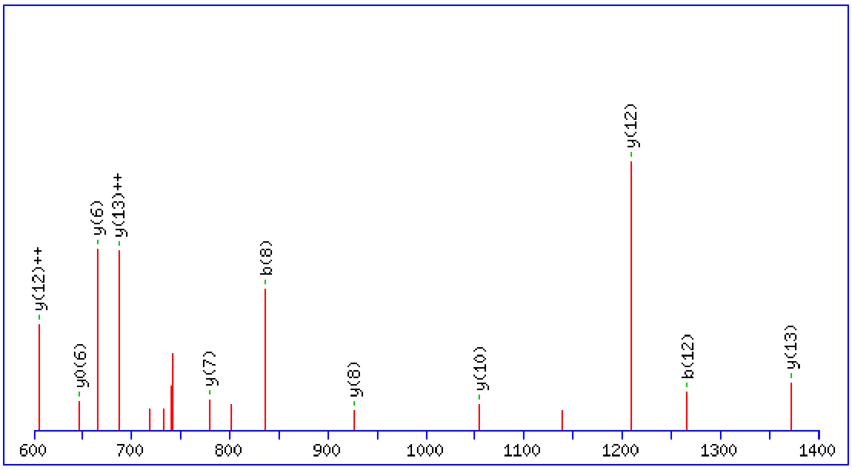
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KYPGGAFDPLGYSK**
Found in **AT3G54890.1** in **TAIR_Arabidopsis**, Symbols: LHCA1 | LHCA1; chlorophyll binding | chr3:20350684-20351900 REVERSE

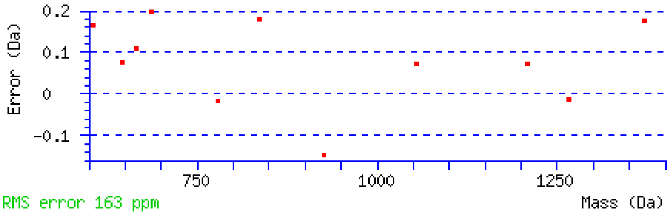
Match to Query 6797: 1498.742180 from(750.378366,2+) index(5794)
Title: Elution from: 51.011 to 51.011 scan no 7182 cid35.00 polarity:+
Data file 0-1_1.mgf

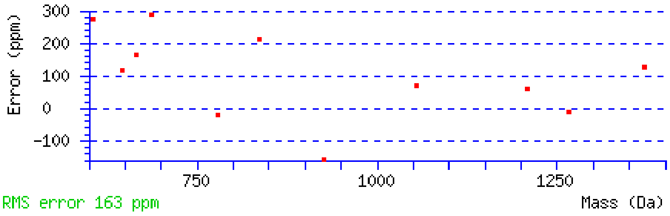
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1498.7456
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 2.7e-005
Matches : 11/140 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	292.1656	146.5864	275.1390	138.0731			Y	***1371.6579***	686.3326	1354.6314	677.8193	1353.6474	677.3273	13
3	389.2183	195.1128	372.1918	186.5995			P	***1208.5946***	604.8009	1191.5681	596.2877	1190.5841	595.7957	12
4	446.2398	223.6235	429.2132	215.1103			G	1111.5419	556.2746	1094.5153	547.7613	1093.5313	547.2693	11
5	503.2613	252.1343	486.2347	243.6210			G	***1054.5204***	527.7638	1037.4938	519.2506	1036.5098	518.7585	10
6	574.2984	287.6528	557.2718	279.1396			A	997.4989	499.2531	980.4724	490.7398	979.4884	490.2478	9
7	721.3668	361.1870	704.3402	352.6738			F	***926.4618***	463.7345	909.4353	455.2213	908.4512	454.7293	8
8	**836.3937**	418.7005	819.3672	410.1872	818.3832	409.6952	D	***779.3934***	390.2003	762.3668	381.6871	761.3828	381.1951	7
9	933.4465	467.2269	916.4199	458.7136	915.4359	458.2216	P	***664.3665***	332.6869	647.3399	324.1736	646.3559	323.6816	6
10	1046.5306	523.7689	1029.5040	515.2556	1028.5200	514.7636	L	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	5
11	1103.5520	552.2796	1086.5255	543.7664	1085.5415	543.2744	G	454.2296	227.6185	437.2031	219.1052	436.2191	218.6132	4
12	**1266.6154**	633.8113	1249.5888	625.2980	1248.6048	624.8060	Y	397.2082	199.1077	380.1816	190.5944	379.1976	190.1024	3
13	1353.6474	677.3273	1336.6208	668.8141	1335.6368	668.3220	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KYPGGAFDPLGYSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G54890.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.4	1498.7456	-0.0034	KYPGGAFDPLGYSK
1.7	1498.7416	0.0006	GESVGYQSSFILGR

Mascot: http://www.matrixscience.com/

AT3G54900.1

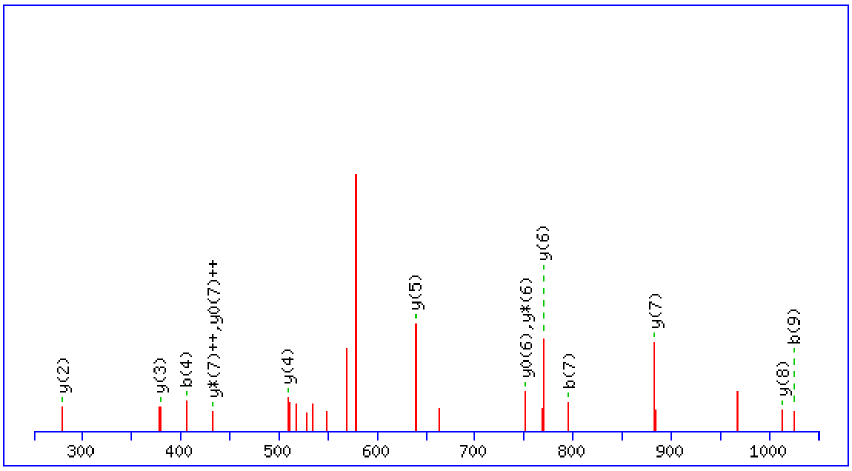
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGELQEEVEK**
Found in **AT3G54900.1** in **TAIR_Arabidopsis**, Symbols: CXIP1 | CXIP1 (CAX INTERACTING PROTEIN 1) | chr3:20352828-20353349 REVERSE

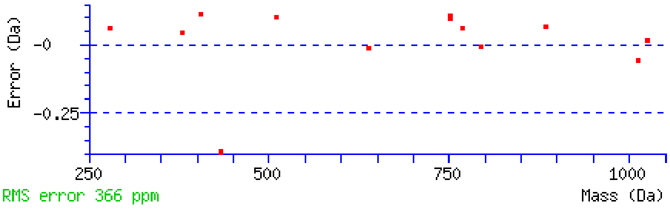
Match to Query 3865: 1172.518856 from(587.266704,2+) index(1421)
Title: Elution from: 18.449 to 18.449 scan no 1885 cid35.00 polarity:+
Data file 0-2_3.mgf

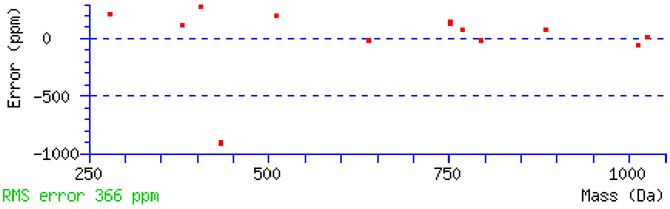
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1172.5205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.1e-006
Matches : 14/98 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							10
2	161.0705	81.0389			143.0599	72.0336	G	1071.4831	536.2452	1053.4595	527.2334	1053.4725	527.2399	9
3	291.1101	146.0587			273.0996	137.0534	E	***1013.4646***	507.2359	995.4410	498.2241	995.4540	498.2306	8
4	**405.1912**	203.0992			387.1807	194.0940	L	***883.4250***	442.2161	865.4014	433.2043	865.4144	433.2108	7
5	535.2439	268.1256	517.2203	259.1138	517.2333	259.1203	Q	***769.3439***	385.1756	751.3203	376.1638	751.3333	376.1703	6
6	665.2835	333.1454	647.2599	324.1336	647.2729	324.1401	E	***639.2912***	320.1492	621.2676	311.1374	621.2806	311.1440	5
7	**795.3231**	398.1652	777.2995	389.1534	777.3126	389.1599	E	***509.2516***	255.1294	491.2280	246.1176	491.2410	246.1241	4
8	895.3886	448.1979	877.3650	439.1861	877.3780	439.1926	V	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	3
9	**1025.4282**	513.2177	1007.4046	504.2059	1007.4176	504.2125	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TGELQEEVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G54900.1

Score	Mr(calc)	Delta	Sequence
61.1	1172.5205	-0.0016	TGELQEEVEK
8.0	1172.5184	0.0004	MEHQILSQR
4.1	1172.5158	0.0031	CGTLQPEDLK
3.8	1172.5180	0.0008	SLSLFYEMR
3.6	1172.5180	0.0009	WMDVDPLTGK
2.2	1172.5158	0.0031	LCDDPDIKGK
1.9	1172.5155	0.0034	RENGANHVTR
1.5	1172.5184	0.0004	MDISGHPKTR
0.5	1172.5158	0.0031	NQLSDDIPMK
0.2	1172.5158	0.0031	MQEIGVQPDK

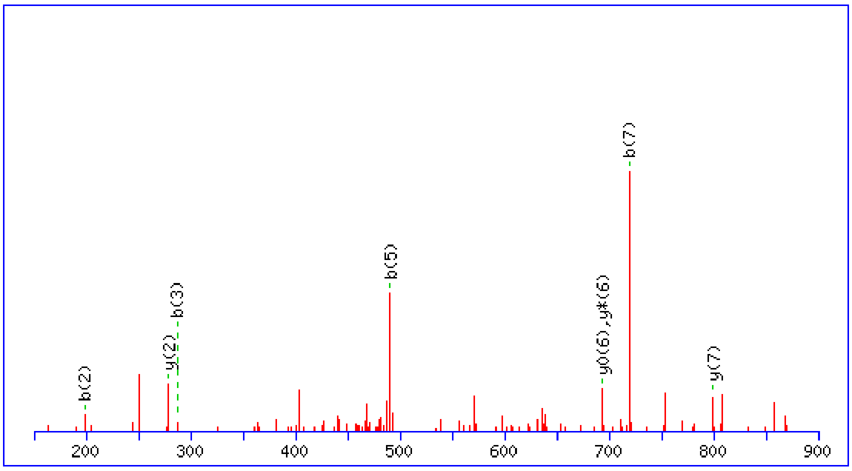
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHSSDLLVR**
Found in **AT3G54910.1** in **TAIR_Arabidopsis**, Symbols: | similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT4G10400.2); similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT4G10400.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN74740.1); contains InterPro do

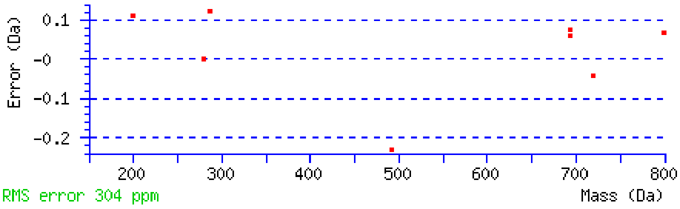
Match to Query 2413: 996.476040 from(499.245296,2+) index(3497)
Title: Elution from: 34.011 to 34.011 scan no 4369 cid35.00 polarity:+
Data file D6h-3_1.mgf

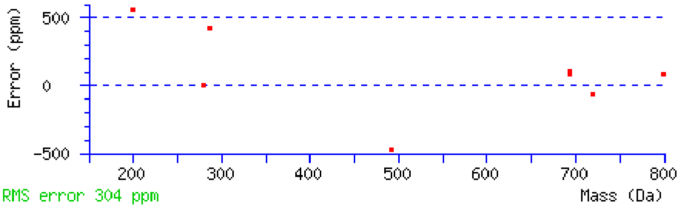
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 996.4781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.048
Matches : 8/68 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			G							9
2	***199.0758***	100.0415			H	939.4669	470.2371	921.4433	461.2253	921.4563	461.2318	8
3	***287.1049***	144.0561	269.0943	135.0508	S	**799.4168**	400.2121	781.3933	391.2003	781.4063	391.2068	7
4	375.1339	188.0706	357.1234	179.0653	S	711.3878	356.1975	693.3642	347.1857	693.3772	347.1922	6
5	***491.1579***	246.0826	473.1473	237.0773	D	623.3587	312.1830	605.3351	303.1712	605.3482	303.1777	5
6	605.2390	303.1231	587.2284	294.1179	L	507.3347	254.1710	489.3112	245.1592			4
7	***719.3201***	360.1637	701.3095	351.1584	L	393.2536	197.1305	375.2301	188.1187			3
8	819.3855	410.1964	801.3750	401.1911	V	**279.1725**	140.0899	261.1490	131.0781			2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GHSSDLLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G54910.1

20.0	996.4781	-0.0020	GHSSDLLVR
7.2	996.4776	-0.0016	DWSLIPEK
5.2	996.4754	0.0006	ALDPQVSEK
2.9	996.4781	-0.0020	TSNSYRKK
2.7	996.4776	-0.0016	LYDYKGTK
0.9	996.4754	0.0006	DANTLVPEK
0.6	996.4781	-0.0020	SNVASHLQK
0.6	996.4734	0.0027	CANHPKKK

AT3G54930.1

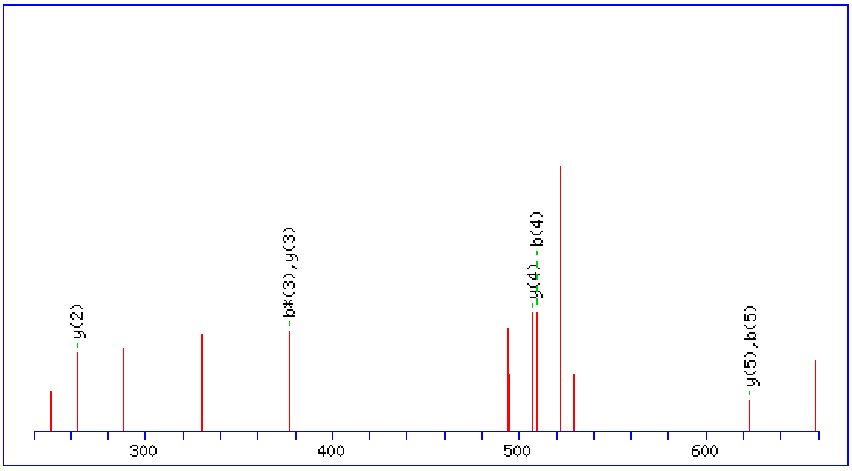
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNKIIK**
Found in **AT3G54930.1** in **TAIR_Arabidopsis**, Symbols: | serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative | chr3:20362062-20363637 REVERSE

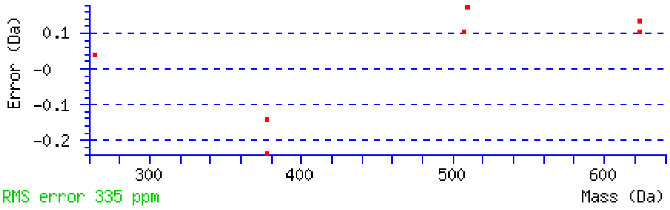
Match to Query 881: 770.452640 from(386.233596,2+) index(5253)
Title: Elution from: 45.663 to 45.663 scan no 6590 cid35.00 polarity:+
Data file D1d-3_3.mgf

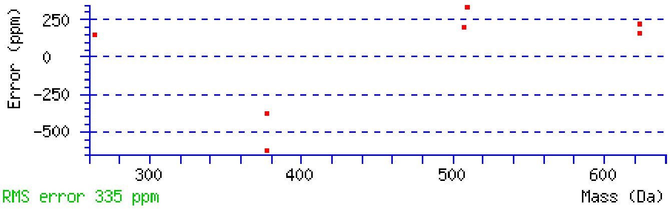
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 240 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.4533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.021
Matches : 7/38 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	149.0727	75.0400			F					6
2	265.1097	133.0585	247.0861	124.0467	N	***623.3951***	312.2012	605.3715	303.1894	5
3	395.1988	198.1030	377.1752	189.0912	K	***507.3581***	254.1827	489.3345	245.1709	4
4	**509.2799**	255.1436	491.2563	246.1318	I	***377.2691***	189.1382	359.2455	180.1264	3
5	**623.3610**	312.1841	605.3374	303.1723	I	***263.1880***	132.0976	245.1644	123.0858	2
6					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of FNKIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.0	770.4533	-0.0006	FNKIIK
23.9	770.4533	-0.0006	LFLKNK
14.0	770.4533	-0.0006	FIKGGIK

AT3G54930.1

13.8	770.4533	-0.0006	IFKNIK
12.7	770.4533	-0.0006	LFKINK
10.4	770.4533	-0.0006	IFQVKK
10.4	770.4533	-0.0006	LFNLKK
9.4	770.4511	0.0016	LASKSKK
8.7	770.4533	-0.0006	NKFLIK
8.3	770.4533	-0.0006	LIFGGKK

AT3G55060.1

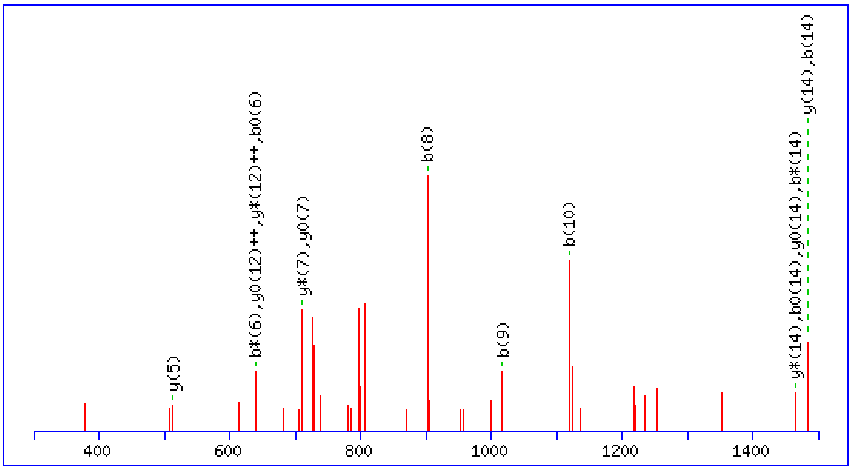
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGETSKNELTTSATK**
Found in **AT3G55060.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G39300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41551.1) | chr3:20414166-20417199 REVERSE

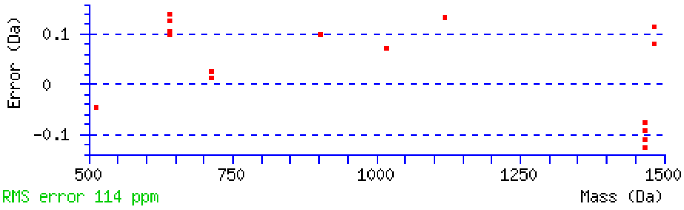
Match to Query 7002: 1630.743050 from(816.378801,2+) index(6290)
Title: Elution from: 59.010 to 59.010 scan no 8251 cid35.00 polarity:+
Data file D1d-2_2.mgf

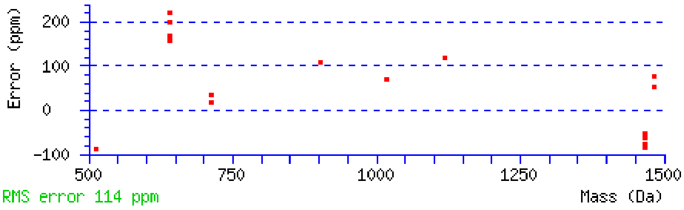
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1630.7410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.031
Matches : 16/152 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					F							15
2	207.0912	104.0492					G	**1483.6829**	742.3451	1465.6593	733.3333	1465.6723	733.3398	14
3	337.1309	169.0691			319.1203	160.0638	E	1425.6644	713.3358	1407.6408	704.3240	1407.6538	704.3305	13
4	439.1756	220.0914			421.1650	211.0861	T	1295.6248	648.3160	1277.6012	639.3042	1277.6142	639.3107	12
5	527.2046	264.1060			509.1941	255.1007	S	1193.5800	597.2937	1175.5565	588.2819	1175.5695	588.2884	11
6	657.2937	329.1505	639.2701	320.1387	639.2831	320.1452	K	1105.5510	553.2791	1087.5274	544.2673	1087.5404	544.2738	10
7	773.3307	387.1690	755.3071	378.1572	755.3201	378.1637	N	975.4619	488.2346	957.4384	479.2228	957.4514	479.2293	9
8	***903.3703***	452.1888	885.3467	443.1770	885.3597	443.1835	E	859.4250	430.2161	841.4014	421.2043	841.4144	421.2108	8
9	***1017.4514***	509.2293	999.4278	500.2175	999.4408	500.2240	L	729.3853	365.1963	711.3617	356.1845	711.3748	356.1910	7
10	***1119.4961***	560.2517	1101.4725	551.2399	1101.4855	551.2464	T	615.3042	308.1558	597.2806	299.1440	597.2937	299.1505	6
11	1221.5408	611.2740	1203.5172	602.2623	1203.5302	602.2688	T	**513.2595**	257.1334	495.2359	248.1216	495.2489	248.1281	5
12	1309.5699	655.2886	1291.5463	646.2768	1291.5593	646.2833	S	411.2148	206.1110	393.1912	197.0992	393.2042	197.1058	4
13	1381.6040	691.3056	1363.5804	682.2939	1363.5935	682.3004	A	323.1857	162.0965	305.1622	153.0847	305.1752	153.0912	3
14	***1483.6487***	742.3280	1465.6252	733.3162	1465.6382	733.3227	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT3G55060.1

NCBI **BLAST** search of FGETSKNELTTSATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.2	1630.7410	0.0020	FGETSKNELTTSATK
24.1	1630.7424	0.0007	MLSCKQELSSRVR
18.5	1630.7385	0.0045	IYVQGGCDGIQYIK
8.5	1630.7437	-0.0007	GSSFETIDIATSARR
6.6	1630.7460	-0.0029	YATGNNTLFGNVNVK
3.9	1630.7446	-0.0015	CLCGKGYIRNLEK
3.9	1630.7430	0.0000	FDEIMKWFLGWK
3.1	1630.7390	0.0041	EMQDSSAFAARKLR
2.5	1630.7386	0.0045	LKPYCSFEDSLVR
1.7	1630.7390	0.0041	YVMDTDNNVVRKR

AT3G55070.1

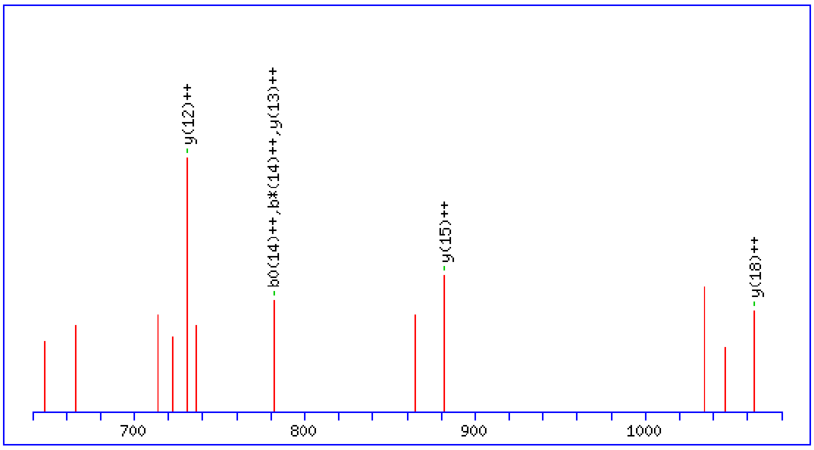
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDHLDSVDVENITEWNNTK**
Found in **AT3G55070.1** in **TAIR_Arabidopsis**, Symbols: | similar to protein binding / zinc ion binding [Arabidopsis thaliana] (TAIR:AT4G37880.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41552.1); contains InterPro domain CT11-RanBPM (InterPro:IPR013144); contains InterPro d

Match to Query 9864: 2241.054669 from(748.025499,3+) index(10404)
Title: Elution from: 99.777 to 99.777 scan no 14667 cid35.00 polarity:+
Data file D6h-2_2.mgf

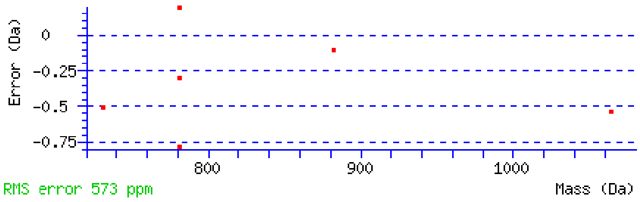
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 640 to 1080 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

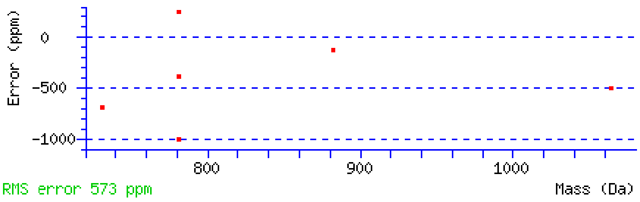


Monoisotopic mass of neutral peptide Mr(calc): 2241.0549
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.0079
Matches : 6/192 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							19
2	229.1183	115.0628			211.1077	106.0575	D	2128.9782	1064.9927	2111.9516	1056.4794	2110.9676	1055.9874	18
3	366.1772	183.5922			348.1666	174.5870	H	2013.9512	1007.4792	1996.9247	998.9660	1995.9407	998.4740	17
4	479.2613	240.1343			461.2507	231.1290	L	1876.8923	938.9498	1859.8658	930.4365	1858.8817	929.9445	16
5	594.2882	297.6477			576.2776	288.6425	D	1763.8082	882.4078	1746.7817	873.8945	1745.7977	873.4025	15
6	681.3202	341.1638			663.3097	332.1585	S	1648.7813	824.8943	1631.7548	816.3810	1630.7707	815.8890	14
7	780.3886	390.6980			762.3781	381.6927	V	1561.7493	781.3783	1544.7227	772.8650	1543.7387	772.3730	13
8	895.4156	448.2114			877.4050	439.2061	D	1462.6809	731.8441	1445.6543	723.3308	1444.6703	722.8388	12
9	994.4840	497.7456			976.4734	488.7404	V	1347.6539	674.3306	1330.6274	665.8173	1329.6434	665.3253	11
10	1123.5266	562.2669			1105.5160	553.2617	E	1248.5855	624.7964	1231.5590	616.2831	1230.5749	615.7911	10
11	1237.5695	619.2884	1220.5430	610.7751	1219.5590	610.2831	N	1119.5429	560.2751	1102.5164	551.7618	1101.5323	551.2698	9
12	1350.6536	675.8304	1333.6270	667.3172	1332.6430	666.8251	I	1005.5000	503.2536	988.4734	494.7404	987.4894	494.2483	8
13	1451.7013	726.3543	1434.6747	717.8410	1433.6907	717.3490	T	892.4159	446.7116	875.3894	438.1983	874.4054	437.7063	7
14	1580.7439	790.8756	1563.7173	782.3623	1562.7333	781.8703	E	791.3682	396.1878	774.3417	387.6745	773.3577	387.1825	6
15	1766.8232	883.9152	1749.7966	875.4019	1748.8126	874.9099	W	662.3257	331.6665	645.2991	323.1532	644.3151	322.6612	5
16	1880.8661	940.9367	1863.8395	932.4234	1862.8555	931.9314	N	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
17	1994.9090	997.9581	1977.8825	989.4449	1976.8985	988.9529	N	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
18	2095.9567	1048.4820	2078.9302	1039.9687	2077.9461	1039.4767	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT3G55070.1





NCBI **BLAST** search of IDHLDSVDVENITEWNNTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.3	2241.0549	-0.0003	IDHLDSVDVENITEWNNTK
14.1	2241.0525	0.0022	GFFEVTHDISNLTCADFLR
2.8	2241.0524	0.0022	AVHNFSIQTGEEFSLEFMR
2.6	2241.0509	0.0037	NLDDIKDISDNYDRSTTTR
0.8	2241.0484	0.0063	ACLFTVNSQLNNEASFSPSR

AT3G55120.1

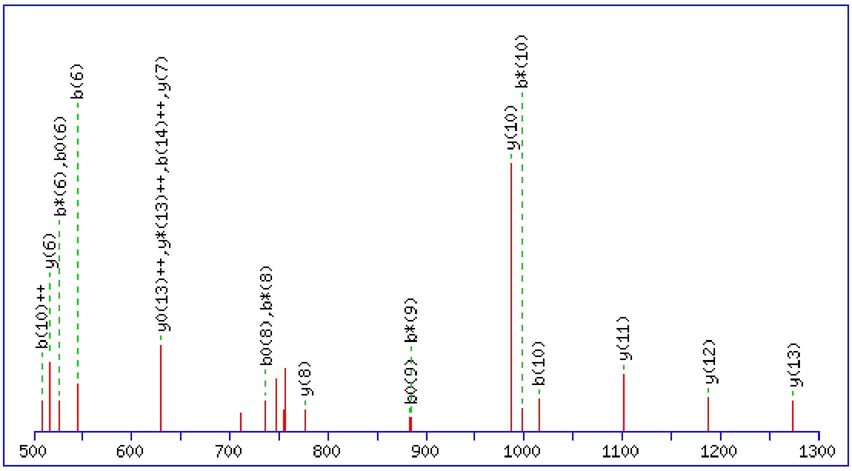
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPASSNPLFLGGAGVR**
Found in **AT3G55120.1** in **TAIR_Arabidopsis**, Symbols: TT5, A11, CFI | A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone isomerase | chr3:20441225-20442392 REVERSE

Match to Query 6892: 1528.799176 from(765.406864,2+) index(6525)
Title: Elution from: 56.681 to 56.681 scan no 8289 cid35.00 polarity:+
Data file C7-1_1.mgf

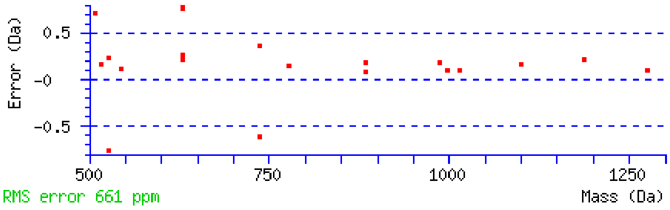
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

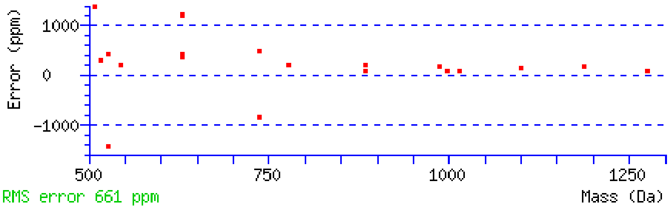


Monoisotopic mass of neutral peptide Mr(calc): 1528.7998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 4.7e-007
Matches : 20/148 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	185.0921	93.0497			167.0815	84.0444	P	1442.7750	721.8912	1425.7485	713.3779	1424.7645	712.8859	15
3	256.1292	128.5682			238.1186	119.5629	A	1345.7223	673.3648	1328.6957	664.8515	1327.7117	664.3595	14
4	343.1612	172.0842			325.1506	163.0790	S	***1274.6852***	637.8462	1257.6586	629.3329	1256.6746	628.8409	13
5	430.1932	215.6003			412.1827	206.5950	S	***1187.6531***	594.3302	1170.6266	585.8169	1169.6426	585.3249	12
6	**544.2362**	272.6217	527.2096	264.1084	526.2256	263.6164	N	***1100.6211***	550.8142	1083.5946	542.3009			11
7	641.2889	321.1481	624.2624	312.6348	623.2784	312.1428	P	***986.5782***	493.7927	969.5516	485.2795			10
8	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	L	889.5254	445.2663	872.4989	436.7531			9
9	901.4414	451.2243	884.4149	442.7111	883.4308	442.2191	F	***776.4413***	388.7243	759.4148	380.2110			8
10	**1014.5255**	**507.7664**	997.4989	499.2531	996.5149	498.7611	L	***629.3729***	315.1901	612.3464	306.6768			7
11	1071.5469	536.2771	1054.5204	527.7638	1053.5364	527.2718	G	***516.2889***	258.6481	499.2623	250.1348			6
12	1128.5684	564.7878	1111.5419	556.2746	1110.5578	555.7826	G	459.2674	230.1373	442.2409	221.6241			5
13	1199.6055	600.3064	1182.5790	591.7931	1181.5949	591.3011	A	402.2459	201.6266	385.2194	193.1133			4
14	1256.6270	**628.8171**	1239.6004	620.3039	1238.6164	619.8118	G	331.2088	166.1081	314.1823	157.5948			3
15	1355.6954	678.3513	1338.6688	669.8381	1337.6848	669.3461	V	274.1874	137.5973	257.1608	129.0840			2
16							R	175.1190	88.0631	158.0924	79.5498			1

AT3G55120.1





NCBI **BLAST** search of SPASSNPLFLGGAGVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.5	1528.7998	-0.0006	SPASSNPLFLGGAGVR
3.3	1528.7966	0.0025	AVLMLSLRCTGHR
1.9	1528.7985	0.0007	DVIQSLVDDDLVAK
0.6	1528.7997	-0.0006	SRNLHEFLEKEK
0.5	1528.7984	0.0007	IEEVIDSDLQGLAK

Mascot: http://www.matrixscience.com/

AT3G55280.1

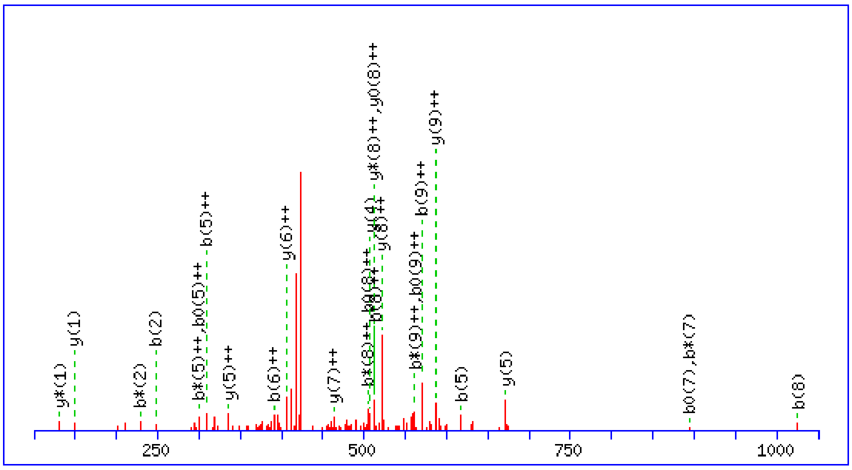
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NKLDHYQILK**
Found in **AT3G55280.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L23A (RPL23aB) | chr3:20511644-20512496 FORWARD

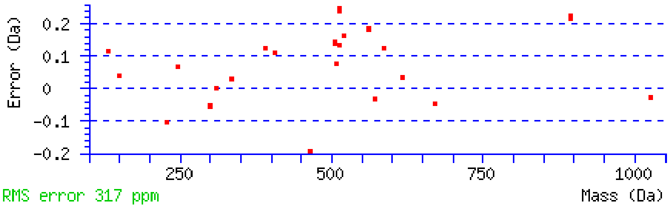
Match to Query 4524: 1286.657415 from(429.893081,3+) index(2112)
Title: Elution from: 22.987 to 22.987 scan no 2656 cid35.00 polarity:+
Data file 0-2_3.mgf

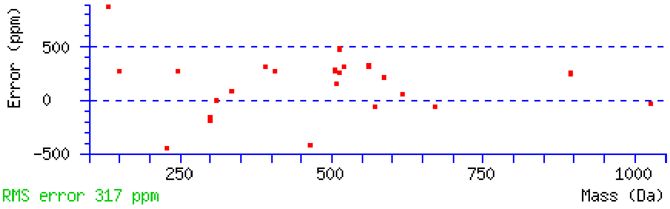
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1286.6559
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0066
Matches : 27/90 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							10
2	**247.1333**	124.0703	229.1097	115.0585			K	1171.6262	586.3167	1153.6026	577.3050	1153.6156	577.3115	9
3	361.2144	181.1108	343.1908	172.0990			L	1041.5372	521.2722	1023.5136	512.2604	1023.5266	512.2669	8
4	477.2384	239.1228	459.2148	230.1110	459.2278	230.1175	D	927.4561	464.2317	909.4325	455.2199	909.4455	455.2264	7
5	**617.2884**	***309.1478***	599.2648	300.1360	599.2778	300.1426	H	811.4321	406.2197	793.4085	397.2079			6
6	781.3488	***391.1780***	763.3252	382.1662	763.3382	382.1727	Y	**671.3821**	336.1947	653.3585	327.1829			5
7	911.4014	456.2043	893.3778	447.1926	893.3908	447.1991	Q	**507.3217**	254.1645	489.2981	245.1527			4
8	**1025.4825**	***513.2449***	1007.4589	504.2331	1007.4719	504.2396	I	377.2691	189.1382	359.2455	180.1264			3
9	1139.5636	***570.2854***	1121.5400	561.2737	1121.5530	561.2802	L	263.1880	132.0976	245.1644	123.0858			2
10							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NKLDHYQILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G55280.1

30.8	1286.6559	0.0015	NKLDHYQILK
12.2	1286.6590	-0.0016	KPPQRGRGGGVR
12.1	1286.6537	0.0037	QRTIEALTNPK
9.1	1286.6537	0.0037	GLTGDSLNRIPK
5.8	1286.6559	0.0015	EHLELYARIK
5.1	1286.6559	0.0015	NFVSHLEKGLK
4.9	1286.6559	0.0015	GGKIWVVDVNGK
3.7	1286.6537	0.0037	AVATSGPSSRPLK
3.7	1286.6537	0.0037	ETLPGGLSVNRK
3.4	1286.6537	0.0037	KQEEPSGLVRK

AT3G55410.1

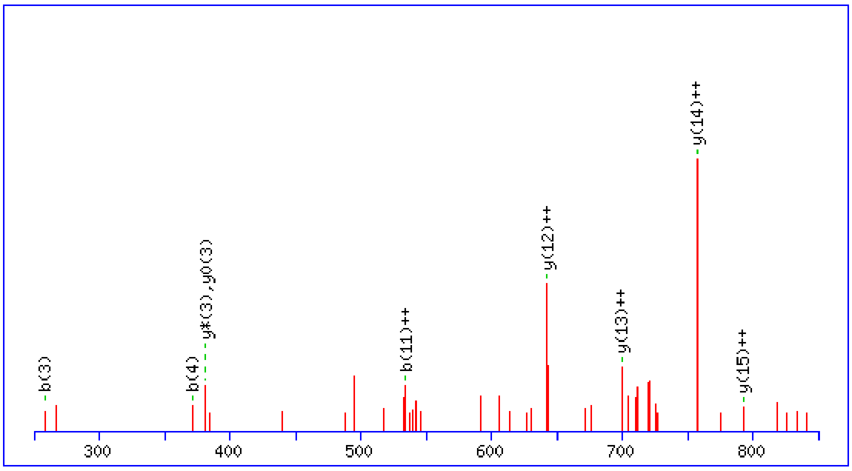
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AADLGVESIVIGMSHR**
Found in **AT3G55410.1** in **TAIR_Arabidopsis**, Symbols: | 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative | chr3:20552874-20556705 FORWARD

Match to Query 7512: 1653.847938 from(552.289922,3+) index(8149)
Title: Elution from: 72.626 to 72.626 scan no 10837 cid35.00 polarity:+
Data file D12h-3_2.mgf

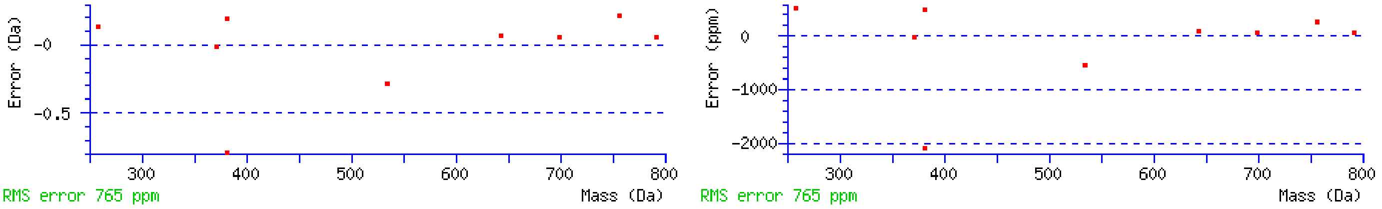
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1653.8508
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.047
Matches : 9/142 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							16
2	143.0815	72.0444			A	1583.8210	792.4141	1566.7945	783.9009	1565.8104	783.4089	15
3	**258.1084**	129.5579	240.0979	120.5526	D	1512.7839	756.8956	1495.7573	748.3823	1494.7733	747.8903	14
4	**371.1925**	186.0999	353.1819	177.0946	L	1397.7569	699.3821	1380.7304	690.8688	1379.7464	690.3768	13
5	428.2140	214.6106	410.2034	205.6053	G	1284.6729	642.8401	1267.6463	634.3268	1266.6623	633.8348	12
6	527.2824	264.1448	509.2718	255.1396	V	1227.6514	614.3293	1210.6249	605.8161	1209.6409	605.3241	11
7	656.3250	328.6661	638.3144	319.6608	E	1128.5830	564.7951	1111.5565	556.2819	1110.5724	555.7899	10
8	743.3570	372.1821	725.3464	363.1769	S	999.5404	500.2738	982.5139	491.7606	981.5298	491.2686	9
9	856.4411	428.7242	838.4305	419.7189	I	912.5084	456.7578	895.4818	448.2446	894.4978	447.7525	8
10	955.5095	478.2584	937.4989	469.2531	V	799.4243	400.2158	782.3978	391.7025	781.4138	391.2105	7
11	1068.5936	534.8004	1050.5830	525.7951	I	700.3559	350.6816	683.3294	342.1683	682.3453	341.6763	6
12	1125.6150	563.3111	1107.6045	554.3059	G	587.2718	294.1396	570.2453	285.6263	569.2613	285.1343	5
13	1256.6555	628.8314	1238.6449	619.8261	M	530.2504	265.6288	513.2238	257.1156	512.2398	256.6235	4
14	1343.6875	672.3474	1325.6770	663.3421	S	399.2099	200.1086	382.1833	191.5953	381.1993	191.1033	3
15	1480.7464	740.8769	1462.7359	731.8716	H	312.1779	156.5926	295.1513	148.0793			2
16					R	175.1190	88.0631	158.0924	79.5498			1

AT3G55410.1



NCBI **BLAST** search of AADLGVESIVIGMSHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.4	1653.8508	-0.0029	AADLGVESIVIGMSHR

Mascot: http://www.matrixscience.com/

AT3G55440.1

MATRIX SCIENCE

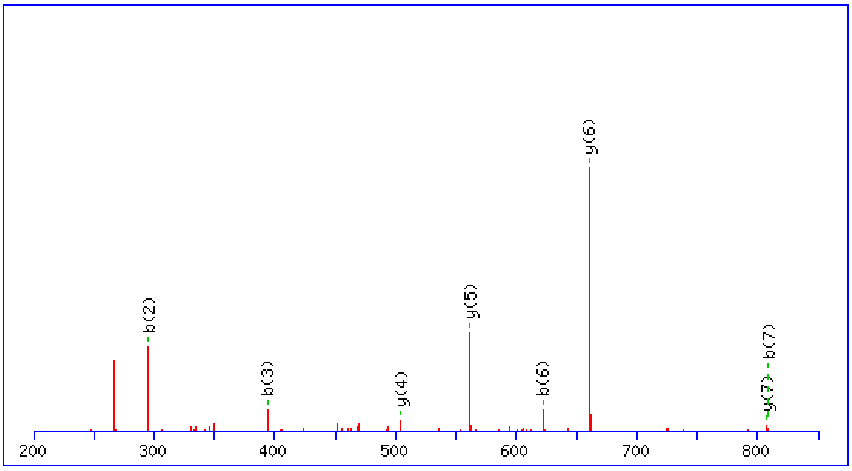
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFVGGNWK**
Found in **AT3G55440.1** in **TAIR_Arabidopsis**, Symbols: TPI, ATCTIMC | ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20564771-20567055 FORWARD

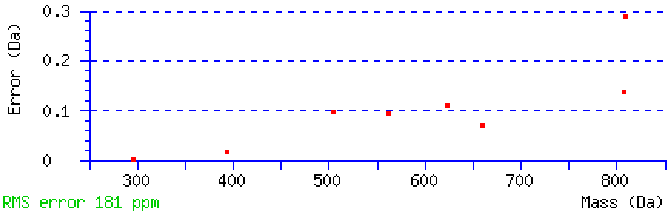
Match to Query 2031: 953.476072 from(477.745312,2+) index(5561)
Title: Elution from: 50.382 to 50.382 scan no 7100 cid35.00 polarity:+
Data file 0-1_2.mgf

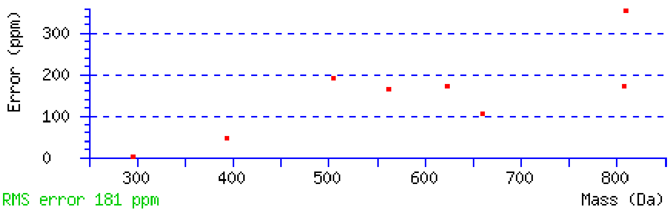
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 953.4760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00018
Matches : 8/46 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	148.0757	74.5415			F					8
2	***295.1441***	148.0757			F	***807.4148***	404.2110	790.3883	395.6978	7
3	***394.2125***	197.6099			V	***660.3464***	330.6768	643.3198	322.1636	6
4	451.2340	226.1206			G	***561.2780***	281.1426	544.2514	272.6293	5
5	508.2554	254.6314			G	***504.2565***	252.6319	487.2300	244.1186	4
6	***622.2984***	311.6528	605.2718	303.1395	N	447.2350	224.1212	430.2085	215.6079	3
7	***808.3777***	404.6925	791.3511	396.1792	W	333.1921	167.0997	316.1656	158.5864	2
8					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of FFVGGNWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.3	953.4760	0.0001	FFVGGNWK

AT3G55440.1

14.1	953.4753	0.0008	MFQQRTK
2.8	953.4753	0.0008	YMTEVRR

Mascot: http://www.matrixscience.com/

AT3G55500.1

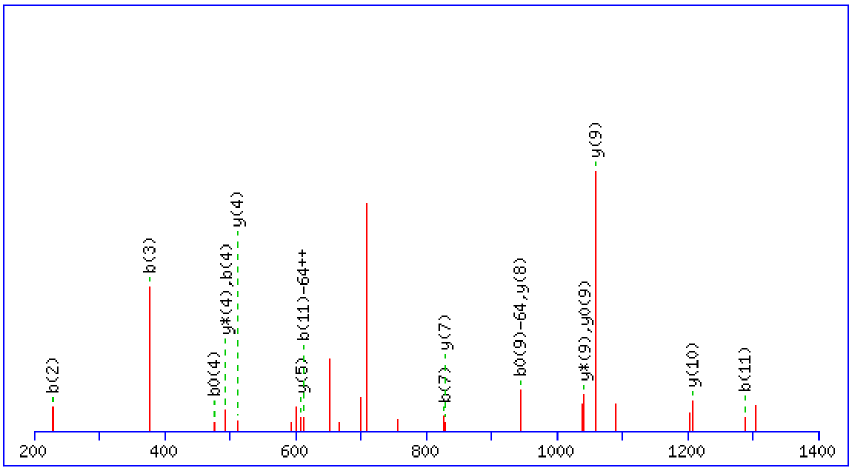
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHFDLAMPVFLK**
Found in **AT3G55500.1** in **TAIR_Arabidopsis**, Symbols: EXP16, ATEXP16, ATHEXP ALPHA 1.7, ATEXPA16 | ATEXPA16 (ARABIDOPSIS THALIANA EXPANSIN A16) | chr3:20586052-20587081 REVERSE

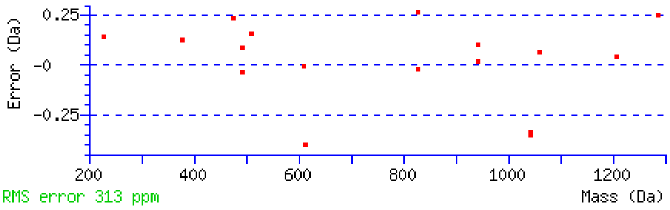
Match to Query 5724: 1434.675910 from(718.345231,2+) index(5930)
Title: Elution from: 52.477 to 52.477 scan no 7543 cid35.00 polarity:+
Data file C7-1_2.mgf

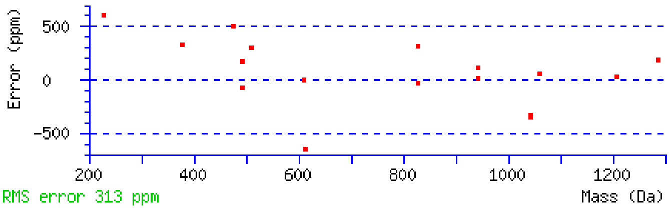
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1434.6776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 45 **Expect:** 0.00035
Matches : 17/144 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							12
2	***229.0864***	115.0468	211.0758	106.0415	H	1347.6558	674.3315	1329.6322	665.3197	1329.6452	665.3263	11
3	***377.1518***	189.0795	359.1412	180.0743	F	***1207.6058***	604.3065	1189.5822	595.2947	1189.5952	595.3012	10
4	***493.1758***	247.0915	475.1652	238.0862	D	***1059.5403***	530.2738	1041.5167	521.2620	1041.5298	521.2685	9
5	607.2569	304.1321	589.2463	295.1268	L	***943.5164***	472.2618	925.4928	463.2500			8
6	679.2910	340.1492	661.2805	331.1439	A	***829.4353***	415.2213	811.4117	406.2095			7
7	***827.3235***	414.1654	809.3129	405.1601	M	757.4011	379.2042	739.3775	370.1924			6
8	925.3733	463.1903	907.3627	454.1850	P	***609.3687***	305.1880	591.3451	296.1762			5
9	1025.4387	513.2230	1007.4281	504.2177	V	***511.3189***	256.1631	493.2953	247.1513			4
10	1173.5042	587.2557	1155.4936	578.2504	F	411.2534	206.1303	393.2298	197.1186			3
11	***1287.5853***	644.2963	1269.5747	635.2910	L	263.1880	132.0976	245.1644	123.0858			2
12					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SHFDLAMPVFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G55500.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.7	1434.6776	-0.0017	SHFDLAMPVFLK
10.7	1434.6778	-0.0019	QDEIDKLSSEKK
10.7	1434.6801	-0.0042	VDEFLQSLVNEK
7.6	1434.6779	-0.0019	LIENKSEKSDEK
5.9	1434.6753	0.0006	MEDIGLVKQGWK
5.5	1434.6731	0.0028	RQVTDPLSLMDK
4.7	1434.6731	0.0028	ELMEGEKGKELR
1.6	1434.6731	0.0028	TGTLTTNHMTVVK
1.5	1434.6731	0.0028	VMAAEAISEITQR
1.3	1434.6778	-0.0019	NQKLEEIETTSK

AT3G55700.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEKKEIEK**
Found in **AT3G55700.1** in **TAIR_Arabidopsis**, Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr3:20682181-20684257 FORWARD

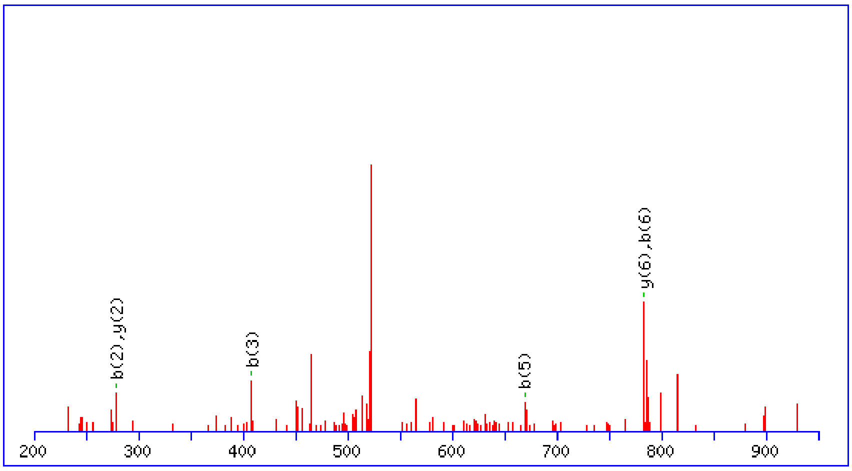
Match to Query 3004: 1060.508064 from(531.261308,2+) index(5126)
Title: Elution from: 46.869 to 46.869 scan no 6505 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

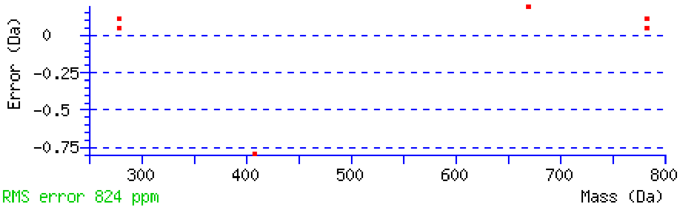
Label all possible matches ○ Label matches used for scoring ●

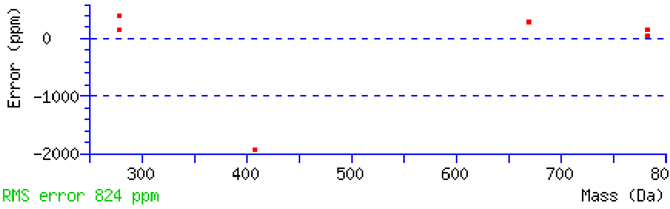
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1060.5101
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.022
Matches : 6/112 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							8
2	*279.0793*	140.0433			261.0688	131.0380	E	913.4849	457.2461	895.4613	448.2343	895.4744	448.2408	7
3	*409.1684*	205.0878	391.1448	196.0760	391.1578	196.0825	K	**783.4453**	392.2263	765.4217	383.2145	765.4347	383.2210	6
4	539.2574	270.1323	521.2338	261.1205	521.2468	261.1271	K	653.3563	327.1818	635.3327	318.1700	635.3457	318.1765	5
5	*669.2970*	335.1522	651.2734	326.1404	651.2865	326.1469	E	523.2672	262.1373	505.2436	253.1255	505.2567	253.1320	4
6	*783.3781*	392.1927	765.3545	383.1809	765.3676	383.1874	I	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	913.4178	457.2125	895.3942	448.2007	895.4072	448.2072	E	**279.1465**	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MEKKEIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G55700.1

27.3	1060.5101	-0.0020	MEKKEIEK
7.7	1060.5101	-0.0020	KDMTVLEAK
4.3	1060.5067	0.0014	FEALEDAKK
4.3	1060.5067	0.0014	FQKEIEEK
4.2	1060.5067	0.0014	YVEALAEQK
2.3	1060.5101	-0.0020	LKAMSDLEK
2.1	1060.5067	0.0014	EFLVETANK
2.1	1060.5053	0.0027	QMLELMIR
2.0	1060.5071	0.0009	LSNSGDAKVR
1.5	1060.5094	-0.0013	HPTVHSIEK

AT3G55800.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTGITGGDQVAAAMGIYGPR**
Found in **AT3G55800.1** in **TAIR_Arabidopsis**, Symbols: SBPASE | SBPASE (SEDOHEPTULOSE-BISPHOSPHATASE); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase | chr3:20720619-20722400 FORWARD

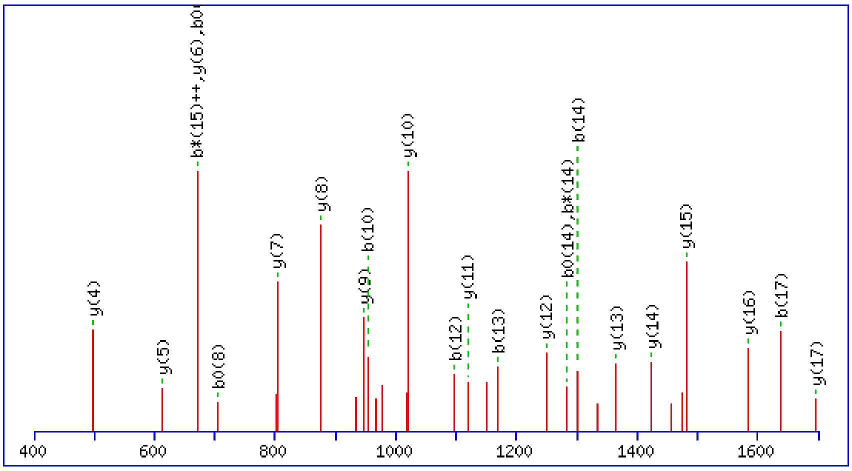
Match to Query 8996: 1970.920996 from(986.467774,2+) index(8356)
Title: Elution from: 74.719 to 74.719 scan no 11174 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

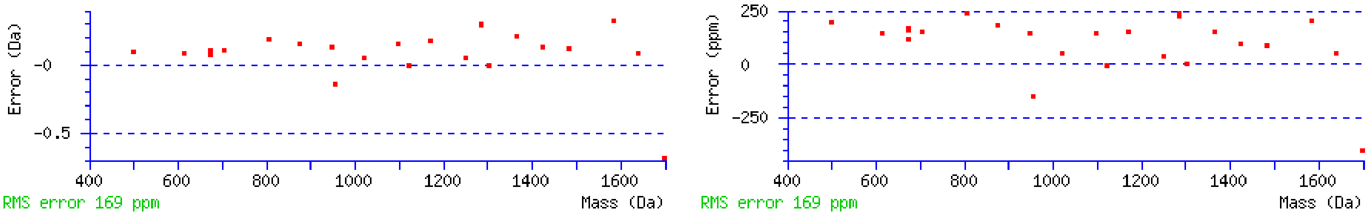
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1970.9172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 157 **Expect:** 1.8e-015
Matches : 24/186 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							20
2	217.1331	109.0702			199.1225	100.0649	T	1857.8434	929.4253	1839.8198	920.4136	1839.8329	920.4201	19
3	275.1516	138.0794			257.1410	129.0741	G	1755.7987	878.4030	1737.7751	869.3912	1737.7881	869.3977	18
4	389.2327	195.1200			371.2221	186.1147	I	***1697.7802***	849.3937	1679.7566	840.3819	1679.7696	840.3885	17
5	491.2774	246.1423			473.2668	237.1371	T	***1583.6991***	792.3532	1565.6755	783.3414	1565.6885	783.3479	16
6	549.2959	275.1516			531.2853	266.1463	G	***1481.6544***	741.3308	1463.6308	732.3190	1463.6438	732.3256	15
7	607.3144	304.1608			589.3038	295.1556	G	***1423.6359***	712.3216	1405.6123	703.3098	1405.6253	703.3163	14
8	723.3384	362.1728			705.3278	353.1675	D	***1365.6174***	683.3123	1347.5938	674.3005	1347.6068	674.3071	13
9	853.3910	427.1991	835.3674	418.1874	835.3805	418.1939	Q	***1249.5934***	625.3003	1231.5698	616.2886			12
10	**953.4565**	477.2319	935.4329	468.2201	935.4459	468.2266	V	***1119.5408***	560.2740	1101.5172	551.2622			11
11	1025.4906	513.2489	1007.4670	504.2372	1007.4801	504.2437	A	***1019.4753***	510.2413	1001.4517	501.2295			10
12	**1097.5248**	549.2660	1079.5012	540.2542	1079.5142	540.2607	A	***947.4412***	474.2242	929.4176	465.2124			9
13	**1169.5589**	585.2831	1151.5353	576.2713	1151.5484	576.2778	A	***875.4070***	438.2071	857.3834	429.1954			8
14	**1301.5964**	651.3019	1283.5729	642.2901	1283.5859	642.2966	M	***803.3729***	402.1901	785.3493	393.1783			7
15	1359.6149	680.3111	1341.5914	671.2993	1341.6044	671.3058	G	***671.3354***	336.1713	653.3118	327.1595			6
16	1473.6960	737.3517	1455.6725	728.3399	1455.6855	728.3464	I	***613.3169***	307.1621	595.2933	298.1503			5
17	**1637.7564**	819.3818	1619.7328	810.3700	1619.7458	810.3766	Y	***499.2358***	250.1215	481.2122	241.1097			4
18	1695.7749	848.3911	1677.7513	839.3793	1677.7643	839.3858	G	335.1754	168.0913	317.1518	159.0795			3
19	1793.8247	897.4160	1775.8011	888.4042	1775.8141	888.4107	P	277.1569	139.0821	259.1333	130.0703			2
20							R	179.1071	90.0572	161.0835	81.0454			1

AT3G55800.1



NCBI **BLAST** search of LTGITGGDQVAAAMGIYGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
156.7	1970.9172	0.0038	LTGITGGDQVAAAMGIYGPR

Mascot: http://www.matrixscience.com/

AT3G56070.1

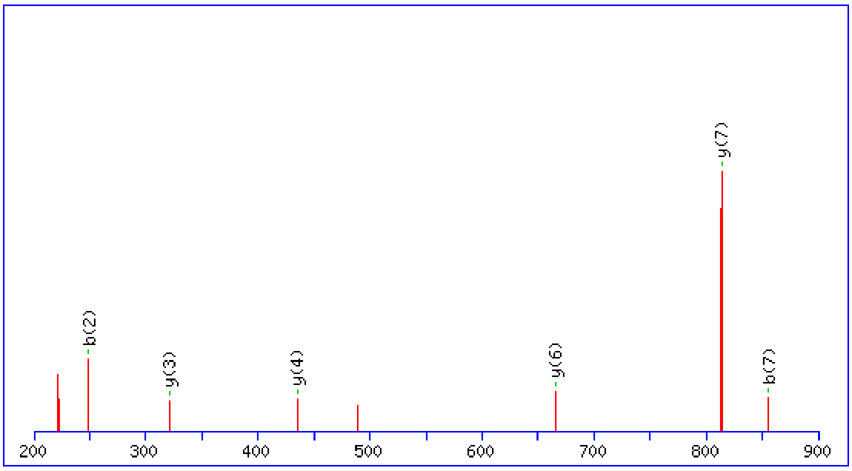
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFFDILIGK**
Found in **AT3G56070.1** in **TAIR_Arabidopsis**, Symbols: ROC2 | ROC2 (rotamase CyP 2); peptidyl-prolyl cis-trans isomerase | chr3:20817966-20818496 REVERSE

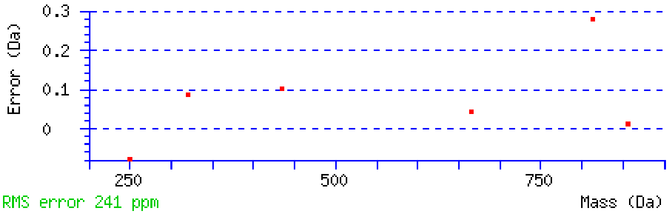
Match to Query 2970: 1060.580802 from(531.297677,2+) index(9957)
Title: Elution from: 91.419 to 91.419 scan no 13847 cid35.00 polarity:+
Data file C7-1_2.mgf

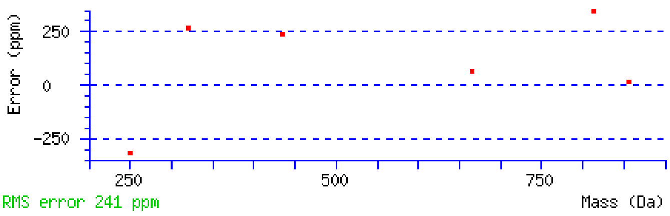
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1060.5817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00079
Matches : 6/64 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							9
2	**249.1382**	125.0727			F	961.5235	481.2654	943.5000	472.2536	943.5130	472.2601	8
3	397.2036	199.1054			F	***813.4581***	407.2327	795.4345	398.2209	795.4475	398.2274	7
4	513.2276	257.1174	495.2170	248.1122	D	***665.3926***	333.2000	647.3691	324.1882	647.3821	324.1947	6
5	627.3087	314.1580	609.2981	305.1527	I	549.3687	275.1880	531.3451	266.1762			5
6	741.3898	371.1985	723.3792	362.1933	L	***435.2876***	218.1474	417.2640	209.1356			4
7	**855.4709**	428.2391	837.4603	419.2338	I	***321.2065***	161.1069	303.1829	152.0951			3
8	913.4894	457.2483	895.4788	448.2431	G	207.1254	104.0663	189.1018	95.0545			2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VFFDILIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G56070.1

38.1	1060.5817	-0.0009	VFFDILIGK

Mascot: http://www.matrixscience.com/

Mascot Search Results

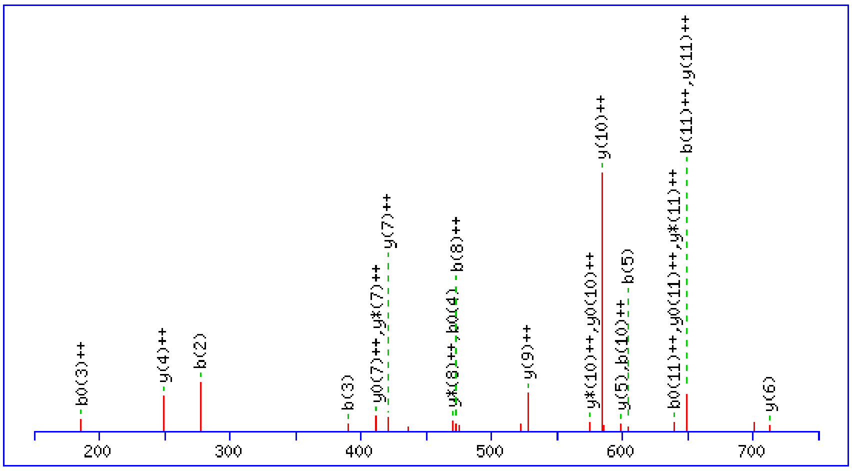
Peptide View

MS/MS Fragmentation of **FELVDQLTHLTK**
Found in **AT3G56150.1** in **TAIR_Arabidopsis**, Symbols: ATEIF3C-1, EIF3C-1, ATTIF3C1, TIF3C1, EIF3C | EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3) | chr3:20844769-20847799 REVERSE

Match to Query 5354: 1442.777268 from(481.933032,3+) index(7994)
Title: Elution from: 71.520 to 71.520 scan no 10582 cid35.00 polarity:+
Data file D12h-2_3.mgf

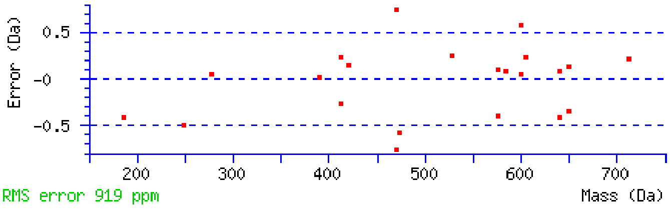
Click mouse within plot area to zoom in by factor of two about that point

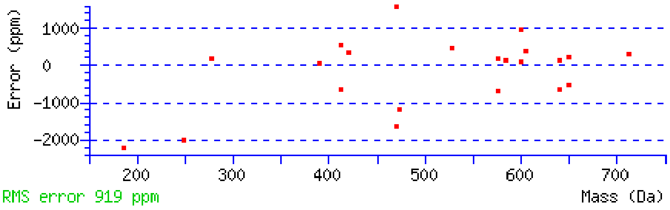
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1442.7769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.0001
Matches : 23/118 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					**F**							**12**
2	**277.1183**	139.0628			259.1077	130.0575	**E**	1296.7158	648.8615	1279.6892	640.3483	1278.7052	639.8563	**11**
3	**390.2023**	195.6048			372.1918	186.5995	**L**	1167.6732	584.3402	1150.6467	575.8270	1149.6626	575.3350	**10**
4	489.2708	245.1390			471.2602	236.1337	**V**	1054.5891	527.7982	1037.5626	519.2849	1036.5786	518.7929	**9**
5	**604.2977**	302.6525			586.2871	293.6472	**D**	955.5207	478.2640	938.4942	469.7507	937.5102	469.2587	**8**
6	732.3563	366.6818	715.3297	358.1685	714.3457	357.6765	**Q**	840.4938	420.7505	823.4672	412.2373	822.4832	411.7452	**7**
7	845.4403	423.2238	828.4138	414.7105	827.4298	414.2185	**L**	**712.4352**	356.7212	695.4087	348.2080	694.4246	347.7160	**6**
8	946.4880	***473.7477***	929.4615	465.2344	928.4775	464.7424	**T**	**599.3511**	300.1792	582.3246	291.6659	581.3406	291.1739	**5**
9	1083.5469	542.2771	1066.5204	533.7638	1065.5364	533.2718	**H**	498.3035	249.6554	481.2769	241.1421	480.2929	240.6501	**4**
10	1196.6310	***598.8191***	1179.6045	590.3059	1178.6204	589.8139	**L**	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
11	1297.6787	***649.3430***	1280.6521	640.8297	1279.6681	640.3377	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
12							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of FELVDQLTHLTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G56150.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.2	1442.7769	0.0003	FELVDQLTHLTK
17.8	1442.7803	-0.0030	GKAIPLPMKDTEK
17.4	1442.7737	0.0035	QRIGPLLMQMEK
0.8	1442.7769	0.0004	TFLSHLIEALDGK
0.2	1442.7809	-0.0037	KLFYEFLNVSAL

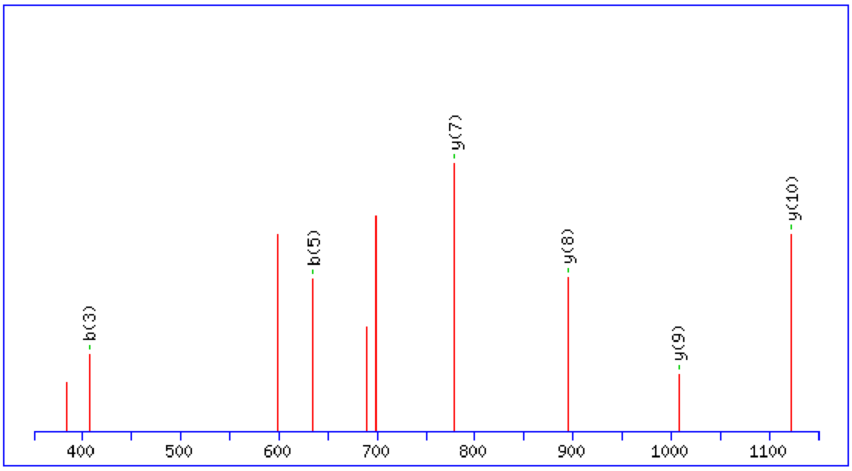
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQDLDPTFTGTR**
Found in **AT3G56190.1** in **TAIR_Arabidopsis**, Symbols: ASNAP, ALPHA-SNAP2 | ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN); soluble NSF attachment protein | chr3:20857098-20859335 REVERSE

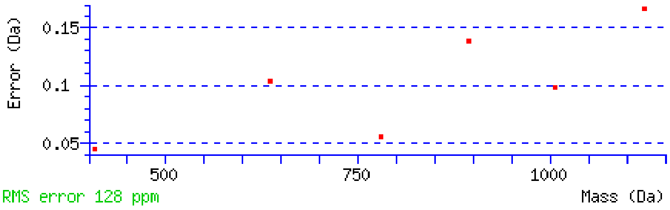
Match to Query 5549: 1412.657738 from(707.336145,2+) index(4362)
Title: Elution from: 40.196 to 40.196 scan no 5454 cid35.00 polarity:+
Data file D12h-1_2.mgf

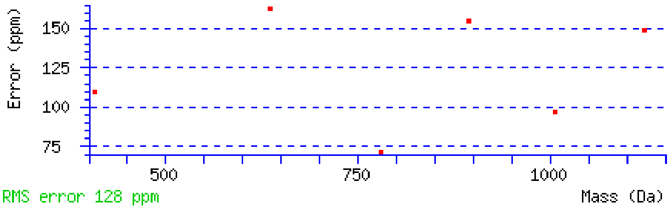
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1412.6572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0037
Matches : 6/124 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							12
2	292.1292	146.5682	275.1026	138.0550			Q	1250.6012	625.8042	1233.5746	617.2909	1232.5906	616.7989	11
3	**407.1561**	204.0817	390.1296	195.5684	389.1456	195.0764	D	***1122.5426***	561.7749	1105.5160	553.2617	1104.5320	552.7696	10
4	520.2402	260.6237	503.2136	252.1105	502.2296	251.6185	L	***1007.5156***	504.2615	990.4891	495.7482	989.5051	495.2562	9
5	**635.2671**	318.1372	618.2406	309.6239	617.2566	309.1319	D	***894.4316***	447.7194	877.4050	439.2062	876.4210	438.7141	8
6	732.3199	366.6636	715.2933	358.1503	714.3093	357.6583	P	***779.4046***	390.2060	762.3781	381.6927	761.3941	381.2007	7
7	833.3676	417.1874	816.3410	408.6742	815.3570	408.1821	T	682.3519	341.6796	665.3253	333.1663	664.3413	332.6743	6
8	980.4360	490.7216	963.4094	482.2084	962.4254	481.7164	F	581.3042	291.1557	564.2776	282.6425	563.2936	282.1504	5
9	1081.4837	541.2455	1064.4571	532.7322	1063.4731	532.2402	T	434.2358	217.6215	417.2092	209.1083	416.2252	208.6162	4
10	1138.5051	569.7562	1121.4786	561.2429	1120.4946	560.7509	G	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
11	1239.5528	620.2800	1222.5263	611.7668	1221.5422	611.2748	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YQDLDPTFTGTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G56190.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.0	1412.6572	0.0005	YQDLDPTFTGTR

AT3G56240.1

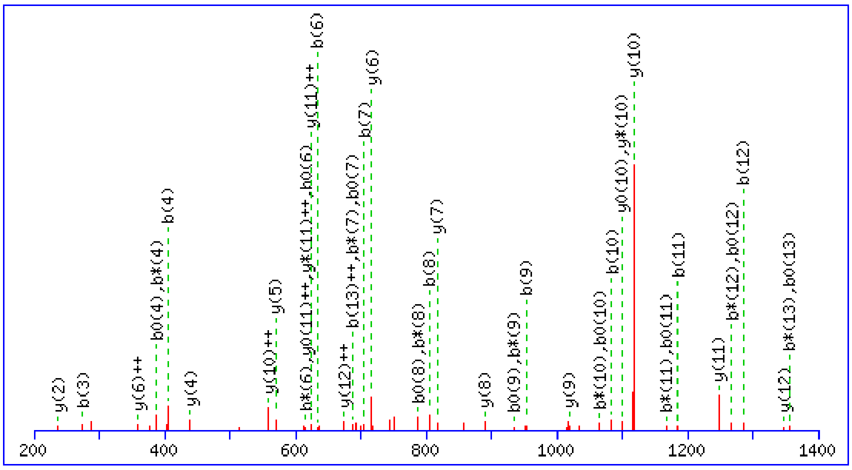
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVEPEAVFQTVSK**
Found in **AT3G56240.1** in **TAIR_Arabidopsis**, Symbols: CCH | CCH (COPPER CHAPERONE) | chr3:20874439-20875381 REVERSE

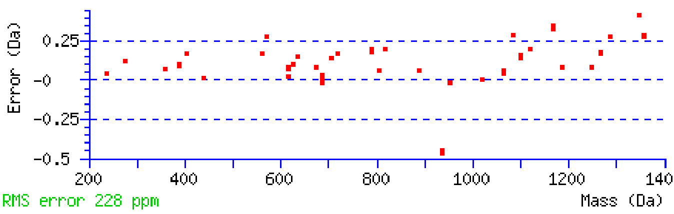
Match to Query 6812: 1520.704374 from(761.359463,2+) index(6289)
Title: Elution from: 54.675 to 54.675 scan no 7956 cid35.00 polarity:+
Data file C7-1_1.mgf

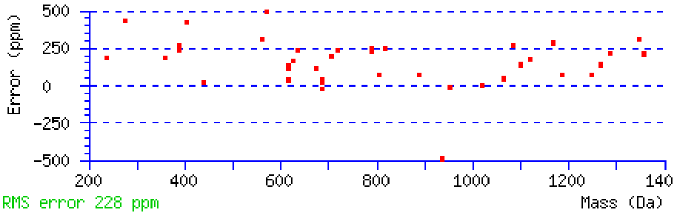
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1520.7065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 3.3e-008
Matches : 46/146 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							14
2	175.0628	88.0350	157.0392	79.0232			N	1463.6953	732.3513	1445.6717	723.3395	1445.6847	723.3460	13
3	***275.1282***	138.0677	257.1046	129.0560			V	***1347.6583***	674.3328	1329.6347	665.3210	1329.6477	665.3275	12
4	***405.1678***	203.0876	387.1443	194.0758	387.1573	194.0823	E	***1247.5928***	624.3001	1229.5693	615.2883	1229.5823	615.2948	11
5	503.2176	252.1125	485.1941	243.1007	485.2071	243.1072	P	***1117.5532***	559.2802	1099.5296	550.2685	1099.5427	550.2750	10
6	***633.2573***	317.1323	615.2337	308.1205	615.2467	308.1270	E	***1019.5034***	510.2553	1001.4798	501.2436	1001.4929	501.2501	9
7	***705.2914***	353.1494	687.2678	344.1376	687.2809	344.1441	A	***889.4638***	445.2355	871.4402	436.2237	871.4532	436.2303	8
8	***805.3569***	403.1821	787.3333	394.1703	787.3463	394.1768	V	***817.4296***	409.2185	799.4061	400.2067	799.4191	400.2132	7
9	***953.4223***	477.2148	935.3987	468.2030	935.4118	468.2095	F	***717.3642***	359.1857	699.3406	350.1739	699.3536	350.1805	6
10	***1083.4750***	542.2411	1065.4514	533.2293	1065.4644	533.2358	Q	***569.2987***	285.1530	551.2752	276.1412	551.2882	276.1477	5
11	***1185.5197***	593.2635	1167.4961	584.2517	1167.5091	584.2582	T	***439.2461***	220.1267	421.2225	211.1149	421.2355	211.1214	4
12	***1285.5851***	643.2962	1267.5615	634.2844	1267.5746	634.2909	V	337.2014	169.1043	319.1778	160.0925	319.1908	160.0990	3
13	1373.6142	687.3107	1355.5906	678.2989	1355.6036	678.3055	S	***237.1359***	119.0716	219.1124	110.0598	219.1254	110.0663	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GNVEPEAVFQTVSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G56240.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.7	1520.7065	-0.0021	GNVEPEAVFQTVSK

Mascot: http://www.matrixscience.com/

AT3G56310.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVIMKK**
Found in **AT3G56310.1** in **TAIR_Arabidopsis**, Symbols: | alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative | chr3:20893865-20896724 FORWARD

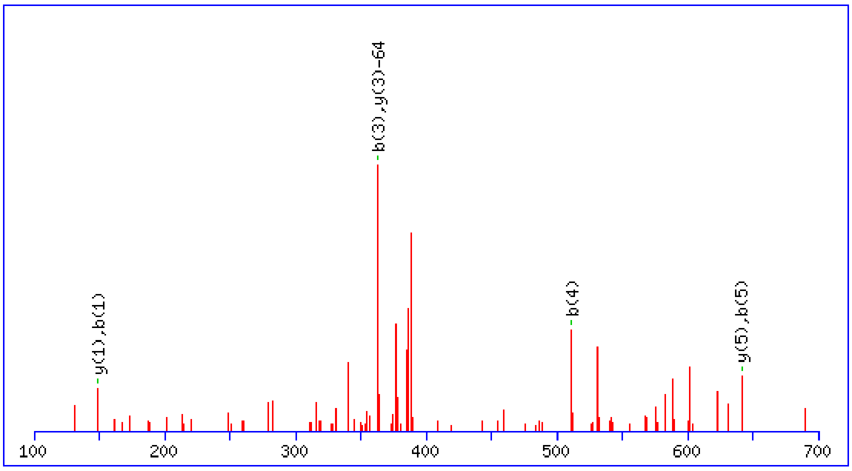
Match to Query 935: 788.398104 from(395.206328,2+) index(1577)
Title: Elution from: 19.449 to 19.449 scan no 2050 cid35.00 polarity:+
Data file C7-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

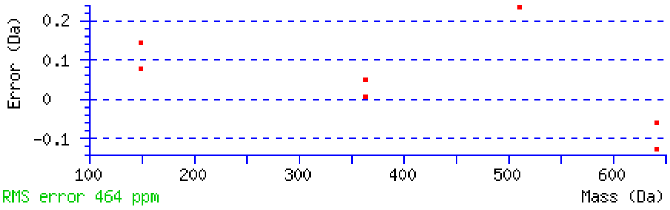
Label all possible matches ○ Label matches used for scoring ●

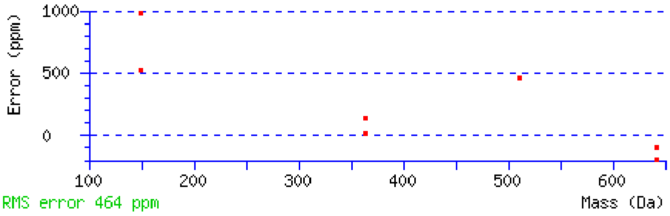
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 788.4001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.013
Matches : 7/56 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	*149.0397*	75.0235			M					6
2	249.1052	125.0562			V	**641.3749**	321.1911	623.3513	312.1793	5
3	*363.1863*	182.0968			I	541.3094	271.1584	523.2859	262.1466	4
4	*511.2187*	256.1130			M	427.2283	214.1178	409.2048	205.1060	3
5	*641.3077*	321.1575	623.2841	312.1457	K	279.1959	140.1016	261.1723	131.0898	2
6					K	**149.1069**	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MVIMKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.4	788.4001	-0.0020	MIVMKK

27.4	788.4001	-0.0020	MVIMKK
17.0	788.3967	0.0014	MQIFVK
14.1	788.3971	0.0010	ARQMKK
13.0	788.4001	-0.0020	MMKVIK
13.0	788.4001	-0.0020	MMKVLK
10.2	788.4001	-0.0020	VMMLKK
10.0	788.3971	0.0010	MVRTVR
9.0	788.3967	0.0014	MVGFALK
8.6	788.3967	0.0014	MGIAFVK

AT3G56320.1

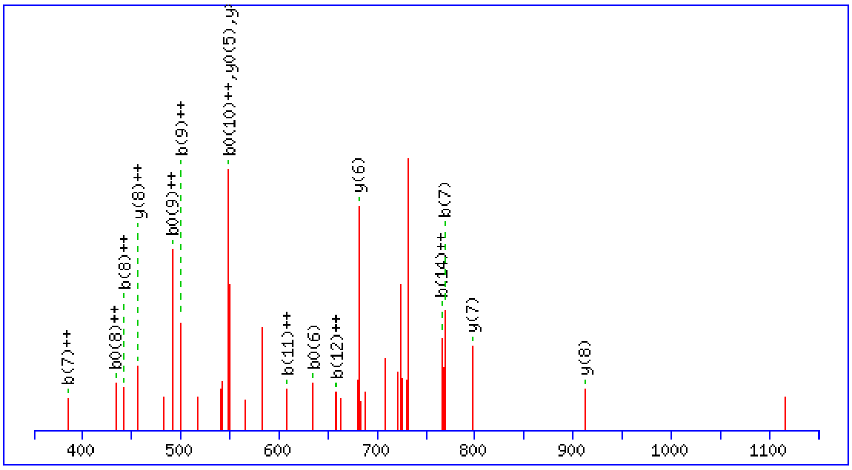
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYLPDGDIDLTVLTK**
Found in **AT3G56320.1** in **TAIR_Arabidopsis**, Symbols: | nucleotidyltransferase family protein | chr3:20897172-20899603 REVERSE

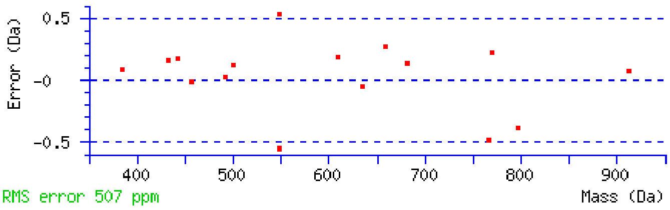
Match to Query 8068: 1678.827102 from(560.616310,3+) index(9553)
Title: Elution from: 87.646 to 87.646 scan no 13039 cid35.00 polarity:+
Data file D6h-2_1.mgf

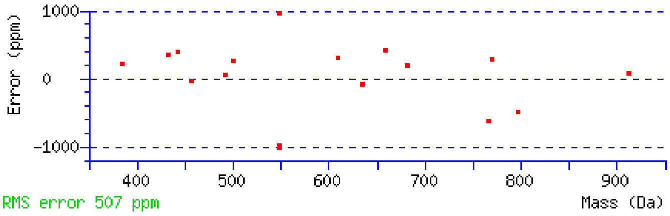
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1678.8241
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0079
Matches : 17/138 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							15
2	267.1124	134.0598	249.1018	125.0545	Y	1577.7867	789.3970	1559.7632	780.3852	1559.7762	780.3917	14
3	381.1935	191.1004	363.1829	182.0951	L	1413.7264	707.3668	1395.7028	698.3550	1395.7158	698.3615	13
4	479.2433	240.1253	461.2327	231.1200	P	1299.6453	650.3263	1281.6217	641.3145	1281.6347	641.3210	12
5	595.2672	298.1373	577.2567	289.1320	D	1201.5955	601.3014	1183.5719	592.2896	1183.5849	592.2961	11
6	653.2857	327.1465	635.2752	318.1412	G	1085.5715	543.2894	1067.5479	534.2776	1067.5609	534.2841	10
7	769.3097	***385.1585***	751.2991	376.1532	D	1027.5530	514.2801	1009.5294	505.2683	1009.5424	505.2749	9
8	883.3908	***442.1990***	865.3802	433.1938	I	**911.5290**	456.2681	893.5054	447.2564	893.5185	447.2629	8
9	999.4148	***500.2110***	981.4042	491.2057	D	**797.4479**	399.2276	779.4243	390.2158	779.4374	390.2223	7
10	1113.4959	557.2516	1095.4853	548.2463	L	**681.4239**	341.2156	663.4004	332.2038	663.4134	332.2103	6
11	1215.5406	***608.2739***	1197.5300	599.2687	T	567.3428	284.1751	549.3193	275.1633	549.3323	275.1698	5
12	1315.6060	***658.3067***	1297.5955	649.3014	V	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
13	1429.6871	715.3472	1411.6766	706.3419	L	365.2327	183.1200	347.2091	174.1082	347.2221	174.1147	3
14	1531.7319	***766.3696***	1513.7213	757.3643	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
15					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TYLPDGDIDLTVLTK

AT3G56320.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	1678.8241	0.0030	TYLPDGDIDLTVLTK
17.8	1678.8268	0.0003	KLVYEELDPEAAKR
10.8	1678.8302	-0.0031	SVEGMKGVSKVTVDPK
10.5	1678.8268	0.0003	NVSLAGPTLFSNVVDK
7.2	1678.8248	0.0023	DMVIGRNLGNWILR
6.5	1678.8246	0.0025	DSIDDKSKANVVQIK
5.4	1678.8221	0.0050	NTALARMVPYLDPAK
2.8	1678.8295	-0.0024	TVDIGGWIDIAVSRR
2.2	1678.8273	-0.0002	GGAVVRALQNESGASIK
1.8	1678.8273	-0.0002	SQRDKVAGLQQEVAK

AT3G56450.1

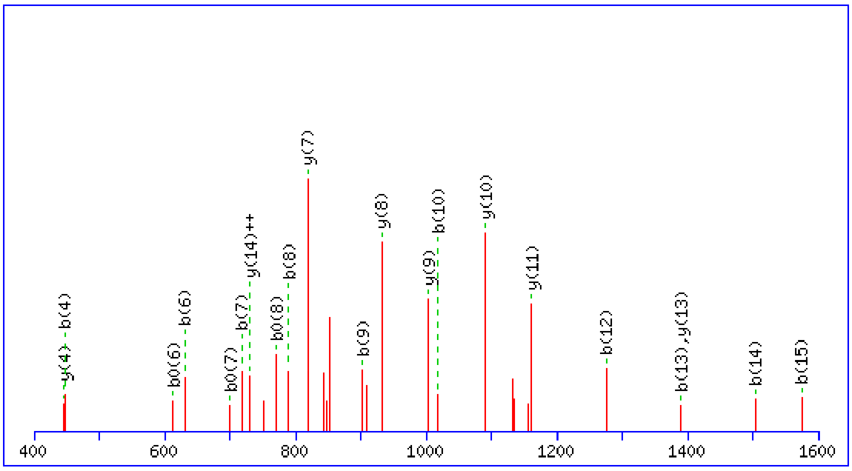
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLADLASAIDEEDIAK**
Found in **AT3G56450.1** in **TAIR_Arabidopsis**, Symbols: ALPHA-SNAP1 | ALPHA-SNAP1 (alpha-soluble NSF attachment protein 1); soluble NSF attachment protein | chr3:20941536-20943848 FORWARD

Match to Query 7729: 1719.860606 from(860.937579,2+) index(8937)
Title: Elution from: 85.053 to 85.053 scan no 12388 cid35.00 polarity:+
Data file D1d-1-2.mgf

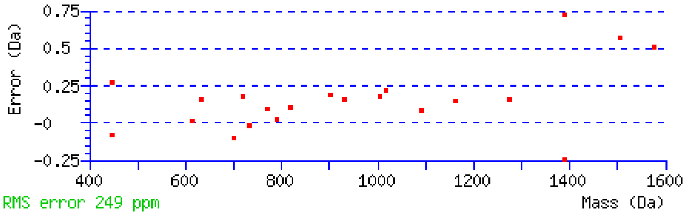
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

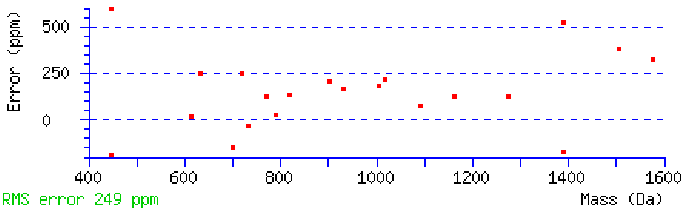


Monoisotopic mass of neutral peptide Mr(calc): 1719.8567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90 **Expect:** 6.6e-009
Matches : 21/138 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415			F							16
2	261.1598	131.0835			L	1573.7956	787.4014	1556.7690	778.8881	1555.7850	778.3961	15
3	332.1969	166.6021			A	1460.7115	730.8594	1443.6849	722.3461	1442.7009	721.8541	14
4	***447.2238***	224.1155	429.2132	215.1103	D	**1389.6744**	695.3408	1372.6478	686.8276	1371.6638	686.3355	13
5	560.3079	280.6576	542.2973	271.6523	L	1274.6474	637.8274	1257.6209	629.3141	1256.6369	628.8221	12
6	***631.3450***	316.1761	613.3344	307.1708	A	**1161.5634**	581.2853	1144.5368	572.7721	1143.5528	572.2800	11
7	***718.3770***	359.6921	700.3665	350.6869	S	**1090.5263**	545.7668	1073.4997	537.2535	1072.5157	536.7615	10
8	***789.4141***	395.2107	771.4036	386.2054	A	**1003.4942**	502.2508	986.4677	493.7375	985.4837	493.2455	9
9	***902.4982***	451.7527	884.4876	442.7475	I	**932.4571**	466.7322	915.4306	458.2189	914.4466	457.7269	8
10	***1017.5251***	509.2662	999.5146	500.2609	D	**819.3731**	410.1902	802.3465	401.6769	801.3625	401.1849	7
11	1146.5677	573.7875	1128.5572	564.7822	E	704.3461	352.6767	687.3196	344.1634	686.3355	343.6714	6
12	***1275.6103***	638.3088	1257.5998	629.3035	E	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
13	***1390.6373***	695.8223	1372.6267	686.8170	D	**446.2609**	223.6341	429.2344	215.1208	428.2504	214.6288	4
14	***1503.7213***	752.3643	1485.7108	743.3590	I	331.2340	166.1206	314.2074	157.6074			3
15	***1574.7584***	787.8829	1556.7479	778.8776	A	218.1499	109.5786	201.1234	101.0653			2
16					K	147.1128	74.0600	130.0863	65.5468			1

AT3G56450.1





NCBI **BLAST** search of FLADLASAIDEEDIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.2	1719.8567	0.0039	FLADLASAIDEEDIAK
0.5	1719.8648	-0.0042	LKDLPASSGIMQTMGR

Mascot: http://www.matrixscience.com/

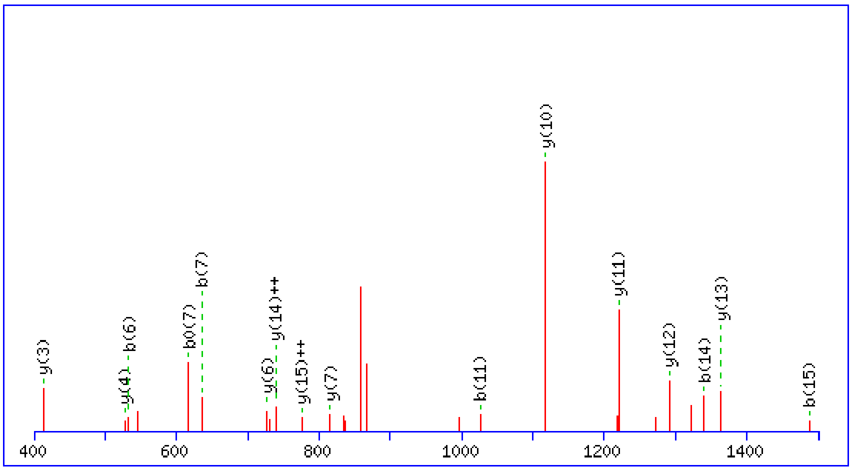
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAALAATPSDSPTIFDK**
Found in **AT3G56490.1** in **TAIR_Arabidopsis**, Symbols: | zinc-binding protein, putative / protein kinase C inhibitor, putative | chr3:20952511-20954108 FORWARD

Match to Query 8392: 1750.800322 from(876.407437,2+) index(5807)
Title: Elution from: 54.558 to 54.558 scan no 7511 cid35.00 polarity:+
Data file D12h-2_1.mgf

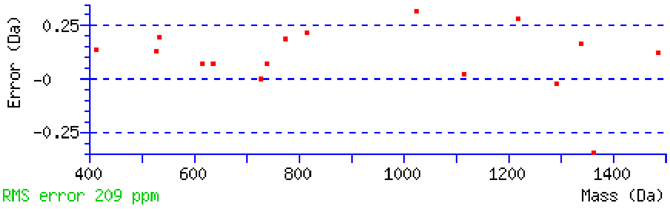
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

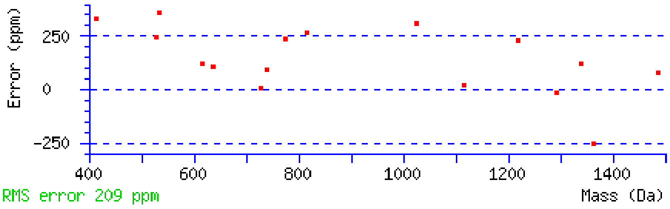


Monoisotopic mass of neutral peptide Mr(calc): 1750.7986
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 4.2e-007
Matches : 16/158 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							17
2	203.0811	102.0442	185.0705	93.0389	A	1621.7662	811.3867	1603.7426	802.3750	1603.7557	802.3815	16
3	275.1152	138.0612	257.1046	129.0560	A	1549.7321	775.3697	1531.7085	766.3579	1531.7215	766.3644	15
4	389.1963	195.1018	371.1857	186.0965	L	1477.6979	739.3526	1459.6743	730.3408	1459.6874	730.3473	14
5	461.2305	231.1189	443.2199	222.1136	A	***1363.6168***	682.3121	1345.5932	673.3003	1345.6063	673.3068	13
6	**533.2646**	267.1359	515.2540	258.1307	A	***1291.5827***	646.2950	1273.5591	637.2832	1273.5721	637.2897	12
7	**635.3093**	318.1583	617.2987	309.1530	T	***1219.5485***	610.2779	1201.5249	601.2661	1201.5380	601.2726	11
8	733.3591	367.1832	715.3485	358.1779	P	***1117.5038***	559.2555	1099.4802	550.2438	1099.4932	550.2503	10
9	821.3882	411.1977	803.3776	402.1924	S	1019.4540	510.2306	1001.4304	501.2189	1001.4435	501.2254	9
10	937.4122	469.2097	919.4016	460.2044	D	931.4250	466.2161	913.4014	457.2043	913.4144	457.2108	8
11	**1025.4412**	513.2242	1007.4307	504.2190	S	***815.4010***	408.2041	797.3774	399.1923	797.3904	399.1988	7
12	1123.4910	562.2491	1105.4804	553.2439	P	***727.3719***	364.1896	709.3483	355.1778	709.3613	355.1843	6
13	1225.5357	613.2715	1207.5252	604.2662	T	629.3221	315.1647	611.2985	306.1529	611.3115	306.1594	5
14	**1339.6168**	670.3121	1321.6063	661.3068	I	***527.2774***	264.1423	509.2538	255.1305	509.2668	255.1371	4
15	**1487.6823**	744.3448	1469.6717	735.3395	F	***413.1963***	207.1018	395.1727	198.0900	395.1857	198.0965	3
16	1603.7063	802.3568	1585.6957	793.3515	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
17					K	149.1069	75.0571	131.0833	66.0453			1

AT3G56490.1





NCBI **BLAST** search of EAALAATPSDSPTIFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.8	1750.7986	0.0018	EAALAATPSDSPTIFDK
3.0	1750.7986	0.0018	LTNDTSSTYIAASYVK

Mascot: http://www.matrixscience.com/

AT3G56760.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGYISMQNYKTAILKSSTEATK**
Found in **AT3G56760.1** in **TAIR_Arabidopsis**, Symbols: | calcium-dependent protein kinase, putative / CDPK, putative | chr3:21031640-21034735 REVERSE

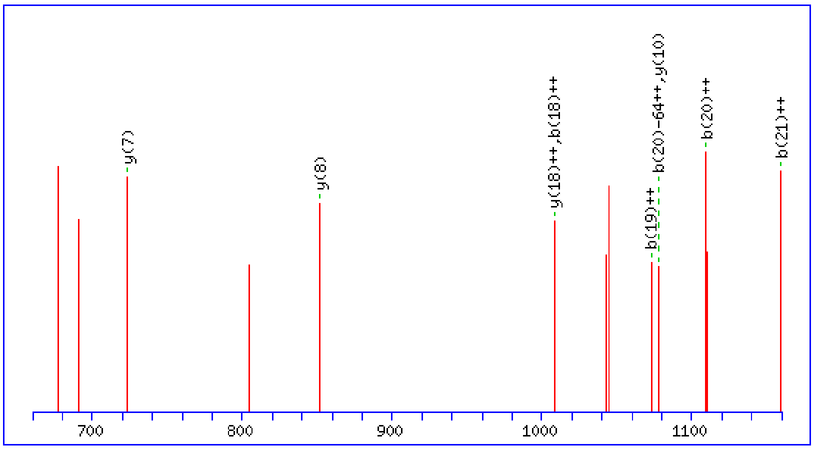
Match to Query 10464: 2463.228561 from(822.083463,3+) index(9646)
Title: Elution from: 87.058 to 87.058 scan no 13193 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 660 to 1160 Da Full range

Label all possible matches ○ Label matches used for scoring ●

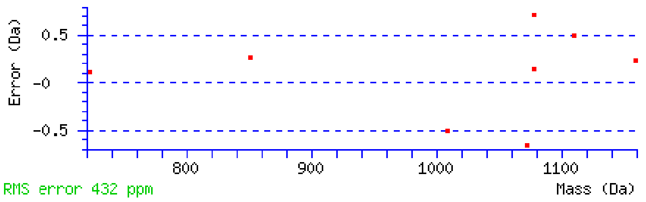
Show Y-axis ☐

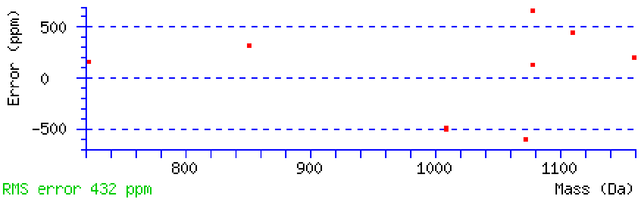


Monoisotopic mass of neutral peptide Mr(calc): 2463.2315
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.019
Matches : 9/368 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							22
2	172.0717	86.5395	155.0451	78.0262			G	2350.1959	1175.6016	2333.1693	1167.0883	2332.1853	1166.5963	21
3	335.1350	168.0711	318.1084	159.5579			Y	2293.1744	1147.0909	2276.1479	1138.5776	2275.1639	1138.0856	20
4	448.2191	224.6132	431.1925	216.0999			I	2130.1111	1065.5592	2113.0845	1057.0459	2112.1005	1056.5539	19
5	535.2511	268.1292	518.2245	259.6159	517.2405	259.1239	S	2017.0270	1009.0172	2000.0005	1000.5039	1999.0165	1000.0119	18
6	682.2865	341.6469	665.2599	333.1336	664.2759	332.6416	M	1929.9950	965.5011	1912.9685	956.9879	1911.9844	956.4959	17
7	810.3451	405.6762	793.3185	397.1629	792.3345	396.6709	Q	1782.9596	891.9834	1765.9331	883.4702	1764.9490	882.9782	16
8	924.3880	462.6976	907.3614	454.1844	906.3774	453.6924	N	1654.9010	827.9542	1637.8745	819.4409	1636.8905	818.9489	15
9	1087.4513	544.2293	1070.4248	535.7160	1069.4408	535.2240	Y	1540.8581	770.9327	1523.8316	762.4194	1522.8475	761.9274	14
10	1215.5463	608.2768	1198.5197	599.7635	1197.5357	599.2715	K	1377.7948	689.4010	1360.7682	680.8877	1359.7842	680.3957	13
11	1316.5940	658.8006	1299.5674	650.2873	1298.5834	649.7953	T	1249.6998	625.3535	1232.6733	616.8403	1231.6892	616.3483	12
12	1387.6311	694.3192	1370.6045	685.8059	1369.6205	685.3139	A	1148.6521	574.8297	1131.6256	566.3164	1130.6416	565.8244	11
13	1500.7151	750.8612	1483.6886	742.3479	1482.7046	741.8559	I	***1077.6150***	539.3111	1060.5885	530.7979	1059.6045	530.3059	10
14	1613.7992	807.4032	1596.7727	798.8900	1595.7886	798.3980	L	964.5310	482.7691	947.5044	474.2558	946.5204	473.7638	9
15	1741.8942	871.4507	1724.8676	862.9374	1723.8836	862.4454	K	***851.4469***	426.2271	834.4203	417.7138	833.4363	417.2218	8
16	1828.9262	914.9667	1811.8996	906.4535	1810.9156	905.9615	S	***723.3519***	362.1796	706.3254	353.6663	705.3414	353.1743	7
17	1915.9582	958.4828	1898.9317	949.9695	1897.9477	949.4775	S	636.3199	318.6636	619.2933	310.1503	618.3093	309.6583	6
18	2017.0059	***1009.0066***	1999.9794	1000.4933	1998.9953	1000.0013	T	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
19	2146.0485	***1073.5279***	2129.0219	1065.0146	2128.0379	1064.5226	E	448.2402	224.6237	431.2136	216.1105	430.2296	215.6185	4
20	2217.0856	***1109.0464***	2200.0591	1100.5332	2199.0750	1100.0412	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
21	2318.1333	***1159.5703***	2301.1067	1151.0570	2300.1227	1150.5650	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
22							K	147.1128	74.0600	130.0863	65.5468			1

AT3G56760.1





NCBI **BLAST** search of NGYISMQNYKTAILKSSTEATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.3	2463.2315	-0.0029	NGYISMQNYKTAILKSSTEATK
5.6	2463.2250	0.0036	NCGENVYQLIIDRGLLNDMVK
5.2	2463.2275	0.0011	SSADMNTELIKIQKQEELSQR
4.9	2463.2349	-0.0063	RMEVLKEGCEGNSTLLLELEK
1.0	2463.2315	-0.0030	SGTDGHMIEEAKFINLSLTSLGK
0.5	2463.2218	0.0068	LMPMLASTYAYHFATVYLVEK
0.5	2463.2218	0.0068	LMPMLASTYAYHFATVYLVEK

Mascot: http://www.matrixscience.com/

AT3G56910.1

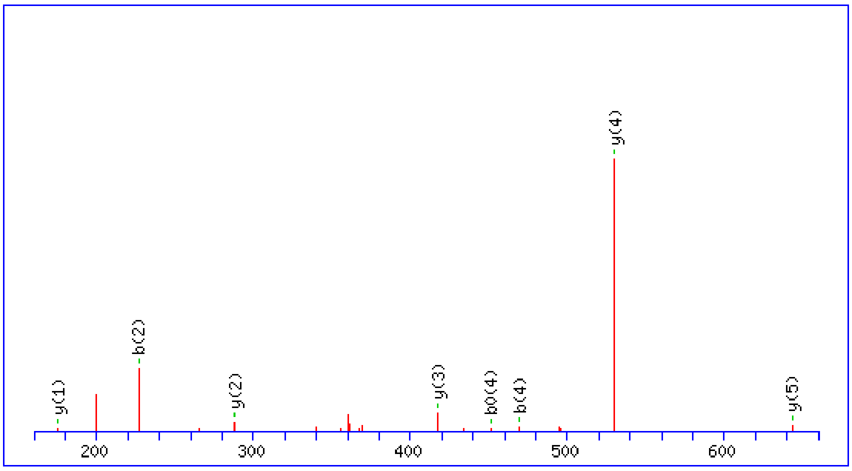
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLELR**
Found in **AT3G56910.1** in **TAIR_Arabidopsis**, Symbols: PSRP5 | PSRP5 (PLASTID-SPECIFIC 50S RIBOSOMAL PROTEIN 5) | chr3:21080537-21081236 REVERSE

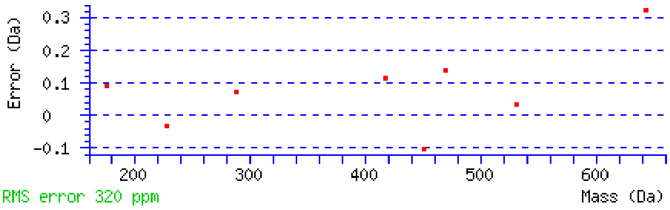
Match to Query 757: 755.490904 from(378.752728,2+) index(5746)
Title: Elution from: 51.801 to 51.801 scan no 7267 cid35.00 polarity:+
Data file 0-3_1.mgf

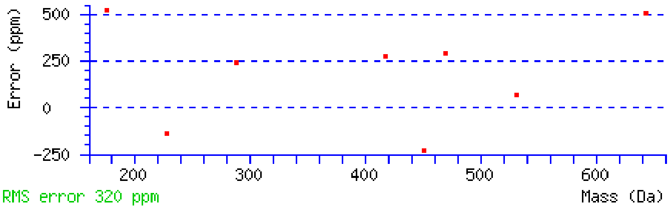
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 755.4905
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 8.5e-005
Matches : 8/40 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							6
2	**227.1754**	114.0913			L	***643.4137***	322.2105	626.3872	313.6972	625.4032	313.2052	5
3	340.2595	170.6334			L	***530.3297***	265.6685	513.3031	257.1552	512.3191	256.6632	4
4	**469.3021**	235.1547	451.2915	226.1494	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
5	582.3861	291.6967	564.3756	282.6914	L	***288.2030***	144.6051	271.1765	136.0919			2
6					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LLLELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.0	755.4905	0.0004	LILELR
46.0	755.4905	0.0004	LLLELR
31.4	755.4905	0.0004	IIEIIR

AT3G56910.1

31.4	755.4905	0.0004	LIELIR
8.2	755.4905	0.0004	LELILR
1.6	755.4905	0.0004	EIIILR
1.6	755.4905	0.0004	EILILR
1.6	755.4905	0.0004	ELLLLR

AT3G57140.1

Mascot Search Results

Peptide View

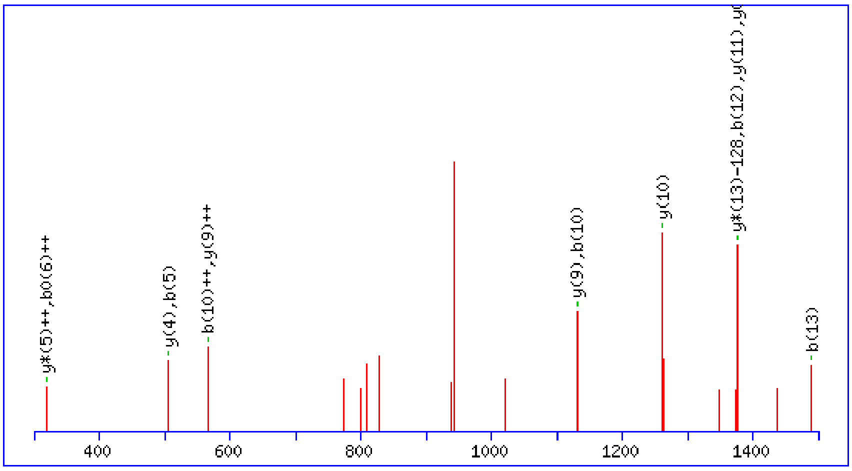
MS/MS Fragmentation of **DGSLEMDLPMIQLK**
Found in **AT3G57140.1** in **TAIR_Arabidopsis**, Symbols: SDP1-LIKE | SDP1-LIKE (SDP1-LIKE); GTP binding | chr3:21161721-21164294 REVERSE

Match to Query 7292: 1636.726358 from(819.370455,2+) index(10509)
Title: Elution from: 104.393 to 104.393 scan no 15334 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

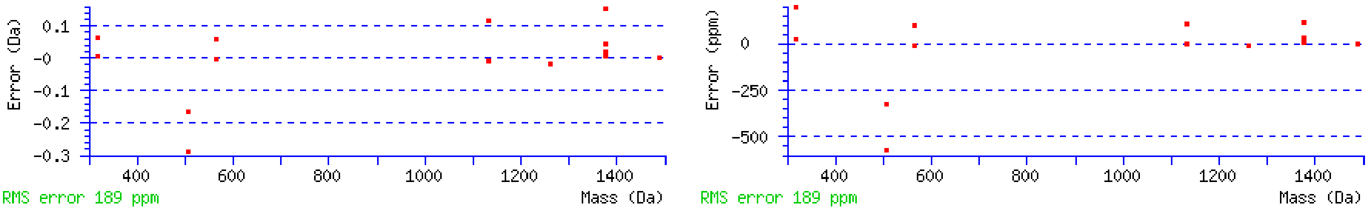
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1636.7265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.012
Matches : 14/204 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							14
2	175.0498	88.0285			157.0392	79.0232	G	1521.7098	761.3585	1503.6862	752.3467	1503.6992	752.3532	13
3	263.0788	132.0430			245.0683	123.0378	S	1463.6913	732.3493	1445.6677	723.3375	1445.6807	723.3440	12
4	377.1599	189.0836			359.1493	180.0783	L	***1375.6622***	688.3347	1357.6386	679.3229	1357.6516	679.3295	11
5	***507.1995***	254.1034			489.1890	245.0981	E	***1261.5811***	631.2942	1243.5575	622.2824	1243.5705	622.2889	10
6	655.2320	328.1196			637.2214	319.1143	M	***1131.5415***	566.2744	1113.5179	557.2626	1113.5309	557.2691	9
7	771.2560	386.1316			753.2454	377.1263	D	983.5090	492.2582	965.4854	483.2464	965.4985	483.2529	8
8	885.3371	443.1722			867.3265	434.1669	L	867.4851	434.2462	849.4615	425.2344			7
9	983.3869	492.1971			965.3763	483.1918	P	753.4040	377.2056	735.3804	368.1938			6
10	***1131.4193***	566.2133			1113.4087	557.2080	M	655.3542	328.1807	637.3306	319.1689			5
11	1245.5004	623.2538			1227.4898	614.2485	I	***507.3217***	254.1645	489.2981	245.1527			4
12	***1375.5530***	688.2802	1357.5295	679.2684	1357.5425	679.2749	Q	393.2406	197.1239	375.2170	188.1122			3
13	***1489.6341***	745.3207	1471.6105	736.3089	1471.6236	736.3154	L	263.1880	132.0976	245.1644	123.0858			2
14							K	149.1069	75.0571	131.0833	66.0453			1

AT3G57140.1



NCBI **BLAST** search of DGSLEMDLPMIQLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.2	1636.7265	-0.0001	DGSLEMDLPMIQLK
4.9	1636.7273	-0.0009	LFSGGGSLWVDWHR
4.2	1636.7292	-0.0028	SSLNDLNHMSMLLK
4.2	1636.7292	-0.0028	SSLNDLNHMSMLLK
2.6	1636.7217	0.0046	MELVVMSMEAIHSK
2.6	1636.7217	0.0046	MELVVMSMEAIHSK
1.6	1636.7309	-0.0045	VDRSDKPRGDDVEK
1.3	1636.7235	0.0028	EMSVNGKANLSPAGDK
1.2	1636.7231	0.0033	MSGFDAPPTDLETLK
0.5	1636.7237	0.0026	NCPKAYHPACIKR

Mascot: http://www.matrixscience.com/

AT3G57150.1

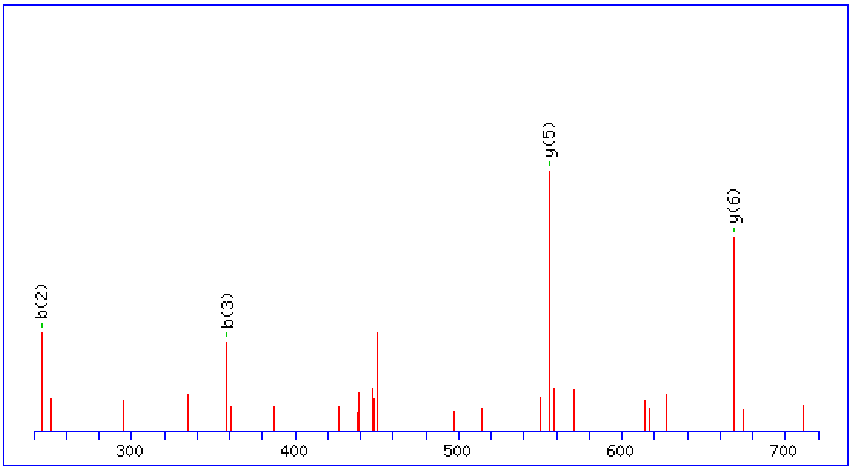
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMIPGLLR**
Found in **AT3G57150.1** in **TAIR_Arabidopsis**, Symbols: ATNAP57, CBF5, ATCBF5, NAP57 | NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57) | chr3:21165234-21166931 REVERSE

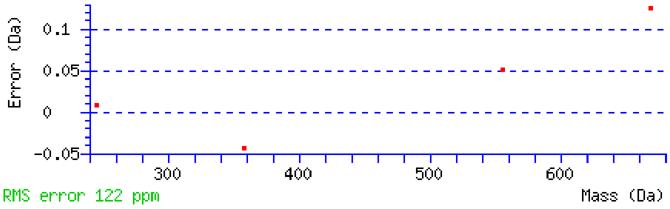
Match to Query 1603: 911.562804 from(456.788678,2+) index(7579)
Title: Elution from: 67.377 to 67.377 scan no 9925 cid35.00 polarity:+
Data file C7-1_3.mgf

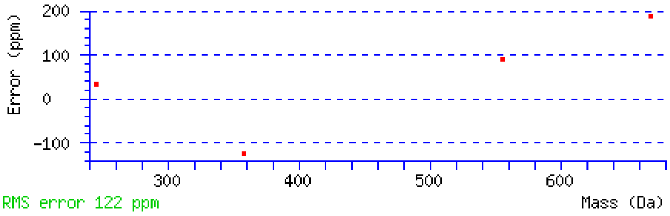
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 240 to 720 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 911.5626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.037
Matches : 4/42 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.0913	57.5493	L					8
2	***245.1318***	123.0696	M	799.4859	400.2466	782.4593	391.7333	7
3	***358.2159***	179.6116	I	***668.4454***	334.7263	651.4188	326.2130	6
4	455.2687	228.1380	P	***555.3613***	278.1843	538.3348	269.6710	5
5	512.2901	256.6487	G	458.3085	229.6579	441.2820	221.1446	4
6	625.3742	313.1907	L	401.2871	201.1472	384.2605	192.6339	3
7	738.4582	369.7328	L	288.2030	144.6051	271.1765	136.0919	2
8			R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of LMIPGLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.3	911.5626	0.0002	LMIPGLLR

AT3G57150.1

Mascot: http://www.matrixscience.com/

AT3G57610.1

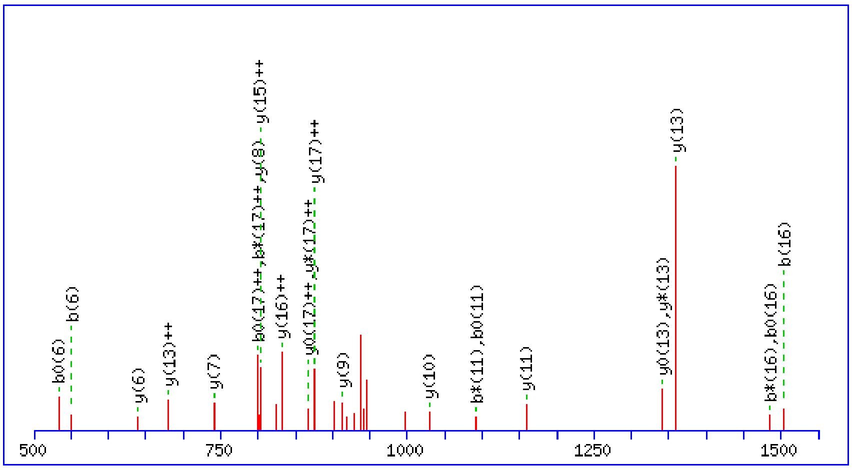
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSGPFPTENLGTGGDLLR**
Found in **AT3G57610.1** in **TAIR_Arabidopsis**, Symbols: ATPURA | ATPURA; adenylosuccinate synthase | chr3:21345496-21347580 REVERSE

Match to Query 8674: 1908.883746 from(955.449149,2+) index(7540)
Title: Elution from: 69.431 to 69.431 scan no 9975 cid35.00 polarity:+
Data file D12h-2_2.mgf

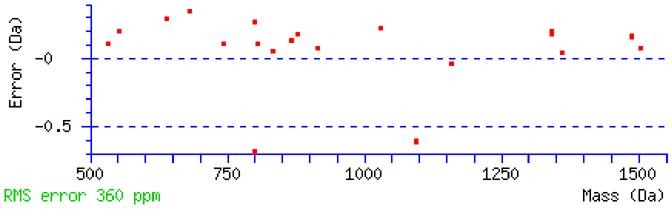
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1550 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

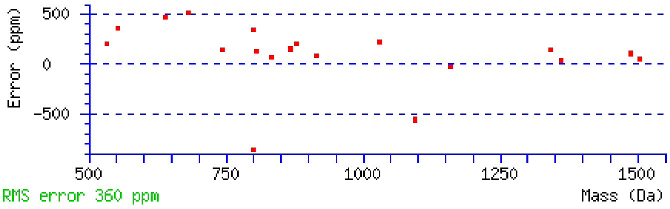


Monoisotopic mass of neutral peptide Mr(calc): 1908.8852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 7.5e-006
Matches : 24/188 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							19
2	159.0912	80.0492					G	1809.8270	905.4171	1791.8034	896.4054	1791.8165	896.4119	18
3	247.1203	124.0638			229.1097	115.0585	S	1751.8085	876.4079	1733.7849	867.3961	1733.7980	867.4026	17
4	305.1388	153.0730			287.1282	144.0677	G	1663.7795	832.3934	1645.7559	823.3816	1645.7689	823.3881	16
5	403.1886	202.0979			385.1780	193.0926	P	1605.7610	803.3841	1587.7374	794.3723	1587.7504	794.3788	15
6	**551.2540**	276.1307			533.2435	267.1254	F	1507.7112	754.3592	1489.6876	745.3474	1489.7006	745.3539	14
7	649.3038	325.1556			631.2933	316.1503	P	***1359.6457***	680.3265	1341.6221	671.3147	1341.6351	671.3212	13
8	751.3485	376.1779			733.3380	367.1726	T	1261.5959	631.3016	1243.5723	622.2898	1243.5854	622.2963	12
9	881.3882	441.1977			863.3776	432.1924	E	***1159.5512***	580.2792	1141.5276	571.2674	1141.5406	571.2740	11
10	997.4252	499.2162	979.4016	490.2044	979.4146	490.2109	N	***1029.5116***	515.2594	1011.4880	506.2476	1011.5010	506.2541	10
11	1111.5063	556.2568	1093.4827	547.2450	1093.4957	547.2515	L	***913.4746***	457.2409	895.4510	448.2291	895.4640	448.2356	9
12	1169.5248	585.2660	1151.5012	576.2542	1151.5142	576.2607	G	***799.3935***	400.2004	781.3699	391.1886	781.3829	391.1951	8
13	1271.5695	636.2884	1253.5459	627.2766	1253.5589	627.2831	T	***741.3750***	371.1911	723.3514	362.1793	723.3644	362.1858	7
14	1329.5880	665.2976	1311.5644	656.2858	1311.5774	656.2923	G	***639.3303***	320.1688	621.3067	311.1570	621.3197	311.1635	6
15	1387.6065	694.3069	1369.5829	685.2951	1369.5959	685.3016	G	581.3118	291.1595	563.2882	282.1477	563.3012	282.1542	5
16	**1503.6305**	752.3189	1485.6069	743.3071	1485.6199	743.3136	D	523.2933	262.1503	505.2697	253.1385	505.2827	253.1450	4
17	1617.7116	809.3594	1599.6880	800.3476	1599.7010	800.3541	L	407.2693	204.1383	389.2457	195.1265			3
18	1731.7927	866.4000	1713.7691	857.3882	1713.7821	857.3947	L	293.1882	147.0977	275.1646	138.0859			2
19							R	179.1071	90.0572	161.0835	81.0454			1

AT3G57610.1





NCBI **BLAST** search of VGSGPFPTENLGTGGDLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.8	1908.8852	-0.0014	VGSGPFPTENLGTGGDLLR
1.6	1908.8809	0.0029	DMDAELAPRREGLRPR
0.7	1908.8802	0.0035	TTETLEADKETNGGVPVK
0.4	1908.8838	-0.0001	KAHMMEIQINGGTIAQK
0.4	1908.8838	-0.0001	KAHMMEIQINGGTIAQK

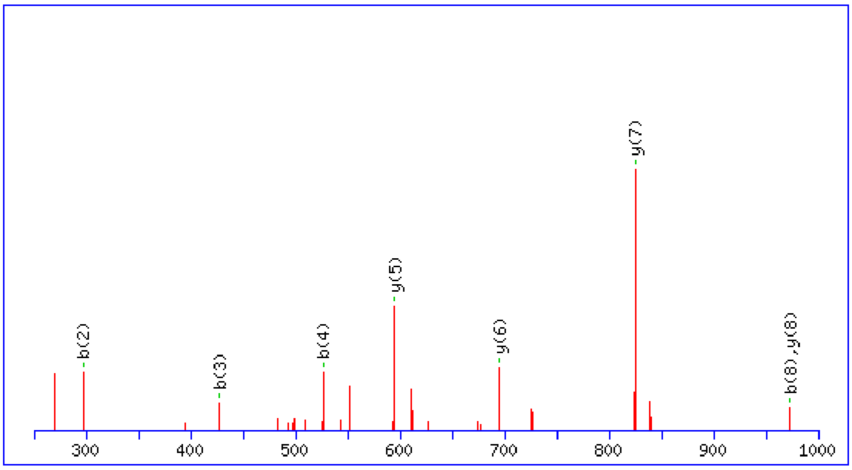
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MMEVAKELK**
Found in **AT3G57740.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr3:21403648-21404721 FORWARD

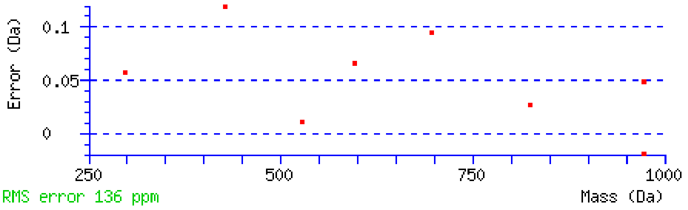
Match to Query 2965: 1120.516812 from(561.265682,2+) index(6989)
Title: Elution from: 64.314 to 64.314 scan no 9268 cid35.00 polarity:+
Data file D1d-1_3.mgf

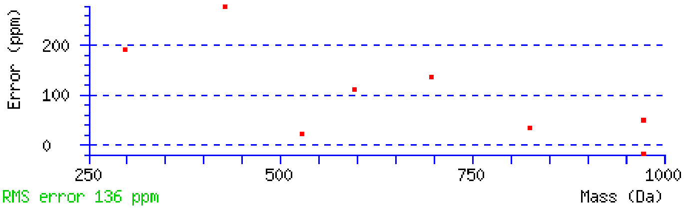
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1120.5135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 41 **Expect:** 0.00071
Matches : 8/118 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							9
2	*297.0721*	149.0397					M	*973.4883*	487.2478	955.4647	478.2360	955.4777	478.2425	8
3	*427.1118*	214.0595			409.1012	205.0542	E	*825.4559*	413.2316	807.4323	404.2198	807.4453	404.2263	7
4	*527.1772*	264.0922			509.1667	255.0870	V	*695.4162*	348.2118	677.3926	339.2000	677.4057	339.2065	6
5	599.2114	300.1093			581.2008	291.1040	A	*595.3508*	298.1790	577.3272	289.1672	577.3402	289.1737	5
6	729.3004	365.1538	711.2768	356.1420	711.2898	356.1486	K	523.3166	262.1620	505.2930	253.1502	505.3061	253.1567	4
7	859.3400	430.1737	841.3164	421.1619	841.3295	421.1684	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
8	*973.4211*	487.2142	955.3975	478.2024	955.4106	478.2089	L	263.1880	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MMEVAKELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G57740.1

Score	Mr(calc)	Delta	Sequence
41.1	1120.5135	0.0034	MMEVAKELK
18.7	1120.5135	0.0033	LMSLENLMK
15.2	1120.5135	0.0034	MEDMKSLIK
12.9	1120.5197	-0.0029	VAADSQFPFK
8.5	1120.5175	-0.0007	KNGEATDVFK
8.2	1120.5154	0.0014	HGMFGGKRSK
5.5	1120.5197	-0.0029	IYHDSALYK
4.3	1120.5175	-0.0007	YTAGQNEVVK
2.9	1120.5184	-0.0015	AGMWQLMKK
2.3	1120.5175	-0.0007	FKTEEDAIR

AT3G58140.1

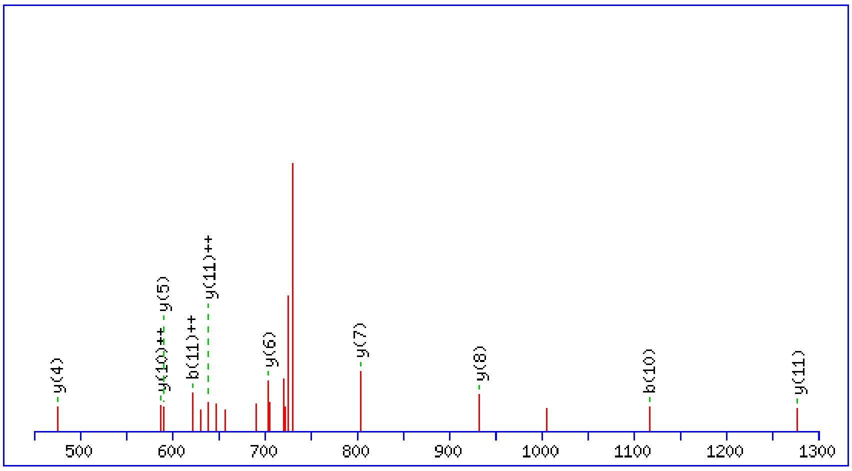
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLTDEEVNDLQSK**
Found in **AT3G58140.1** in **TAIR_Arabidopsis**, Symbols: | phenylalanyl-tRNA synthetase class IIc family protein | chr3:21540965-21543363 REVERSE

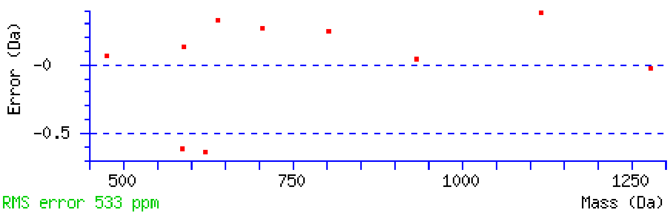
Match to Query 6320: 1476.696078 from(739.355315,2+) index(3562)
Title: Elution from: 34.889 to 34.889 scan no 4442 cid35.00 polarity:+
Data file D12h-3_1.mgf

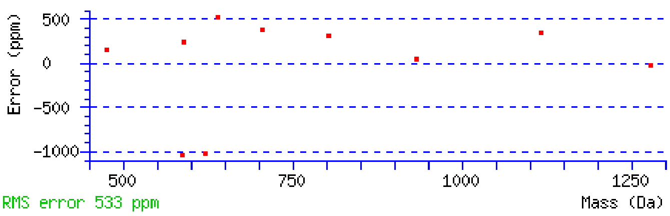
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1476.6944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0004
Matches : 10/128 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**13**
2	201.1234	101.0653			183.1128	92.0600	**L**	1390.6696	695.8385	1373.6431	687.3252	1372.6591	686.8332	**12**
3	302.1710	151.5892			284.1605	142.5839	**T**	***1277.5856***	639.2964	1260.5590	630.7831	1259.5750	630.2911	**11**
4	417.1980	209.1026			399.1874	200.0974	**D**	1176.5379	588.7726	1159.5113	580.2593	1158.5273	579.7673	**10**
5	546.2406	273.6239			528.2300	264.6186	**E**	1061.5109	531.2591	1044.4844	522.7458	1043.5004	522.2538	**9**
6	675.2832	338.1452			657.2726	329.1399	**E**	***932.4684***	466.7378	915.4418	458.2245	914.4578	457.7325	**8**
7	774.3516	387.6794			756.3410	378.6742	**V**	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	**7**
8	888.3945	444.7009	871.3680	436.1876	870.3840	435.6956	**N**	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	**6**
9	1003.4215	502.2144	986.3949	493.7011	985.4109	493.2091	**D**	***590.3144***	295.6608	573.2879	287.1476	572.3039	286.6556	**5**
10	1116.5055	558.7564	1099.4790	550.2431	1098.4950	549.7511	**L**	***475.2875***	238.1474	458.2609	229.6341	457.2769	229.1421	**4**
11	1244.5641	622.7857	1227.5376	614.2724	1226.5535	613.7804	**Q**	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	**3**
12	1331.5961	666.3017	1314.5696	657.7884	1313.5856	657.2964	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
13							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SLTDEEVNDLQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G58140.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.9	1476.6944	0.0017	SLTDEEVNDLQSK
12.4	1476.6990	-0.0030	ANNVENKMEEKR
2.1	1476.6917	0.0044	HRSSTSTVSGSSER
0.8	1476.6957	0.0004	ASHSDFSVTARDGK
0.7	1476.6918	0.0042	ALQMTEWLDENK
0.1	1476.6997	-0.0036	AISRAYDNYNYK

AT3G58200.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQEMKVFKQK**
Found in **AT3G58200.1** in **TAIR_Arabidopsis**, Symbols: | meprin and TRAF homology domain-containing protein / MATH domain-containing protein | chr3:21571063-21572335 REVERSE

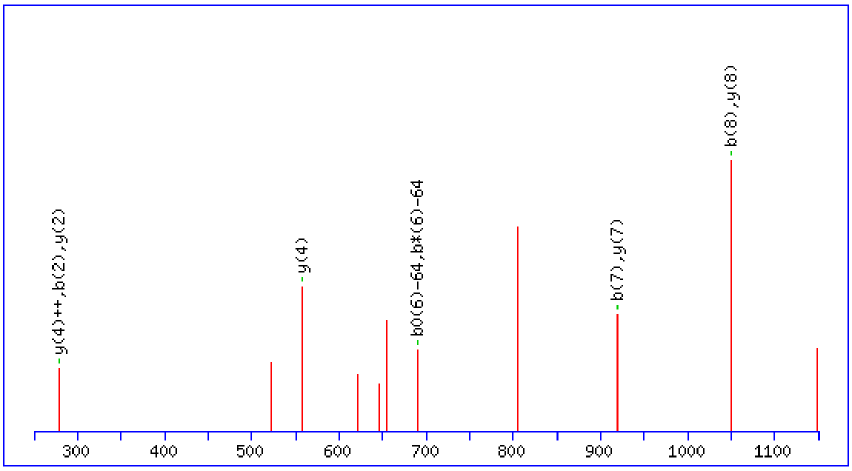
Match to Query 5201: 1326.620398 from(664.317475,2+) index(9342)
Title: Elution from: 82.660 to 82.660 scan no 12505 cid35.00 polarity:+
Data file D1d-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1150 Da Full range

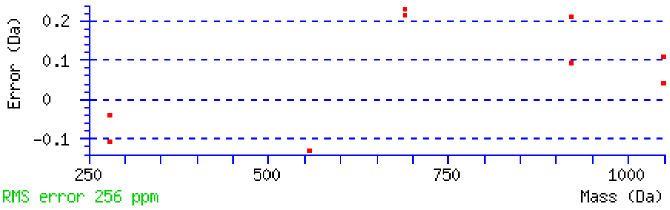
Label all possible matches ○ Label matches used for scoring ●

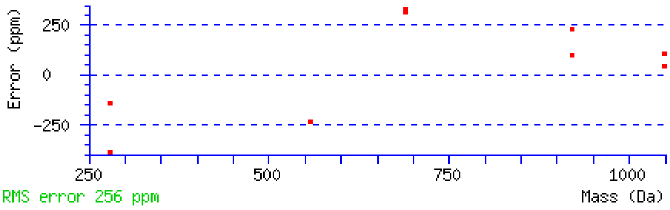
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1326.6234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.021
Matches : 10/136 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							10
2	**279.0924**	140.0498	261.0688	131.0380			Q	1179.5983	590.3028	1161.5747	581.2910	1161.5877	581.2975	9
3	409.1320	205.0696	391.1084	196.0578	391.1214	196.0643	E	***1049.5456***	525.2765	1031.5220	516.2647	1031.5351	516.2712	8
4	541.1695	271.0884	523.1459	262.0766	523.1589	262.0831	M	***919.5060***	460.2566	901.4824	451.2448			7
5	671.2585	336.1329	653.2350	327.1211	653.2480	327.1276	K	787.4685	394.2379	769.4449	385.2261			6
6	771.3240	386.1656	753.3004	377.1538	753.3134	377.1603	V	657.3795	329.1934	639.3559	320.1816			5
7	**919.3894**	460.1984	901.3659	451.1866	901.3789	451.1931	F	***557.3140***	279.1606	539.2904	270.1488			4
8	**1049.4785**	525.2429	1031.4549	516.2311	1031.4679	516.2376	K	409.2486	205.1279	391.2250	196.1161			3
9	1179.5311	590.2692	1161.5075	581.2574	1161.5206	581.2639	Q	***279.1595***	140.0834	261.1359	131.0716			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MQEMKVFKQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G58200.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
25.1	1326.6234	-0.0030	MQEMKVFKQK	Oxidation M1 95.12%
21.2	1326.6201	0.0003	FQELAMIYAAR	
16.7	1326.6200	0.0004	YMQFLAGDLVR	
14.9	1326.6171	0.0033	TWARQSTGFVR	
12.2	1326.6201	0.0003	FLARCIFEEK	
12.2	1326.6234	-0.0030	MQEMKVFKQK	Oxidation M4 4.88%
11.8	1326.6178	0.0026	MKKSDSSFPLR	
8.7	1326.6178	0.0026	MQGDALITYRK	
3.0	1326.6178	0.0026	EMKAFTDVARK	
2.2	1326.6178	0.0026	LYDAMKISQSR	

AT3G58610.1

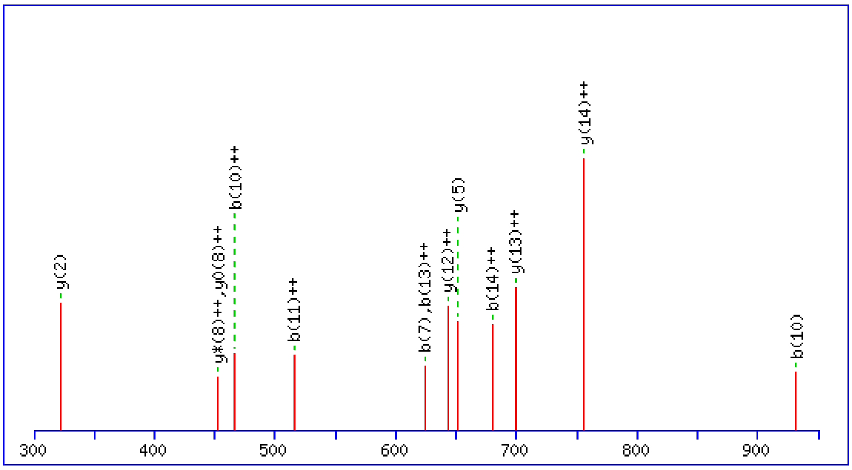
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GILLGAVHGIVESLFR**
Found in **AT3G58610.1** in **TAIR_Arabidopsis**, Symbols: | ketol-acid reductoisomerase | chr3:21682538-21685616 FORWARD

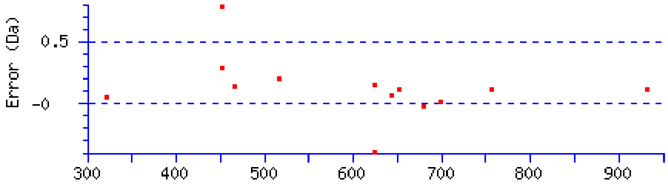
Match to Query 7654: 1679.971869 from(560.997899,3+) index(10625)
Title: Elution from: 111.445 to 111.445 scan no 15724 cid35.00 polarity:+
Data file C7-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

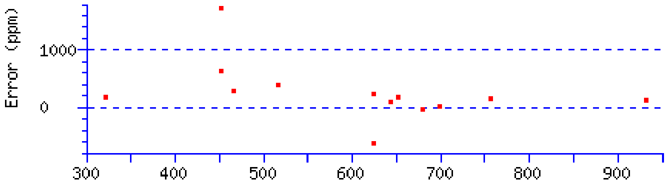


Monoisotopic mass of neutral peptide Mr(calc): 1679.9723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 2.1e-005
Matches : 13/122 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							16
2	171.1128	86.0600			I	1623.9581	812.4827	1606.9315	803.9694	1605.9475	803.4774	15
3	284.1969	142.6021			L	1510.8740	755.9407	1493.8475	747.4274	1492.8635	746.9354	14
4	397.2809	199.1441			L	1397.7900	699.3986	1380.7634	690.8853	1379.7794	690.3933	13
5	454.3024	227.6548			G	1284.7059	642.8566	1267.6793	634.3433	1266.6953	633.8513	12
6	525.3395	263.1734			A	1227.6844	614.3459	1210.6579	605.8326	1209.6739	605.3406	11
7	**624.4079**	312.7076			V	1156.6473	578.8273	1139.6208	570.3140	1138.6368	569.8220	10
8	761.4668	381.2371			H	1057.5789	529.2931	1040.5524	520.7798	1039.5683	520.2878	9
9	818.4883	409.7478			G	920.5200	460.7636	903.4934	452.2504	902.5094	451.7584	8
10	**931.5724**	***466.2898***			I	863.4985	432.2529	846.4720	423.7396	845.4880	423.2476	7
11	1030.6408	***515.8240***			V	750.4145	375.7109	733.3879	367.1976	732.4039	366.7056	6
12	1159.6834	580.3453	1141.6728	571.3400	E	**651.3461**	326.1767	634.3195	317.6634	633.3355	317.1714	5
13	1246.7154	***623.8613***	1228.7048	614.8561	S	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
14	1359.7995	***680.4034***	1341.7889	671.3981	L	435.2714	218.1394	418.2449	209.6261			3
15	1506.8679	753.9376	1488.8573	744.9323	F	**322.1874**	161.5973	305.1608	153.0840			2
16					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 568 ppm



RMS error 568 ppm

AT3G58610.1

NCBI **BLAST** search of GILLGAVHGIVESLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.1	1679.9723	-0.0004	GILLGAVHGIVESLFR
2.9	1679.9722	-0.0004	VLHNYANILELLLR

Mascot: http://www.matrixscience.com/

AT3G58660.1

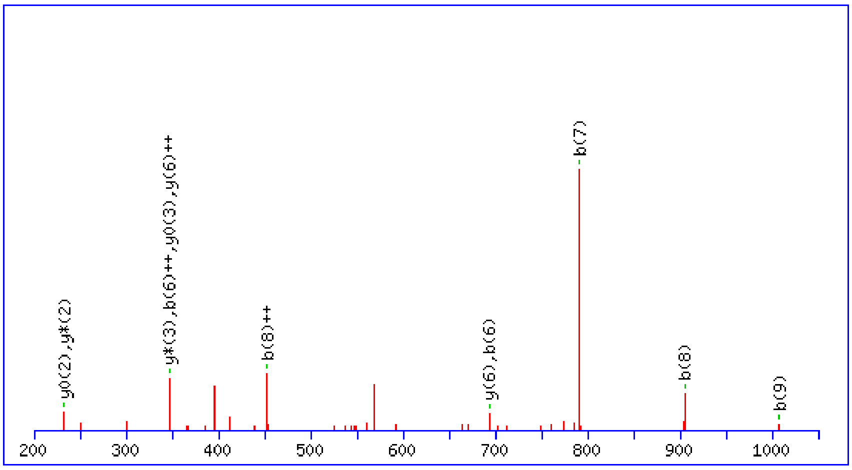
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IKSENIPITK**
Found in **AT3G58660.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein-related | chr3:21712551-21713891 FORWARD

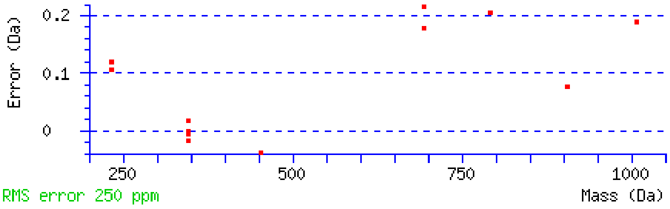
Match to Query 3849: 1154.628682 from(578.321617,2+) index(7401)
Title: Elution from: 65.618 to 65.618 scan no 9698 cid35.00 polarity:+
Data file D12h-3_2.mgf

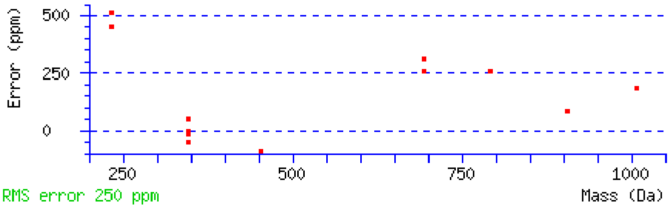
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.6321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0018
Matches : 12/100 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							10
2	245.1774	123.0923	227.1538	114.0805			K	1041.5583	521.2828	1023.5347	512.2710	1023.5477	512.2775	9
3	333.2065	167.1069	315.1829	158.0951	315.1959	158.1016	S	911.4693	456.2383	893.4457	447.2265	893.4587	447.2330	8
4	463.2461	232.1267	445.2225	223.1149	445.2355	223.1214	E	823.4402	412.2237	805.4166	403.2120	805.4296	403.2185	7
5	579.2831	290.1452	561.2595	281.1334	561.2725	281.1399	N	693.4006	347.2039	675.3770	338.1921	675.3900	338.1986	6
6	***693.3642***	**347.1857**	675.3406	338.1739	675.3536	338.1805	I	577.3636	289.1854	559.3400	280.1736	559.3530	280.1801	5
7	***791.4140***	396.2106	773.3904	387.1988	773.4034	387.2054	P	463.2825	232.1449	445.2589	223.1331	445.2719	223.1396	4
8	***905.4951***	**453.2512**	887.4715	444.2394	887.4845	444.2459	I	365.2327	183.1200	347.2091	174.1082	347.2221	174.1147	3
9	***1007.5398***	504.2735	989.5162	495.2617	989.5292	495.2683	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IKSENIPITK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G58660.1

33.5	1154.6321	-0.0035	IKSENIPITK
10.9	1154.6321	-0.0034	TLKELVPNTK
2.6	1154.6321	-0.0034	VPEGSKSVLVK

AT3G58790.1

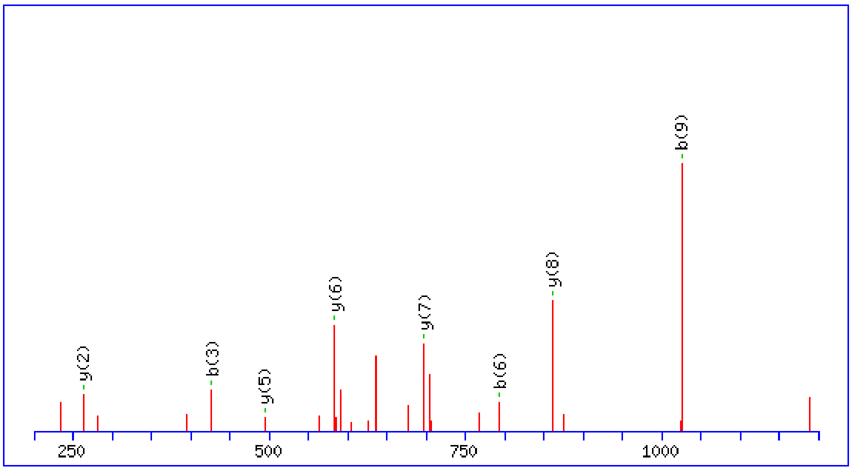
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKFYISATGIK**
Found in **AT3G58790.1** in **TAIR_Arabidopsis**, Symbols: GAUT15 | GAUT15 (Galacturonosyltransferase 15); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr3:21753432-21756949 REVERSE

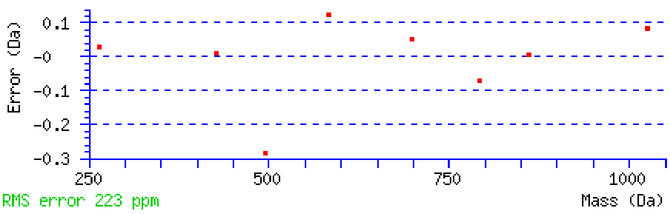
Match to Query 4581: 1286.633872 from(644.324212,2+) index(7875)
Title: Elution from: 70.246 to 70.246 scan no 10414 cid35.00 polarity:+
Data file D6h-1_3.mgf

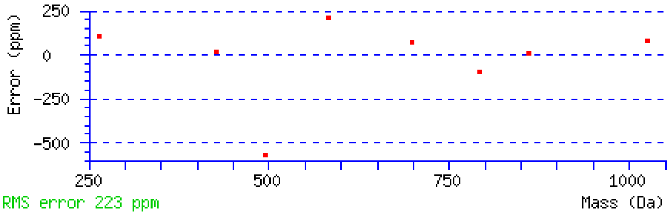
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1286.6355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 43 **Expect:** 0.0003
Matches : 8/150 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							11
2	279.1287	140.0680	261.1052	131.0562			K	1139.6103	570.3088	1121.5868	561.2970	1121.5998	561.3035	10
3	**427.1942**	214.1007	409.1706	205.0889			F	1009.5213	505.2643	991.4977	496.2525	991.5107	496.2590	9
4	591.2546	296.1309	573.2310	287.1191			Y	***861.4559***	431.2316	843.4323	422.2198	843.4453	422.2263	8
5	705.3357	353.1715	687.3121	344.1597			I	***697.3955***	349.2014	679.3719	340.1896	679.3849	340.1961	7
6	**793.3647**	397.1860	775.3411	388.1742	775.3542	388.1807	S	***583.3144***	292.1608	565.2908	283.1490	565.3038	283.1556	6
7	865.3989	433.2031	847.3753	424.1913	847.3883	424.1978	A	***495.2853***	248.1463	477.2617	239.1345	477.2748	239.1410	5
8	967.4436	484.2254	949.4200	475.2136	949.4330	475.2201	T	423.2512	212.1292	405.2276	203.1174	405.2406	203.1239	4
9	**1025.4621**	513.2347	1007.4385	504.2229	1007.4515	504.2294	G	321.2065	161.1069	303.1829	152.0951			3
10	1139.5432	570.2752	1121.5196	561.2634	1121.5326	561.2699	I	***263.1880***	132.0976	245.1644	123.0858			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MKFYISATGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G58790.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.4	1286.6355	-0.0016	MKFYISATGIK
3.8	1286.6359	-0.0021	MINDAHIKKGK
3.6	1286.6303	0.0035	IKRTTSYSASR
1.7	1286.6321	0.0017	NVYSLGAYFIK

AT3G59080.1

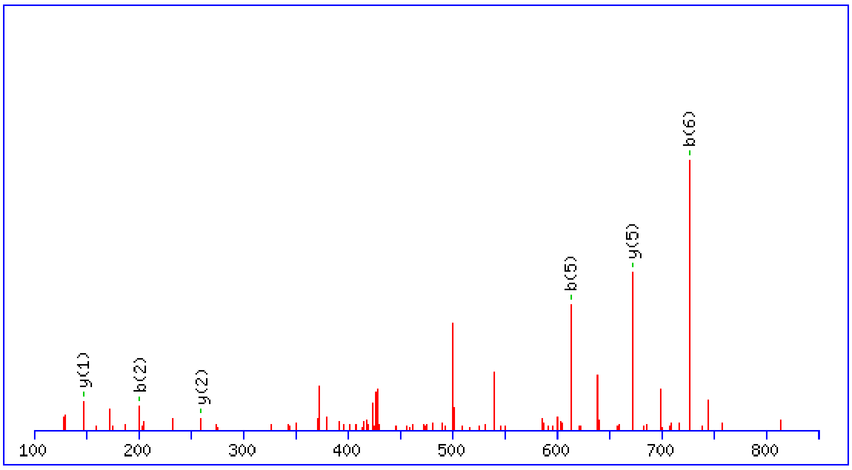
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVKFHLK**
Found in **AT3G59080.1** in **TAIR_Arabidopsis**, Symbols: | aspartyl protease family protein | chr3:21847789-21849396 FORWARD

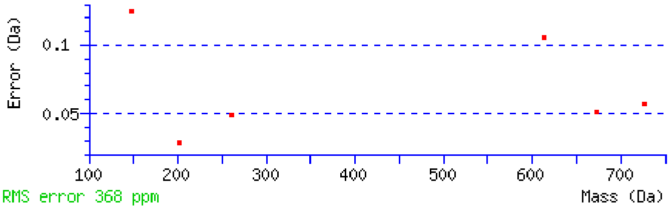
Match to Query 1377: 871.527594 from(436.771073,2+) index(1938)
Title: Elution from: 22.720 to 22.720 scan no 2491 cid35.00 polarity:+
Data file D6h-3_2.mgf

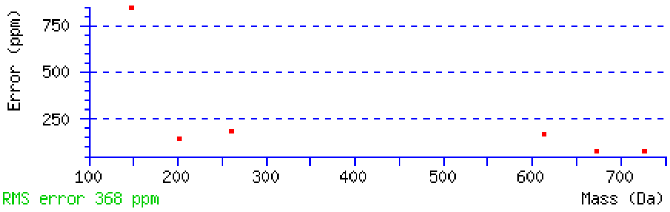
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 871.5280
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.046
Matches : 6/56 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					7
2	***201.1234***	101.0653			183.1128	92.0600	V	771.4876	386.2474	754.4610	377.7341	6
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	K	***672.4192***	336.7132	655.3926	328.1999	5
4	476.2867	238.6470	459.2602	230.1337	458.2762	229.6417	F	544.3242	272.6657	527.2976	264.1525	4
5	***613.3457***	307.1765	596.3191	298.6632	595.3351	298.1712	H	397.2558	199.1315	380.2292	190.6183	3
6	***726.4297***	363.7185	709.4032	355.2052	708.4192	354.7132	L	***260.1969***	130.6021	243.1703	122.0888	2
7							K	***147.1128***	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of TVKFHLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.2	871.5280	-0.0004	TVKFHLK
9.2	871.5279	-0.0003	YHKLALK
8.5	871.5280	-0.0004	IQGWKLK

AT3G59080.1

8.5	871.5280	-0.0004	LFSKHLK
8.5	871.5280	-0.0004	LWGQKLK
8.5	871.5279	-0.0003	YLHKALK
5.6	871.5280	-0.0004	KWIQAVK

AT3G59400.1

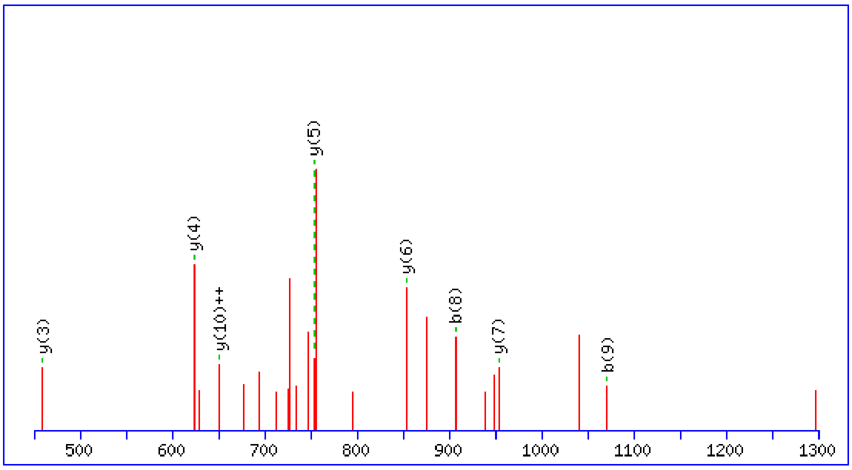
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDTEVVQYNYR**
Found in **AT3G59400.1** in **TAIR_Arabidopsis**, Symbols: GUN4 | GUN4 (Genomes uncoupled 4) | chr3:21959858-21960655 REVERSE

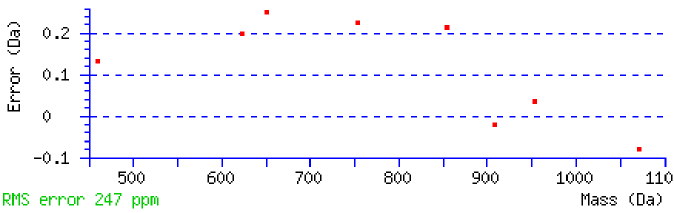
Match to Query 6360: 1528.709824 from(765.362188,2+) index(5697)
Title: Elution from: 50.484 to 50.484 scan no 7241 cid35.00 polarity:+
Data file D12h-1_3.mgf

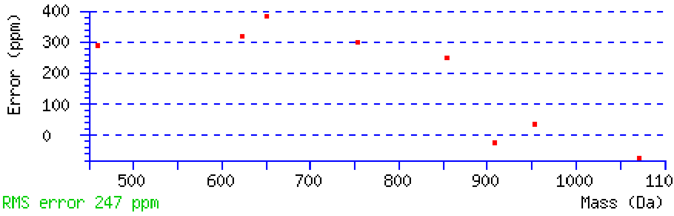
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1528.7116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.024
Matches : 8/100 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							12
2	229.1695	115.0884					L	1415.6378	708.3225	1397.6142	699.3107	1397.6272	699.3172	11
3	345.1935	173.1004			327.1829	164.0951	D	1301.5567	651.2820	1283.5331	642.2702	1283.5461	642.2767	10
4	447.2382	224.1227			429.2276	215.1174	T	1185.5327	593.2700	1167.5091	584.2582	1167.5221	584.2647	9
5	577.2778	289.1425			559.2672	280.1373	E	1083.4880	542.2476	1065.4644	533.2358	1065.4774	533.2424	8
6	677.3432	339.1753			659.3327	330.1700	V	***953.4484***	477.2278	935.4248	468.2160			7
7	777.4087	389.2080			759.3981	380.2027	V	***853.3829***	427.1951	835.3593	418.1833			6
8	**907.4613**	454.2343	889.4378	445.2225	889.4508	445.2290	Q	***753.3175***	377.1624	735.2939	368.1506			5
9	**1071.5217**	536.2645	1053.4981	527.2527	1053.5111	527.2592	Y	***623.2648***	312.1360	605.2412	303.1243			4
10	1187.5587	594.2830	1169.5351	585.2712	1169.5481	585.2777	N	***459.2045***	230.1059	441.1809	221.0941			3
11	1351.6191	676.3132	1333.5955	667.3014	1333.6085	667.3079	Y	343.1675	172.0874	325.1439	163.0756			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LLDTEVVQYNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G59400.1

Score	Mr(calc)	Delta	Sequence
25.1	1528.7116	-0.0018	LLDTEVVQYNYR
0.5	1528.7068	0.0030	NPVTGMRFFLEGK

AT3G59760.1

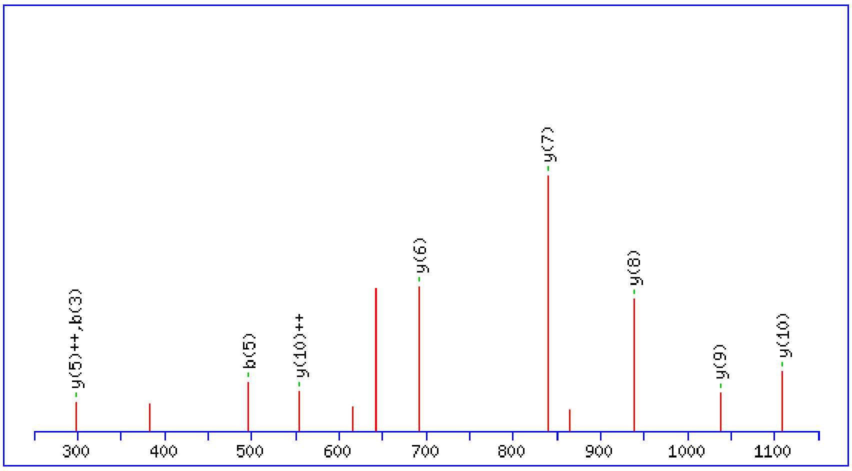
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIAVVFPSFGER**
Found in **AT3G59760.1** in **TAIR_Arabidopsis**, Symbols: ATCS-C, OASC | OASC (O-ACETYLSERINE (THIOL) LYASE ISOFORM C); cysteine synthase | chr3:22083096-22086322 REVERSE

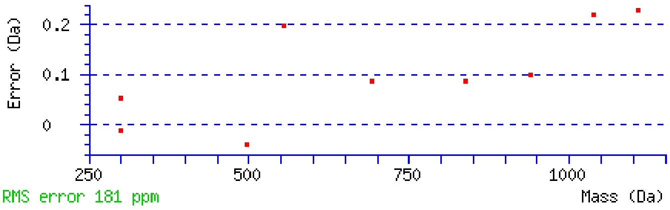
Match to Query 5349: 1333.738646 from(667.876599,2+) index(9693)
Title: Elution from: 86.236 to 86.236 scan no 12997 cid35.00 polarity:+
Data file D12h-1_1.mgf

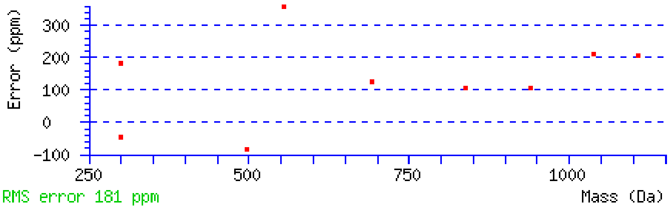
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1333.7394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 6.2e-005
Matches : 9/94 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							12
2	227.1754	114.0913			I	1221.6626	611.3350	1204.6361	602.8217	1203.6521	602.3297	11
3	**298.2125**	149.6099			A	***1108.5786***	554.7929	1091.5520	546.2796	1090.5680	545.7876	10
4	397.2809	199.1441			V	***1037.5415***	519.2744	1020.5149	510.7611	1019.5309	510.2691	9
5	**496.3493**	248.6783			V	***938.4730***	469.7402	921.4465	461.2269	920.4625	460.7349	8
6	643.4178	322.2125			F	***839.4046***	420.2060	822.3781	411.6927	821.3941	411.2007	7
7	740.4705	370.7389			P	***692.3362***	346.6717	675.3097	338.1585	674.3257	337.6665	6
8	827.5026	414.2549	809.4920	405.2496	S	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	5
9	974.5710	487.7891	956.5604	478.7838	F	508.2514	254.6293	491.2249	246.1161	490.2409	245.6241	4
10	1031.5924	516.2999	1013.5819	507.2946	G	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
11	1160.6350	580.8211	1142.6245	571.8159	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LIAVVFPSFGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G59760.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.5	1333.7394	-0.0008	LIAVVFPSFGER
7.5	1333.7354	0.0032	LNRGLSVVDSFK
3.3	1333.7363	0.0024	MRIMIKGGVWK
3.3	1333.7363	0.0024	MRIMIKGGVWK

AT3G59770.1

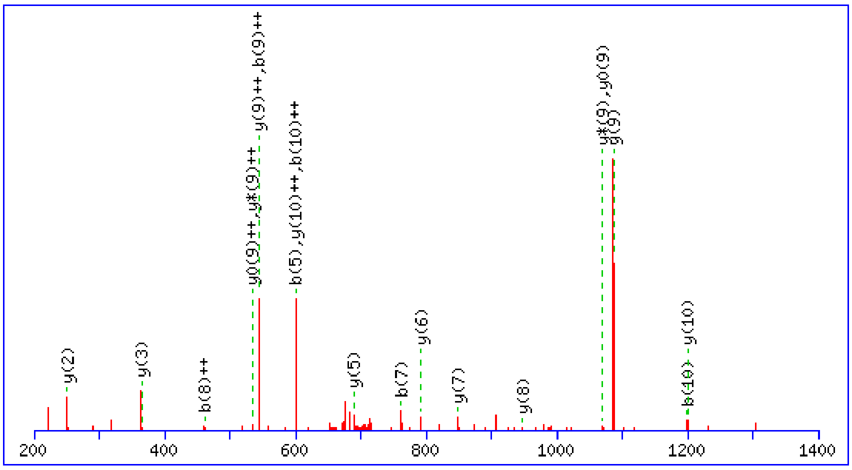
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SRLHPGTRYLAR**
Found in **AT3G59770.1** in **TAIR_Arabidopsis**, Symbols: SAC9 | SAC9 (suppressor of actin 9) | chr3:22090258-22096651 REVERSE

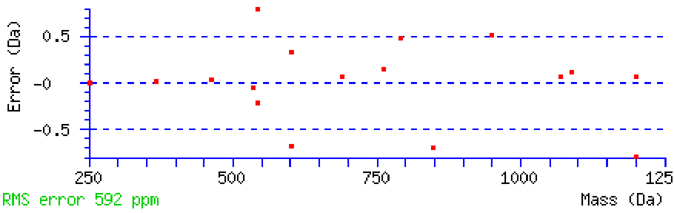
Match to Query 5560: 1448.731424 from(725.372988,2+) index(8182)
Title: Elution from: 73.270 to 73.270 scan no 10880 cid35.00 polarity:+
Data file C7-1_3.mgf

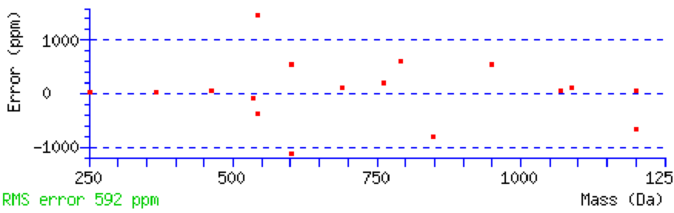
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1448.7271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0025
Matches : 20/120 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	249.1256	125.0664	231.1020	116.0546	231.1150	116.0612	R	1361.7053	681.3563	1343.6817	672.3445	1343.6948	672.3510	11
3	363.2067	182.1070	345.1831	173.0952	345.1961	173.1017	L	***1201.6161***	601.3117	1183.5925	592.2999	1183.6055	592.3064	10
4	503.2567	252.1320	485.2331	243.1202	485.2461	243.1267	H	***1087.5350***	544.2711	1069.5114	535.2593	1069.5244	535.2658	9
5	**601.3065**	301.1569	583.2829	292.1451	583.2959	292.1516	P	***947.4850***	474.2461	929.4614	465.2343	929.4744	465.2408	8
6	659.3250	330.1661	641.3014	321.1543	641.3144	321.1609	G	***849.4352***	425.2212	831.4116	416.2094	831.4246	416.2159	7
7	**761.3697**	381.1885	743.3461	372.1767	743.3592	372.1832	T	***791.4167***	396.2120	773.3931	387.2002	773.4061	387.2067	6
8	921.4590	**461.2331**	903.4354	452.2213	903.4484	452.2278	R	***689.3720***	345.1896	671.3484	336.1778			5
9	1085.5193	**543.2633**	1067.4957	534.2515	1067.5088	534.2580	Y	529.2827	265.1450	511.2591	256.1332			4
10	**1199.6004**	**600.3039**	1181.5768	591.2921	1181.5899	591.2986	L	***365.2223***	183.1148	347.1988	174.1030			3
11	1271.6346	636.3209	1253.6110	627.3091	1253.6240	627.3156	A	***251.1412***	126.0743	233.1177	117.0625			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SRLHPGTRYLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G59770.1

Score	Mr(calc)	Delta	Sequence
35.2	1448.7271	0.0043	SRLHPGTRYLAR
2.7	1448.7355	-0.0041	EMVSKKEDLLVK
2.7	1448.7321	-0.0007	LYVTNQEDIIVK
1.1	1448.7348	-0.0034	DHNLPGTLPQIVK

AT3G59920.1

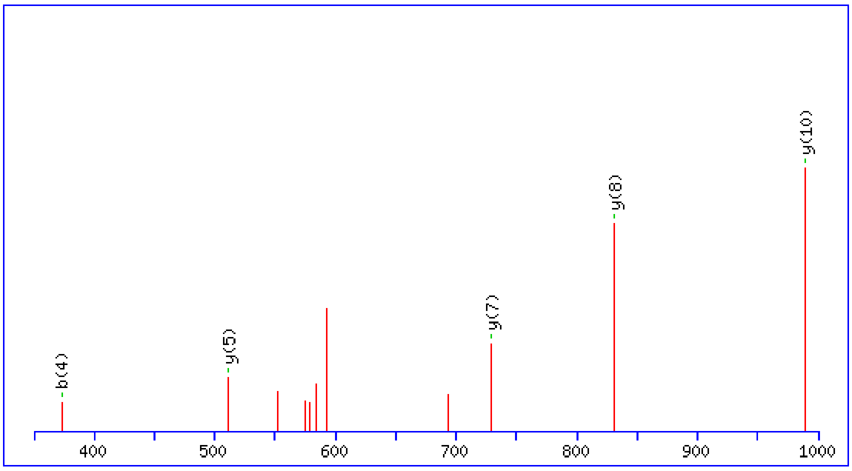
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIGVTSEGETAK**
Found in **AT3G59920.1** in **TAIR_Arabidopsis**, Symbols: ATGDI2 | ATGDI2 (RAB GDP DISSOCIATION INHIBITOR 2); RAB GDP-dissociation inhibitor | chr3:22146134-22149198 FORWARD

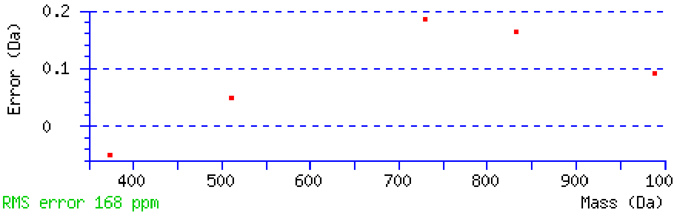
Match to Query 4442: 1202.580920 from(602.297736,2+) index(1361)
Title: Elution from: 19.106 to 19.106 scan no 1865 cid35.00 polarity:+
Data file D6h-1_1.mgf

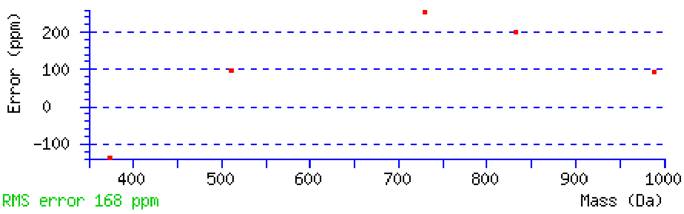
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1202.5805
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0046
Matches : 5/98 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400			V							12
2	215.1538	108.0805			I	1103.5223	552.2648	1085.4987	543.2530	1085.5117	543.2595	11
3	273.1723	137.0898			G	***989.4412***	495.2242	971.4176	486.2125	971.4307	486.2190	10
4	373.2378	187.1225			V	931.4227	466.2150	913.3991	457.2032	913.4122	457.2097	9
5	475.2825	238.1449	457.2719	229.1396	T	***831.3573***	416.1823	813.3337	407.1705	813.3467	407.1770	8
6	563.3115	282.1594	545.3010	273.1541	S	***729.3126***	365.1599	711.2890	356.1481	711.3020	356.1546	7
7	693.3512	347.1792	675.3406	338.1739	E	641.2835	321.1454	623.2599	312.1336	623.2729	312.1401	6
8	751.3697	376.1885	733.3591	367.1832	G	***511.2439***	256.1256	493.2203	247.1138	493.2333	247.1203	5
9	881.4093	441.2083	863.3987	432.2030	E	453.2254	227.1163	435.2018	218.1045	435.2148	218.1110	4
10	983.4540	492.2306	965.4435	483.2254	T	323.1857	162.0965	305.1622	153.0847	305.1752	153.0912	3
11	1055.4882	528.2477	1037.4776	519.2424	A	221.1410	111.0741	203.1174	102.0624			2
12					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VIGVTSEGETAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G59920.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.8	1202.5805	0.0005	VIGVTSEGETAK
4.9	1202.5827	-0.0018	DPKEFLSLDK
0.5	1202.5832	-0.0023	NRSEGSSLLPK

AT3G59970.3

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDSPAIGWGGPGGYVYQK**
Found in **AT3G59970.3** in **TAIR_Arabidopsis**, Symbols: MTHFR1 | MTHFR1 (METHYLENETETRAHYDROFOLATE REDUCTASE 1); methylenetetrahydrofolate reductase (NADPH) | chr3:22162280-22165300 FORWARD

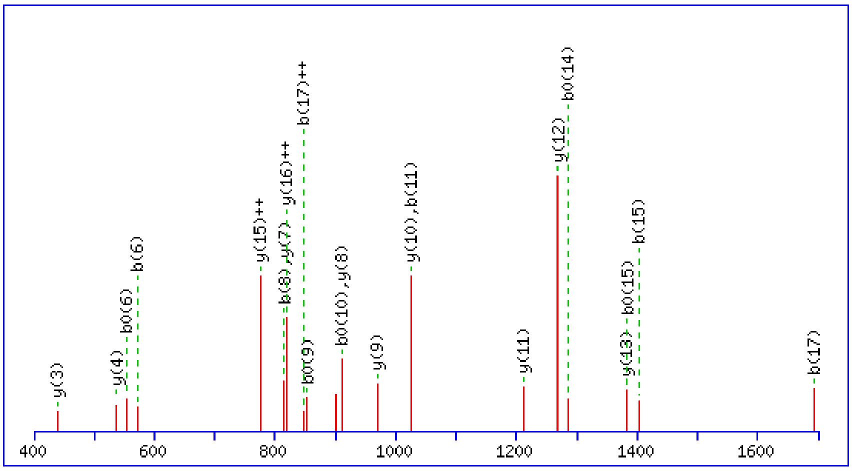
Match to Query 9178: 1837.861716 from(919.938134,2+) index(6962)
Title: Elution from: 60.567 to 60.567 scan no 8834 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

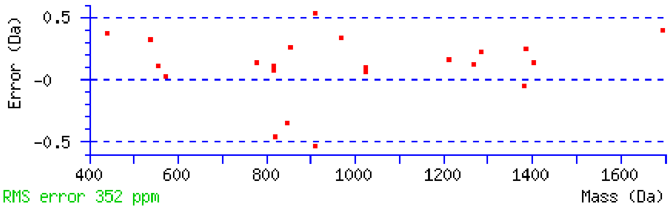
Show Y-axis ☐

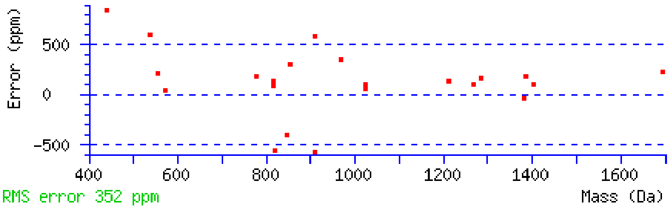


Monoisotopic mass of neutral peptide Mr(calc): 1837.8635
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 5.3e-009
Matches : 22/142 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							18
2	203.0662	102.0368			185.0557	93.0315	D	1751.8388	876.4230	1734.8122	867.9097	1733.8282	867.4177	17
3	290.0983	145.5528			272.0877	136.5475	S	1636.8118	818.9095	1619.7853	810.3963	1618.8013	809.9043	16
4	387.1510	194.0792			369.1405	185.0739	P	1549.7798	775.3935	1532.7532	766.8803			15
5	458.1882	229.5977			440.1776	220.5924	A	1452.7270	726.8672	1435.7005	718.3539			14
6	**571.2722**	286.1397			553.2617	277.1345	I	***1381.6899***	691.3486	1364.6634	682.8353			13
7	628.2937	314.6505			610.2831	305.6452	G	***1268.6059***	634.8066	1251.5793	626.2933			12
8	**814.3730**	407.6901			796.3624	398.6849	W	***1211.5844***	606.2958	1194.5578	597.7826			11
9	871.3945	436.2009			853.3839	427.1956	G	***1025.5051***	513.2562	1008.4785	504.7429			10
10	928.4159	464.7116			910.4054	455.7063	G	***968.4836***	484.7454	951.4571	476.2322			9
11	**1025.4687**	513.2380			1007.4581	504.2327	P	***911.4621***	456.2347	894.4356	447.7214			8
12	1082.4902	541.7487			1064.4796	532.7434	G	***814.4094***	407.7083	797.3828	399.1951			7
13	1139.5116	570.2594			1121.5010	561.2542	G	757.3879	379.1976	740.3614	370.6843			6
14	1302.5749	651.7911			1284.5644	642.7858	Y	700.3665	350.6869	683.3399	342.1736			5
15	**1401.6434**	701.3253			1383.6328	692.3200	V	***537.3031***	269.1552	520.2766	260.6419			4
16	1564.7067	782.8570			1546.6961	773.8517	Y	***438.2347***	219.6210	421.2082	211.1077			3
17	**1692.7653**	846.8863	1675.7387	838.3730	1674.7547	837.8810	Q	275.1714	138.0893	258.1448	129.5761			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT3G59970.3





NCBI **BLAST** search of SDSPAIGWGGPGGYVYQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
87.4	1837.8635	-0.0018	SDSPAIGWGGPGGYVYQK
8.1	1837.8595	0.0022	GNLGNGDITSDGYHKYK
5.0	1837.8588	0.0029	NKNVDQSCSTSKQQSK
4.8	1837.8653	-0.0036	ELKSSEDGDLGSSSSRGK
1.9	1837.8669	-0.0052	MASASFSAVSSLSYQFR
0.3	1837.8628	-0.0011	VNGENNSNVYELMIRA

Mascot: http://www.matrixscience.com/

AT3G60240.2

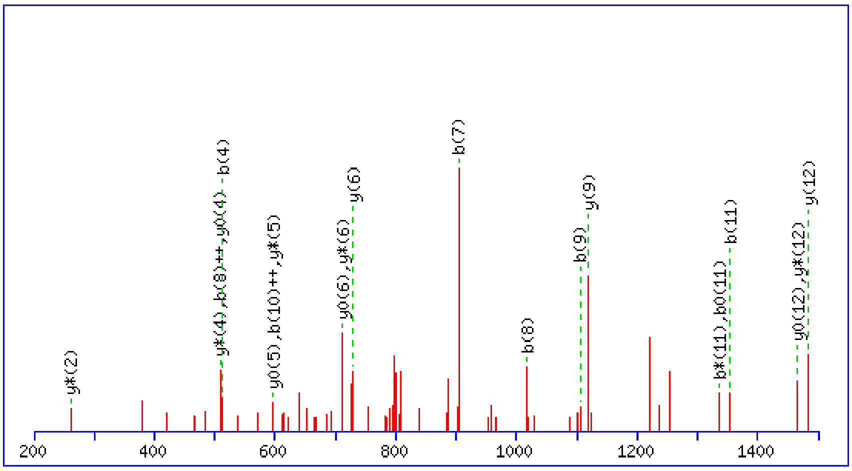
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLSCKQELSSRVR**
Found in **AT3G60240.2** in **TAIR_Arabidopsis**, Symbols: CUM2, EIF4G | EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G) | chr3:22272817-22279270 FORWARD

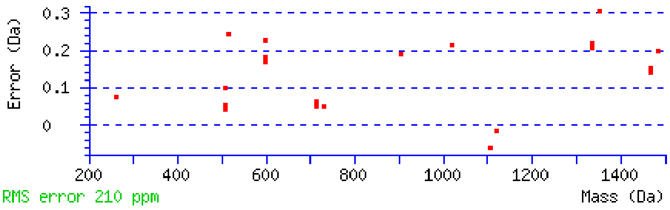
Match to Query 6966: 1630.744066 from(816.379309,2+) index(6250)
Title: Elution from: 59.154 to 59.154 scan no 8194 cid35.00 polarity:+
Data file D1d-1-2.mgf

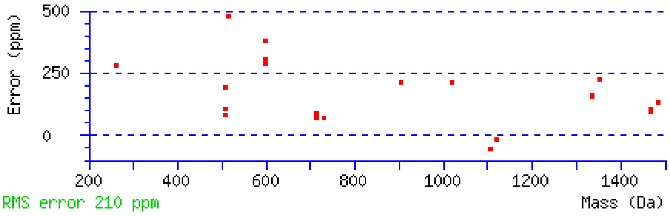
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1630.7424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 0.01
Matches : 21/186 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							13
2	263.1208	132.0640					L	**1483.7172**	742.3622	1465.6936	733.3504	1465.7066	733.3570	12
3	351.1499	176.0786			333.1393	167.0733	S	1369.6361	685.3217	1351.6125	676.3099	1351.6255	676.3164	11
4	***513.1746***	257.0909			495.1640	248.0857	C	1281.6070	641.3072	1263.5835	632.2954	1263.5965	632.3019	10
5	643.2636	322.1354	625.2400	313.1237	625.2531	313.1302	K	**1119.5823**	560.2948	1101.5587	551.2830	1101.5718	551.2895	9
6	773.3163	387.1618	755.2927	378.1500	755.3057	378.1565	Q	989.4933	495.2503	971.4697	486.2385	971.4827	486.2450	8
7	***903.3559***	452.1816	885.3323	443.1698	885.3453	443.1763	E	859.4406	430.2240	841.4171	421.2122	841.4301	421.2187	7
8	***1017.4370***	**509.2221**	999.4134	500.2103	999.4264	500.2169	L	**729.4010**	365.2041	711.3774	356.1924	711.3905	356.1989	6
9	***1105.4661***	553.2367	1087.4425	544.2249	1087.4555	544.2314	S	615.3199	308.1636	597.2963	299.1518	597.3094	299.1583	5
10	1193.4951	**597.2512**	1175.4715	588.2394	1175.4846	588.2459	S	527.2909	264.1491	509.2673	255.1373	509.2803	255.1438	4
11	***1353.5844***	677.2958	1335.5608	668.2840	1335.5738	668.2905	R	439.2618	220.1345	421.2382	211.1227			3
12	1453.6498	727.3285	1435.6262	718.3168	1435.6393	718.3233	V	279.1725	140.0899	261.1490	131.0781			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MLSCKQELSSRVR

AT3G60240.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.0	1630.7424	0.0017	MLSCKQELSSRVR
22.0	1630.7489	-0.0048	VYLEQDDFVKTMK
21.0	1630.7410	0.0030	FGETSKNELTTSATK
6.4	1630.7437	0.0004	GSSFETIDIATSARR
3.7	1630.7435	0.0006	FVHPNIDHMIFNK
0.4	1630.7430	0.0011	FDEIMKWFLGWK

AT3G60380.1

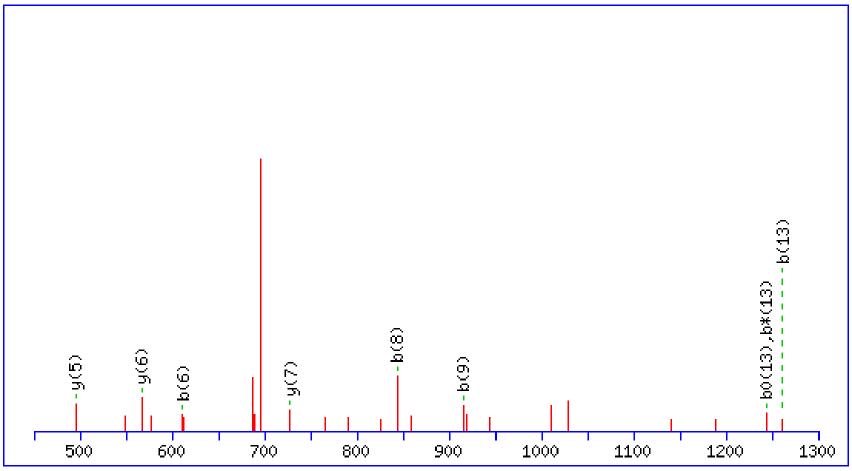
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDESVSARASVVGK**
Found in **AT3G60380.1** in **TAIR_Arabidopsis**, Symbols: | similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT4G16790.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70557.1) | chr3:22327888-22330119 REVERSE

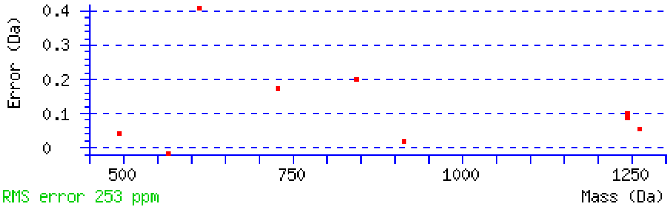
Match to Query 5077: 1408.649368 from(705.331960,2+) index(3175)
Title: Elution from: 32.155 to 32.155 scan no 4021 cid35.00 polarity:+
Data file D1d-2_3.mgf

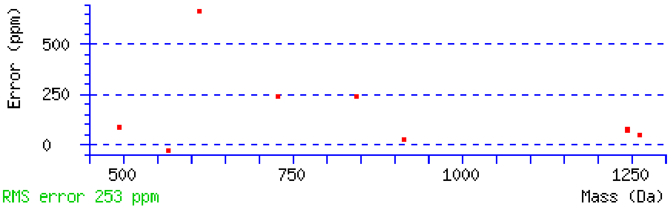
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1408.6518
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.043
Matches : 9/134 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							14
2	205.0603	103.0338			187.0498	94.0285	D	1321.6301	661.3187	1303.6065	652.3069	1303.6195	652.3134	13
3	335.0999	168.0536			317.0894	159.0483	E	1205.6061	603.3067	1187.5825	594.2949	1187.5955	594.3014	12
4	423.1290	212.0681			405.1184	203.0629	S	1075.5665	538.2869	1057.5429	529.2751	1057.5559	529.2816	11
5	523.1945	262.1009			505.1839	253.0956	V	987.5374	494.2723	969.5138	485.2605	969.5268	485.2671	10
6	***611.2235***	306.1154			593.2130	297.1101	S	887.4719	444.2396	869.4484	435.2278	869.4614	435.2343	9
7	683.2577	342.1325			665.2471	333.1272	A	799.4429	400.2251	781.4193	391.2133	781.4323	391.2198	8
8	***843.3469***	422.1771	825.3233	413.1653	825.3364	413.1718	R	***727.4087***	364.2080	709.3851	355.1962	709.3982	355.2027	7
9	***915.3811***	458.1942	897.3575	449.1824	897.3705	449.1889	A	***567.3195***	284.1634	549.2959	275.1516	549.3089	275.1581	6
10	1003.4101	502.2087	985.3865	493.1969	985.3996	493.2034	S	***495.2853***	248.1463	477.2617	239.1345	477.2748	239.1410	5
11	1103.4756	552.2414	1085.4520	543.2296	1085.4650	543.2361	V	407.2563	204.1318	389.2327	195.1200			4
12	1203.5410	602.2742	1185.5174	593.2624	1185.5305	593.2689	V	307.1908	154.0990	289.1672	145.0873			3
13	***1261.5595***	631.2834	1243.5359	622.2716	1243.5490	622.2781	G	207.1254	104.0663	189.1018	95.0545			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SDESVSARASVVGK

AT3G60380.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.4	1408.6518	-0.0025	SDESVSARASVVGK
16.9	1408.6514	-0.0020	KSYILDAEVDDK
13.3	1408.6467	0.0027	SICEAAKVEYPK
11.1	1408.6527	-0.0033	TMTHRMILTQK
10.8	1408.6471	0.0023	MASPRVVSEDRK
10.0	1408.6516	-0.0022	FTEKHFCKAPK
8.8	1408.6494	0.0000	ETMNRALNLWK
7.7	1408.6514	-0.0021	SSVESSVIPSFEK
7.3	1408.6518	-0.0025	TREASQTETLQK
7.3	1408.6516	-0.0022	MQITVAFNHFGK

AT3G60750.1

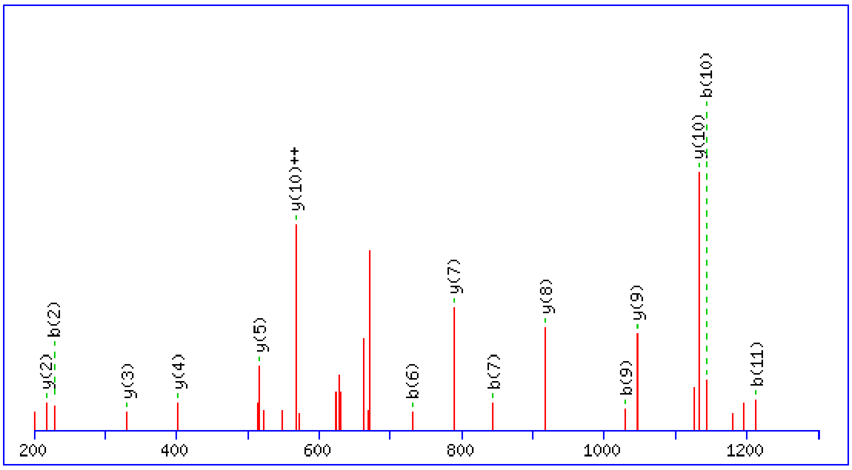
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLSQQCLNALAK**
Found in **AT3G60750.1** in **TAIR_Arabidopsis**, Symbols: | transketolase, putative | chr3:22464979-22467799 FORWARD

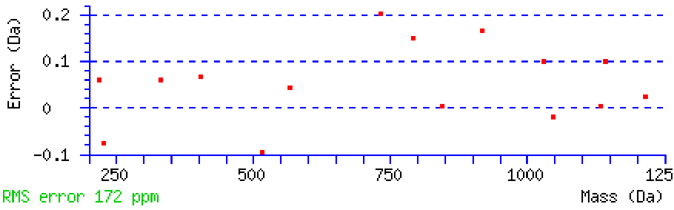
Match to Query 4979: 1358.698836 from(680.356694,2+) index(3811)
Title: Elution from: 35.110 to 35.110 scan no 4730 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

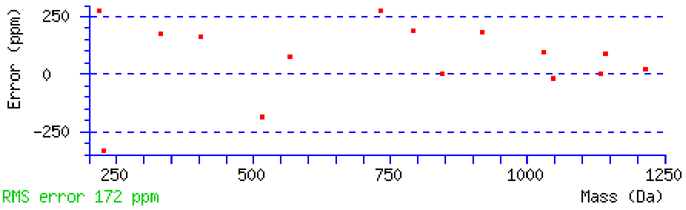


Monoisotopic mass of neutral peptide Mr(calc): 1358.6976
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 6.6e-009
Matches : 15/110 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	***228.1343***	114.5708	211.1077	106.0575			L	1245.6620	623.3346	1228.6354	614.8214	1227.6514	614.3293	11
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	S	***1132.5779***	566.7926	1115.5514	558.2793	1114.5674	557.7873	10
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	Q	***1045.5459***	523.2766	1028.5193	514.7633			9
5	571.2835	286.1454	554.2569	277.6321	553.2729	277.1401	Q	***917.4873***	459.2473	900.4608	450.7340			8
6	***731.3141***	366.1607	714.2876	357.6474	713.3035	357.1554	C	***789.4287***	395.2180	772.4022	386.7047			7
7	***844.3982***	422.7027	827.3716	414.1894	826.3876	413.6974	L	629.3981	315.2027	612.3715	306.6894			6
8	958.4411	479.7242	941.4145	471.2109	940.4305	470.7189	N	***516.3140***	258.6606	499.2875	250.1474			5
9	***1029.4782***	515.2427	1012.4517	506.7295	1011.4676	506.2375	A	***402.2711***	201.6392	385.2445	193.1259			4
10	***1142.5623***	571.7848	1125.5357	563.2715	1124.5517	562.7795	L	***331.2340***	166.1206	314.2074	157.6074			3
11	***1213.5994***	607.3033	1196.5728	598.7901	1195.5888	598.2980	A	***218.1499***	109.5786	201.1234	101.0653			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 172 ppm



RMS error 172 ppm

NCBI **BLAST** search of NLSQQCLNALAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G60750.1

Score	Mr(calc)	Delta	Sequence
87.0	1358.6976	0.0012	NLSQQCLNALAK
1.8	1358.6976	0.0012	QVAELQMERQK
0.2	1358.7023	-0.0035	MMHSVSRLARR
0.2	1358.7023	-0.0035	MMHSVSRLARR

Mascot: http://www.matrixscience.com/

AT3G60770.1

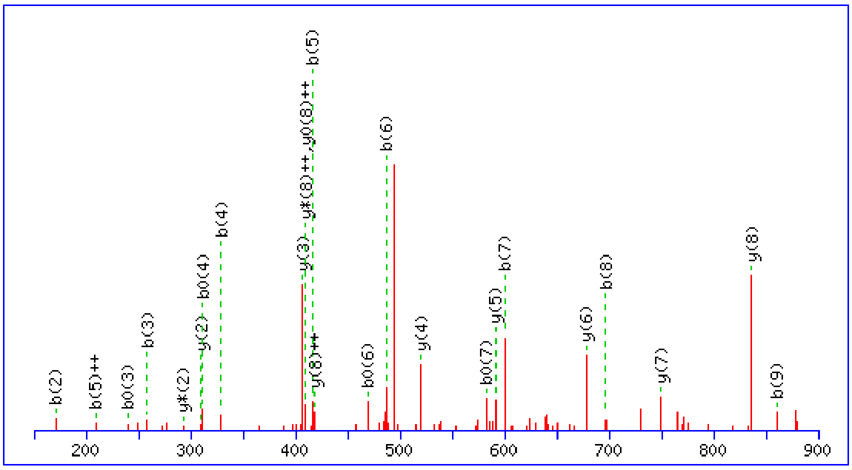
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GISASALPYK**
Found in **AT3G60770.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S13 (RPS13A) | chr3:22471500-22472631 REVERSE

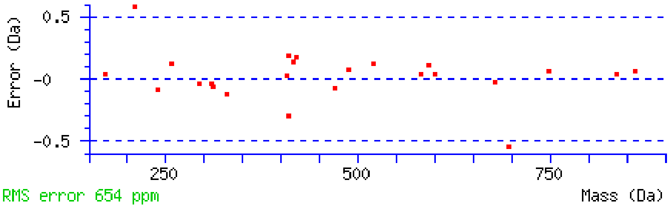
Match to Query 2336: 1005.550358 from(503.782455,2+) index(3300)
Title: Elution from: 31.257 to 31.257 scan no 4065 cid35.00 polarity:+
Data file D6h-3_3.mgf

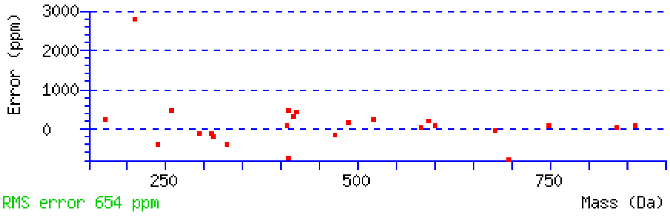
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1005.5495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 4.2e-006
Matches : 24/76 fragment ions using 37 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180			G							10
2	***171.1128***	86.0600			I	949.5353	475.2713	932.5088	466.7580	931.5247	466.2660	9
3	***258.1448***	129.5761	240.1343	120.5708	S	**836.4512**	418.7293	819.4247	410.2160	818.4407	409.7240	8
4	***329.1819***	165.0946	311.1714	156.0893	A	**749.4192**	375.2132	732.3927	366.7000	731.4087	366.2080	7
5	***416.2140***	208.6106	398.2034	199.6053	S	**678.3821**	339.6947	661.3556	331.1814	660.3715	330.6894	6
6	***487.2511***	244.1292	469.2405	235.1239	A	**591.3501**	296.1787	574.3235	287.6654			5
7	***600.3352***	300.6712	582.3246	291.6659	L	**520.3130**	260.6601	503.2864	252.1468			4
8	***697.3879***	349.1976	679.3774	340.1923	P	**407.2289**	204.1181	390.2023	195.6048			3
9	***860.4512***	430.7293	842.4407	421.7240	Y	**310.1761**	155.5917	293.1496	147.0784			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GISASALPYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT3G60770.1

61.3	1005.5495	0.0009	GISASALPYK
11.0	1005.5528	-0.0025	EKAMLALSK
2.4	1005.5495	0.0009	GLDYALLNK
0.2	1005.5495	0.0009	GEVKSVPYK

AT3G60820.1

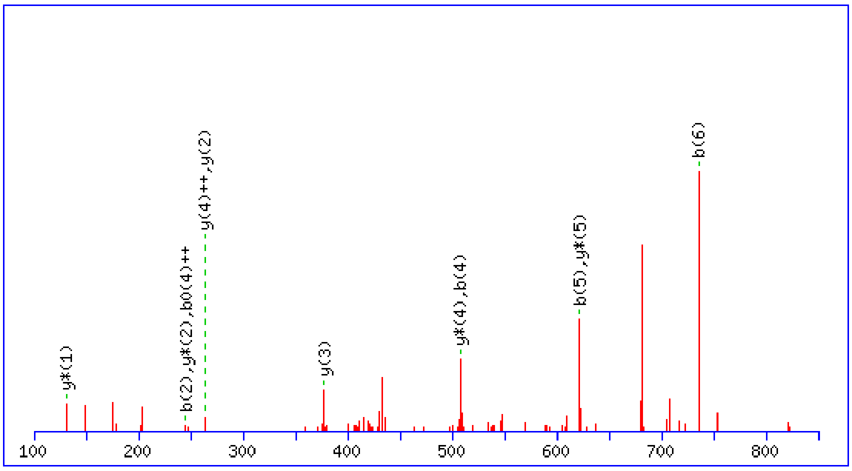
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEIMILK**
Found in **AT3G60820.1** in **TAIR_Arabidopsis**, Symbols: PBF1 | PBF1 (20S proteasome beta subunit F1); peptidase | chr3:22483013-22484784 REVERSE

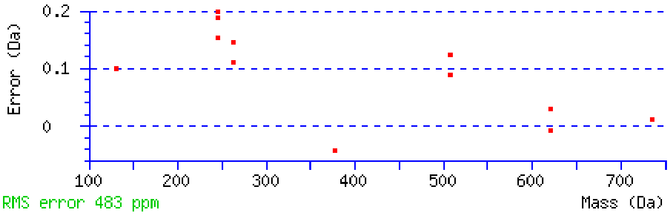
Match to Query 1636: 882.496730 from(442.255641,2+) index(1983)
Title: Elution from: 22.249 to 22.249 scan no 2514 cid35.00 polarity:+
Data file D1d-3_2.mgf

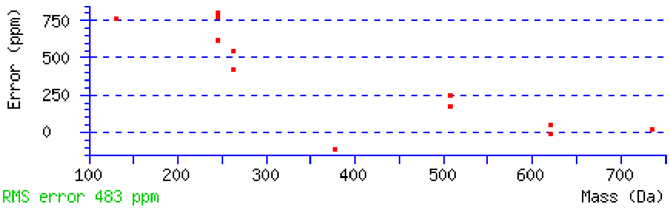
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 882.4961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.011
Matches : 12/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							7
2	***245.1280***	123.0676	227.1174	114.0624	E	769.4222	385.2148	751.3986	376.2030	751.4117	376.2095	6
3	359.2091	180.1082	341.1985	171.1029	I	639.3826	320.1949	621.3590	311.1831			5
4	***507.2415***	254.1244	489.2310	245.1191	M	525.3015	263.1544	507.2779	254.1426			4
5	***621.3226***	311.1650	603.3121	302.1597	I	**377.2691**	189.1382	359.2455	180.1264			3
6	***735.4037***	368.2055	717.3932	359.2002	L	**263.1880**	132.0976	245.1644	123.0858			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LEIMILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.5	882.4961	0.0007	LEIMILK

AT3G60820.1

19.3	882.4954	0.0014	FLLLNPR
12.9	882.4954	0.0014	LFSKHLK
12.9	882.4987	-0.0020	MKPKQIK
12.4	882.4953	0.0014	TVKFHLK
9.2	882.4987	-0.0020	MVLPRIK
8.8	882.4953	0.0014	IQGWKLK
8.4	882.4953	0.0014	KWIQAVK
6.3	882.4953	0.0014	LFLVQPR
1.6	882.4953	0.0014	LWGQKLK

AT3G61440.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLSSVLFDELRK**
Found in **AT3G61440.1** in **TAIR_Arabidopsis**, Symbols: ARATH;BSAS3;1, ATCYSC1 | ATCYSC1 (BETA-SUBSTITUTED ALA SYNTHASE 3;1); L-3-cyanoalanine synthase/ cysteine synthase | chr3:22746860-22748767 FORWARD

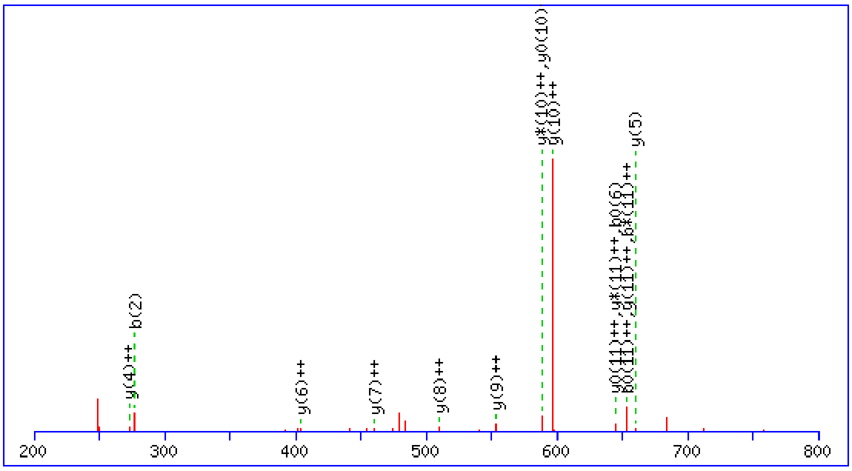
Match to Query 5969: 1468.792986 from(490.604938,3+) index(7817)
Title: Elution from: 70.068 to 70.068 scan no 10227 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 800 Da Full range

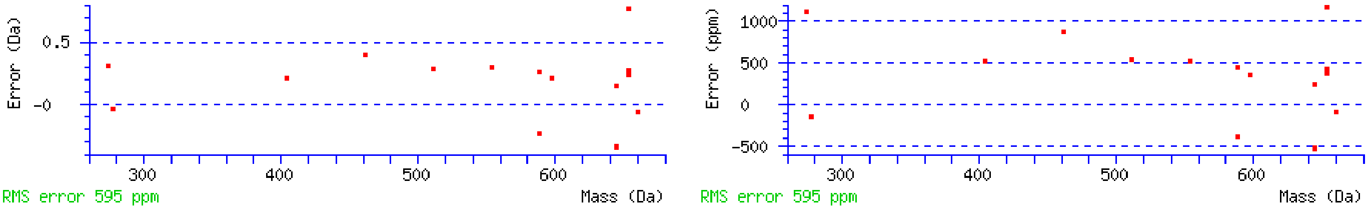
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.7926
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0042
Matches : 16/102 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							12
2	277.1547	139.0810					L	1306.7365	653.8719	1289.7100	645.3586	1288.7260	644.8666	11
3	364.1867	182.5970			346.1761	173.5917	S	1193.6525	597.3299	1176.6259	588.8166	1175.6419	588.3246	10
4	451.2187	226.1130			433.2082	217.1077	S	1106.6204	553.8139	1089.5939	545.3006	1088.6099	544.8086	9
5	550.2871	275.6472			532.2766	266.6419	V	1019.5884	510.2978	1002.5619	501.7846	1001.5778	501.2926	8
6	663.3712	332.1892			645.3606	323.1840	L	920.5200	460.7636	903.4934	452.2504	902.5094	451.7584	7
7	810.4396	405.7234			792.4291	396.7182	F	807.4359	404.2216	790.4094	395.7083	789.4254	395.2163	6
8	925.4666	463.2369			907.4560	454.2316	D	660.3675	330.6874	643.3410	322.1741	642.3569	321.6821	5
9	1054.5092	527.7582			1036.4986	518.7529	E	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	4
10	1167.5932	584.3002			1149.5827	575.2950	L	416.2980	208.6526	399.2714	200.1394			3
11	1323.6943	662.3508	1306.6678	653.8375	1305.6838	653.3455	R	303.2139	152.1106	286.1874	143.5973			2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of YLSSVLFDELRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G61440.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.4	1468.7926	0.0004	YLSSVLFDELRK
15.9	1468.7973	-0.0043	YNPRMNPIIPVR
3.4	1468.7959	-0.0029	MPTQIIKVGEPEK

AT3G61470.1

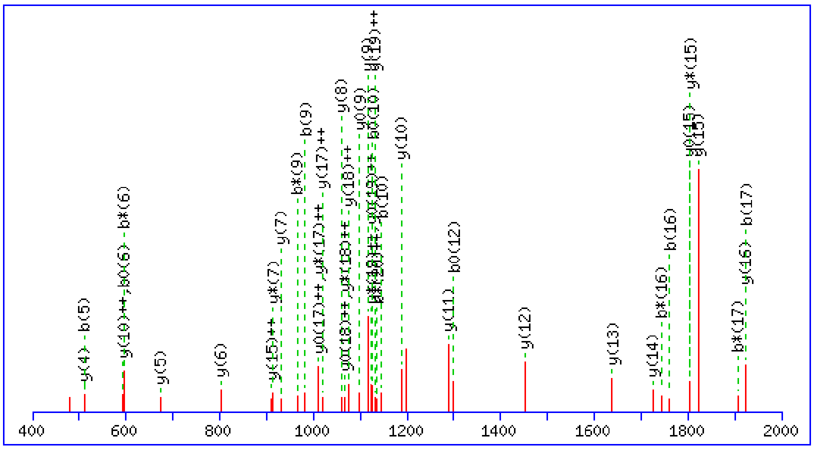
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGILNTPSWYTAGEQEYFTDK**
Found in **AT3G61470.1** in **TAIR_Arabidopsis**, Symbols: LHCA2 | LHCA2 (Photosystem I light harvesting complex gene 2); chlorophyll binding | chr3:22756711-22758007 FORWARD

Match to Query 10123: 2432.146418 from(1217.080485,2+) index(9352)
Title: Elution from: 89.286 to 89.286 scan no 13138 cid35.00 polarity:+
Data file D1d-2_2.mgf

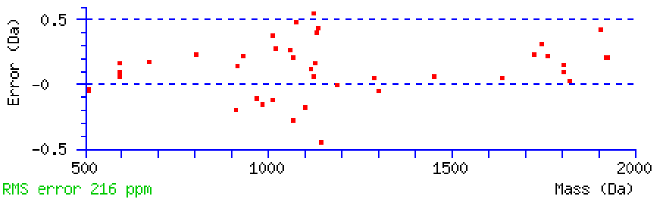
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

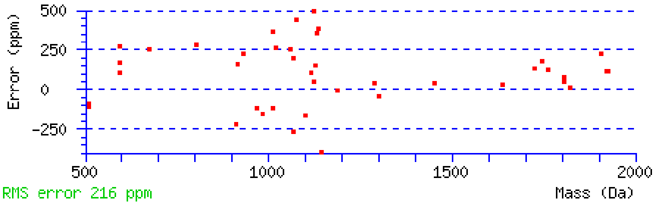


Monoisotopic mass of neutral peptide Mr(calc): 2432.1536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 5.7e-011
Matches : 41/220 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							21
2	171.1128	86.0600					G	2320.0768	1160.5420	2303.0503	1152.0288	2302.0663	1151.5368	20
3	284.1969	142.6021					I	2263.0554	1132.0313	2246.0288	1123.5180	2245.0448	1123.0260	19
4	397.2809	199.1441					L	2149.9713	1075.4893	2132.9447	1066.9760	2131.9607	1066.4840	18
5	**511.3239**	256.1656	494.2973	247.6523			N	2036.8872	1018.9473	2019.8607	1010.4340	2018.8767	1009.9420	17
6	612.3715	306.6894	595.3450	298.1761	594.3610	297.6841	T	***1922.8443***	961.9258	1905.8178	953.4125	1904.8337	952.9205	16
7	709.4243	355.2158	692.3978	346.7025	691.4137	346.2105	P	***1821.7966***	911.4019	1804.7701	902.8887	1803.7861	902.3967	15
8	796.4563	398.7318	779.4298	390.2185	778.4458	389.7265	S	***1724.7439***	862.8756	1707.7173	854.3623	1706.7333	853.8703	14
9	**982.5356**	491.7715	965.5091	483.2582	964.5251	482.7662	W	***1637.7118***	819.3596	1620.6853	810.8463	1619.7013	810.3543	13
10	**1145.5990**	573.3031	1128.5724	564.7898	1127.5884	564.2978	Y	***1451.6325***	726.3199	1434.6060	717.8066	1433.6220	717.3146	12
11	1246.6467	623.8270	1229.6201	615.3137	1228.6361	614.8217	T	***1288.5692***	644.7882	1271.5426	636.2750	1270.5586	635.7830	11
12	1317.6838	659.3455	1300.6572	650.8322	1299.6732	650.3402	A	***1187.5215***	594.2644	1170.4950	585.7511	1169.5109	585.2591	10
13	1374.7052	687.8563	1357.6787	679.3430	1356.6947	678.8510	G	***1116.4844***	558.7458	1099.4578	550.2326	1098.4738	549.7406	9
14	1503.7478	752.3775	1486.7213	743.8643	1485.7373	743.3723	E	***1059.4629***	530.2351	1042.4364	521.7218	1041.4524	521.2298	8
15	1631.8064	816.4068	1614.7799	807.8936	1613.7958	807.4016	Q	***930.4203***	465.7138	913.3938	457.2005	912.4098	456.7085	7
16	**1760.8490**	880.9281	1743.8224	872.4149	1742.8384	871.9229	E	***802.3618***	401.6845	785.3352	393.1712	784.3512	392.6792	6
17	**1923.9123**	962.4598	1906.8858	953.9465	1905.9018	953.4545	Y	***673.3192***	337.1632	656.2926	328.6499	655.3086	328.1579	5
18	2070.9807	1035.9940	2053.9542	1027.4807	2052.9702	1026.9887	F	***510.2558***	255.6316	493.2293	247.1183	492.2453	246.6263	4
19	2172.0284	1086.5178	2155.0019	1078.0046	2154.0178	1077.5126	T	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
20	2287.0554	1144.0313	2270.0288	1135.5180	2269.0448	1135.0260	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT3G61470.1





NCBI **BLAST** search of IGILNTPSWYTAGEQEYFTDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
107.6	2432.1536	-0.0072	IGILNTPSWYTAGEQEYFTDK

Mascot: http://www.matrixscience.com/

AT3G61540.1

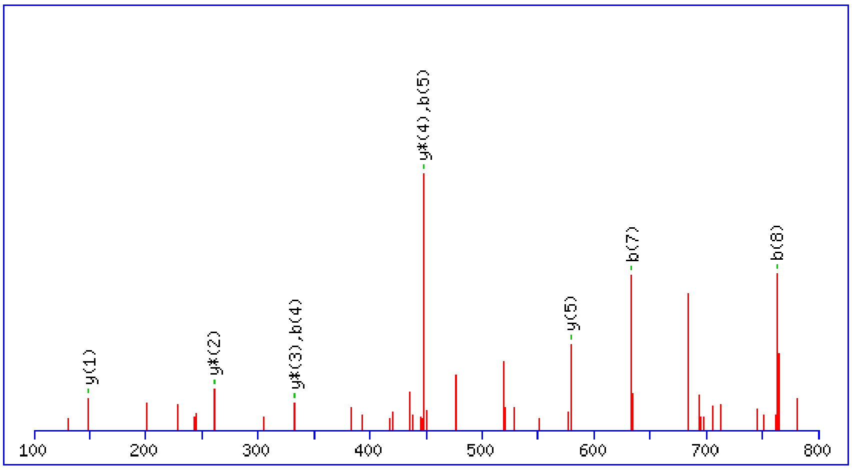
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAADLLAKK**
Found in **AT3G61540.1** in **TAIR_Arabidopsis**, Symbols: | peptidase family protein | chr3:22784374-22786674 FORWARD

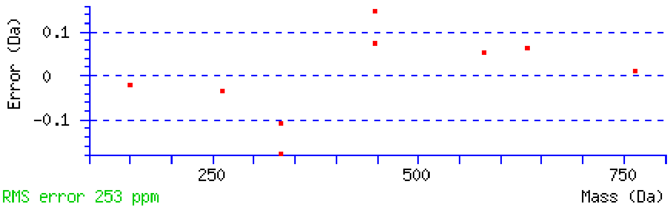
Match to Query 1680: 910.509230 from(456.261891,2+) index(1463)
Title: Elution from: 21.145 to 21.145 scan no 2041 cid35.00 polarity:+
Data file 0-3_1.mgf

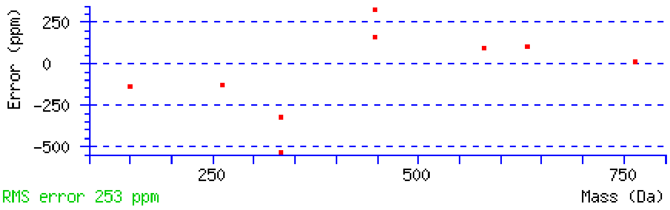
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 910.5114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0012
Matches : 9/66 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							9
2	145.0756	73.0414					A	839.4845	420.2459	821.4609	411.2341	821.4740	411.2406	8
3	217.1097	109.0585					A	767.4504	384.2288	749.4268	375.2170	749.4398	375.2235	7
4	***333.1337***	167.0705			315.1231	158.0652	D	695.4162	348.2118	677.3926	339.2000	677.4057	339.2065	6
5	***447.2148***	224.1110			429.2042	215.1058	L	**579.3923**	290.1998	561.3687	281.1880			5
6	561.2959	281.1516			543.2853	272.1463	L	465.3112	233.1592	447.2876	224.1474			4
7	***633.3300***	317.1687			615.3195	308.1634	A	351.2301	176.1187	333.2065	167.1069			3
8	***763.4191***	382.2132	745.3955	373.2014	745.4085	373.2079	K	279.1959	140.1016	261.1723	131.0898			2
9							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AAADLLAKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.9	910.5114	-0.0022	AAADLLAKK

AT3G61540.1

26.1	910.5114	-0.0022	AEKTVPKK
26.1	910.5114	-0.0022	EKAKSIPK
23.6	910.5114	-0.0022	QEVVGLKK
18.7	910.5067	0.0026	MKKHVLK
18.6	910.5114	-0.0022	ELRLIEK
18.1	910.5114	-0.0022	AQQLSILK
16.5	910.5114	-0.0022	KLSSLQPK
14.6	910.5114	-0.0021	QTVGVGVIK
13.3	910.5114	-0.0022	AIQELAKK

AT3G61570.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNLTSTSAALK**
Found in **AT3G61570.1** in **TAIR_Arabidopsis**, Symbols: GC3, GDAP1 | GC3/GDAP1 (GRIP-RELATED ARF-BINDING DOMAIN-CONTAINING ARABIDOPSIS PROTEIN 1); oxidoreductase/ transition metal ion binding | chr3:22790612-22794617 REVERSE

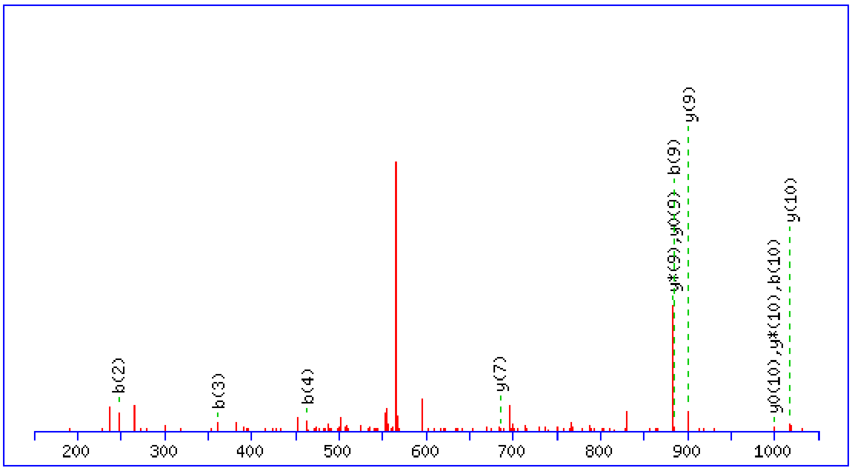
Match to Query 3247: 1146.566050 from(574.290301,2+) index(4520)
Title: Elution from: 45.068 to 45.068 scan no 5828 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1050 Da Full range

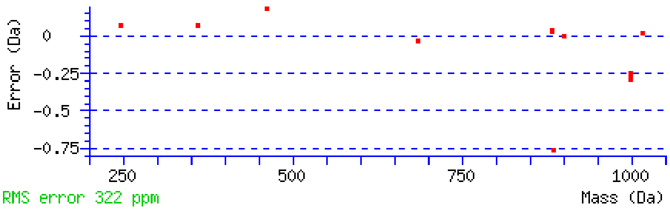
Label all possible matches ○ Label matches used for scoring ●

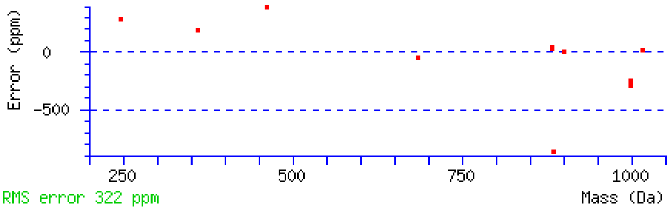
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1146.5673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.042
Matches : 12/106 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							11
2	***247.0969***	124.0521	229.0733	115.0403			N	**1017.5219**	509.2646	999.4983	500.2528	999.5114	500.2593	10
3	***361.1780***	181.0926	343.1544	172.0809			L	**901.4849**	451.2461	883.4613	442.2343	883.4744	442.2408	9
4	***463.2227***	232.1150	445.1991	223.1032	445.2122	223.1097	T	787.4038	394.2055	769.3802	385.1938	769.3933	385.2003	8
5	551.2518	276.1295	533.2282	267.1177	533.2412	267.1243	S	**685.3591**	343.1832	667.3355	334.1714	667.3485	334.1779	7
6	653.2965	327.1519	635.2729	318.1401	635.2859	318.1466	T	597.3300	299.1687	579.3065	290.1569	579.3195	290.1634	6
7	741.3256	371.1664	723.3020	362.1546	723.3150	362.1611	S	495.2853	248.1463	477.2617	239.1345	477.2748	239.1410	5
8	813.3597	407.1835	795.3361	398.1717	795.3492	398.1782	A	407.2563	204.1318	389.2327	195.1200			4
9	***885.3939***	443.2006	867.3703	434.1888	867.3833	434.1953	A	335.2221	168.1147	317.1985	159.1029			3
10	***999.4750***	500.2411	981.4514	491.2293	981.4644	491.2358	L	263.1880	132.0976	245.1644	123.0858			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QNLTSTSAALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G61570.1

Score	Mr(calc)	Delta	Sequence
18.8	1146.5673	-0.0012	QNLTSTSAALK
16.4	1146.5673	-0.0012	NKDTSLSIGAK
9.5	1146.5673	-0.0012	SKLQKAESDK
8.4	1146.5673	-0.0012	KKGVEESTQK
7.1	1146.5673	-0.0012	DKSALAAQTTK
6.3	1146.5673	-0.0012	SSGGSGLGLAISK
2.3	1146.5655	0.0006	MLLKMEEVK
1.9	1146.5648	0.0013	DFMKPLNLR
1.6	1146.5682	-0.0021	MPKKMGLNSK
1.6	1146.5682	-0.0021	NLEMLKMVR

AT3G61670.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPIHGR**
Found in **AT3G61670.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G46380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65830.1) | chr3:22830027-22832845 FORWARD

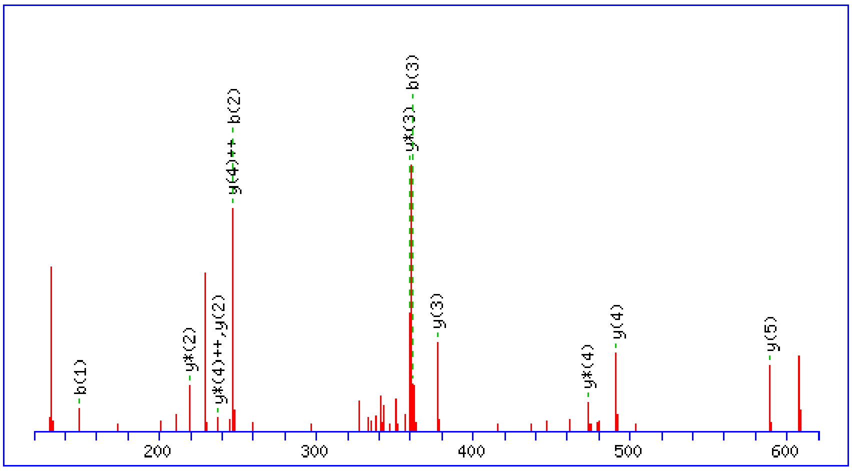
Match to Query 725: 736.365090 from(369.189821,2+) index(416)
Title: Elution from: 9.607 to 9.607 scan no 654 cid35.00 polarity:+
Data file C7-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 120 to 620 Da Full range

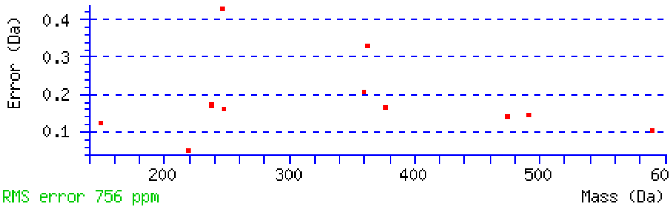
Label all possible matches ○ Label matches used for scoring ●

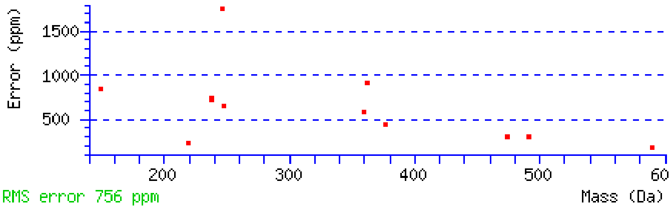
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 736.3647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.0081
Matches : 12/30 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**149.0727**	75.0400	**F**					**6**
2	**247.1225**	124.0649	**P**	***589.3065***	295.1569	571.2829	286.1451	**5**
3	**361.2036**	181.1054	**I**	***491.2567***	246.1320	473.2331	237.1202	**4**
4	501.2536	251.1305	**H**	***377.1756***	189.0914	359.1520	180.0796	**3**
5	559.2721	280.1397	**G**	***237.1256***	119.0664	219.1020	110.0546	**2**
6			**R**	179.1071	90.0572	161.0835	81.0454	**1**





NCBI **BLAST** search of FPIHGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.9	736.3647	0.0004	FPIHGR
3.8	736.3647	0.0004	IFPHGR
2.8	736.3647	0.0004	QKHWK

AT3G61670.1

1.8	736.3654	-0.0003	MPEPKK

Mascot: http://www.matrixscience.com/

AT3G61730.1

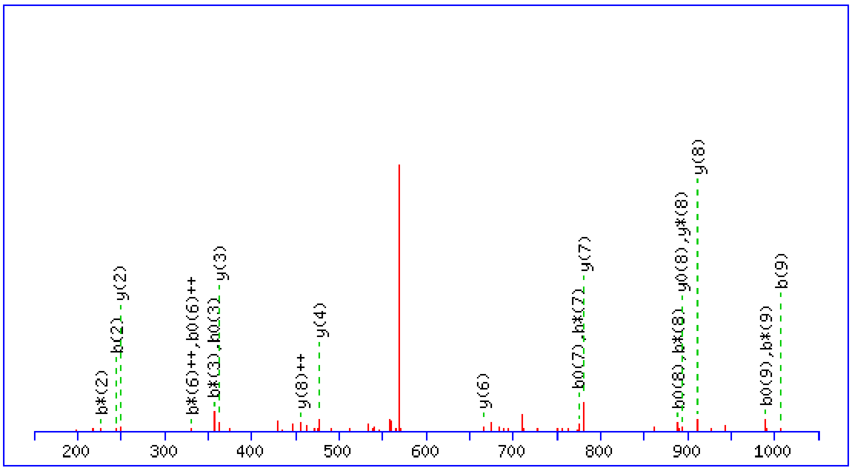
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQENEGILVK**
Found in **AT3G61730.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G36000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39758.1); contains domain F-box domain (SSF81383) | chr3:22859402-22861450 REVERSE

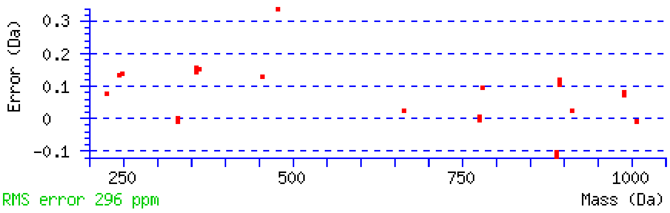
Match to Query 3379: 1154.595530 from(578.305041,2+) index(3108)
Title: Elution from: 33.737 to 33.737 scan no 3990 cid35.00 polarity:+
Data file D1d-2_2.mgf

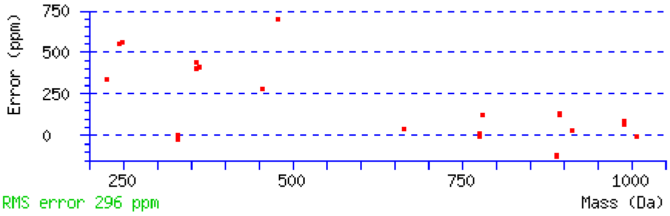
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1154.5957
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00024
Matches : 22/92 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							10
2	**245.1410**	123.0741	227.1174	114.0624			Q	1041.5219	521.2646	1023.4983	512.2528	1023.5114	512.2593	9
3	375.1806	188.0940	357.1571	179.0822	357.1701	179.0887	E	***911.4693***	456.2383	893.4457	447.2265	893.4587	447.2330	8
4	491.2176	246.1125	473.1941	237.1007	473.2071	237.1072	N	***781.4296***	391.2185	763.4061	382.2067	763.4191	382.2132	7
5	621.2573	311.1323	603.2337	302.1205	603.2467	302.1270	E	***665.3926***	333.2000	647.3691	324.1882	647.3821	324.1947	6
6	679.2758	340.1415	661.2522	331.1297	661.2652	331.1362	G	535.3530	268.1801	517.3294	259.1684			5
7	793.3569	397.1821	775.3333	388.1703	775.3463	388.1768	I	***477.3345***	239.1709	459.3109	230.1591			4
8	907.4380	454.2226	889.4144	445.2108	889.4274	445.2173	L	***363.2534***	182.1303	345.2298	173.1186			3
9	**1007.5034**	504.2553	989.4798	495.2436	989.4929	495.2501	V	***249.1723***	125.0898	231.1487	116.0780			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LQENEGILVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G61730.1

Score	Mr(calc)	Delta	Sequence
41.8	1154.5957	-0.0002	LQENEGILVK
37.4	1154.5957	-0.0002	QLQAEDVIVK
13.4	1154.5958	-0.0002	APPSKSVSIEK
11.9	1154.5957	-0.0002	KLPEKGDEVK
11.7	1154.5957	-0.0002	VSSPAINEVVK
10.6	1154.5957	-0.0002	VPEGTNSVLVK
9.5	1154.5966	-0.0011	QLLMMHLLK
8.8	1154.5984	-0.0029	EQLPILRDR
7.6	1154.5957	-0.0002	VKVPDLASDAK
6.3	1154.5957	-0.0002	LEAQIAELQK

Mascot: http://www.matrixscience.com/

AT3G62000.1

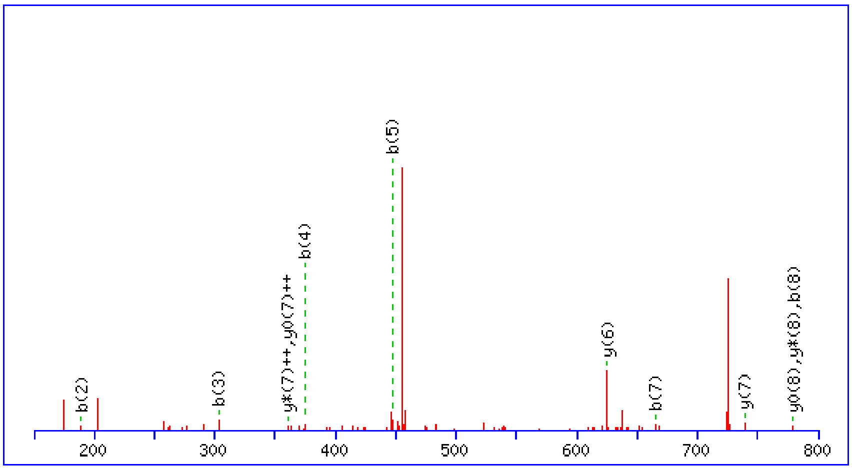
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGLAAESLK**
Found in **AT3G62000.1** in **TAIR_Arabidopsis**, Symbols: | O-methyltransferase family 3 protein | chr3:22970416-22972155 REVERSE

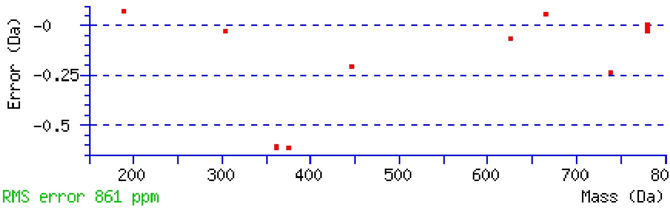
Match to Query 1795: 926.472356 from(464.243454,2+) index(2975)
Title: Elution from: 29.776 to 29.776 scan no 3713 cid35.00 polarity:+
Data file C7-3_3.mgf

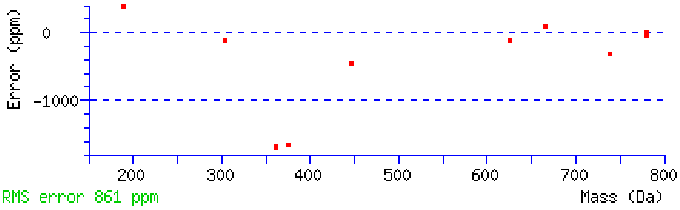
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 926.4699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0069
Matches : 12/82 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							9
2	***189.0784***	95.0428	171.0548	86.0311			G	797.4246	399.2159	779.4010	390.2041	779.4140	390.2106	8
3	***303.1595***	152.0834	285.1359	143.0716			L	**739.4061**	370.2067	721.3825	361.1949	721.3955	361.2014	7
4	***375.1937***	188.1005	357.1701	179.0887			A	**625.3250**	313.1661	607.3014	304.1543	607.3144	304.1608	6
5	***447.2278***	224.1175	429.2042	215.1058			A	553.2908	277.1490	535.2672	268.1373	535.2802	268.1438	5
6	577.2674	289.1374	559.2439	280.1256	559.2569	280.1321	E	481.2567	241.1320	463.2331	232.1202	463.2461	232.1267	4
7	***665.2965***	333.1519	647.2729	324.1401	647.2859	324.1466	S	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
8	***779.3776***	390.1924	761.3540	381.1807	761.3670	381.1872	L	263.1880	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QGLAAESLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.2	926.4699	0.0024	QGLAAESLK

AT3G62000.1

24.8	926.4699	0.0024	NATIEQLK
24.8	926.4699	0.0024	NATLQEIK
24.1	926.4699	0.0024	AEVSAIQAK
16.0	926.4699	0.0024	GGALSDGVIK
15.6	926.4699	0.0024	QAEAEKLK
15.1	926.4699	0.0024	SVIASTPNK
14.6	926.4699	0.0024	NATQELLK
13.6	926.4699	0.0024	AEVEIISR
13.6	926.4699	0.0024	ISVEEALR

Mascot: http://www.matrixscience.com/

AT3G62030.1

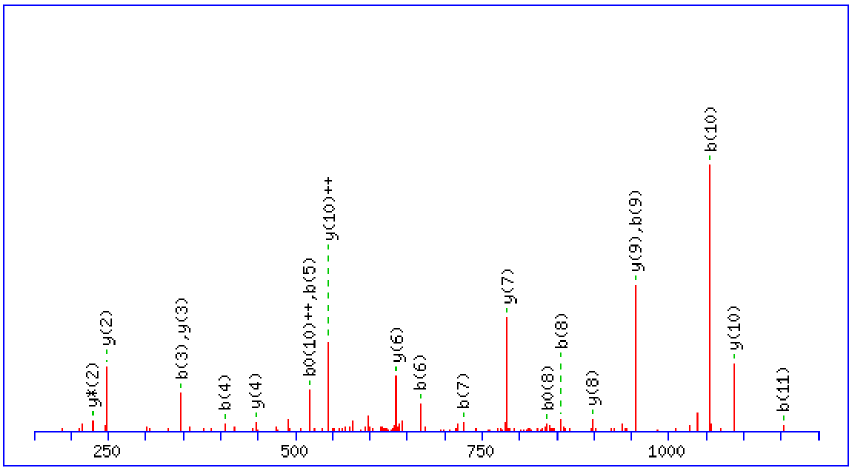
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVMGLFGEVVPK**
Found in **AT3G62030.1** in **TAIR_Arabidopsis**, Symbols: ROC4 | ROC4 (ROTAMASE CYP 4); peptidyl-prolyl cis-trans isomerase | chr3:22984683-22986114 FORWARD

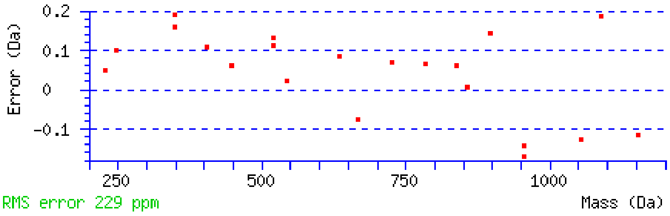
Match to Query 4281: 1300.683846 from(651.349199,2+) index(8485)
Title: Elution from: 79.285 to 79.285 scan no 11557 cid35.00 polarity:+
Data file D1d-2_2.mgf

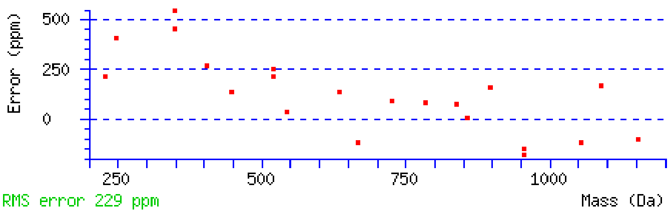
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1300.6875
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 101 **Expect:** 4e-010
Matches : 21/88 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478			**I**							**12**
2	215.1538	108.0805			**V**	1187.6137	594.3105	1169.5901	585.2987	1169.6031	585.3052	**11**
3	***347.1913***	174.0993			**M**	***1087.5483***	544.2778	1069.5247	535.2660	1069.5377	535.2725	**10**
4	***405.2098***	203.1086			**G**	***955.5107***	478.2590	937.4872	469.2472	937.5002	469.2537	**9**
5	***519.2909***	260.1491			**L**	***897.4922***	449.2498	879.4687	440.2380	879.4817	440.2445	**8**
6	***667.3564***	334.1818			**F**	***783.4111***	392.2092	765.3876	383.1974	765.4006	383.2039	**7**
7	***725.3749***	363.1911			**G**	***635.3457***	318.1765	617.3221	309.1647	617.3351	309.1712	**6**
8	***855.4145***	428.2109	837.4040	419.2056	**E**	577.3272	289.1672	559.3036	280.1554	559.3166	280.1620	**5**
9	***955.4800***	478.2436	937.4694	469.2383	**V**	***447.2876***	224.1474	429.2640	215.1356			**4**
10	***1055.5454***	528.2763	1037.5349	519.2711	**V**	***347.2221***	174.1147	329.1985	165.1029			**3**
11	***1153.5952***	577.3012	1135.5846	568.2960	**P**	***247.1567***	124.0820	229.1331	115.0702			**2**
12					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of IVMGLFGEVVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G62030.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.5	1300.6875	-0.0037	IVMGLFGEVVPK
16.8	1300.6846	-0.0007	LTQLGVRSWPK
11.5	1300.6853	-0.0015	QLLMLSSLASPK
1.2	1300.6823	0.0015	DQILRILQER

AT3G62250.1

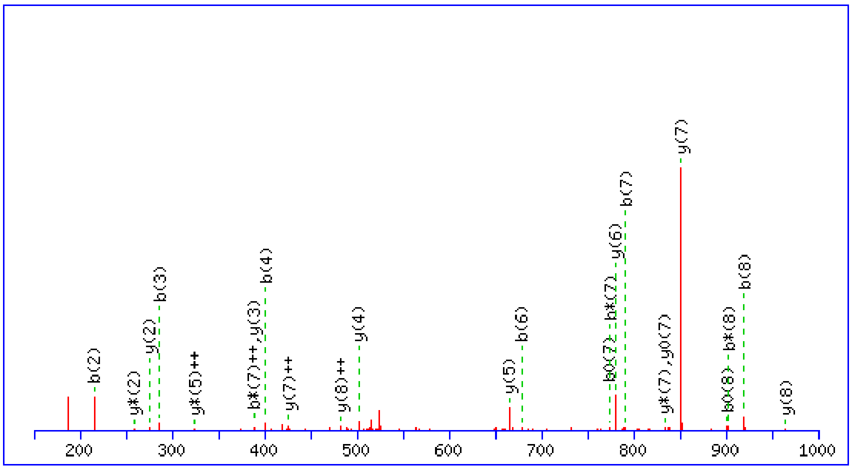
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLADYNIQK**
Found in **AT3G62250.1** in **TAIR_Arabidopsis**, Symbols: UBQ5 | UBQ5 (UBIQUITIN 5); protein binding | chr3:23048113-23048586 FORWARD

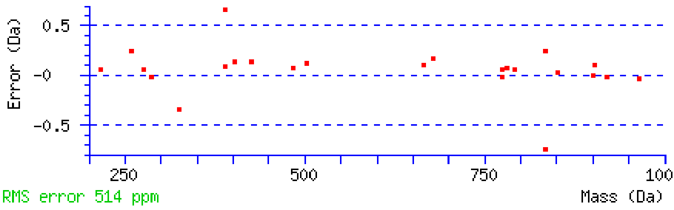
Match to Query 2904: 1064.548908 from(533.281730,2+) index(2485)
Title: Elution from: 25.948 to 25.948 scan no 3109 cid35.00 polarity:+
Data file 0-3_3.mgf

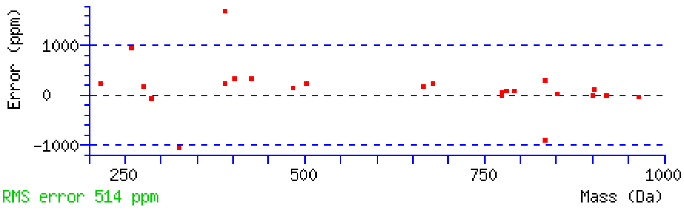
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1064.5502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.00011
Matches : 24/76 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							9
2	***215.1390***	108.0731			197.1285	99.0679	L	***964.5098***	482.7585	947.4833	474.2453	946.4993	473.7533	8
3	***286.1761***	143.5917			268.1656	134.5864	A	***851.4258***	426.2165	834.3992	417.7032	833.4152	417.2112	7
4	***401.2031***	201.1052			383.1925	192.0999	D	***780.3886***	390.6980	763.3621	382.1847	762.3781	381.6927	6
5	564.2664	282.6368			546.2558	273.6316	Y	***665.3617***	333.1845	648.3352	324.6712			5
6	***678.3093***	339.6583	661.2828	331.1450	660.2988	330.6530	N	***502.2984***	251.6528	485.2718	243.1395			4
7	***791.3934***	396.2003	774.3668	387.6871	773.3828	387.1951	I	***388.2554***	194.6314	371.2289	186.1181			3
8	***919.4520***	460.2296	902.4254	451.7164	901.4414	451.2243	Q	***275.1714***	138.0893	258.1448	129.5761			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TLADYNIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.8	1064.5502	-0.0013	TLADYNIQK

AT3G62250.1

5.7	1064.5462	0.0027	SSQSVASSGKK
4.8	1064.5502	-0.0013	DVASELYLR
4.7	1064.5502	-0.0013	FEKDEAAKK
4.0	1064.5502	-0.0013	VDNFSKDLK
2.7	1064.5502	-0.0013	NYDLGDLKK
1.8	1064.5502	-0.0013	TNEVAGLYAK
1.1	1064.5462	0.0027	ETERSSTKK

AT3G62410.1

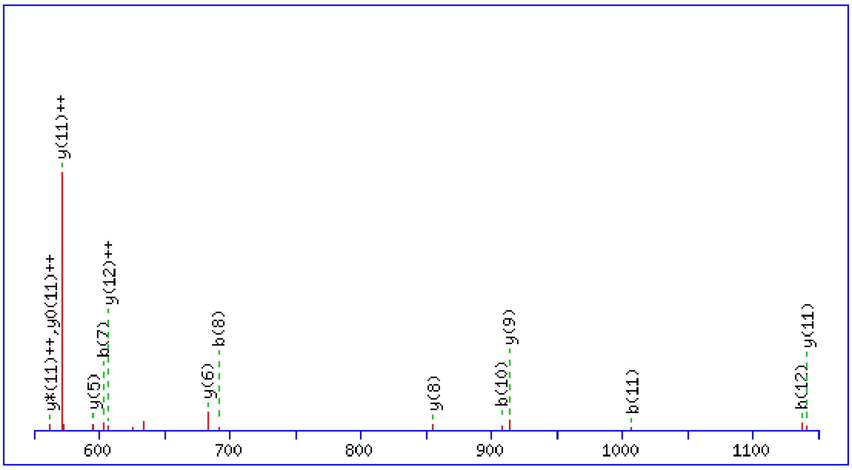
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAPEGGISDVVEK**
Found in **AT3G62410.1** in **TAIR_Arabidopsis**, Symbols: CP12, CP12-2 | CP12-2 | chr3:23101982-23102377 FORWARD

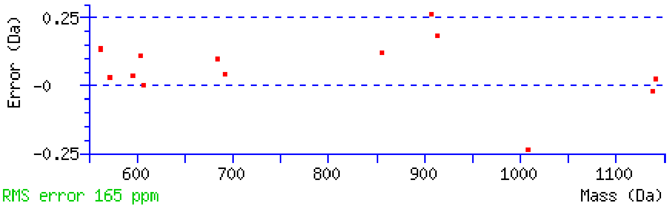
Match to Query 4597: 1284.598062 from(643.306307,2+) index(2779)
Title: Elution from: 29.277 to 29.277 scan no 3517 cid35.00 polarity:+
Data file D6h-1_2.mgf

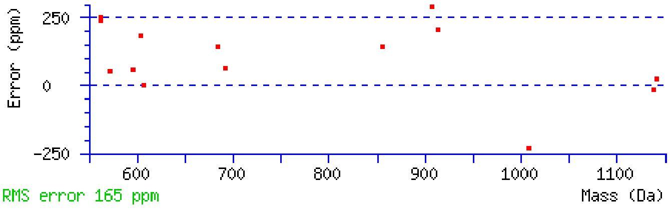
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1284.5990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 5.6e-006
Matches : 14/112 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							13
2	145.0756	73.0414			A	1213.5721	607.2897	1195.5485	598.2779	1195.5615	598.2844	12
3	243.1254	122.0663			P	***1141.5380***	571.2726	1123.5144	562.2608	1123.5274	562.2673	11
4	373.1650	187.0861	355.1544	178.0809	E	1043.4882	522.2477	1025.4646	513.2359	1025.4776	513.2424	10
5	431.1835	216.0954	413.1729	207.0901	G	***913.4485***	457.2279	895.4250	448.2161	895.4380	448.2226	9
6	489.2020	245.1046	471.1914	236.0994	G	***855.4300***	428.2187	837.4065	419.2069	837.4195	419.2134	8
7	***603.2831***	302.1452	585.2725	293.1399	I	797.4115	399.2094	779.3880	390.1976	779.4010	390.2041	7
8	***691.3122***	346.1597	673.3016	337.1544	S	***683.3304***	342.1689	665.3069	333.1571	665.3199	333.1636	6
9	807.3361	404.1717	789.3256	395.1664	D	***595.3014***	298.1543	577.2778	289.1425	577.2908	289.1490	5
10	***907.4016***	454.2044	889.3910	445.1991	V	479.2774	240.1423	461.2538	231.1305	461.2668	231.1371	4
11	***1007.4670***	504.2372	989.4565	495.2319	V	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	***1137.5067***	569.2570	1119.4961	560.2517	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AAPEGGISDVVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G62410.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.3	1284.5990	-0.0009	AAPEGGISDVVEK
7.1	1284.5969	0.0012	MERYAQARVK
6.1	1284.5991	-0.0011	TCRSGVKFWK
0.3	1284.6016	-0.0036	QAHKEDDAKVK

AT3G62530.1

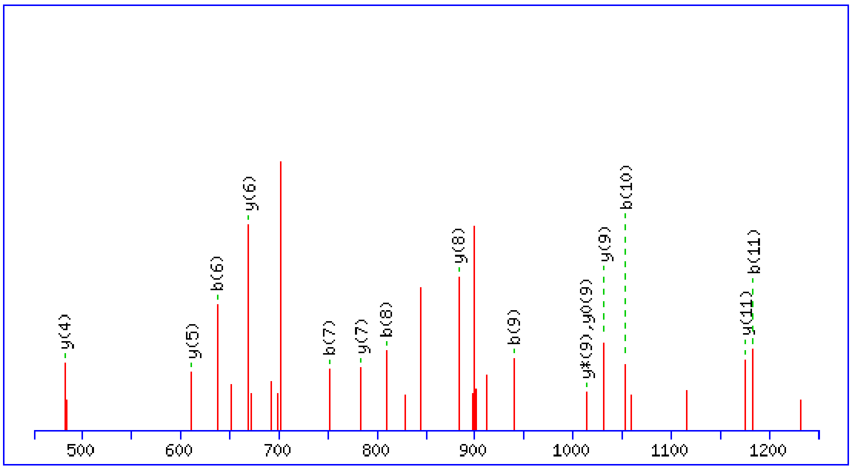
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEAAFVLGQLESK**
Found in **AT3G62530.1** in **TAIR_Arabidopsis**, Symbols: | PBS lyase HEAT-like repeat-containing protein | chr3:23143195-23144097 FORWARD

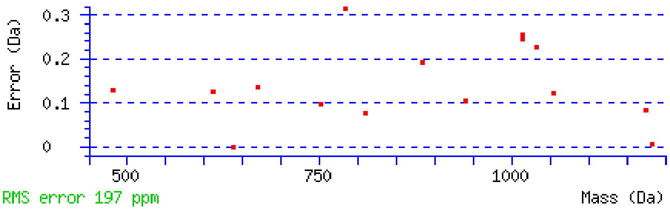
Match to Query 5863: 1418.721868 from(710.368210,2+) index(8815)
Title: Elution from: 76.716 to 76.716 scan no 11587 cid35.00 polarity:+
Data file C7-1_1.mgf

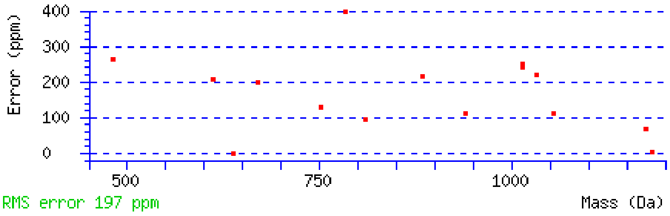
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1418.7215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 5.6e-006
Matches : 15/124 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							13
2	245.1280	123.0676			227.1174	114.0624	E	1305.6477	653.3275	1287.6241	644.3157	1287.6372	644.3222	12
3	317.1622	159.0847			299.1516	150.0794	A	***1175.6081***	588.3077	1157.5845	579.2959	1157.5975	579.3024	11
4	389.1963	195.1018			371.1857	186.0965	A	1103.5740	552.2906	1085.5504	543.2788	1085.5634	543.2853	10
5	537.2618	269.1345			519.2512	260.1292	F	***1031.5398***	516.2735	1013.5162	507.2617	1013.5292	507.2683	9
6	***637.3272***	319.1672			619.3166	310.1620	V	***883.4744***	442.2408	865.4508	433.2290	865.4638	433.2355	8
7	***751.4083***	376.2078			733.3977	367.2025	L	***783.4089***	392.2081	765.3853	383.1963	765.3983	383.2028	7
8	***809.4268***	405.2170			791.4162	396.2118	G	***669.3278***	335.1675	651.3042	326.1558	651.3172	326.1623	6
9	***939.4794***	470.2434	921.4559	461.2316	921.4689	461.2381	Q	***611.3093***	306.1583	593.2857	297.1465	593.2987	297.1530	5
10	***1053.5605***	527.2839	1035.5370	518.2721	1035.5500	518.2786	L	***481.2567***	241.1320	463.2331	232.1202	463.2461	232.1267	4
11	***1183.6002***	592.3037	1165.5766	583.2919	1165.5896	583.2984	E	367.1756	184.0914	349.1520	175.0796	349.1650	175.0861	3
12	1271.6292	636.3183	1253.6057	627.3065	1253.6187	627.3130	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IEAAFVLGQLESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT3G62530.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.0	1418.7215	0.0003	IEAAFVLGQLESK
11.5	1418.7249	-0.0030	MLEEKLGTEKVK
11.2	1418.7193	0.0026	IASLQTEVSSLQK
7.2	1418.7193	0.0026	TTKSDEIVNAVVK
1.5	1418.7242	-0.0024	LLDYRNPKPGTK
1.2	1418.7242	-0.0024	DIIYVNGNRIPK
0.5	1418.7193	0.0025	SDNLLISADKSIK
0.5	1418.7242	-0.0023	ALQQSTLKAWAGK
0.5	1418.7242	-0.0024	NPKGYTIPLDKR

AT3G62590.1

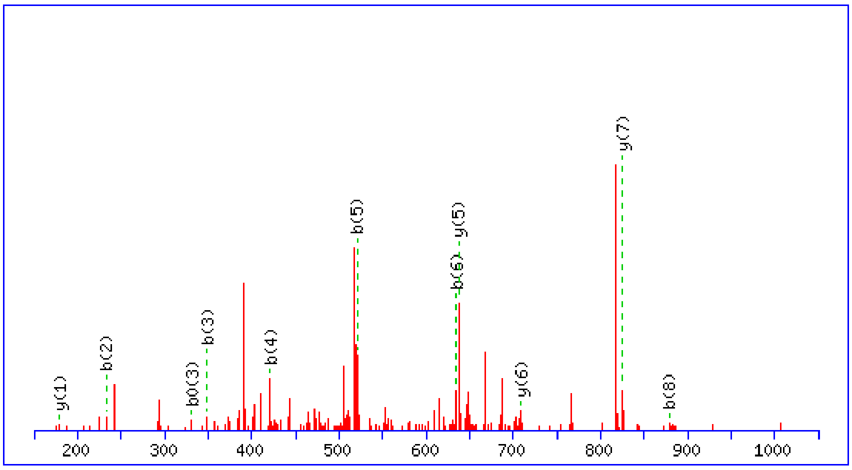
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDDAVLLER**
Found in **AT3G62590.1** in **TAIR_Arabidopsis**, Symbols: | lipase class 3 family protein | chr3:23158949-23161145 REVERSE

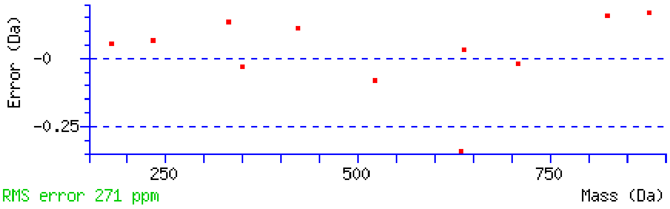
Match to Query 2942: 1056.476126 from(529.245339,2+) index(3363)
Title: Elution from: 32.773 to 32.773 scan no 4178 cid35.00 polarity:+
Data file D12h-3_2.mgf

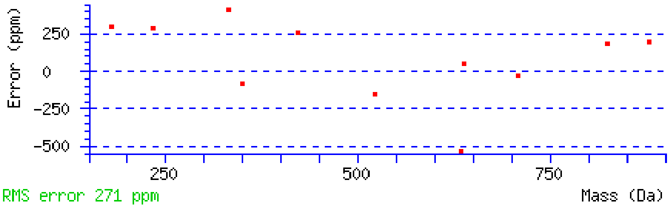
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.4731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.039
Matches : 11/78 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							9
2	***233.0552***	117.0313	215.0447	108.0260	D	941.4565	471.2319	923.4329	462.2201	923.4459	462.2266	8
3	***349.0792***	175.0432	331.0686	166.0380	D	**825.4325**	413.2199	807.4089	404.2081	807.4219	404.2146	7
4	***421.1134***	211.0603	403.1028	202.0550	A	**709.4085**	355.2079	691.3849	346.1961	691.3980	346.2026	6
5	***521.1788***	261.0930	503.1682	252.0878	V	**637.3744**	319.1908	619.3508	310.1790	619.3638	310.1855	5
6	***635.2599***	318.1336	617.2493	309.1283	L	537.3089	269.1581	519.2853	260.1463	519.2984	260.1528	4
7	749.3410	375.1741	731.3304	366.1689	L	423.2278	212.1175	405.2042	203.1058	405.2173	203.1123	3
8	***879.3806***	440.1940	861.3701	431.1887	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
9					R	**179.1071**	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DDDAVLLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1056.4731	0.0030	DDDAVLLER

AT3G62590.1

11.0	1056.4758	0.0003	REQDPELR
2.3	1056.4758	0.0003	VETSSHVQR
1.7	1056.4758	0.0003	QQANTDIPR
1.4	1056.4758	0.0003	QERDPIER

AT3G62870.1

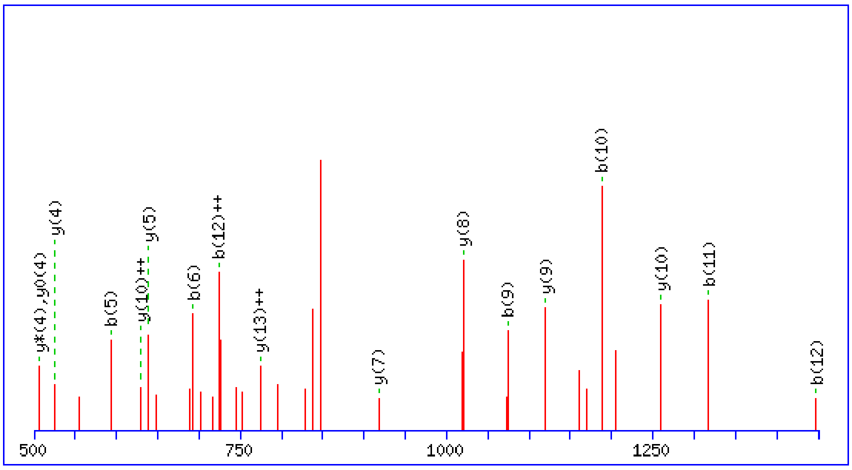
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGLNHVTYLIEQNK**
Found in **AT3G62870.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L7A (RPL7aB) | chr3:23253837-23255248 REVERSE

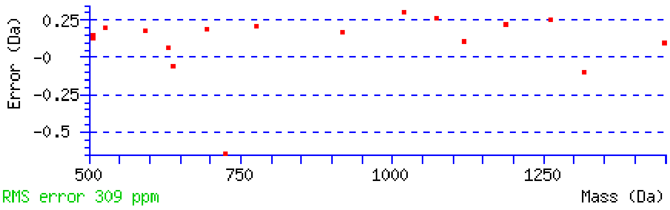
Match to Query 8174: 1710.807620 from(856.411086,2+) index(5555)
Title: Elution from: 52.561 to 52.561 scan no 7177 cid35.00 polarity:+
Data file D12h-2_1.mgf

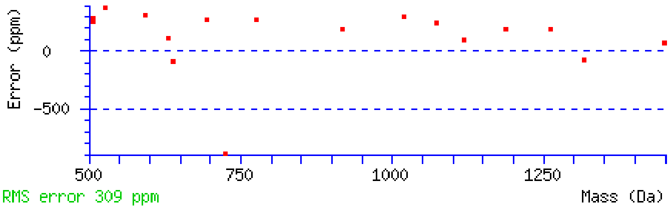
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1710.8086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.9e-005
Matches : 17/132 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							14
2	223.0861	112.0467					G	1547.7555	774.3814	1529.7319	765.3696	1529.7449	765.3761	13
3	337.1672	169.0873					L	1489.7370	745.3721	1471.7134	736.3603	1471.7264	736.3668	12
4	453.2042	227.1058	435.1807	218.0940			N	1375.6559	688.3316	1357.6323	679.3198	1357.6453	679.3263	11
5	***593.2543***	297.1308	575.2307	288.1190			H	***1259.6189***	630.3131	1241.5953	621.3013	1241.6083	621.3078	10
6	***693.3197***	347.1635	675.2961	338.1517			V	***1119.5689***	560.2881	1101.5453	551.2763	1101.5583	551.2828	9
7	795.3644	398.1858	777.3408	389.1741	777.3538	389.1806	T	***1019.5034***	510.2553	1001.4798	501.2436	1001.4929	501.2501	8
8	959.4248	480.2160	941.4012	471.2042	941.4142	471.2107	Y	***917.4587***	459.2330	899.4351	450.2212	899.4481	450.2277	7
9	***1073.5059***	537.2566	1055.4823	528.2448	1055.4953	528.2513	L	753.3983	377.2028	735.3748	368.1910	735.3878	368.1975	6
10	***1187.5870***	594.2971	1169.5634	585.2853	1169.5764	585.2918	I	***639.3172***	320.1623	621.2937	311.1505	621.3067	311.1570	5
11	***1317.6266***	659.3169	1299.6030	650.3051	1299.6160	650.3117	E	***525.2361***	263.1217	507.2126	254.1099	507.2256	254.1164	4
12	***1447.6793***	724.3433	1429.6557	715.3315	1429.6687	715.3380	Q	395.1965	198.1019	377.1729	189.0901			3
13	1563.7162	782.3618	1545.6927	773.3500	1545.7057	773.3565	N	265.1439	133.0756	247.1203	124.0638			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YGLNHVTYLIEQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT3G62870.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.2	1710.8086	-0.0009	YGLNHVTYLIEQNK
27.1	1710.8041	0.0035	KEQLSGSQNSLQKDK
2.5	1710.8079	-0.0003	VTMMKLKVDLDCPK
2.5	1710.8079	-0.0003	VTMMKLKVDLDCPK
2.4	1710.8108	-0.0032	GLKFYGFHGAIPEEK
2.1	1710.8086	-0.0009	EIFIYLSDRDPAPR
2.1	1710.8099	-0.0022	MIRVMWSVRAPDAR
1.9	1710.8093	-0.0016	MEKVDVYDELVNLK
1.7	1710.8119	-0.0043	YLQDIVPGCNKVTGK
1.5	1710.8059	0.0017	IAFIGDGPYKEDLEK

AT3G63140.1

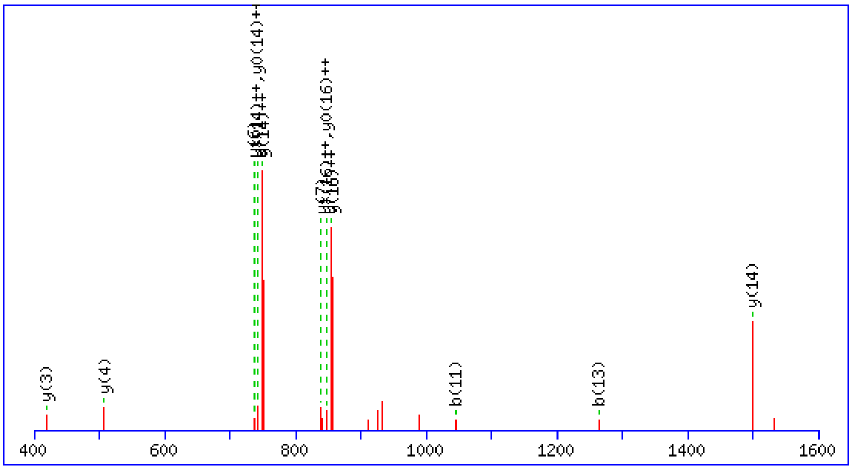
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVPIPGSGLQLTNISHVR**
Found in **AT3G63140.1** in **TAIR_Arabidopsis**, Symbols: | mRNA-binding protein, putative | chr3:23337981-23339595 REVERSE

Match to Query 8757: 1882.973116 from(942.493834,2+) index(6612)
Title: Elution from: 58.913 to 58.913 scan no 8560 cid35.00 polarity:+
Data file D6h-1_3.mgf

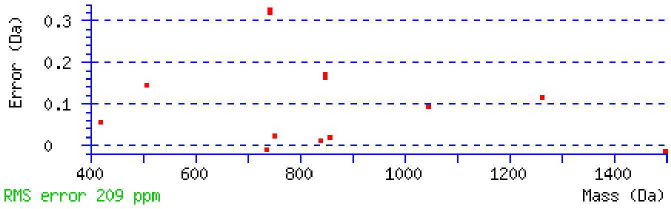
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

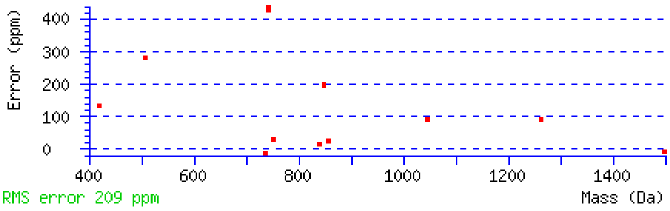


Monoisotopic mass of neutral peptide Mr(calc): 1882.9684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0012
Matches : 13/168 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							18
2	173.1069	87.0571					V	1811.9415	906.4744	1793.9179	897.4626	1793.9309	897.4691	17
3	271.1567	136.0820					P	1711.8760	856.4417	1693.8524	847.4299	1693.8655	847.4364	16
4	385.2378	193.1225					I	1613.8262	807.4168	1595.8026	798.4050	1595.8157	798.4115	15
5	483.2876	242.1474					P	***1499.7451***	750.3762	1481.7216	741.3644	1481.7346	741.3709	14
6	541.3061	271.1567					G	1401.6953	701.3513	1383.6718	692.3395	1383.6848	692.3460	13
7	629.3351	315.1712			611.3246	306.1659	S	1343.6768	672.3421	1325.6533	663.3303	1325.6663	663.3368	12
8	687.3536	344.1805			669.3431	335.1752	G	1255.6478	628.3275	1237.6242	619.3157	1237.6372	619.3222	11
9	801.4347	401.2210			783.4242	392.2157	L	1197.6293	599.3183	1179.6057	590.3065	1179.6187	590.3130	10
10	931.4874	466.2473	913.4638	457.2355	913.4768	457.2420	Q	1083.5482	542.2777	1065.5246	533.2659	1065.5376	533.2724	9
11	**1045.5685**	523.2879	1027.5449	514.2761	1027.5579	514.2826	L	953.4955	477.2514	935.4719	468.2396	935.4850	468.2461	8
12	1147.6132	574.3102	1129.5896	565.2984	1129.6026	565.3050	T	***839.4144***	420.2109	821.3908	411.1991	821.4039	411.2056	7
13	**1263.6502**	632.3287	1245.6266	623.3169	1245.6396	623.3234	N	***737.3697***	369.1885	719.3461	360.1767	719.3592	360.1832	6
14	1377.7313	689.3693	1359.7077	680.3575	1359.7207	680.3640	I	621.3327	311.1700	603.3091	302.1582	603.3222	302.1647	5
15	1465.7603	733.3838	1447.7368	724.3720	1447.7498	724.3785	S	***507.2516***	254.1294	489.2280	245.1177	489.2411	245.1242	4
16	1605.8104	803.4088	1587.7868	794.3970	1587.7998	794.4035	H	***419.2226***	210.1149	401.1990	201.1031			3
17	1705.8758	853.4415	1687.8522	844.4298	1687.8652	844.4363	V	279.1725	140.0899	261.1490	131.0781			2
18							R	179.1071	90.0572	161.0835	81.0454			1

AT3G63140.1





NCBI **BLAST** search of AVPIPGSGLQLTNISHVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.6	1882.9684	0.0048	AVPIPGSGLQLTNISHVR
2.0	1882.9706	0.0025	KIHRLPIEPIDFPER
1.1	1882.9787	-0.0056	AVDISPSIAHELIQVLR

Mascot: http://www.matrixscience.com/

AT3G63160.1

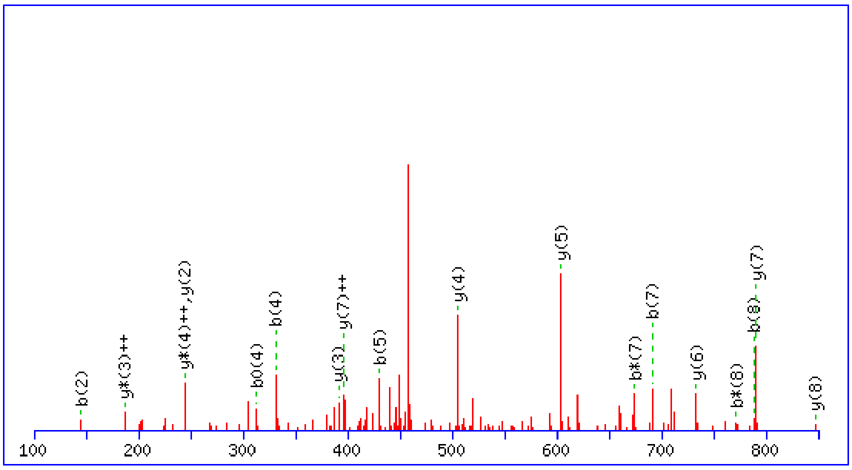
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGGEVNFPK**
Found in **AT3G63160.1** in **TAIR_Arabidopsis**, Symbols: | unknown protein | chr3:23344748-23344957 REVERSE

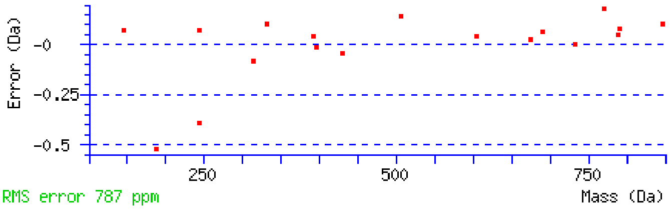
Match to Query 1948: 933.457526 from(467.736039,2+) index(1864)
Title: Elution from: 22.568 to 22.568 scan no 2423 cid35.00 polarity:+
Data file D12h-1_2.mgf

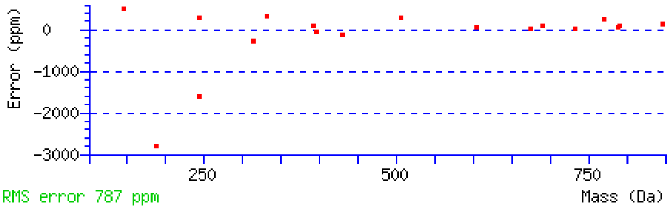
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 933.4556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00021
Matches : 18/76 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	**145.0608**	73.0340			127.0502	64.0287	G	***847.4308***	424.2191	830.4043	415.7058	829.4203	415.2138	8
3	202.0822	101.5448			184.0717	92.5395	G	***790.4094***	395.7083	773.3828	387.1951	772.3988	386.7030	7
4	**331.1248**	166.0661			313.1143	157.0608	E	***733.3879***	367.1976	716.3614	358.6843	715.3774	358.1923	6
5	**430.1932**	215.6003			412.1827	206.5950	V	***604.3453***	302.6763	587.3188	294.1630			5
6	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	N	***505.2769***	253.1421	488.2504	244.6288			4
7	**691.3046**	346.1559	674.2780	337.6427	673.2940	337.1506	F	***391.2340***	196.1206	374.2074	187.6074			3
8	**788.3573**	394.6823	771.3308	386.1690	770.3468	385.6770	P	***244.1656***	122.5864	227.1390	114.0731			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SGGEVNFPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.0	933.4556	0.0019	SGGEVNFPK

AT3G63160.1

10.2	933.4596	-0.0021	FELDWPK
9.2	933.4590	-0.0014	DSKCTVPK
4.8	933.4589	-0.0014	SGIMEIER
4.6	933.4590	-0.0014	MENGVIAGK
3.3	933.4589	-0.0014	MADLNLNK
3.3	933.4589	-0.0014	MGELNLNK
3.3	933.4590	-0.0014	NTMNLTPK
3.0	933.4603	-0.0028	SRCGWLR
1.8	933.4589	-0.0014	LGCKEAEK

AT3G63170.1

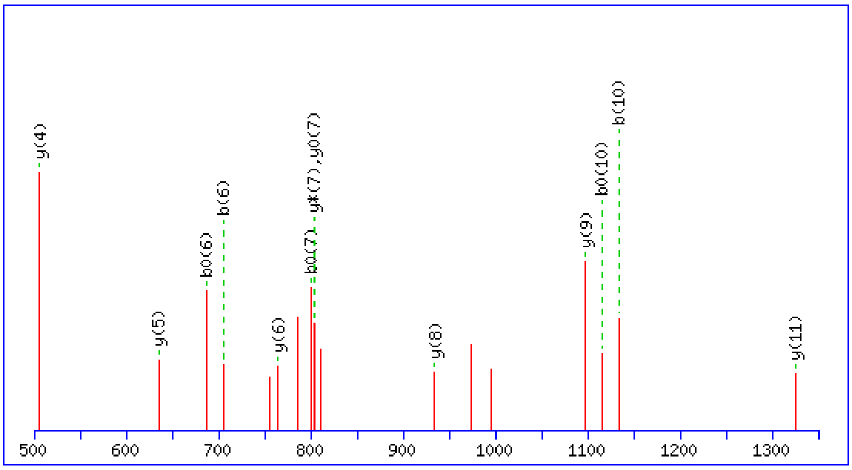
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILDLYIGEEPFDK**
Found in **AT3G63170.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22529.1); contains InterPro domain Chalcone isomerase-like (InterPro:IPR016087) | chr3:23345650-23346968 FO

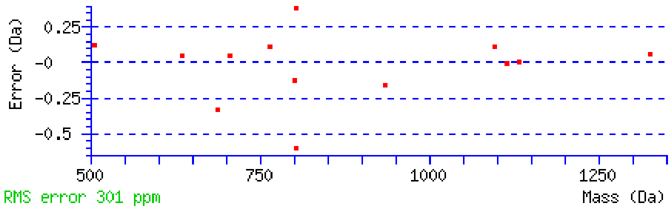
Match to Query 6908: 1637.815398 from(819.914975,2+) index(9620)
Title: Elution from: 92.467 to 92.467 scan no 13732 cid35.00 polarity:+
Data file D1d-1_3.mgf

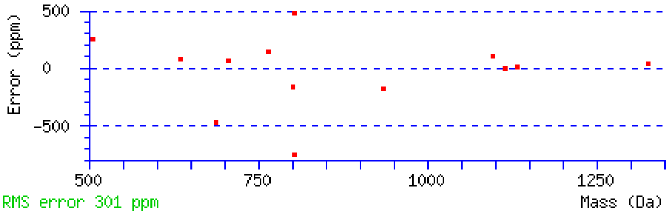
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1637.8188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00011
Matches : 13/128 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							14
2	201.1234	101.0653	183.1128	92.0600	I	1551.7941	776.4007	1534.7676	767.8874	1533.7835	767.3954	13
3	314.2074	157.6074	296.1969	148.6021	L	1438.7100	719.8587	1421.6835	711.3454	1420.6995	710.8534	12
4	429.2344	215.1208	411.2238	206.1155	D	***1325.6260***	663.3166	1308.5994	654.8034	1307.6154	654.3113	11
5	542.3184	271.6629	524.3079	262.6576	L	1210.5990	605.8032	1193.5725	597.2899	1192.5885	596.7979	10
6	**705.3818**	353.1945	687.3712	344.1892	Y	***1097.5150***	549.2611	1080.4884	540.7478	1079.5044	540.2558	9
7	818.4658	409.7366	800.4553	400.7313	I	***934.4516***	467.7295	917.4251	459.2162	916.4411	458.7242	8
8	875.4873	438.2473	857.4767	429.2420	G	821.3676	411.1874	804.3410	402.6742	803.3570	402.1821	7
9	1004.5299	502.7686	986.5193	493.7633	E	***764.3461***	382.6767	747.3196	374.1634	746.3355	373.6714	6
10	**1133.5725**	567.2899	1115.5619	558.2846	E	***635.3035***	318.1554	618.2770	309.6421	617.2930	309.1501	5
11	1230.6252	615.8163	1212.6147	606.8110	P	***506.2609***	253.6341	489.2344	245.1208	488.2504	244.6288	4
12	1377.6937	689.3505	1359.6831	680.3452	F	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
13	1492.7206	746.8639	1474.7100	737.8587	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
14					K	147.1128	74.0600	130.0863	65.5468			1





AT3G63170.1

NCBI **BLAST** search of SILDLYIGEEPFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.3	1637.8188	-0.0034	SILDLYIGEEPFDK
3.1	1637.8161	-0.0007	QHAKVAEDAVAGWEK
0.3	1637.8195	-0.0041	TTKGGKVMNPTDAYR

AT3G63190.1

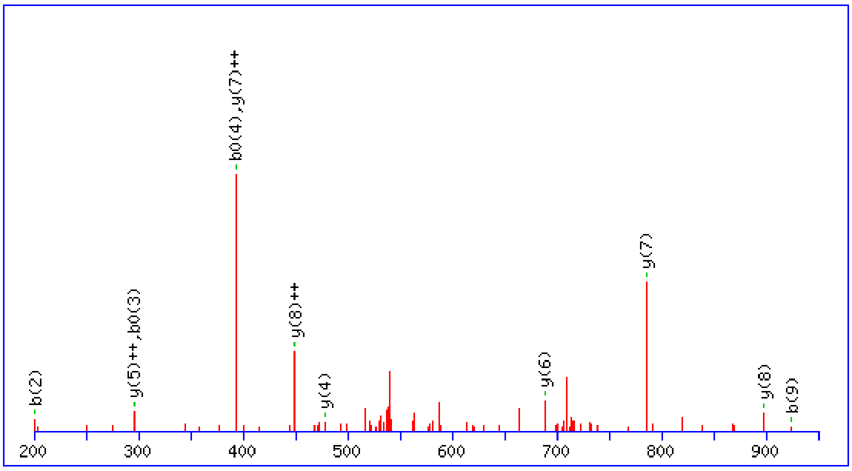
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSLPPLTSDR**
Found in **AT3G63190.1** in **TAIR_Arabidopsis**, Symbols: RRF | RRF (RIBOSOME RECYCLING FACTOR, CHLOROPLAST PRECURSOR) | chr3:23353836-23355615 REVERSE

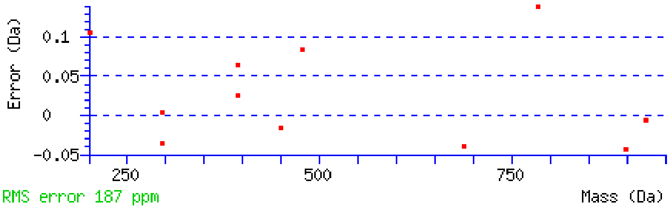
Match to Query 3430: 1097.609312 from(549.811932,2+) index(5731)
Title: Elution from: 50.158 to 50.158 scan no 7237 cid35.00 polarity:+
Data file C7-3_2.mgf

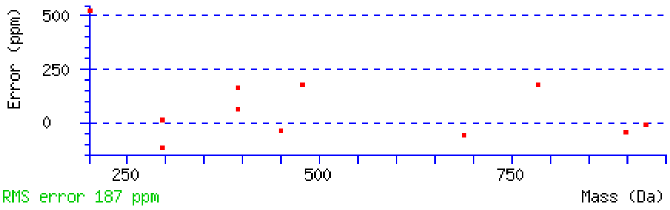
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1097.6081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.003
Matches : 11/86 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							10
2	201.1234	101.0653	183.1128	92.0600	S	985.5313	493.2693	968.5047	484.7560	967.5207	484.2640	9
3	314.2074	157.6074	296.1969	148.6021	L	898.4993	449.7533	881.4727	441.2400	880.4887	440.7480	8
4	411.2602	206.1337	393.2496	197.1285	P	785.4152	393.2112	768.3886	384.6980	767.4046	384.2060	7
5	508.3130	254.6601	490.3024	245.6548	P	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	6
6	621.3970	311.2022	603.3865	302.1969	L	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
7	722.4447	361.7260	704.4341	352.7207	T	478.2256	239.6164	461.1991	231.1032	460.2150	230.6112	4
8	809.4767	405.2420	791.4662	396.2367	S	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
9	924.5037	462.7555	906.4931	453.7502	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
10					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LSLPPLTSDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT3G63190.1

Score	Mr(calc)	Delta	Sequence
28.5	1097.6081	0.0012	LSLPPLTSDR
3.8	1097.6081	0.0012	KAVDPSVGTPK

Mascot: http://www.matrixscience.com/

AT3G63410.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVSAGSIEYWPDPQR**
Found in **AT3G63410.1** in **TAIR_Arabidopsis**, Symbols: VTE3, APG1 | APG1 (ALBINO OR PALE GREEN MUTANT 1); methyltransferase | chr3:23426791-23427977 REVERSE

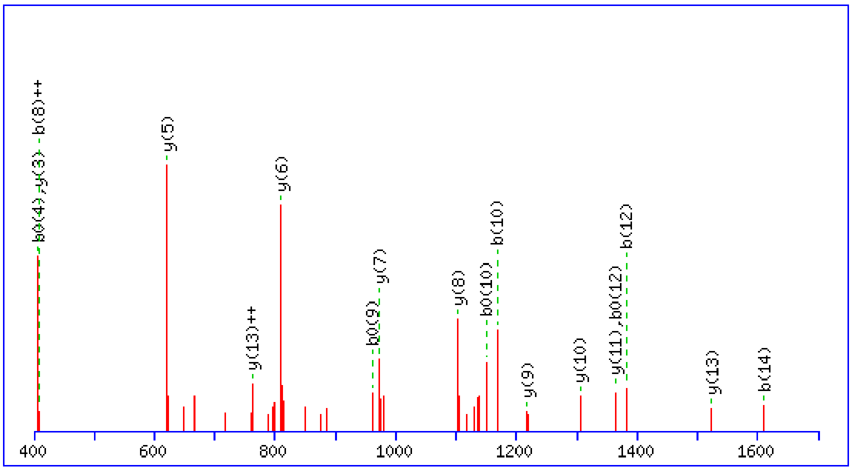
Match to Query 8377: 1786.764590 from(894.389571,2+) index(6776)
Title: Elution from: 59.693 to 59.693 scan no 8763 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1700 Da Full range

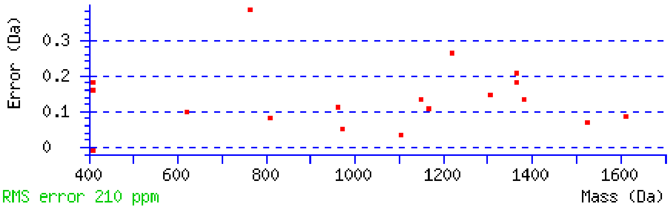
Label all possible matches ○ Label matches used for scoring ●

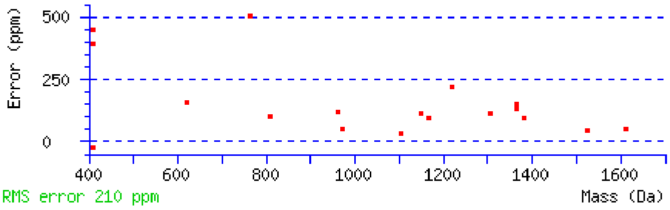
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1786.7671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 1.9e-006
Matches : 18/132 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	165.0676	83.0375					Y							15
2	265.1331	133.0702					V	1623.7140	812.3606	1605.6904	803.3489	1605.7034	803.3554	14
3	353.1622	177.0847			335.1516	168.0794	S	***1523.6486***	762.3279	1505.6250	753.3161	1505.6380	753.3226	13
4	425.1963	213.1018			407.1857	204.0965	A	1435.6195	718.3134	1417.5959	709.3016	1417.6089	709.3081	12
5	483.2148	242.1110			465.2042	233.1058	G	***1363.5854***	682.2963	1345.5618	673.2845	1345.5748	673.2910	11
6	571.2439	286.1256			553.2333	277.1203	S	***1305.5669***	653.2871	1287.5433	644.2753	1287.5563	644.2818	10
7	685.3250	343.1661			667.3144	334.1608	I	***1217.5378***	609.2725	1199.5142	600.2607	1199.5272	600.2672	9
8	815.3646	408.1859			797.3540	399.1807	E	***1103.4567***	552.2320	1085.4331	543.2202	1085.4461	543.2267	8
9	979.4250	490.2161			961.4144	481.2108	Y	***973.4171***	487.2122	955.3935	478.2004	955.4065	478.2069	7
10	**1167.4983**	584.2528			1149.4878	575.2475	W	***809.3567***	405.1820	791.3331	396.1702	791.3461	396.1767	6
11	1265.5481	633.2777			1247.5376	624.2724	P	***621.2833***	311.1453	603.2597	302.1335	603.2727	302.1400	5
12	**1381.5721**	691.2897			1363.5615	682.2844	D	523.2335	262.1204	505.2099	253.1086	505.2230	253.1151	4
13	1479.6219	740.3146			1461.6113	731.3093	P	***407.2095***	204.1084	389.1860	195.0966			3
14	**1609.6746**	805.3409	1591.6510	796.3291	1591.6640	796.3356	Q	309.1597	155.0835	291.1362	146.0717			2
15							R	179.1071	90.0572	161.0835	81.0454			1





AT3G63410.1

NCBI **BLAST** search of YVSAGSIEYWPDPQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.6	1786.7671	-0.0025	YVSAGSIEYWPDPQR
5.9	1786.7608	0.0038	GTLMQMIGADWISSDK

AT3G63460.1

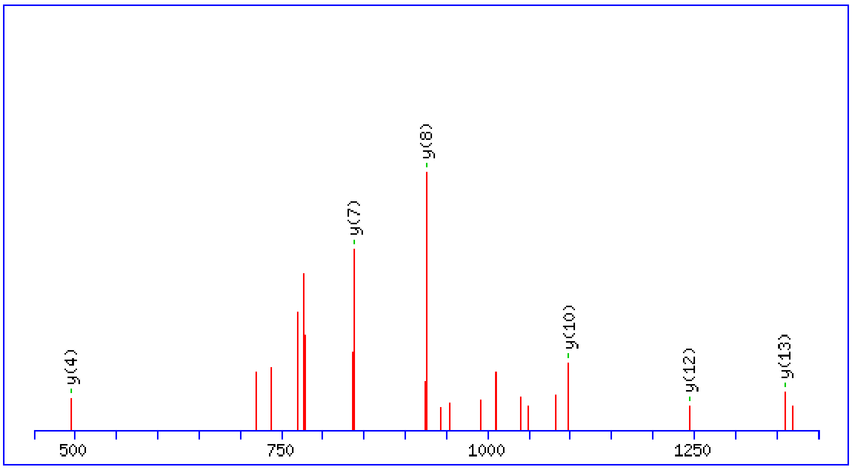
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLDSGGLSPELSILR**
Found in **AT3G63460.1** in **TAIR_Arabidopsis**, Symbols: | WD-40 repeat family protein | chr3:23441984-23448216 REVERSE

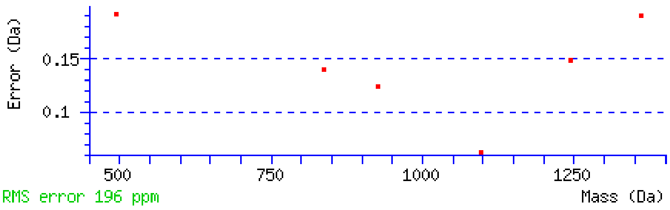
Match to Query 6826: 1572.803786 from(787.409169,2+) index(8369)
Title: Elution from: 73.760 to 73.760 scan no 11167 cid35.00 polarity:+
Data file C7-2_3.mgf

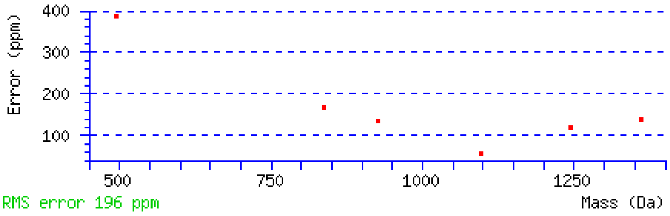
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1572.8084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 3.1e-005
Matches : 6/130 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							15
2	215.1538	108.0805			L	1473.7502	737.3787	1455.7266	728.3669	1455.7396	728.3734	14
3	331.1778	166.0925	313.1672	157.0873	D	***1359.6691***	680.3382	1341.6455	671.3264	1341.6585	671.3329	13
4	419.2069	210.1071	401.1963	201.1018	S	***1243.6451***	622.3262	1225.6215	613.3144	1225.6345	613.3209	12
5	477.2254	239.1163	459.2148	230.1110	G	1155.6160	578.3117	1137.5925	569.2999	1137.6055	569.3064	11
6	535.2439	268.1256	517.2333	259.1203	G	***1097.5975***	549.3024	1079.5740	540.2906	1079.5870	540.2971	10
7	649.3250	325.1661	631.3144	316.1608	L	1039.5790	520.2932	1021.5555	511.2814	1021.5685	511.2879	9
8	737.3540	369.1807	719.3435	360.1754	S	***925.4979***	463.2526	907.4744	454.2408	907.4874	454.2473	8
9	835.4038	418.2056	817.3933	409.2003	P	***837.4689***	419.2381	819.4453	410.2263	819.4583	410.2328	7
10	965.4435	483.2254	947.4329	474.2201	E	739.4191	370.2132	721.3955	361.2014	721.4085	361.2079	6
11	1079.5246	540.2659	1061.5140	531.2606	L	609.3795	305.1934	591.3559	296.1816	591.3689	296.1881	5
12	1167.5536	584.2804	1149.5430	575.2752	S	***495.2984***	248.1528	477.2748	239.1410	477.2878	239.1475	4
13	1281.6347	641.3210	1263.6241	632.3157	I	407.2693	204.1383	389.2457	195.1265			3
14	1395.7158	698.3615	1377.7052	689.3563	L	293.1882	147.0977	275.1646	138.0859			2
15					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VLDSGGLSPELSILR

AT3G63460.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.0	1572.8084	-0.0046	VLDSGGLSPELSILR
2.9	1572.8007	0.0031	RIPRGGSNPIQIDK
1.4	1572.8002	0.0036	IFTHNSTIPGQIVK
0.9	1572.8025	0.0013	AIGLNFIDVYFRK

AT3G63490.1

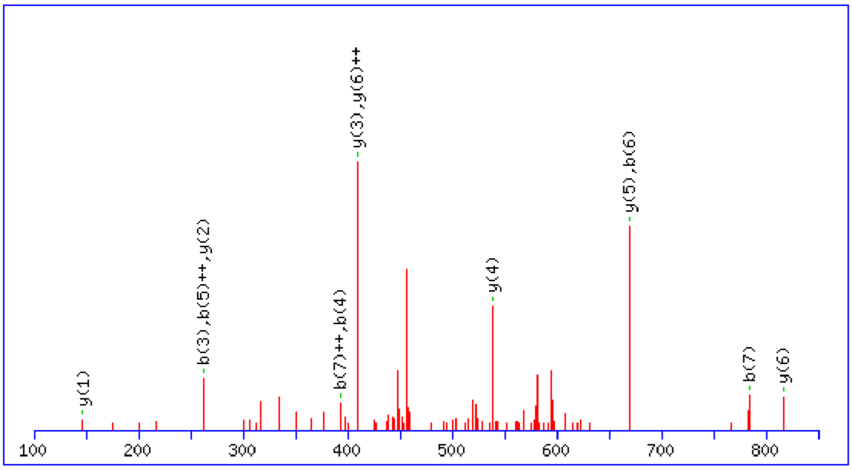
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGFMEFDK**
Found in **AT3G63490.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L1 family protein | chr3:23455244-23456995 FORWARD

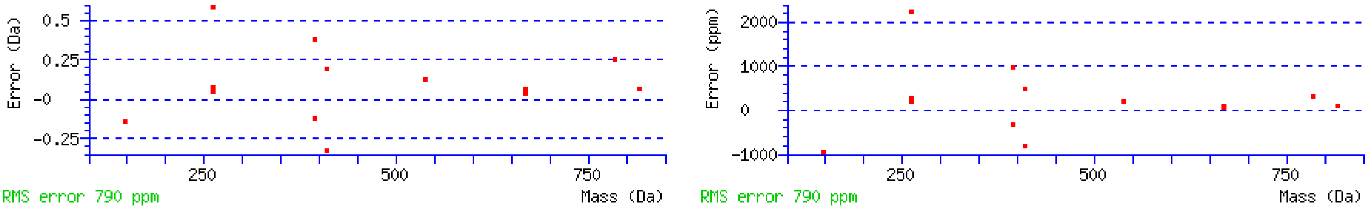
Match to Query 1486: 929.396370 from(465.705461,2+) index(4360)
Title: Elution from: 42.423 to 42.423 scan no 5612 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 929.3953
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 2.1e-005
Matches : 13/60 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							8
2	115.0502	58.0287			G	873.3811	437.1942	856.3546	428.6809	855.3706	428.1889	7
3	**262.1186**	131.5629			F	***816.3597***	408.6835	799.3331	400.1702	798.3491	399.6782	6
4	**393.1591**	197.0832			M	***669.2912***	335.1493	652.2647	326.6360	651.2807	326.1440	5
5	522.2017	**261.6045**	504.1911	252.5992	E	***538.2508***	269.6290	521.2242	261.1157	520.2402	260.6237	4
6	**669.2701**	335.1387	651.2595	326.1334	F	***409.2082***	205.1077	392.1816	196.5944	391.1976	196.1024	3
7	**784.2971**	**392.6522**	766.2865	383.6469	D	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
8					K	***147.1128***	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of GGFMEFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.8	929.3953	0.0011	GGFMEFDK
21.5	929.3938	0.0026	SSSSSSSSSK

9.8	929.3953	0.0010	FCDFVDK
9.6	929.3987	-0.0023	DMMFNLK
1.5	929.3955	0.0009	MMMKAMR
1.5	929.3955	0.0009	MMMKAMR

AT4G00200.1

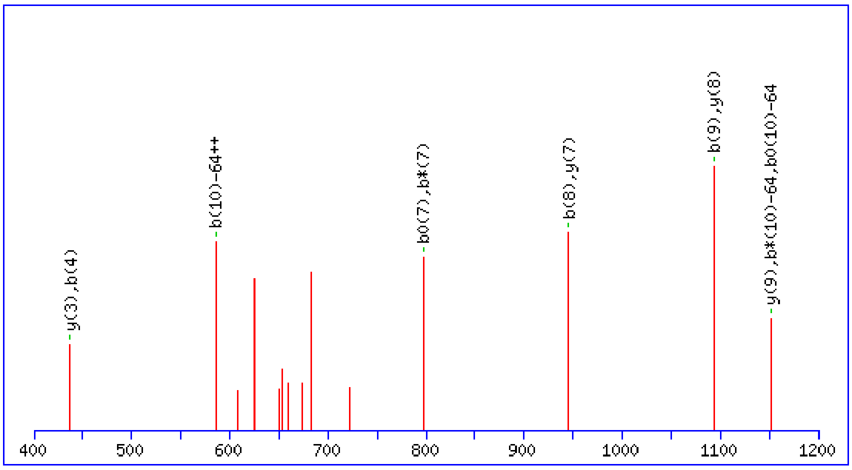
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNGFDMKKMHK**
Found in **AT4G00200.1** in **TAIR_Arabidopsis**, Symbols: | DNA binding | chr4:82653-84104 REVERSE

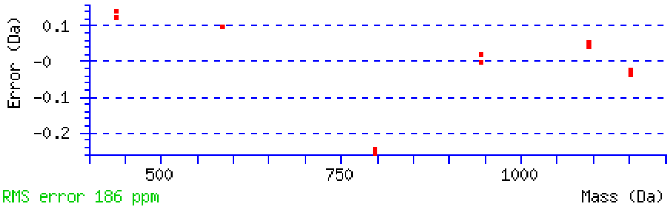
Match to Query 5101: 1380.624198 from(691.319375,2+) index(9978)
Title: Elution from: 93.616 to 93.616 scan no 14141 cid35.00 polarity:+
Data file D12h-1_3.mgf

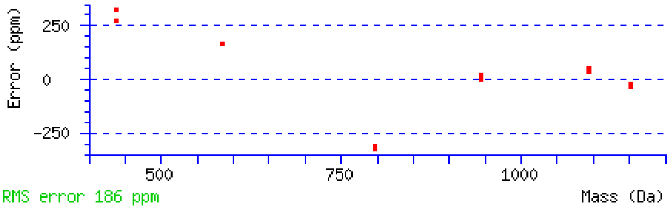
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1380.6237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 **Expect:** 0.0017
Matches : 12/150 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							11
2	231.1254	116.0663	213.1018	107.0545			N	1267.5498	634.2786	1249.5263	625.2668	1249.5393	625.2733	10
3	289.1439	145.0756	271.1203	136.0638			G	***1151.5128***	576.2601	1133.4893	567.2483	1133.5023	567.2548	9
4	***437.2093***	219.1083	419.1857	210.0965			F	***1093.4943***	547.2508	1075.4708	538.2390	1075.4838	538.2455	8
5	553.2333	277.1203	535.2097	268.1085	535.2227	268.1150	D	***945.4289***	473.2181	927.4053	464.2063	927.4183	464.2128	7
6	685.2708	343.1390	667.2472	334.1273	667.2603	334.1338	M	829.4049	415.2061	811.3813	406.1943			6
7	815.3599	408.1836	797.3363	399.1718	797.3493	399.1783	K	697.3674	349.1873	679.3438	340.1755			5
8	***945.4489***	473.2281	927.4253	464.2163	927.4383	464.2228	K	567.2784	284.1428	549.2548	275.1310			4
9	***1093.4813***	547.2443	1075.4577	538.2325	1075.4708	538.2390	M	***437.1893***	219.0983	419.1657	210.0865			3
10	1233.5313	617.2693	1215.5078	608.2575	1215.5208	608.2640	H	289.1569	145.0821	271.1333	136.0703			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LNGFDMKKMHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G00200.1

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.9	1380.6237	0.0005	LNGFDMKKMHK	Oxidation M9 97.11%
21.6	1380.6237	0.0005	LNGFDMKKMHK	Oxidation M6 2.89%
2.6	1380.6228	0.0014	EVGSSWIDSRTK	
2.0	1380.6228	0.0014	ISFPEESSGKQR	
1.8	1380.6210	0.0032	MDLEMFLGVQGK	
0.5	1380.6257	-0.0015	LDTGETVVEFMK	

AT4G00790.1

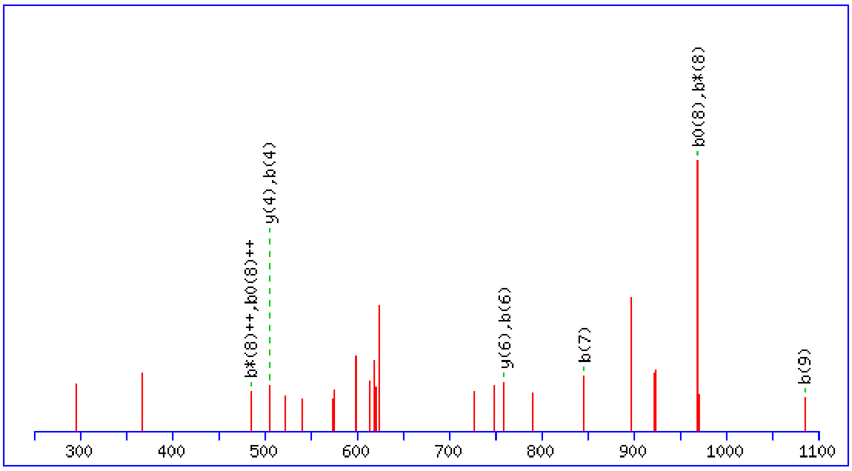
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQEQLHSHPR**
Found in **AT4G00790.1** in **TAIR_Arabidopsis**, Symbols: | DNA binding / binding / protein binding / zinc ion binding | chr4:337114-340602 REVERSE

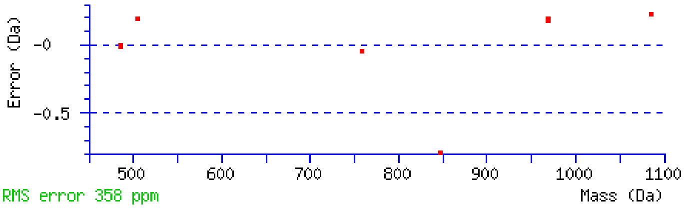
Match to Query 3977: 1262.587172 from(632.300862,2+) index(4566)
Title: Elution from: 45.399 to 45.399 scan no 5884 cid35.00 polarity:+
Data file D1d-1-2.mgf

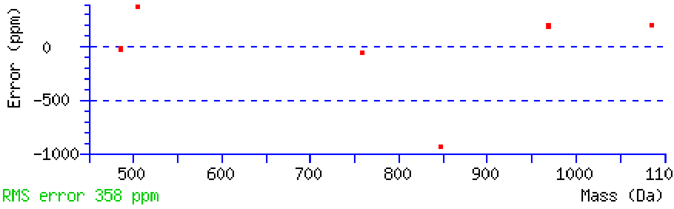
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1262.5858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0074
Matches : 10/96 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							10
2	245.1410	123.0741	227.1174	114.0624			Q	1149.5120	575.2596	1131.4884	566.2479	1131.5014	566.2544	9
3	375.1806	188.0940	357.1571	179.0822	357.1701	179.0887	E	1019.4594	510.2333	1001.4358	501.2215	1001.4488	501.2280	8
4	***505.2333***	253.1203	487.2097	244.1085	487.2227	244.1150	Q	889.4197	445.2135	871.3961	436.2017	871.4092	436.2082	7
5	619.3144	310.1608	601.2908	301.1490	601.3038	301.1556	L	**759.3671**	380.1872	741.3435	371.1754	741.3565	371.1819	6
6	***759.3644***	380.1858	741.3408	371.1741	741.3538	371.1806	H	645.2860	323.1466	627.2624	314.1348	627.2754	314.1413	5
7	***847.3935***	424.2004	829.3699	415.1886	829.3829	415.1951	S	**505.2360**	253.1216	487.2124	244.1098	487.2254	244.1163	4
8	987.4435	494.2254	969.4199	485.2136	969.4329	485.2201	H	417.2069	209.1071	399.1833	200.0953			3
9	***1085.4933***	543.2503	1067.4697	534.2385	1067.4827	534.2450	P	277.1569	139.0821	259.1333	130.0703			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IQEQLHSHPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G00790.1

Score	Mr(calc)	Delta	Sequence
30.5	1262.5858	0.0013	IQEQLHSHPR
3.6	1262.5892	-0.0020	LNADQRPRMK
2.6	1262.5865	0.0007	NTVLVDAISCR
1.6	1262.5865	0.0006	LDESQRPKMK
1.2	1262.5888	-0.0016	CAIPLQYLDR
1.2	1262.5865	0.0007	MVDANGKLLDR
1.2	1262.5836	0.0036	QIRDIQNSNR
0.8	1262.5892	-0.0020	MSETRPVPRR
0.6	1262.5888	-0.0016	FMTLNPGTVPR
0.0	1262.5880	-0.0009	QRDGAPFLWR

AT4G01010.1

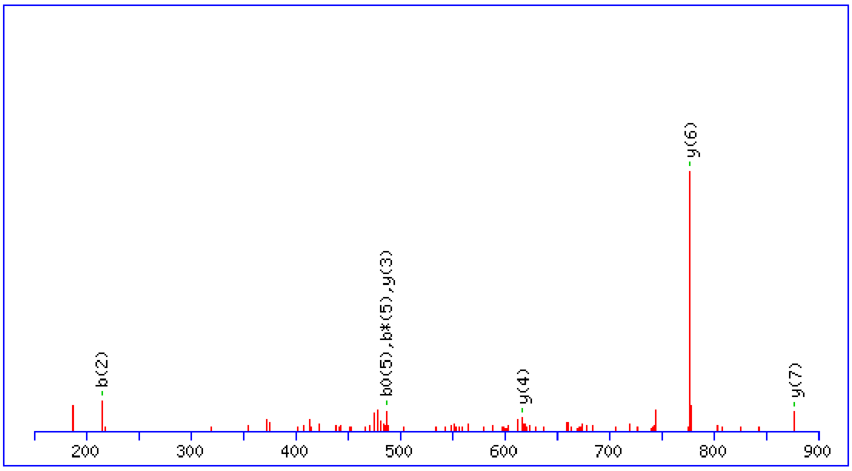
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVASQFRR**
Found in **AT4G01010.1** in **TAIR_Arabidopsis**, Symbols: CNGC13, ATCNGC13 | ATCNGC13 (cyclic nucleotide gated channel 13); calmodulin binding / cyclic nucleotide binding / ion channel | chr4:434569-437242 REVERSE

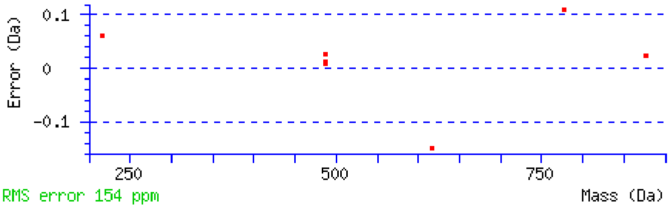
Match to Query 2358: 990.515562 from(496.265057,2+) index(6286)
Title: Elution from: 56.036 to 56.036 scan no 8112 cid35.00 polarity:+
Data file 0-2_2.mgf

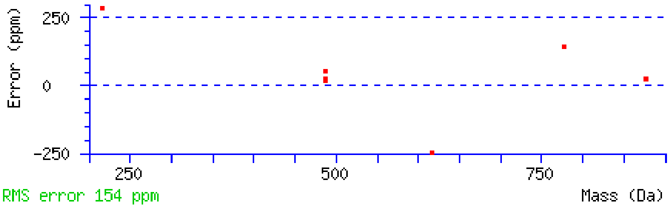
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 990.5169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.016
Matches : 7/62 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							8
2	215.1538	108.0805					V	***877.4431***	439.2252	859.4195	430.2134	859.4325	430.2199	7
3	287.1880	144.0976					A	***777.3777***	389.1925	759.3541	380.1807	759.3671	380.1872	6
4	375.2170	188.1122			357.2065	179.1069	S	705.3435	353.1754	687.3199	344.1636	687.3329	344.1701	5
5	505.2697	253.1385	487.2461	244.1267	487.2591	244.1332	Q	***617.3144***	309.1609	599.2909	300.1491			4
6	653.3351	327.1712	635.3115	318.1594	635.3246	318.1659	F	***487.2618***	244.1345	469.2382	235.1227			3
7	813.4244	407.2158	795.4008	398.2040	795.4138	398.2105	R	339.1963	170.1018	321.1728	161.0900			2
8							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LVASQFRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.6	990.5169	-0.0013	LVASQFRR

AT4G01010.1

4.2	990.5138	0.0018	IVTLFYLD
3.9	990.5142	0.0013	IVINYTTR
3.9	990.5165	-0.0009	IVPGYYLR
3.9	990.5142	0.0013	IVSKVYDR
3.9	990.5165	-0.0009	LVFFPTTR
3.3	990.5143	0.0013	AINASTKFK

AT4G01050.1

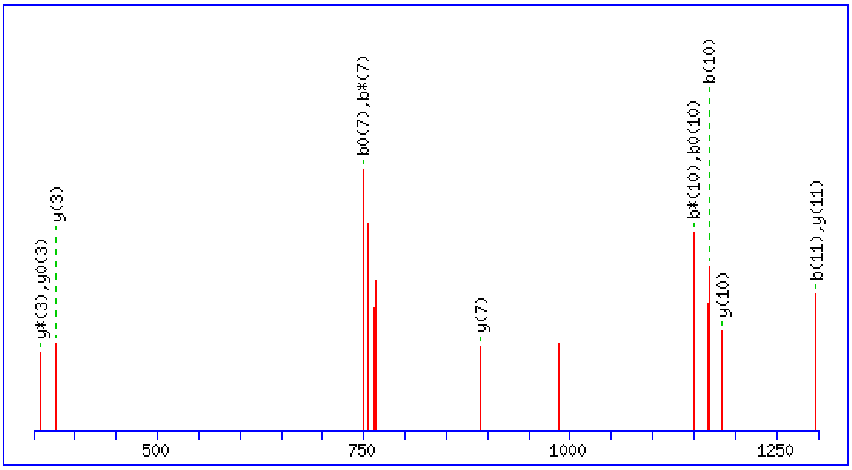
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GWLNSSLPWIEPK**
Found in **AT4G01050.1** in **TAIR_Arabidopsis**, Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:455874-458175 FORWARD

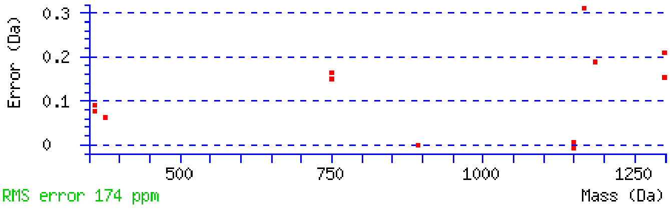
Match to Query 7119: 1542.747106 from(772.380829,2+) index(10311)
Title: Elution from: 93.402 to 93.402 scan no 14204 cid35.00 polarity:+
Data file D6h-1_1.mgf

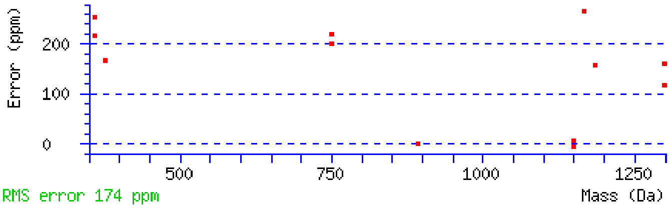
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1542.7425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0071
Matches : 12/126 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							13
2	247.0992	124.0532					W	1485.7313	743.3693	1467.7077	734.3575	1467.7207	734.3640	12
3	361.1803	181.0938					L	1297.6579	649.3326	1279.6343	640.3208	1279.6473	640.3273	11
4	477.2173	239.1123	459.1937	230.1005			N	1183.5768	592.2920	1165.5532	583.2802	1165.5662	583.2868	10
5	565.2463	283.1268	547.2227	274.1150	547.2358	274.1215	S	1067.5398	534.2735	1049.5162	525.2617	1049.5292	525.2683	9
6	653.2754	327.1413	635.2518	318.1295	635.2648	318.1360	S	979.5107	490.2590	961.4872	481.2472	961.5002	481.2537	8
7	767.3565	384.1819	749.3329	375.1701	749.3459	375.1766	L	891.4817	446.2445	873.4581	437.2327	873.4711	437.2392	7
8	865.4063	433.2068	847.3827	424.1950	847.3957	424.2015	P	777.4006	389.2039	759.3770	380.1921	759.3900	380.1986	6
9	1053.4797	527.2435	1035.4561	518.2317	1035.4691	518.2382	W	679.3508	340.1790	661.3272	331.1672	661.3402	331.1737	5
10	1167.5608	584.2840	1149.5372	575.2722	1149.5502	575.2787	I	491.2774	246.1423	473.2538	237.1305	473.2668	237.1371	4
11	1297.6004	649.3038	1279.5768	640.2920	1279.5898	640.2985	E	377.1963	189.1018	359.1727	180.0900	359.1857	180.0965	3
12	1395.6502	698.3287	1377.6266	689.3169	1377.6396	689.3234	P	247.1567	124.0820	229.1331	115.0702			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GWLNSSLPWIEPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G01050.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.1	1542.7425	0.0046	GWLNSSLPWIEPK
3.2	1542.7511	-0.0040	FIRASSSSTSQKPK
1.9	1542.7429	0.0042	NKLRSSFWDTLR
1.1	1542.7436	0.0035	GGEFNKVAMSTKLK
0.9	1542.7484	-0.0013	KALEAGDDPTTALPK
0.7	1542.7437	0.0035	LIEMAYEKSKASR

AT4G01150.1

Mascot Search Results

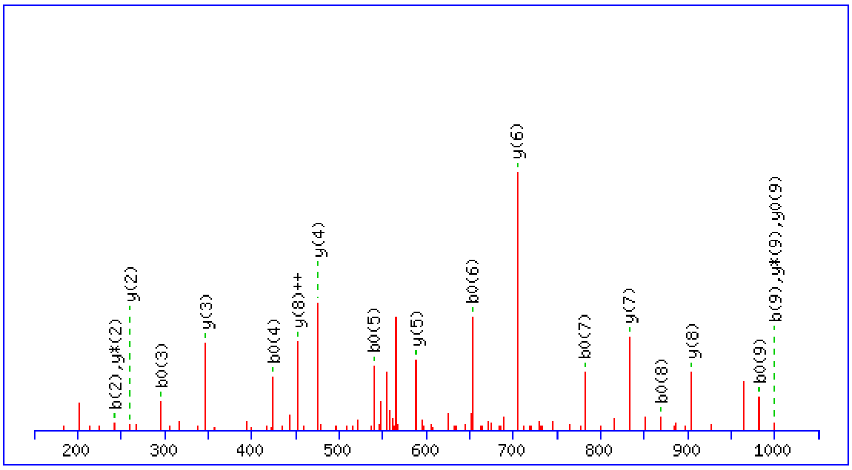
Peptide View

MS/MS Fragmentation of **ELAEDIESLK**
Found in **AT4G01150.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Uncharacterized protein At4g01150, chloroplast precursor [Arabidopsis Thaliana] (GB:O04616;GB:Q38835); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G38100.1); similar to unknown [Populus trichocarpa] (GB:ABK95

Match to Query 3213: 1145.582494 from(573.798523,2+) index(5060)
Title: Elution from: 48.029 to 48.029 scan no 6560 cid35.00 polarity:+
Data file D1d-1_3.mgf

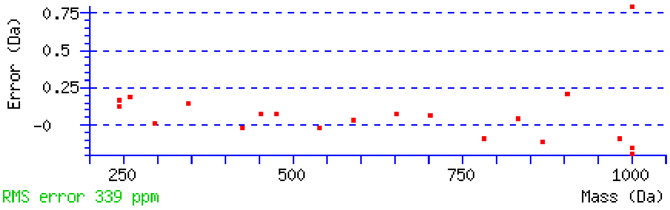
Click mouse within plot area to zoom in by factor of two about that point

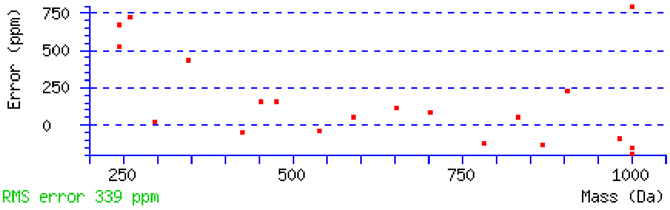
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1145.5815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 6.9e-006
Matches : 20/86 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	**243.1339**	122.0706	225.1234	113.0653	L	1017.5463	509.2768	1000.5197	500.7635	999.5357	500.2715	9
3	314.1710	157.5892	296.1605	148.5839	A	***904.4622***	452.7347	887.4357	444.2215	886.4516	443.7295	8
4	443.2136	222.1105	425.2031	213.1052	E	***833.4251***	417.2162	816.3985	408.7029	815.4145	408.2109	7
5	558.2406	279.6239	540.2300	270.6186	D	***704.3825***	352.6949	687.3559	344.1816	686.3719	343.6896	6
6	671.3246	336.1660	653.3141	327.1607	I	***589.3556***	295.1814	572.3290	286.6681	571.3450	286.1761	5
7	800.3672	400.6873	782.3567	391.6820	E	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	4
8	887.3993	444.2033	869.3887	435.1980	S	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	**1000.4833**	500.7453	982.4728	491.7400	L	***260.1969***	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ELAEDIESLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G01150.1

Score	Mr(calc)	Delta	Sequence
57.1	1145.5815	0.0010	ELAEDIESLK
12.4	1145.5816	0.0009	EALIDEITDK
12.4	1145.5816	0.0009	EALIDEVTEK

AT4G01310.1

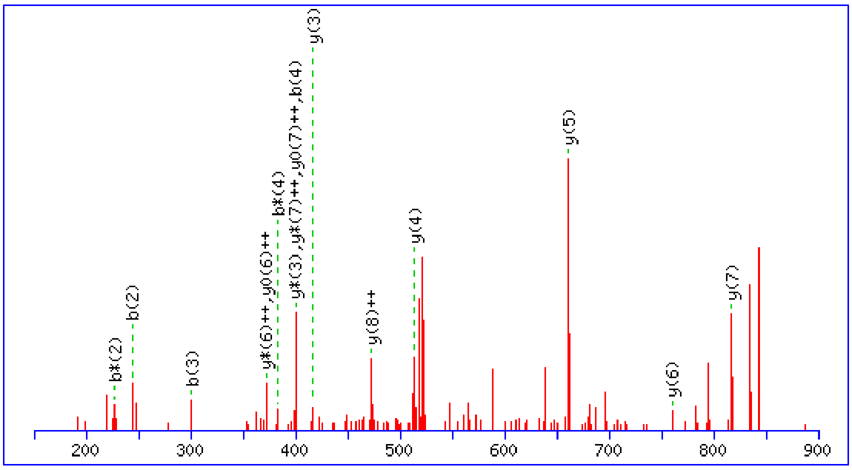
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQGVFPEIR**
Found in **AT4G01310.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L5 family protein | chr4:544166-545480 REVERSE

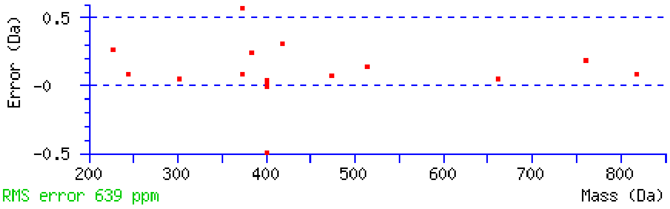
Match to Query 2914: 1059.537018 from(530.775785,2+) index(5364)
Title: Elution from: 47.683 to 47.683 scan no 6737 cid35.00 polarity:+
Data file 0-3_2.mgf

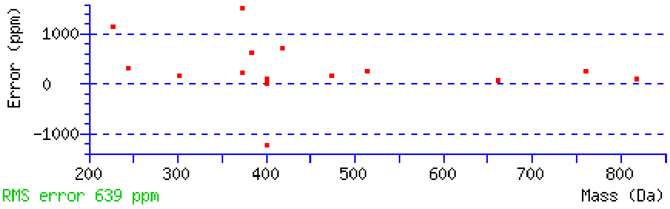
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1059.5349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.027
Matches : 16/90 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							9
2	**244.0928**	122.5500	227.0662	114.0368	226.0822	113.5448	Q	945.5152	473.2613	928.4887	464.7480	927.5047	464.2560	8
3	**301.1143**	151.0608	284.0877	142.5475	283.1037	142.0555	G	***817.4567***	409.2320	800.4301	400.7187	799.4461	400.2267	7
4	**400.1827**	200.5950	383.1561	192.0817	382.1721	191.5897	V	***760.4352***	380.7212	743.4087	372.2080	742.4246	371.7160	6
5	547.2511	274.1292	530.2245	265.6159	529.2405	265.1239	F	***661.3668***	331.1870	644.3402	322.6738	643.3562	322.1817	5
6	644.3039	322.6556	627.2773	314.1423	626.2933	313.6503	P	***514.2984***	257.6528	497.2718	249.1396	496.2878	248.6475	4
7	773.3464	387.1769	756.3199	378.6636	755.3359	378.1716	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
8	886.4305	443.7189	869.4040	435.2056	868.4199	434.7136	I	288.2030	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DQGVFPEIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.2	1059.5349	0.0021	DQGVFPEIR

AT4G01310.1

2.1	1059.5383	-0.0013	GTQSVNVMPK

Mascot: http://www.matrixscience.com/

AT4G01690.1

Mascot Search Results

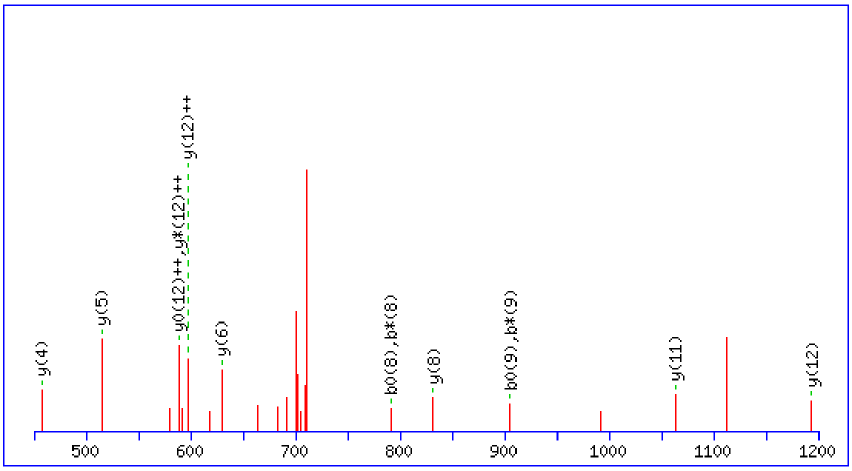
Peptide View

MS/MS Fragmentation of **LEQNGGSIIGGTFK**
Found in **AT4G01690.1** in **TAIR_Arabidopsis**, Symbols: HEMG1, PPOX | PPOX (PROTOPORPHYRINOGEN OXIDASE); protoporphyrinogen oxidase | chr4:729929-732309 FORWARD

Match to Query 5522: 1436.684916 from(719.349734,2+) index(4588)
Title: Elution from: 41.567 to 41.567 scan no 5735 cid35.00 polarity:+
Data file D12h-1_3.mgf

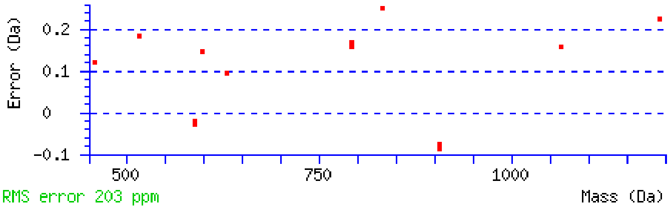
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

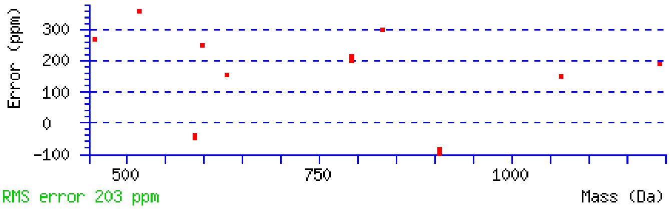


Monoisotopic mass of neutral peptide Mr(calc): 1436.6854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0032
Matches : 13/146 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**14**
2	245.1280	123.0676			227.1174	114.0624	**E**	1323.6116	662.3094	1305.5880	653.2976	1305.6010	653.3041	**13**
3	375.1806	188.0940	357.1571	179.0822	357.1701	179.0887	**Q**	***1193.5719***	597.2896	1175.5484	588.2778	1175.5614	588.2843	**12**
4	491.2176	246.1125	473.1941	237.1007	473.2071	237.1072	**N**	***1063.5193***	532.2633	1045.4957	523.2515	1045.5087	523.2580	**11**
5	549.2361	275.1217	531.2126	266.1099	531.2256	266.1164	**G**	947.4823	474.2448	929.4587	465.2330	929.4717	465.2395	**10**
6	607.2546	304.1310	589.2311	295.1192	589.2441	295.1257	**G**	889.4638	445.2355	871.4402	436.2237	871.4532	436.2303	**9**
7	695.2837	348.1455	677.2601	339.1337	677.2731	339.1402	**S**	***831.4453***	416.2263	813.4217	407.2145	813.4347	407.2210	**8**
8	809.3648	405.1860	791.3412	396.1742	791.3542	396.1808	**I**	743.4162	372.2118	725.3926	363.2000	725.4057	363.2065	**7**
9	923.4459	462.2266	905.4223	453.2148	905.4353	453.2213	**I**	***629.3351***	315.1712	611.3115	306.1594	611.3246	306.1659	**6**
10	981.4644	491.2358	963.4408	482.2240	963.4538	482.2306	**G**	***515.2540***	258.1307	497.2305	249.1189	497.2435	249.1254	**5**
11	1039.4829	520.2451	1021.4593	511.2333	1021.4723	511.2398	**G**	***457.2355***	229.1214	439.2120	220.1096	439.2250	220.1161	**4**
12	1141.5276	571.2674	1123.5040	562.2557	1123.5171	562.2622	**T**	399.2170	200.1122	381.1935	191.1004	381.2065	191.1069	**3**
13	1289.5931	645.3002	1271.5695	636.2884	1271.5825	636.2949	**F**	297.1723	149.0898	279.1487	140.0780			**2**
14							**K**	149.1069	75.0571	131.0833	66.0453			**1**



RMS error 203 ppm



RMS error 203 ppm

NCBI **BLAST** search of LEQNGGSIIGGTFK

AT4G01690.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.4	1436.6854	-0.0004	LEQNGGSIIGGTFK
9.0	1436.6854	-0.0004	EIQAAFRTDEIK
8.8	1436.6827	0.0022	LKELGYEISDEK
5.4	1436.6814	0.0036	KLMMLEKEEQK
5.4	1436.6814	0.0036	KLMMLEKEEQK
4.7	1436.6863	-0.0013	KYMALVIGCPPR
4.7	1436.6840	0.0009	AIGEMRKCVDLK
2.5	1436.6887	-0.0038	ELGKTAGKDVMAGK
2.4	1436.6887	-0.0038	TKGVNGLTMDKEK
1.8	1436.6854	-0.0004	FQKDGLESDLLR

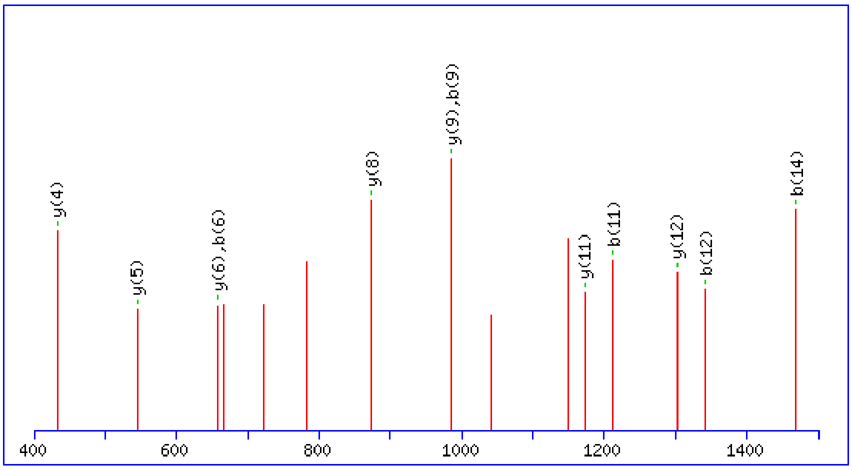
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQVESVINTIIEGAR**
Found in **AT4G01900.1** in **TAIR_Arabidopsis**, Symbols: P11, GLB1 | GLB1 (glutamine synthetase B1) | chr4:821736-823294 FORWARD

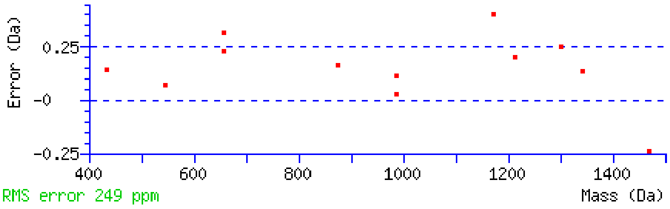
Match to Query 7423: 1642.848522 from(822.431537,2+) index(10743)
Title: Elution from: 106.922 to 106.922 scan no 15588 cid35.00 polarity:+
Data file D1d-1_1.mgf

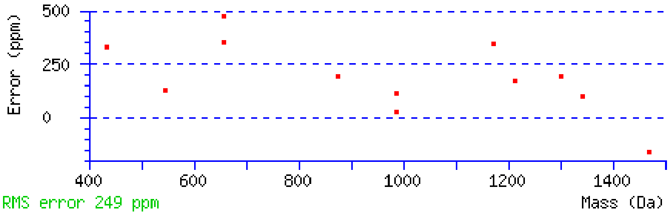
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1642.8526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.2e-005
Matches : 12/160 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**15**
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	**Q**	1528.8329	764.9201	1511.8064	756.4068	1510.8224	755.9148	**14**
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	**V**	1400.7744	700.8908	1383.7478	692.3775	1382.7638	691.8855	**13**
4	472.2038	236.6055	455.1773	228.0923	454.1932	227.6003	**E**	***1301.7060***	651.3566	1284.6794	642.8433	1283.6954	642.3513	**12**
5	559.2358	280.1216	542.2093	271.6083	541.2253	271.1163	**S**	***1172.6634***	586.8353	1155.6368	578.3220	1154.6528	577.8300	**11**
6	***658.3042***	329.6558	641.2777	321.1425	640.2937	320.6505	**V**	1085.6313	543.3193	1068.6048	534.8060	1067.6208	534.3140	**10**
7	771.3883	386.1978	754.3618	377.6845	753.3777	377.1925	**I**	***986.5629***	493.7851	969.5364	485.2718	968.5524	484.7798	**9**
8	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	**N**	***873.4789***	437.2431	856.4523	428.7298	855.4683	428.2378	**8**
9	***986.4789***	493.7431	969.4524	485.2298	968.4684	484.7378	**T**	759.4359	380.2216	742.4094	371.7083	741.4254	371.2163	**7**
10	1099.5630	550.2851	1082.5364	541.7719	1081.5524	541.2798	**I**	***658.3883***	329.6978	641.3617	321.1845	640.3777	320.6925	**6**
11	***1212.6470***	606.8272	1195.6205	598.3139	1194.6365	597.8219	**I**	***545.3042***	273.1557	528.2776	264.6425	527.2936	264.1504	**5**
12	***1341.6896***	671.3485	1324.6631	662.8352	1323.6791	662.3432	**E**	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	**4**
13	1398.7111	699.8592	1381.6846	691.3459	1380.7005	690.8539	**G**	303.1775	152.0924	286.1510	143.5791			**3**
14	***1469.7482***	735.3777	1452.7217	726.8645	1451.7376	726.3725	**A**	246.1561	123.5817	229.1295	115.0684			**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DQVESVINTIIEGAR

AT4G01900.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.6	1642.8526	-0.0041	DQVESVINTIIEGAR
2.4	1642.8514	-0.0029	MAHSLIIHYHLHR

Mascot: http://www.matrixscience.com/

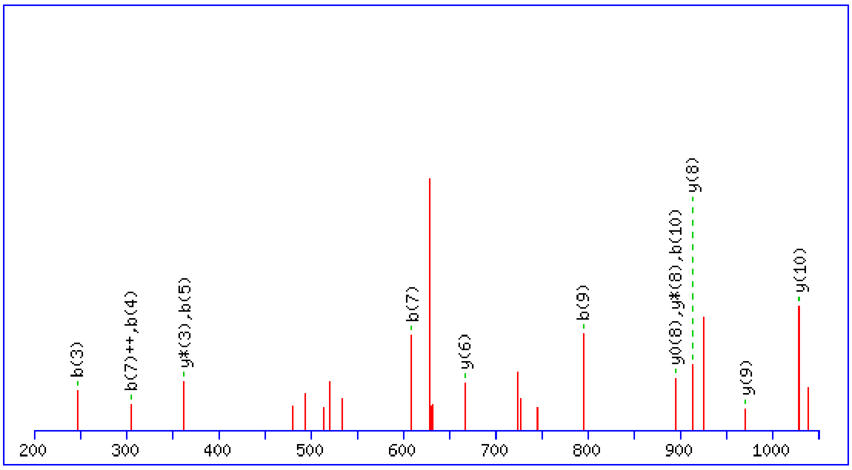
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSGGDQSPVARK**
Found in **AT4G02110.1** in **TAIR_Arabidopsis**, Symbols: | BRCT domain-containing protein | chr4:935191-940191 FORWARD

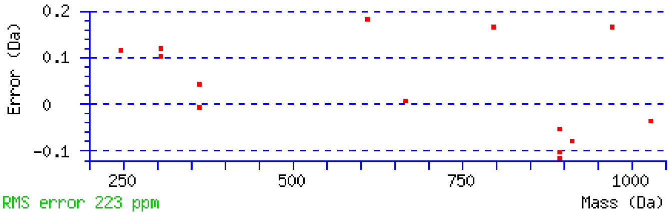
Match to Query 4161: 1274.594486 from(638.304519,2+) index(3511)
Title: Elution from: 34.964 to 34.964 scan no 4464 cid35.00 polarity:+
Data file D12h-2_3.mgf

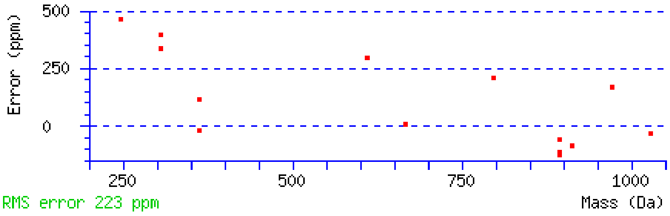
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1274.5939
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0018
Matches : 14/118 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							13
2	159.0912	80.0492					G	1175.5358	588.2715	1157.5122	579.2597	1157.5252	579.2662	12
3	***247.1203***	124.0638			229.1097	115.0585	S	1117.5173	559.2623	1099.4937	550.2505	1099.5067	550.2570	11
4	***305.1388***	153.0730			287.1282	144.0677	G	**1029.4882**	515.2477	1011.4646	506.2360	1011.4776	506.2425	10
5	***363.1573***	182.0823			345.1467	173.0770	G	**971.4697**	486.2385	953.4461	477.2267	953.4591	477.2332	9
6	479.1813	240.0943			461.1707	231.0890	D	**913.4512**	457.2292	895.4276	448.2175	895.4406	448.2240	8
7	***609.2339***	305.1206	591.2103	296.1088	591.2233	296.1153	Q	797.4272	399.2173	779.4036	390.2055	779.4167	390.2120	7
8	697.2630	349.1351	679.2394	340.1233	679.2524	340.1298	S	**667.3746**	334.1909	649.3510	325.1791	649.3640	325.1856	6
9	***795.3128***	398.1600	777.2892	389.1482	777.3022	389.1547	P	579.3455	290.1764	561.3219	281.1646			5
10	***895.3782***	448.1927	877.3546	439.1810	877.3677	439.1875	V	481.2957	241.1515	463.2721	232.1397			4
11	967.4124	484.2098	949.3888	475.1980	949.4018	475.2045	A	381.2303	191.1188	363.2067	182.1070			3
12	1127.5016	564.2544	1109.4780	555.2427	1109.4911	555.2492	R	309.1961	155.1017	291.1725	146.0899			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VGSGGDQSPVARK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G02110.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.8	1274.5939	0.0006	VGSGGDQSPVARK
15.0	1274.5957	-0.0012	DKDFPVIWDK
12.6	1274.5969	-0.0024	VAMDALDEAAKK
10.0	1274.5912	0.0032	ETQNQGELTLK
9.9	1274.5939	0.0006	KVGSGGDQSPVAR
9.9	1274.5912	0.0032	KDDEIVQANTK
9.7	1274.5913	0.0032	EKKTNDPDSVK
7.8	1274.5939	0.0005	RINSEGPESLR
7.0	1274.5912	0.0032	DDEKLSVTTPR
4.5	1274.5969	-0.0024	AETKNDVPMIK

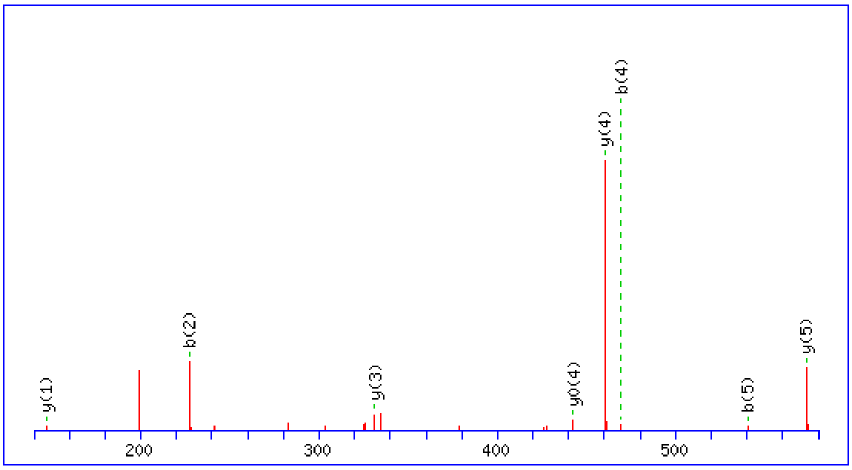
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEIAK**
Found in **AT4G02405.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO40030.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68023.1); contains domain S-adenosyl-L-methionine-dependent methyltransferases (SSF53335) | chr4:1057999-105967

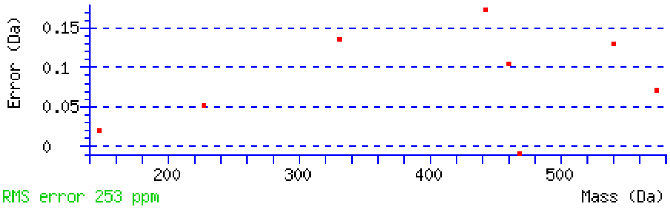
Match to Query 627: 685.437552 from(343.726052,2+) index(2073)
Title: Elution from: 24.493 to 24.493 scan no 2682 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

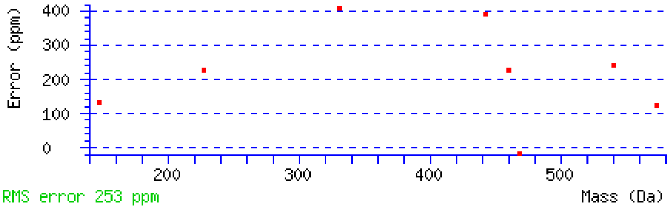


Monoisotopic mass of neutral peptide Mr(calc): 685.4374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0068
Matches : 8/40 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			**L**							**6**
2	***227.1754***	114.0913			**L**	***573.3606***	287.1840	556.3341	278.6707	555.3501	278.1787	**5**
3	356.2180	178.6126	338.2074	169.6074	**E**	***460.2766***	230.6419	443.2500	222.1287	442.2660	221.6366	**4**
4	***469.3021***	235.1547	451.2915	226.1494	**I**	***331.2340***	166.1206	314.2074	157.6074			**3**
5	***540.3392***	270.6732	522.3286	261.6679	**A**	218.1499	109.5786	201.1234	101.0653			**2**
6					**K**	***147.1128***	74.0600	130.0863	65.5468			**1**



RMS error 253 ppm



RMS error 253 ppm

NCBI **BLAST** search of LLEIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.9	685.4374	0.0002	LLEIAK
26.9	685.4374	0.0002	IIEALK

AT4G02405.1

26.9	685.4374	0.0002	ILEAIK
26.9	685.4374	0.0002	ILEALK
26.9	685.4374	0.0002	LIEALK
18.8	685.4374	0.0002	ILAEIK
18.8	685.4374	0.0002	ILAELK
18.3	685.4374	0.0001	LLVDVK
15.3	685.4374	0.0001	LLAVSAI
9.6	685.4374	0.0002	IEILAK

AT4G02450.1

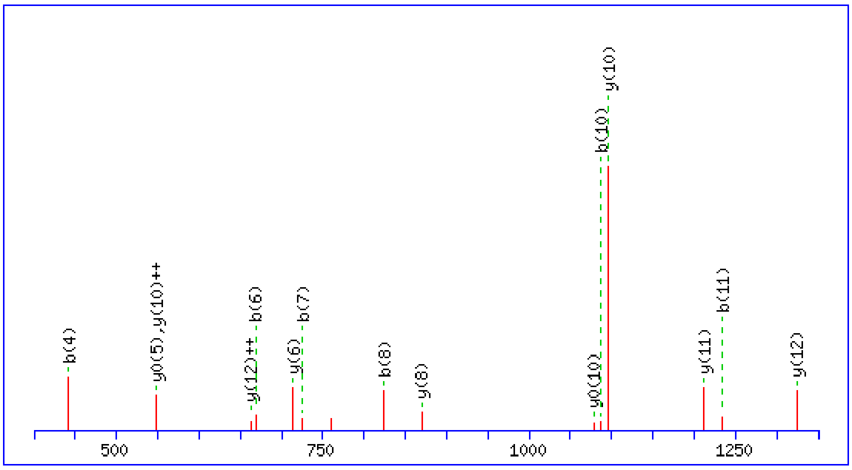
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNLDPEGVFDFSAK**
Found in **AT4G02450.1** in **TAIR_Arabidopsis**, Symbols: | glycine-rich protein | chr4:1073987-1075765 REVERSE

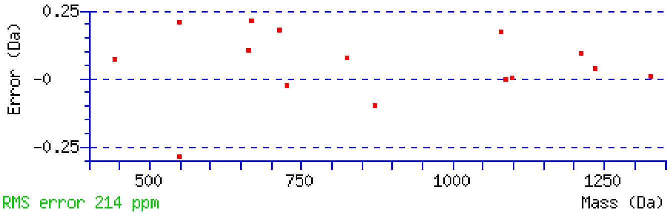
Match to Query 6514: 1536.746866 from(769.380709,2+) index(8846)
Title: Elution from: 80.045 to 80.045 scan no 11998 cid35.00 polarity:+
Data file D6h-1_3.mgf

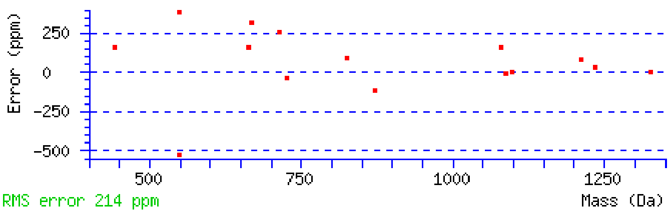
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1536.7460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 3.3e-007
Matches : 15/144 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							14
2	214.1186	107.5629	197.0921	99.0497			N	1438.6849	719.8461	1421.6583	711.3328	1420.6743	710.8408	13
3	327.2027	164.1050	310.1761	155.5917			L	***1324.6420***	662.8246	1307.6154	654.3113	1306.6314	653.8193	12
4	***442.2296***	221.6185	425.2031	213.1052	424.2191	212.6132	D	***1211.5579***	606.2826	1194.5313	597.7693	1193.5473	597.2773	11
5	539.2824	270.1448	522.2558	261.6316	521.2718	261.1395	P	***1096.5310***	548.7691	1079.5044	540.2558	1078.5204	539.7638	10
6	***668.3250***	334.6661	651.2984	326.1529	650.3144	325.6608	E	999.4782	500.2427	982.4516	491.7295	981.4676	491.2374	9
7	***725.3464***	363.1769	708.3199	354.6636	707.3359	354.1716	G	***870.4356***	435.7214	853.4090	427.2082	852.4250	426.7162	8
8	***824.4149***	412.7111	807.3883	404.1978	806.4043	403.7058	V	813.4141	407.2107	796.3876	398.6974	795.4036	398.2054	7
9	971.4833	486.2453	954.4567	477.7320	953.4727	477.2400	F	***714.3457***	357.6765	697.3192	349.1632	696.3352	348.6712	6
10	***1086.5102***	543.7587	1069.4837	535.2455	1068.4997	534.7535	D	567.2773	284.1423	550.2508	275.6290	549.2667	275.1370	5
11	***1233.5786***	617.2930	1216.5521	608.7797	1215.5681	608.2877	F	452.2504	226.6288	435.2238	218.1155	434.2398	217.6235	4
12	1320.6107	660.8090	1303.5841	652.2957	1302.6001	651.8037	S	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
13	1391.6478	696.3275	1374.6212	687.8142	1373.6372	687.3222	A	218.1499	109.5786	201.1234	101.0653			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VNLDPEGVFDFSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G02450.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.2	1536.7460	0.0008	VNLDPEGVFDFSAK

Mascot: http://www.matrixscience.com/

AT4G02520.1

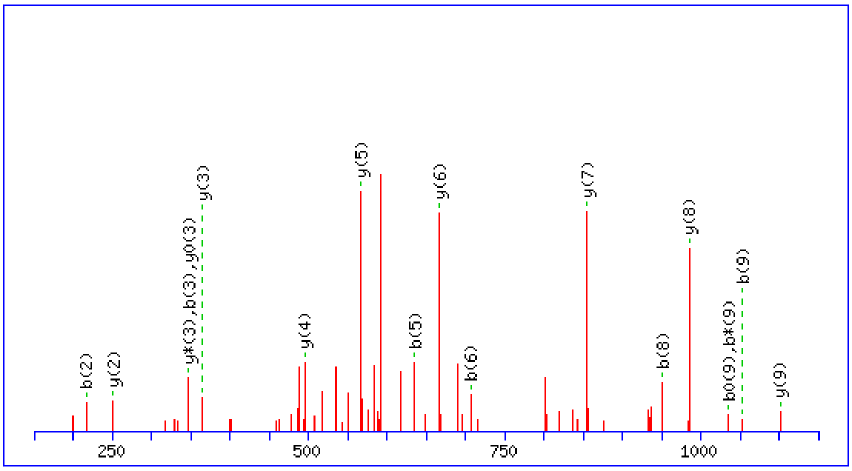
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNEWVAEITK**
Found in **AT4G02520.1** in **TAIR_Arabidopsis**, Symbols: ATPM24.1, ATPM24, GST2, ATGSTF2 | ATGSTF2 (Arabidopsis thaliana Glutathione S-transferase (class phi) 2); glutathione transferase | chr4:1110673-1111531 REVERSE

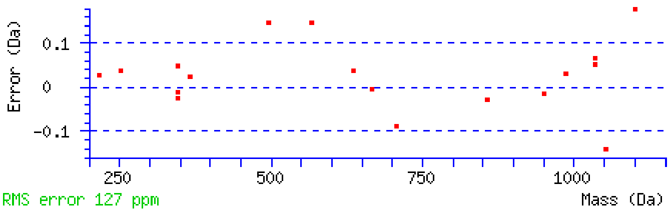
Match to Query 3910: 1200.577118 from(601.295835,2+) index(5706)
Title: Elution from: 50.142 to 50.142 scan no 7281 cid35.00 polarity:+
Data file D6h-3_3.mgf

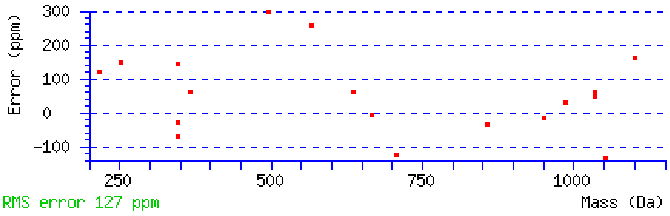
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1200.5801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.7e-007
Matches : 18/100 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400					V							10
2	**217.1097**	109.0585	199.0861	100.0467			N	***1101.5219***	551.2646	1083.4983	542.2528	1083.5114	542.2593	9
3	**347.1493**	174.0783	329.1258	165.0665	329.1388	165.0730	E	***985.4849***	493.2461	967.4613	484.2343	967.4744	484.2408	8
4	535.2227	268.1150	517.1991	259.1032	517.2122	259.1097	W	***855.4453***	428.2263	837.4217	419.2145	837.4347	419.2210	7
5	**635.2882**	318.1477	617.2646	309.1359	617.2776	309.1424	V	***667.3719***	334.1896	649.3483	325.1778	649.3613	325.1843	6
6	**707.3223**	354.1648	689.2987	345.1530	689.3118	345.1595	A	***567.3065***	284.1569	549.2829	275.1451	549.2959	275.1516	5
7	837.3620	419.1846	819.3384	410.1728	819.3514	410.1793	E	***495.2723***	248.1398	477.2487	239.1280	477.2617	239.1345	4
8	**951.4431**	476.2252	933.4195	467.2134	933.4325	467.2199	I	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
9	**1053.4878**	527.2475	1035.4642	518.2357	1035.4772	518.2422	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VNEWVAEITK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G02520.1

Score	Mr(calc)	Delta	Sequence
76.1	1200.5801	-0.0030	VNEWVAEITK
12.5	1200.5805	-0.0034	VQNQDISPKR
11.8	1200.5805	-0.0034	VQNQQQVVNK
10.3	1200.5778	-0.0007	VGGEDVDQLKK
9.2	1200.5778	-0.0007	DIDGKDVALNK
6.5	1200.5778	-0.0007	EDVLKNNDLK
5.1	1200.5778	-0.0007	DKGLDGIVNEK
1.7	1200.5779	-0.0007	VDNSSLITNPK
1.3	1200.5778	-0.0007	EVKPNSGDLTK
0.0	1200.5778	-0.0007	DVLRVDSVPTS

AT4G02530.1

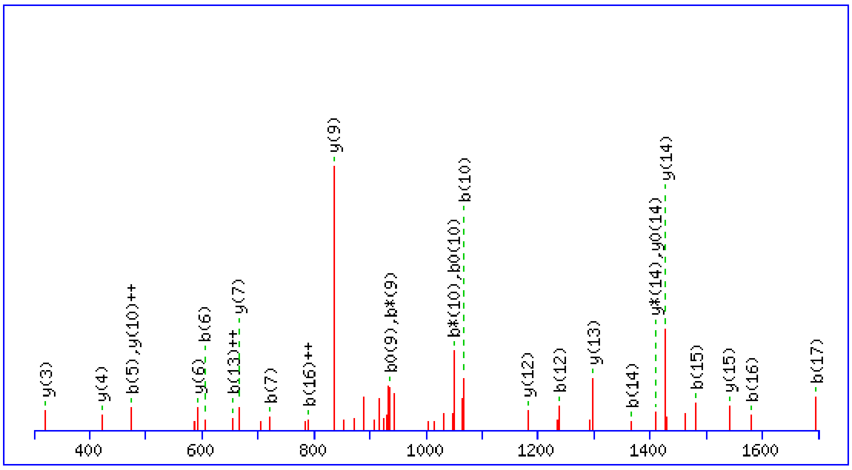
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGQAIENNDLPAAGLVLGK**
Found in **AT4G02530.1** in **TAIR_Arabidopsis**, Symbols: | chloroplast thylakoid lumen protein | chr4:1112335-1114005 REVERSE

Match to Query 9170: 1900.951028 from(951.482790,2+) index(7857)
Title: Elution from: 69.406 to 69.406 scan no 10302 cid35.00 polarity:+
Data file D6h-3_1.mgf

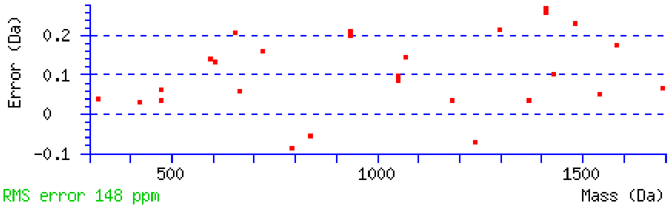
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

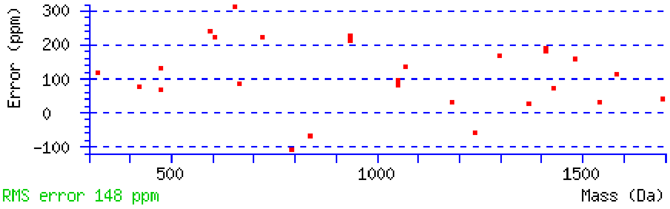


Monoisotopic mass of neutral peptide Mr(calc): 1900.9529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 4.5e-010
Matches : 27/182 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							19
2	159.0912	80.0492					G	1801.8947	901.4510	1783.8711	892.4392	1783.8841	892.4457	18
3	289.1439	145.0756	271.1203	136.0638			Q	1743.8762	872.4417	1725.8526	863.4300	1725.8656	863.4365	17
4	361.1780	181.0926	343.1544	172.0809			A	1613.8236	807.4154	1595.8000	798.4036	1595.8130	798.4101	16
5	***475.2591***	238.1332	457.2355	229.1214			I	***1541.7894***	771.3983	1523.7658	762.3866	1523.7788	762.3931	15
6	***605.2987***	303.1530	587.2752	294.1412	587.2882	294.1477	E	***1427.7083***	714.3578	1409.6847	705.3460	1409.6978	705.3525	14
7	***721.3357***	361.1715	703.3122	352.1597	703.3252	352.1662	N	***1297.6687***	649.3380	1279.6451	640.3262	1279.6581	640.3327	13
8	837.3727	419.1900	819.3492	410.1782	819.3622	410.1847	N	***1181.6317***	591.3195	1163.6081	582.3077	1163.6211	582.3142	12
9	953.3967	477.2020	935.3731	468.1902	935.3862	468.1967	D	1065.5947	533.3010	1047.5711	524.2892	1047.5841	524.2957	11
10	***1067.4778***	534.2425	1049.4542	525.2308	1049.4673	525.2373	L	949.5707	475.2890	931.5471	466.2772			10
11	1165.5276	583.2674	1147.5040	574.2557	1147.5171	574.2622	P	***835.4896***	418.2484	817.4660	409.2367			9
12	***1237.5618***	619.2845	1219.5382	610.2727	1219.5512	610.2792	A	737.4398	369.2235	719.4162	360.2118			8
13	1309.5959	**655.3016**	1291.5723	646.2898	1291.5854	646.2963	A	***665.4057***	333.2065	647.3821	324.1947			7
14	***1367.6144***	684.3108	1349.5908	675.2991	1349.6038	675.3056	G	***593.3715***	297.1894	575.3479	288.1776			6
15	***1481.6955***	741.3514	1463.6719	732.3396	1463.6849	732.3461	L	535.3530	268.1801	517.3294	259.1684			5
16	***1581.7610***	**791.3841**	1563.7374	782.3723	1563.7504	782.3788	V	***421.2719***	211.1396	403.2483	202.1278			4
17	***1695.8421***	848.4247	1677.8185	839.4129	1677.8315	839.4194	L	***321.2065***	161.1069	303.1829	152.0951			3
18	1753.8606	877.4339	1735.8370	868.4221	1735.8500	868.4286	G	207.1254	104.0663	189.1018	95.0545			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT4G02530.1





NCBI **BLAST** search of VGQAIENNDLPAAGLVLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
99.7	1900.9529	-0.0018	VGQAIENNDLPAAGLVLGK
1.0	1900.9466	0.0045	AVGEPPFFLAASAFFAIK
0.9	1900.9556	-0.0045	SIQEKLERSHVTLAHK

Mascot: http://www.matrixscience.com/

AT4G02770.1

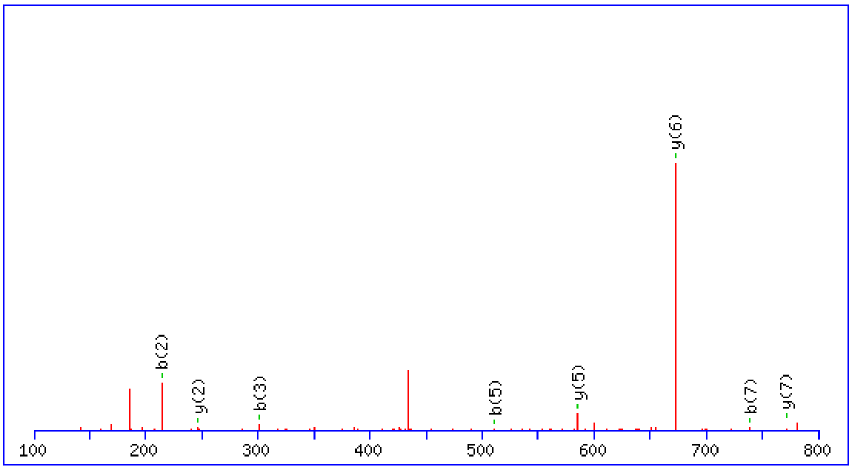
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVSPIEVK**
Found in **AT4G02770.1** in **TAIR_Arabidopsis**, Symbols: PSAD-1 | PSAD-1 (photosystem I subunit D-1) | chr4:1229247-1229873 REVERSE

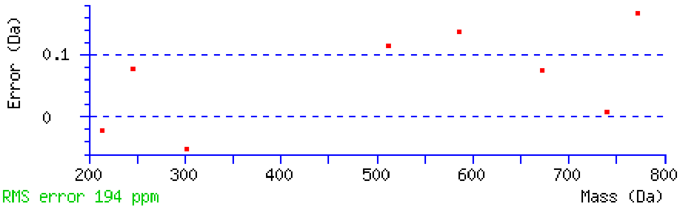
Match to Query 1545: 884.497416 from(443.255984,2+) index(1795)
Title: Elution from: 22.765 to 22.765 scan no 2362 cid35.00 polarity:+
Data file D12h-3_1.mgf

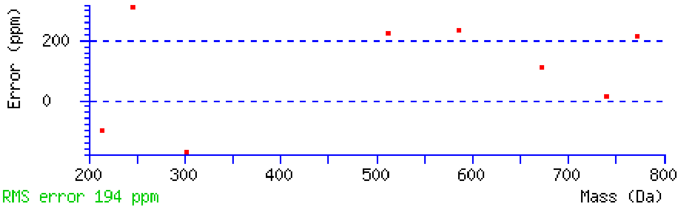
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 884.4967
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00029
Matches : 8/76 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	*214.1186*	107.5629	197.0921	99.0497			V	*771.4611*	386.2342	754.4345	377.7209	753.4505	377.2289	7
3	*301.1506*	151.0790	284.1241	142.5657	283.1401	142.0737	S	*672.3927*	336.7000	655.3661	328.1867	654.3821	327.6947	6
4	398.2034	199.6053	381.1769	191.0921	380.1928	190.6001	P	*585.3606*	293.1840	568.3341	284.6707	567.3501	284.1787	5
5	*511.2875*	256.1474	494.2609	247.6341	493.2769	247.1421	I	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
6	640.3301	320.6687	623.3035	312.1554	622.3195	311.6634	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
7	*739.3985*	370.2029	722.3719	361.6896	721.3879	361.1976	V	*246.1812*	123.5942	229.1547	115.0810			2
8							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NVSPIEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.7	884.4967	0.0007	NVSPIEVK

AT4G02770.1

Mascot: http://www.matrixscience.com/

AT4G02930.1

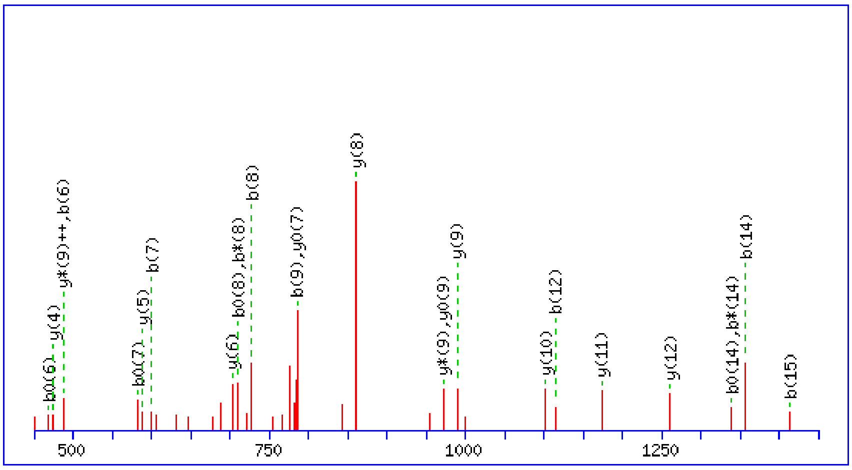
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSALSALQGTNDEIGR**
Found in **AT4G02930.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor Tu, putative / EF-Tu, putative | chr4:1295751-1298354 REVERSE

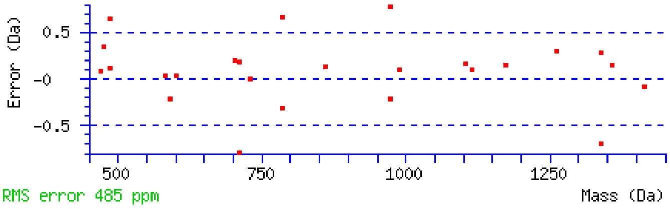
Match to Query 7098: 1587.782396 from(794.898474,2+) index(5080)
Title: Elution from: 46.302 to 46.302 scan no 6424 cid35.00 polarity:+
Data file D6h-1_2.mgf

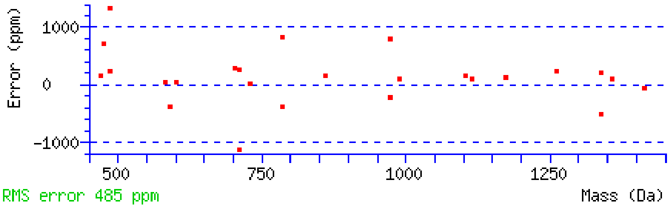
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1587.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 3.1e-009
Matches : 25/158 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							16
2	145.0608	73.0340			127.0502	64.0287	S	1531.7711	766.3892	1514.7445	757.8759	1513.7605	757.3839	15
3	216.0979	108.5526			198.0873	99.5473	A	1444.7390	722.8732	1427.7125	714.3599	1426.7285	713.8679	14
4	329.1819	165.0946			311.1714	156.0893	L	1373.7019	687.3546	1356.6754	678.8413	1355.6914	678.3493	13
5	416.2140	208.6106			398.2034	199.6053	S	***1260.6179***	630.8126	1243.5913	622.2993	1242.6073	621.8073	12
6	***487.2511***	244.1292			469.2405	235.1239	A	***1173.5858***	587.2966	1156.5593	578.7833	1155.5753	578.2913	11
7	***600.3352***	300.6712			582.3246	291.6659	L	***1102.5487***	551.7780	1085.5222	543.2647	1084.5382	542.7727	10
8	***728.3937***	364.7005	711.3672	356.1872	710.3832	355.6952	Q	***989.4647***	495.2360	972.4381	486.7227	971.4541	486.2307	9
9	***785.4152***	393.2112	768.3886	384.6980	767.4046	384.2060	G	***861.4061***	431.2067	844.3795	422.6934	843.3955	422.2014	8
10	886.4629	443.7351	869.4363	435.2218	868.4523	434.7298	T	804.3846	402.6959	787.3581	394.1827	786.3741	393.6907	7
11	1000.5058	500.7565	983.4793	492.2433	982.4952	491.7513	N	***703.3369***	352.1721	686.3104	343.6588	685.3264	343.1668	6
12	***1115.5327***	558.2700	1098.5062	549.7567	1097.5222	549.2647	D	***589.2940***	295.1506	572.2675	286.6374	571.2835	286.1454	5
13	1244.5753	622.7913	1227.5488	614.2780	1226.5648	613.7860	E	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
14	***1357.6594***	679.3333	1340.6329	670.8201	1339.6488	670.3281	I	345.2245	173.1159	328.1979	164.6026			3
15	***1414.6809***	707.8441	1397.6543	699.3308	1396.6703	698.8388	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1





AT4G02930.1

NCBI **BLAST** search of GSALSALQGTNDEIGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.9	1587.7852	-0.0029	GSALSALQGTNDEIGR
2.0	1587.7803	0.0021	FPAFHAGPRMCLGK
0.2	1587.7802	0.0022	MYKSAFWARCLR

AT4G03000.1

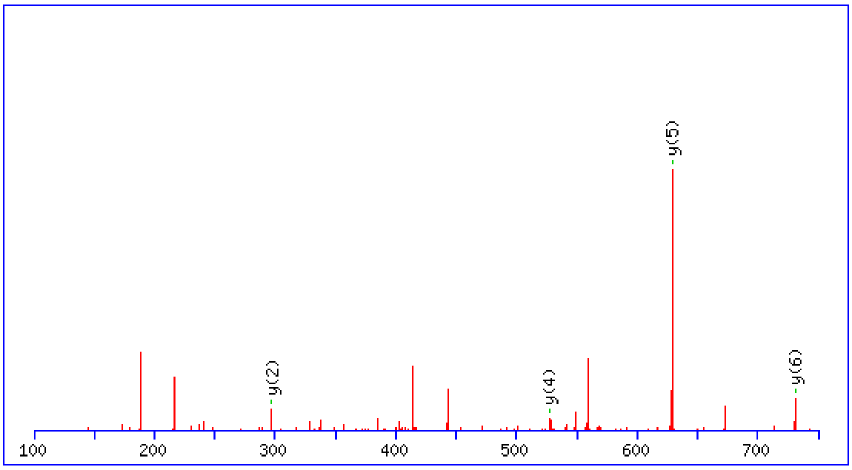
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITTEVMK**
Found in **AT4G03000.1** in **TAIR_Arabidopsis**, Symbols: | protein binding / zinc ion binding | chr4:1324602-1327348 FORWARD

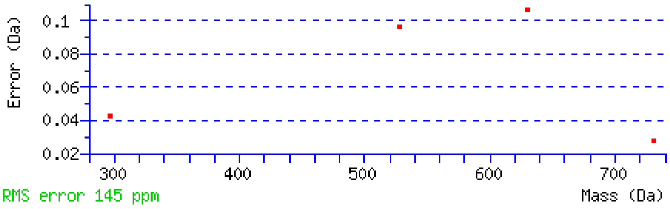
Match to Query 1252: 844.410066 from(423.212309,2+) index(3852)
Title: Elution from: 36.285 to 36.285 scan no 4799 cid35.00 polarity:+
Data file 0-3_2.mgf

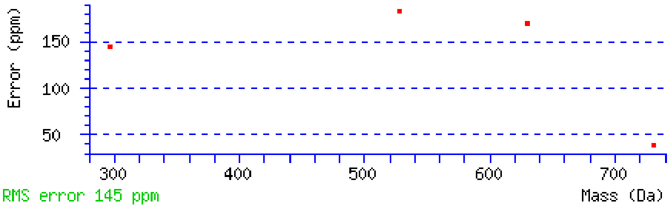
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 844.4076
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 34 **Expect:** 0.0037
Matches : 4/82 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							7
2	217.1331	109.0702	199.1225	100.0649	T	***731.3338***	366.1705	713.3102	357.1588	713.3232	357.1653	6
3	319.1778	160.0925	301.1672	151.0873	T	***629.2891***	315.1482	611.2655	306.1364	611.2785	306.1429	5
4	449.2174	225.1124	431.2069	216.1071	E	***527.2444***	264.1258	509.2208	255.1140	509.2338	255.1205	4
5	549.2829	275.1451	531.2723	266.1398	V	397.2048	199.1060	379.1812	190.0942			3
6	697.3153	349.1613	679.3047	340.1560	M	***297.1393***	149.0733	279.1157	140.0615			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ITTEVMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.1	844.4076	0.0024	ITTEVMK
8.9	844.4076	0.0024	TLLESMK

AT4G03000.1

8.5	844.4076	0.0024	TLSEIMK
8.2	844.4103	-0.0002	ITNMVTR
4.5	844.4103	-0.0002	IGTMSLGR
3.4	844.4092	0.0009	LYGAHFK
2.4	844.4103	-0.0002	LKEMTGR
1.2	844.4103	-0.0003	LPRSMSK

{MATRIX SCIENCE} Mascot Search Results

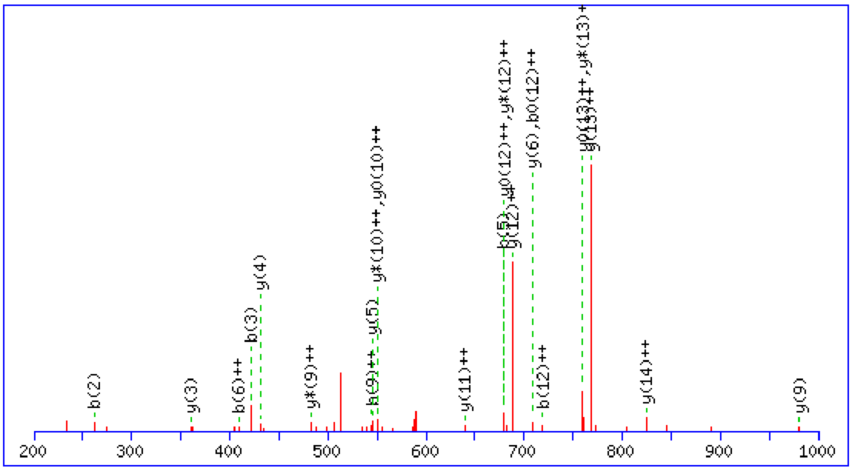
Peptide View

MS/MS Fragmentation of **FLCPCHGSQYNAQGR**
Found in **AT4G03280.1** in **TAIR_Arabidopsis**, Symbols: PGR1, PETC | PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C) | chr4:1440314-1441717 FORWARD

Match to Query 9108: 1793.772108 from(598.931312,3+) index(1851)
Title: Elution from: 23.232 to 23.232 scan no 2440 cid35.00 polarity:+
Data file 0-1_1.mgf

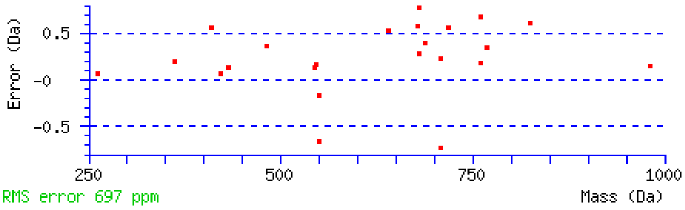
Click mouse within plot area to zoom in by factor of two about that point

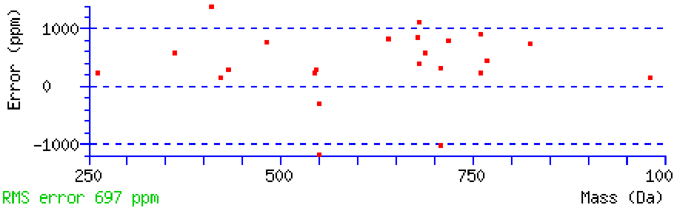
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1793.7726
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.00091
Matches : 23/124 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							15
2	**261.1598**	131.0835					L	1647.7115	824.3594	1630.6849	815.8461	1629.7009	815.3541	14
3	**421.1904**	211.0988					C	1534.6274	767.8173	1517.6009	759.3041	1516.6168	758.8121	13
4	518.2432	259.6252					P	1374.5968	687.8020	1357.5702	679.2887	1356.5862	678.7967	12
5	**678.2738**	339.6405					C	1277.5440	639.2756	1260.5174	630.7624	1259.5334	630.2704	11
6	815.3327	**408.1700**					H	1117.5133	559.2603	1100.4868	550.7470	1099.5028	550.2550	10
7	872.3542	436.6807					G	***980.4544***	490.7309	963.4279	482.2176	962.4439	481.7256	9
8	959.3862	480.1967			941.3757	471.1915	S	923.4330	462.2201	906.4064	453.7068	905.4224	453.2148	8
9	1087.4448	**544.2260**	1070.4182	535.7128	1069.4342	535.2208	Q	836.4009	418.7041	819.3744	410.1908			7
10	1250.5081	625.7577	1233.4816	617.2444	1232.4976	616.7524	Y	***708.3424***	354.6748	691.3158	346.1615			6
11	1364.5511	682.7792	1347.5245	674.2659	1346.5405	673.7739	N	***545.2790***	273.1432	528.2525	264.6299			5
12	1435.5882	**718.2977**	1418.5616	709.7844	1417.5776	709.2924	A	***431.2361***	216.1217	414.2096	207.6084			4
13	1563.6467	782.3270	1546.6202	773.8137	1545.6362	773.3217	Q	***360.1990***	180.6031	343.1724	172.0899			3
14	1620.6682	810.8377	1603.6417	802.3245	1602.6576	801.8325	G	232.1404	116.5738	215.1139	108.0606			2
15							R	175.1190	88.0631	158.0924	79.5498			1





AT4G03280.1

NCBI **BLAST** search of FLCPCHGSQYNAQGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.4	1793.7726	-0.0005	FLCPCHGSQYNAQGR

AT4G03280.2

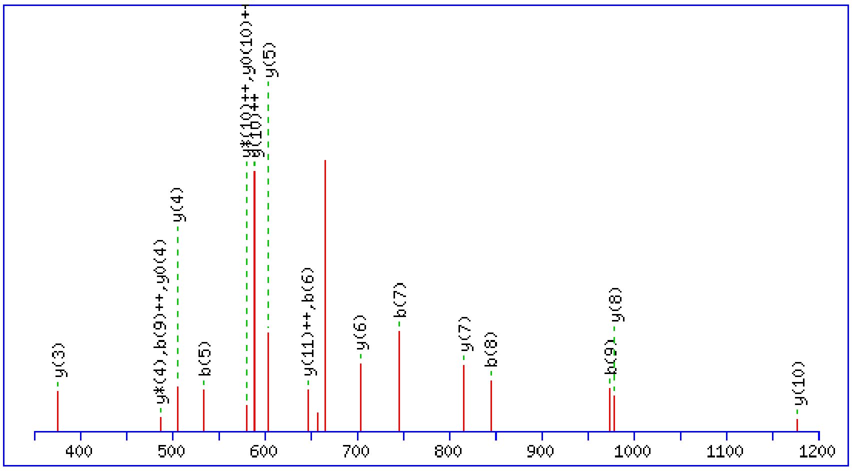
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDPTYLVVENDK**
Found in **AT4G03280.2** in **TAIR_Arabidopsis**, Symbols: PGR1, PETC | PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C) | chr4:1440462-1441717 FORWARD

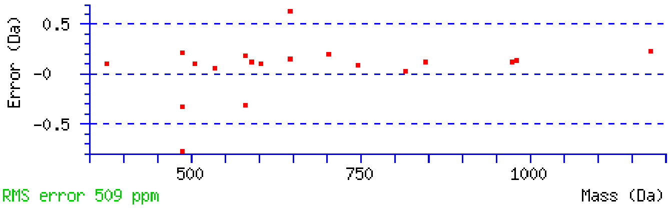
Match to Query 5139: 1348.648024 from(675.331288,2+) index(3984)
Title: Elution from: 36.698 to 36.698 scan no 4968 cid35.00 polarity:+
Data file C7-3_2.mgf

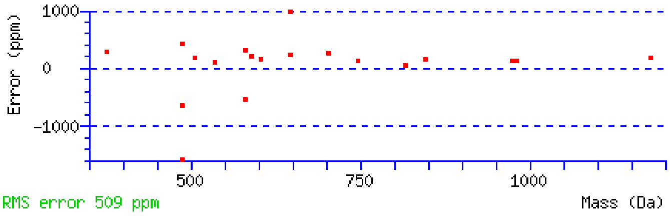
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1348.6511
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1e-007
Matches : 19/110 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							12
2	173.0557	87.0315			155.0451	78.0262	D	1292.6369	646.8221	1275.6103	638.3088	1274.6263	637.8168	11
3	270.1084	135.5579			252.0979	126.5526	P	***1177.6099***	589.3086	1160.5834	580.7953	1159.5994	580.3033	10
4	371.1561	186.0817			353.1456	177.0764	T	1080.5572	540.7822	1063.5306	532.2689	1062.5466	531.7769	9
5	**534.2195**	267.6134			516.2089	258.6081	Y	***979.5095***	490.2584	962.4829	481.7451	961.4989	481.2531	8
6	**647.3035**	324.1554			629.2930	315.1501	L	***816.4462***	408.7267	799.4196	400.2134	798.4356	399.7214	7
7	**746.3719**	373.6896			728.3614	364.6843	V	***703.3621***	352.1847	686.3355	343.6714	685.3515	343.1794	6
8	**845.4403**	423.2238			827.4298	414.2185	V	***604.2937***	302.6505	587.2671	294.1372	586.2831	293.6452	5
9	**974.4829**	487.7451			956.4724	478.7398	E	***505.2253***	253.1163	488.1987	244.6030	487.2147	244.1110	4
10	1088.5259	544.7666	1071.4993	536.2533	1070.5153	535.7613	N	***376.1827***	188.5950	359.1561	180.0817	358.1721	179.5897	3
11	1203.5528	602.2800	1186.5263	593.7668	1185.5422	593.2748	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GDPTYLVVENDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G03280.2

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.4	1348.6511	-0.0030	GDPTYLVVENDK
3.5	1348.6486	-0.0005	VYLLDFTCYR
1.6	1348.6517	-0.0037	DGKVCNSSAGKAR

AT4G03520.1

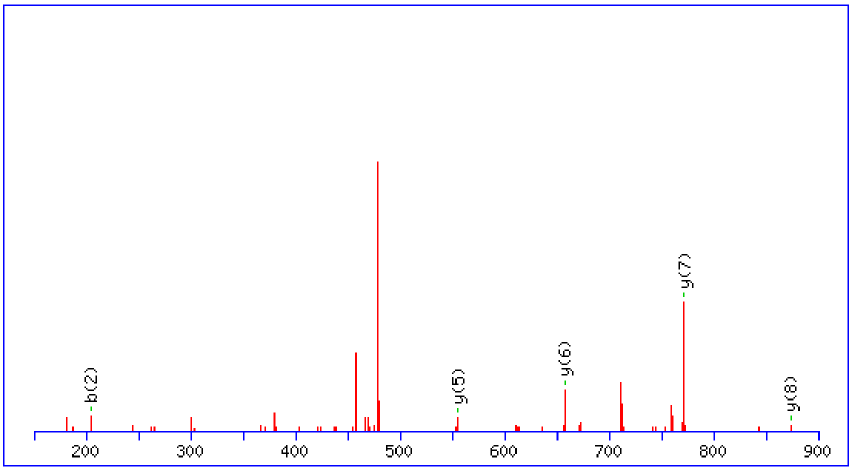
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTLTSSLDK**
Found in **AT4G03520.1** in **TAIR_Arabidopsis**, Symbols: ATHM2 | ATHM2 (Arabidopsis thioredoxin M-type 2); thiol-disulfide exchange intermediate | chr4:1562583-1564053 REVERSE

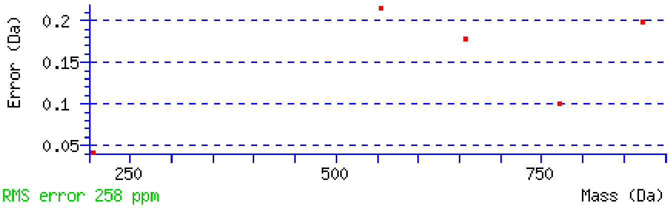
Match to Query 2399: 974.476442 from(488.245497,2+) index(1651)
Title: Elution from: 21.768 to 21.768 scan no 2216 cid35.00 polarity:+
Data file C7-2_1.mgf

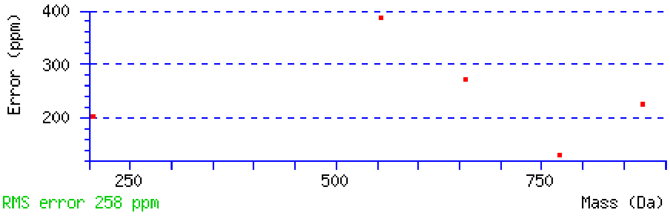
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 974.4780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0071
Matches : 5/78 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							9
2	205.0967	103.0520	187.0861	94.0467	T	***873.4406***	437.2239	855.4170	428.2121	855.4300	428.2187	8
3	319.1778	160.0925	301.1672	151.0873	L	***771.3959***	386.2016	753.3723	377.1898	753.3853	377.1963	7
4	421.2225	211.1149	403.2119	202.1096	T	***657.3148***	329.1610	639.2912	320.1492	639.3042	320.1558	6
5	509.2516	255.1294	491.2410	246.1241	S	***555.2701***	278.1387	537.2465	269.1269	537.2595	269.1334	5
6	597.2806	299.1440	579.2701	290.1387	S	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
7	711.3617	356.1845	693.3512	347.1792	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
8	827.3857	414.1965	809.3752	405.1912	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TTLTSSLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G03520.1

30.3	974.4780	-0.0016	TTLTSSLDK
16.0	974.4760	0.0005	TVNRNVMK
13.4	974.4755	0.0009	MALELFNK
9.3	974.4760	0.0005	SPMTTRLR
5.4	974.4780	-0.0016	TLSSVETTK
5.2	974.4755	0.0009	ITFPSCLK
3.4	974.4789	-0.0025	TMITCVLK
3.1	974.4753	0.0012	QWRNKAR
1.9	974.4755	0.0009	FKTPPTMK
1.8	974.4760	0.0005	MARSLANAK

AT4G04020.1

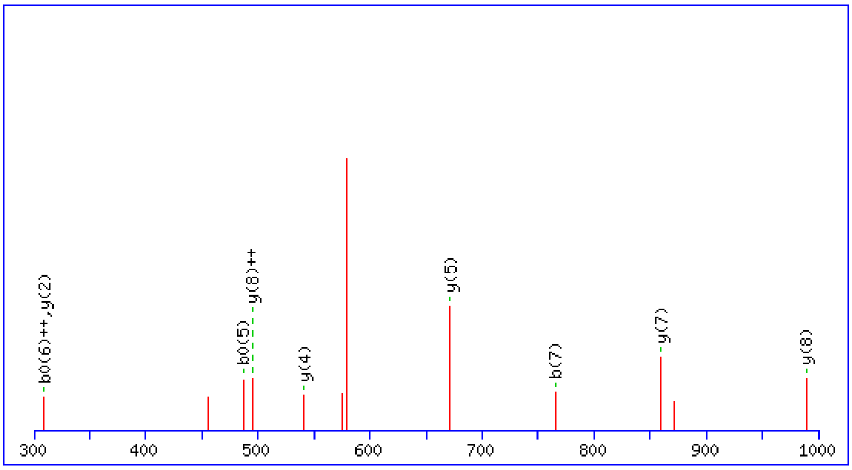
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIESVEETER**
Found in **AT4G04020.1** in **TAIR_Arabidopsis**, Symbols: FIB | FIB (FIBRILLIN); structural molecule | chr4:1932159-1933544 FORWARD

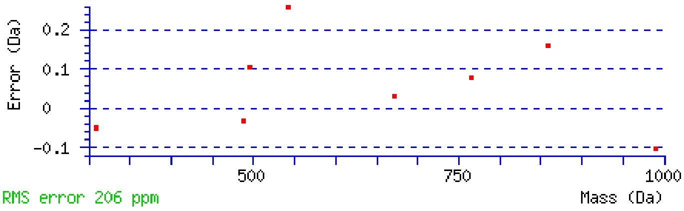
Match to Query 3786: 1174.512770 from(588.263661,2+) index(972)
Title: Elution from: 14.537 to 14.537 scan no 1340 cid35.00 polarity:+
Data file 0-3_3.mgf

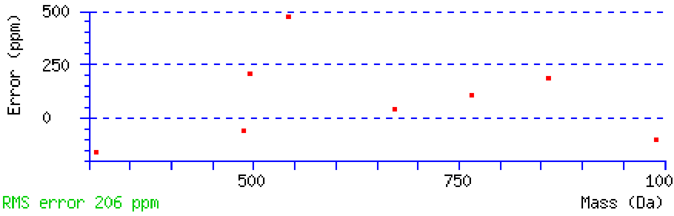
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1174.5128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0044
Matches : 9/84 fragment ions using 12 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244			A							10
2	187.1225	94.0649			I	1103.4859	552.2466	1085.4623	543.2348	1085.4754	543.2413	9
3	317.1622	159.0847	299.1516	150.0794	E	***989.4048***	495.2061	971.3812	486.1943	971.3943	486.2008	8
4	405.1912	203.0992	387.1807	194.0940	S	***859.3652***	430.1862	841.3416	421.1744	841.3546	421.1810	7
5	505.2567	253.1320	487.2461	244.1267	V	771.3361	386.1717	753.3126	377.1599	753.3256	377.1664	6
6	635.2963	318.1518	617.2857	309.1465	E	***671.2707***	336.1390	653.2471	327.1272	653.2601	327.1337	5
7	765.3359	383.1716	747.3254	374.1663	E	***541.2311***	271.1192	523.2075	262.1074	523.2205	262.1139	4
8	867.3806	434.1940	849.3701	425.1887	T	411.1914	206.0994	393.1678	197.0876	393.1809	197.0941	3
9	997.4203	499.2138	979.4097	490.2085	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
10					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AIESVEETER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G04020.1

31.3	1174.5128	-0.0000	AIESVEETER
16.9	1174.5155	-0.0027	VNGQVSSSPER
4.8	1174.5128	-0.0000	IAEASKEGDDK
4.0	1174.5155	-0.0027	LEADGLSGNQR
3.0	1174.5155	-0.0027	NDAAVALSDQR
2.3	1174.5137	-0.0009	VTIHMMSESK
2.1	1174.5130	-0.0002	ALHQFDCLR

AT4G04640.1

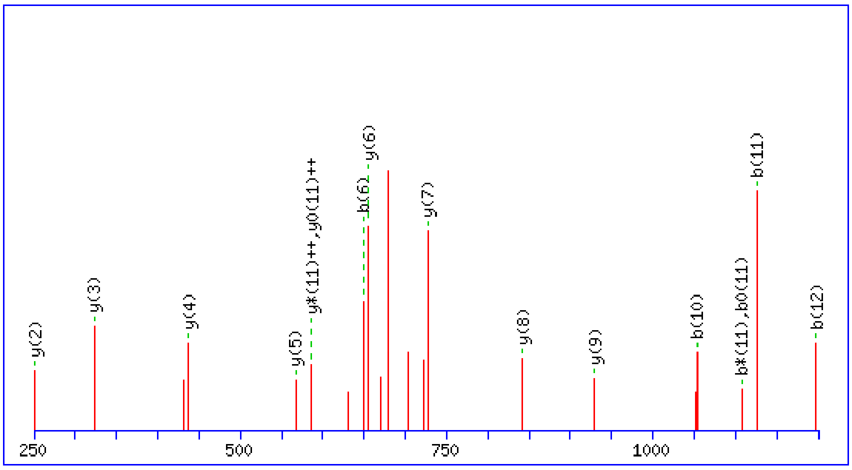
Mascot Search Results

Peptide View

MS/MS Fragmentation of ALQESLASELAAR
Found in AT4G04640.1 in TAIR_Arabidopsis, Symbols: ATPC1 | ATPC1 (ATP synthase gamma chain 1) | chr4:2350759-2351880 REVERSE

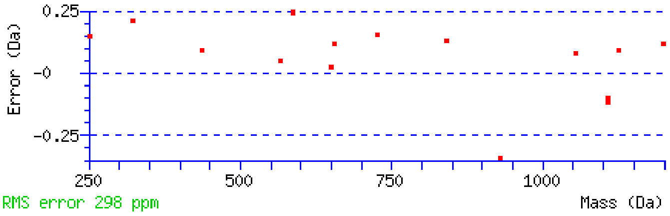
Match to Query 5446: 1374.668970 from(688.341761,2+) index(6016)
Title: Elution from: 53.031 to 53.031 scan no 7570 cid35.00 polarity:+
Data file C7-3_1.mgf

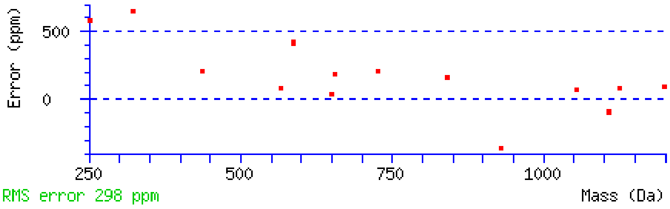
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1374.6697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 7.4e-008
Matches : 16/126 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244					A							13
2	187.1225	94.0649					L	1303.6429	652.3251	1285.6193	643.3133	1285.6323	643.3198	12
3	317.1752	159.0912	299.1516	150.0794			Q	1189.5618	595.2845	1171.5382	586.2727	1171.5512	586.2792	11
4	447.2148	224.1110	429.1912	215.0992	429.2042	215.1058	E	1059.5091	530.2582	1041.4855	521.2464	1041.4986	521.2529	10
5	535.2439	268.1256	517.2203	259.1138	517.2333	259.1203	S	***929.4695***	465.2384	911.4459	456.2266	911.4589	456.2331	9
6	**649.3250**	325.1661	631.3014	316.1543	631.3144	316.1608	L	***841.4404***	421.2239	823.4168	412.2121	823.4299	412.2186	8
7	721.3591	361.1832	703.3355	352.1714	703.3485	352.1779	A	***727.3593***	364.1833	709.3357	355.1715	709.3488	355.1780	7
8	809.3882	405.1977	791.3646	396.1859	791.3776	396.1924	S	***655.3252***	328.1662	637.3016	319.1544	637.3146	319.1609	6
9	939.4278	470.2175	921.4042	461.2057	921.4172	461.2123	E	***567.2961***	284.1517	549.2725	275.1399	549.2856	275.1464	5
10	**1053.5089**	527.2581	1035.4853	518.2463	1035.4983	518.2528	L	***437.2565***	219.1319	419.2329	210.1201			4
11	**1125.5430**	563.2752	1107.5195	554.2634	1107.5325	554.2699	A	***323.1754***	162.0913	305.1518	153.0795			3
12	**1197.5772**	599.2922	1179.5536	590.2804	1179.5666	590.2870	A	***251.1412***	126.0743	233.1177	117.0625			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ALQESLASELAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G04640.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.2	1374.6697	-0.0008	ALQESLASELAAR
23.5	1374.6697	-0.0008	EAEEAKSLAIAAR
14.6	1374.6697	-0.0008	EAKVTLDNEIAR
10.3	1374.6724	-0.0034	AGVVREEAQVAAR
9.0	1374.6672	0.0017	LMLYAGADHVLR
2.9	1374.6720	-0.0030	VDKVLQPFDGNK
2.7	1374.6697	-0.0008	EGAAESPAVKSGKK
2.7	1374.6697	-0.0008	ILSGLRAEGEEGK
2.1	1374.6672	0.0017	NVKMSYLYGKR
0.8	1374.6699	-0.0009	MATSFFRRLAR

AT4G04800.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AILSPEQFR**
Found in **AT4G04800.1** in **TAIR_Arabidopsis**, Symbols: | methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein | chr4:2439572-2440935 FORWARD

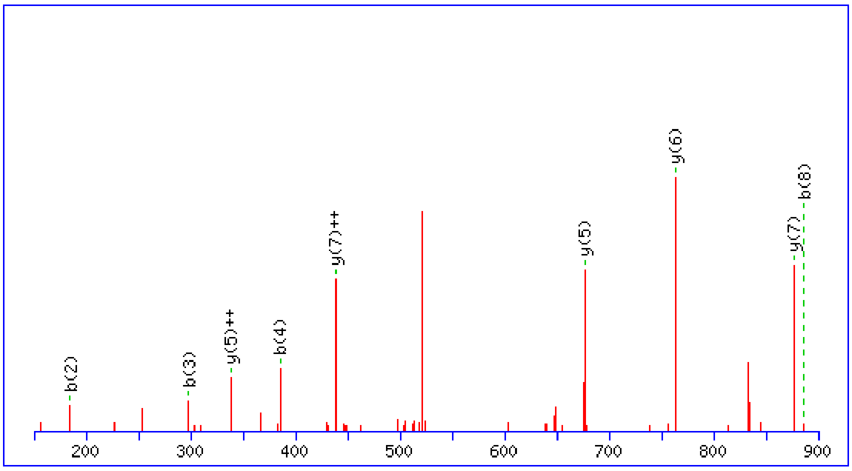
Match to Query 2613: 1059.571546 from(530.793049,2+) index(4396)
Title: Elution from: 41.586 to 41.586 scan no 5631 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

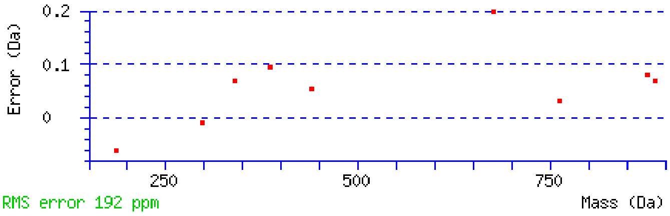
Label all possible matches ○ Label matches used for scoring ●

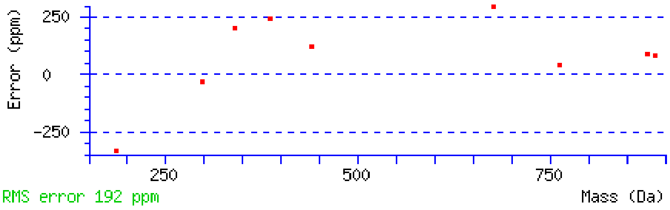
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1059.5713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0085
Matches : 9/72 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							9
2	*185.1285*	93.0679					I	989.5415	495.2744	972.5149	486.7611	971.5309	486.2691	8
3	*298.2125*	149.6099					L	**876.4574**	438.7323	859.4308	430.2191	858.4468	429.7271	7
4	*385.2445*	193.1259			367.2340	184.1206	S	**763.3733**	382.1903	746.3468	373.6770	745.3628	373.1850	6
5	482.2973	241.6523			464.2867	232.6470	P	**676.3413**	338.6743	659.3148	330.1610	658.3307	329.6690	5
6	611.3399	306.1736			593.3293	297.1683	E	579.2885	290.1479	562.2620	281.6346	561.2780	281.1426	4
7	739.3985	370.2029	722.3719	361.6896	721.3879	361.1976	Q	450.2459	225.6266	433.2194	217.1133			3
8	*886.4669*	443.7371	869.4403	435.2238	868.4563	434.7318	F	322.1874	161.5973	305.1608	153.0840			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AILSPEQFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G04800.1

28.2	1059.5713	0.0003	AILSPEQFR
18.8	1059.5746	-0.0031	SPAELKLMR
15.1	1059.5746	-0.0031	AISLPSMAVR
0.3	1059.5713	0.0003	SQYLALTHK

AT4G04955.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMSDGNFLK**
Found in **AT4G04955.1** in **TAIR_Arabidopsis**, Symbols: ATALN | ATALN (ARABIDOPSIS ALLANTOINASE); allantoinase/ hydrolase | chr4:2522299-2525257 REVERSE

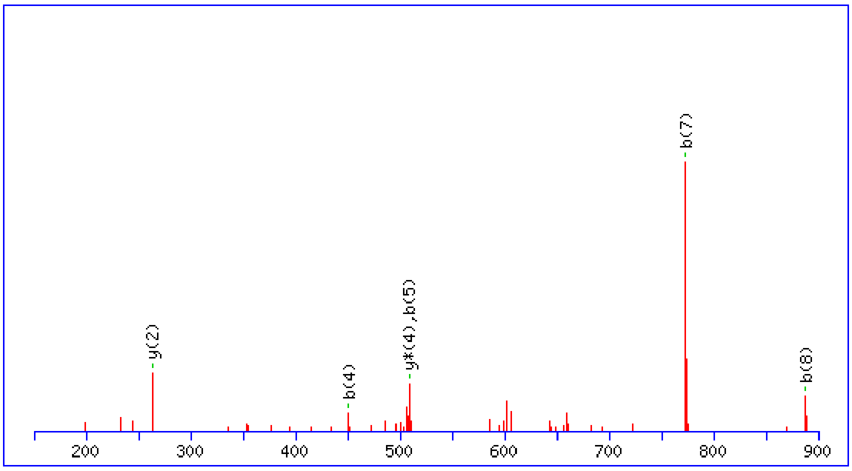
Match to Query 2890: 1034.476170 from(518.245361,2+) index(1655)
Title: Elution from: 20.958 to 20.958 scan no 2184 cid35.00 polarity:+
Data file C7-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

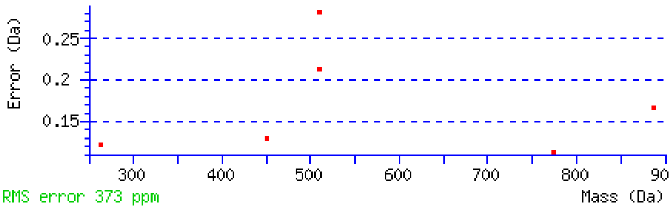
Label all possible matches ○ Label matches used for scoring ●

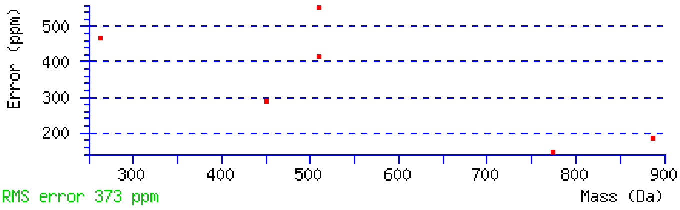
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1034.4733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.027
Matches : 6/72 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							9
2	247.1259	124.0666					M	921.3995	461.2034	903.3759	452.1916	903.3889	452.1981	8
3	335.1550	168.0811			317.1444	159.0758	S	789.3620	395.1846	771.3384	386.1728	771.3514	386.1793	7
4	***451.1789***	226.0931			433.1684	217.0878	D	701.3329	351.1701	683.3093	342.1583	683.3223	342.1648	6
5	***509.1974***	255.1024			491.1869	246.0971	G	585.3089	293.1581	567.2853	284.1463			5
6	625.2344	313.1209	607.2108	304.1091	607.2239	304.1156	N	527.2904	264.1488	509.2668	255.1371			4
7	***773.2999***	387.1536	755.2763	378.1418	755.2893	378.1483	F	411.2534	206.1303	393.2298	197.1186			3
8	***887.3810***	444.1941	869.3574	435.1823	869.3704	435.1888	L	263.1880	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LMSDGNFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G04955.1

25.7	1034.4733	0.0029	LMSDGNFLK
19.3	1034.4760	0.0002	MGASGRWIK
15.6	1034.4733	0.0029	MEKGVGFEK
14.2	1034.4733	0.0029	MAFAQESIK
11.9	1034.4789	-0.0028	LPYNMMLK
11.8	1034.4789	-0.0028	LPYNMMLK
10.8	1034.4789	-0.0027	EMKMVPYK
6.7	1034.4780	-0.0019	ETTSAEFLK
6.7	1034.4785	-0.0023	ASTSGEVSRK
4.2	1034.4760	0.0002	MLFSSHKR

AT4G05180.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRFYIQPLSPTEAAAR**
Found in **AT4G05180.1** in **TAIR_Arabidopsis**, Symbols: PSBQ, PSBQ-2, PSII-Q | PSBQ/PSBQ-2/PSII-Q (PHOTOSYSTEM II SUBUNIT Q-2); calcium ion binding | chr4:2672091-2673168 REVERSE

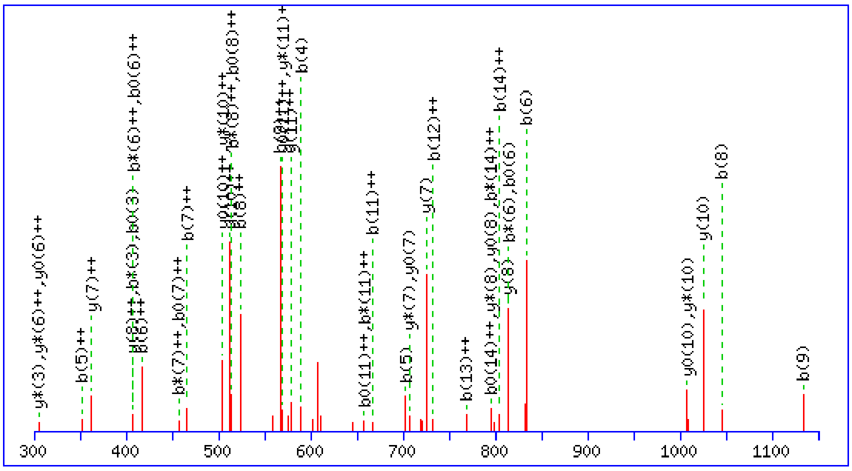
Match to Query 8877: 1856.872587 from(619.964805,3+) index(6010)
Title: Elution from: 53.165 to 53.165 scan no 7659 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1150 Da Full range

Label all possible matches ○ Label matches used for scoring ●

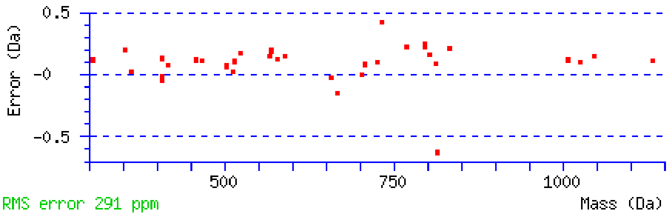
Show Y-axis ☐

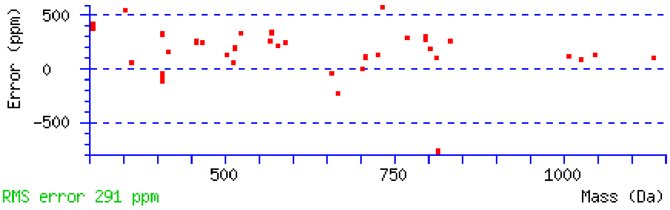


Monoisotopic mass of neutral peptide Mr(calc): 1856.8691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 1.3e-006
Matches : 48/170 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							16
2	277.1205	139.0639	259.0969	130.0521	259.1099	130.0586	R	1741.8525	871.4299	1723.8289	862.4181	1723.8419	862.4246	15
3	425.1860	213.0966	407.1624	204.0848	407.1754	204.0913	F	1581.7632	791.3852	1563.7396	782.3734	1563.7526	782.3800	14
4	**589.2463**	295.1268	571.2227	286.1150	571.2358	286.1215	Y	1433.6978	717.3525	1415.6742	708.3407	1415.6872	708.3472	13
5	**703.3274**	***352.1673***	685.3038	343.1556	685.3169	343.1621	I	1269.6374	635.3223	1251.6138	626.3105	1251.6268	626.3170	12
6	**833.3801**	***417.1937***	815.3565	408.1819	815.3695	408.1884	Q	1155.5563	578.2818	1137.5327	569.2700	1137.5457	569.2765	11
7	931.4299	***466.2186***	913.4063	457.2068	913.4193	457.2133	P	**1025.5036**	513.2555	1007.4801	504.2437	1007.4931	504.2502	10
8	**1045.5110**	***523.2591***	1027.4874	514.2473	1027.5004	514.2538	L	927.4538	464.2306	909.4303	455.2188	909.4433	455.2253	9
9	**1133.5400**	***567.2737***	1115.5164	558.2619	1115.5295	558.2684	S	**813.3727**	407.1900	795.3492	398.1782	795.3622	398.1847	8
10	1231.5898	616.2985	1213.5662	607.2868	1213.5793	607.2933	P	**725.3437**	363.1755	707.3201	354.1637	707.3331	354.1702	7
11	1333.6345	***667.3209***	1315.6110	658.3091	1315.6240	658.3156	T	627.2939	314.1506	609.2703	305.1388	609.2833	305.1453	6
12	1463.6742	***732.3407***	1445.6506	723.3289	1445.6636	723.3354	E	525.2492	263.1282	507.2256	254.1164	507.2386	254.1229	5
13	1535.7083	***768.3578***	1517.6847	759.3460	1517.6977	759.3525	A	395.2095	198.1084	377.1860	189.0966			4
14	1607.7425	***804.3749***	1589.7189	795.3631	1589.7319	795.3696	A	323.1754	162.0913	305.1518	153.0795			3
15	1679.7766	840.3919	1661.7530	831.3802	1661.7660	831.3867	A	251.1412	126.0743	233.1177	117.0625			2
16							R	179.1071	90.0572	161.0835	81.0454			1

AT4G05180.1





NCBI **BLAST** search of DRFYIQPLSPTEAAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.0	1856.8691	0.0034	DRFYIQPLSPTEAAAR
8.6	1856.8747	-0.0022	TSVAIVFSTFMRAYSR
4.6	1856.8703	0.0023	SGVRVSAGESVAMLAQGSK
3.0	1856.8725	0.0001	ETSKQNPINMVTLFGR
1.2	1856.8698	0.0027	AMETFVAELNGVLNVSK
1.2	1856.8698	0.0027	MVEEINDYKLQLQSK
0.3	1856.8772	-0.0046	TVRKEVSDGFGEDLVGK
0.1	1856.8725	0.0001	GKLSEDMSGAQLLWKR

Mascot: http://www.matrixscience.com/

AT4G05200.1

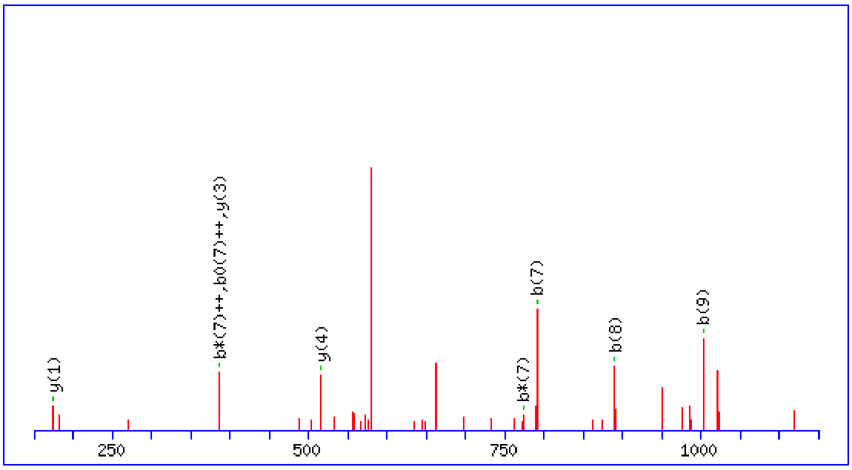
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNFQTNEVIR**
Found in **AT4G05200.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr4:2679791-2682307 REVERSE

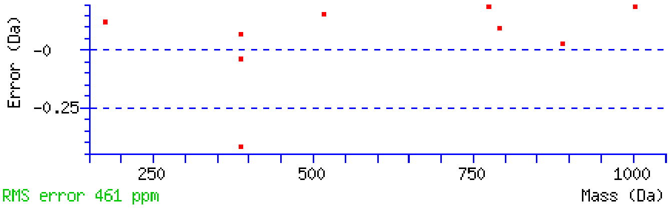
Match to Query 3928: 1176.586874 from(589.300713,2+) index(1839)
Title: Elution from: 22.952 to 22.952 scan no 2424 cid35.00 polarity:+
Data file D6h-1_2.mgf

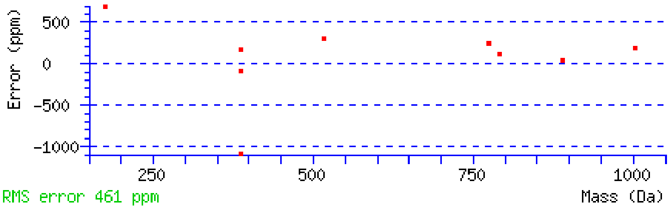
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1176.5887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0066
Matches : 9/92 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							10
2	172.0717	86.5395	155.0451	78.0262			N	1120.5745	560.7909	1103.5480	552.2776	1102.5640	551.7856	9
3	319.1401	160.0737	302.1135	151.5604			F	1006.5316	503.7694	989.5051	495.2562	988.5211	494.7642	8
4	447.1987	224.1030	430.1721	215.5897			Q	859.4632	430.2352	842.4367	421.7220	841.4526	421.2300	7
5	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	T	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	6
6	662.2893	331.6483	645.2627	323.1350	644.2787	322.6430	N	630.3569	315.6821	613.3304	307.1688	612.3464	306.6768	5
7	***791.3319***	396.1696	774.3053	387.6563	773.3213	387.1643	E	***516.3140***	258.6606	499.2875	250.1474	498.3035	249.6554	4
8	***890.4003***	445.7038	873.3737	437.1905	872.3897	436.6985	V	***387.2714***	194.1394	370.2449	185.6261			3
9	***1003.4843***	502.2458	986.4578	493.7325	985.4738	493.2405	I	288.2030	144.6051	271.1765	136.0919			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GNFQTNEVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G05200.1

27.4	1176.5887	-0.0019	GNFQTNEVIR
19.2	1176.5860	0.0009	RNNYNQGRR
18.8	1176.5887	-0.0019	NNGTGDALFLR
11.7	1176.5847	0.0022	KSGNNSASKER
7.2	1176.5887	-0.0018	NLSISTSNWR
7.2	1176.5888	-0.0019	SGGTPVGGGGYIR
6.8	1176.5887	-0.0018	REPQYLTDR
5.1	1176.5856	0.0013	RDPLAMRMR
5.0	1176.5887	-0.0019	QLFVANAGDSR
2.7	1176.5847	0.0022	SSQRSLQSER

AT4G08210.1

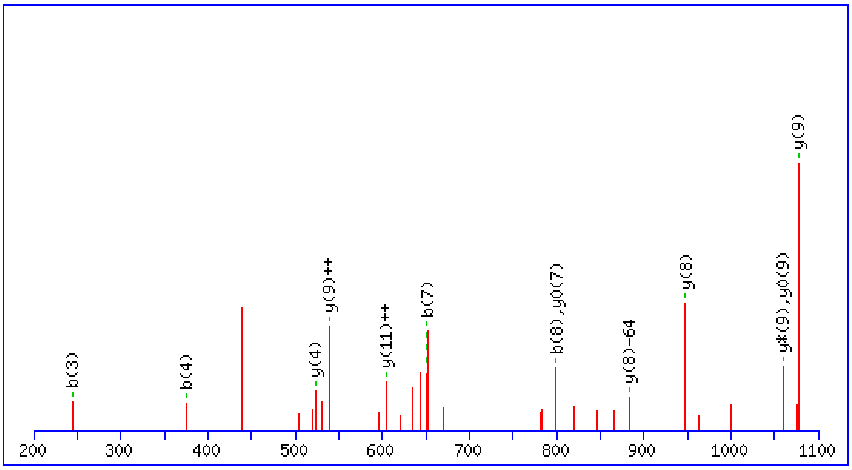
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGAKESGMSWII**
Found in **AT4G08210.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr4:5183810-5185870 REVERSE

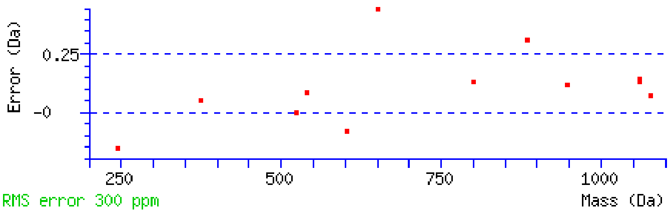
Match to Query 4862: 1320.619092 from(661.316822,2+) index(2925)
Title: Elution from: 29.746 to 29.746 scan no 3668 cid35.00 polarity:+
Data file C7-1_2.mgf

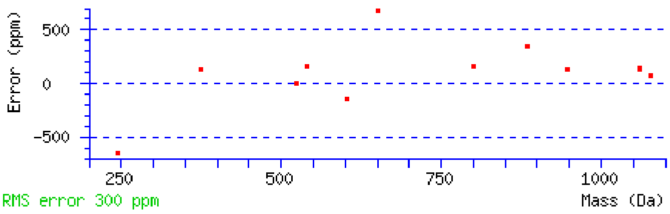
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.6176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 **Expect:** 0.022
Matches : 13/154 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							12
2	173.1069	87.0571					G	1207.5438	604.2755	1189.5202	595.2637	1189.5332	595.2703	11
3	***245.1410***	123.0741					A	1149.5253	575.2663	1131.5017	566.2545	1131.5147	566.2610	10
4	***375.2301***	188.1187	357.2065	179.1069			K	**1077.4911**	539.2492	1059.4676	530.2374	1059.4806	530.2439	9
5	505.2697	253.1385	487.2461	244.1267	487.2591	244.1332	E	**947.4021**	474.2047			929.3915	465.1994	8
6	593.2987	297.1530	575.2752	288.1412	575.2882	288.1477	S	817.3625	409.1849			799.3519	400.1796	7
7	***651.3172***	326.1623	633.2937	317.1505	633.3067	317.1570	G	729.3334	365.1703			711.3229	356.1651	6
8	***799.3497***	400.1785	781.3261	391.1667	781.3391	391.1732	M	671.3149	336.1611			653.3044	327.1558	5
9	887.3787	444.1930	869.3552	435.1812	869.3682	435.1877	S	**523.2825**	262.1449			505.2719	253.1396	4
10	1075.4521	538.2297	1057.4285	529.2179	1057.4416	529.2244	W	435.2534	218.1303					3
11	1189.5332	595.2703	1171.5096	586.2585	1171.5227	586.2650	I	247.1800	124.0937					2
12							I	133.0989	67.0531					1





NCBI **BLAST** search of LGAKESGMSWII
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G08210.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.4	1320.6176	0.0015	LGAKESGMSWII
12.2	1320.6169	0.0022	QIEVNFYVHR
10.6	1320.6154	0.0037	LEERKLEDMK
10.6	1320.6154	0.0037	ELNISGCSSLVK
10.3	1320.6228	-0.0037	LQTDQSSLEKR
5.0	1320.6154	0.0037	ELEAMLDKSVR
5.0	1320.6154	0.0037	ELKDMEKEIR
4.4	1320.6223	-0.0033	EIEAKYDEIAK
4.4	1320.6223	-0.0033	ELETLDLSFNK
4.1	1320.6203	-0.0012	KMEGSKVPSWR

AT4G08390.1

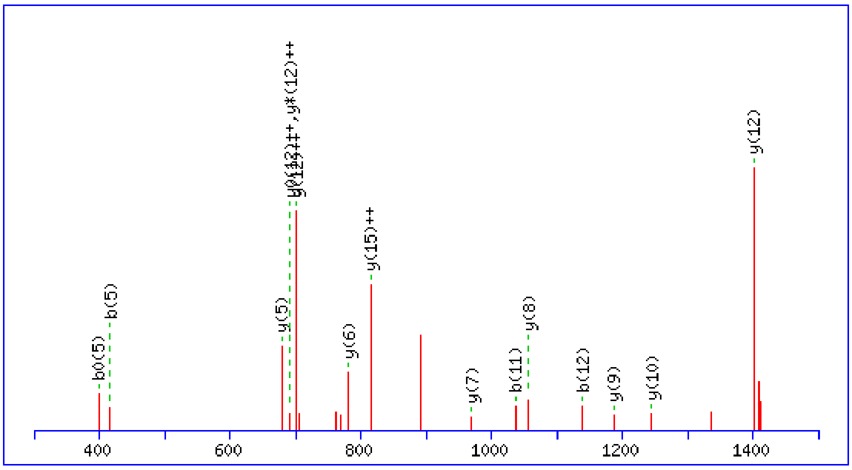
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGPGAPGGQSWTPEWLK**
Found in **AT4G08390.1** in **TAIR_Arabidopsis**, Symbols: SAPX | SAPX; L-ascorbate peroxidase | chr4:5314996-5317068 FORWARD

Match to Query 8285: 1816.796062 from(909.405307,2+) index(7769)
Title: Elution from: 71.626 to 71.626 scan no 10327 cid35.00 polarity:+
Data file D12h-2_2.mgf

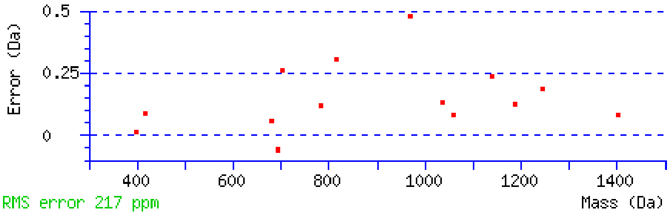
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

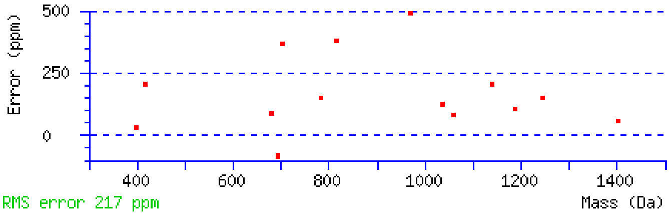


Monoisotopic mass of neutral peptide Mr(calc): 1816.7907
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 8.9e-006
Matches : 15/170 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0469	66.0271			113.0363	57.0218	E							17
2	189.0654	95.0363			171.0548	86.0311	G	1687.7583	844.3828	1669.7347	835.3710	1669.7478	835.3775	16
3	287.1152	144.0612			269.1046	135.0560	P	1629.7398	815.3736	1611.7162	806.3618	1611.7293	806.3683	15
4	345.1337	173.0705			327.1231	164.0652	G	1531.6900	766.3487	1513.6664	757.3369	1513.6795	757.3434	14
5	**417.1678**	209.0876			399.1573	200.0823	A	1473.6715	737.3394	1455.6480	728.3276	1455.6610	728.3341	13
6	515.2176	258.1125			497.2071	249.1072	P	***1401.6374***	701.3223	1383.6138	692.3105	1383.6268	692.3170	12
7	573.2361	287.1217			555.2256	278.1164	G	1303.5876	652.2974	1285.5640	643.2856	1285.5770	643.2921	11
8	631.2546	316.1310			613.2441	307.1257	G	***1245.5691***	623.2882	1227.5455	614.2764	1227.5585	614.2829	10
9	761.3073	381.1573	743.2837	372.1455	743.2967	372.1520	Q	***1187.5506***	594.2789	1169.5270	585.2671	1169.5400	585.2736	9
10	849.3364	425.1718	831.3128	416.1600	831.3258	416.1665	S	***1057.4979***	529.2526	1039.4744	520.2408	1039.4874	520.2473	8
11	**1037.4097**	519.2085	1019.3862	510.1967	1019.3992	510.2032	W	***969.4689***	485.2381	951.4453	476.2263	951.4583	476.2328	7
12	**1139.4545**	570.2309	1121.4309	561.2191	1121.4439	561.2256	T	***781.3955***	391.2014	763.3719	382.1896	763.3849	382.1961	6
13	1237.5043	619.2558	1219.4807	610.2440	1219.4937	610.2505	P	***679.3508***	340.1790	661.3272	331.1672	661.3402	331.1737	5
14	1367.5439	684.2756	1349.5203	675.2638	1349.5333	675.2703	E	581.3010	291.1541	563.2774	282.1423	563.2904	282.1488	4
15	1555.6173	778.3123	1537.5937	769.3005	1537.6067	769.3070	W	451.2614	226.1343	433.2378	217.1225			3
16	1669.6984	835.3528	1651.6748	826.3410	1651.6878	826.3475	L	263.1880	132.0976	245.1644	123.0858			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT4G08390.1





NCBI **BLAST** search of EGPGAPGGQSWTPEWLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.2	1816.7907	0.0054	EGPGAPGGQSWTPEWLK

Mascot: http://www.matrixscience.com/

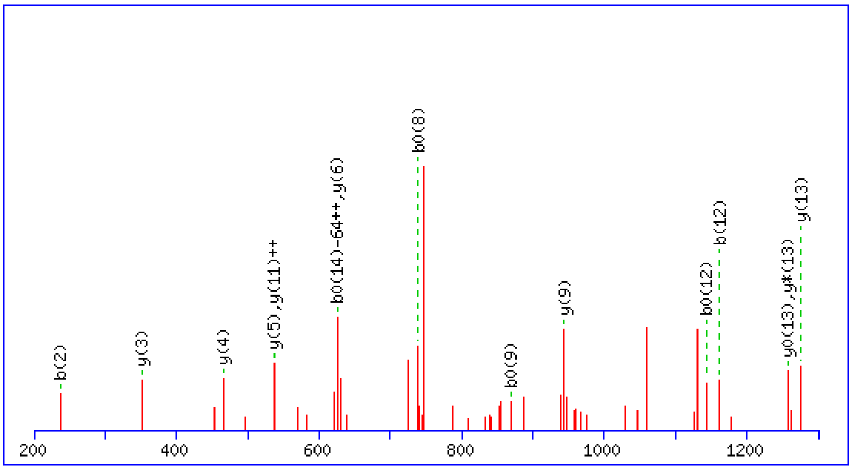
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSVTAGVSESAIAVR**
Found in **AT4G08580.1** in **TAIR_Arabidopsis**, Symbols: | microfibrillar-associated protein-related | chr4:5462187-5463715 FORWARD

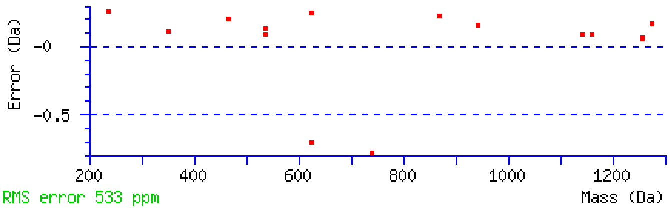
Match to Query 6727: 1510.706152 from(756.360352,2+) index(7103)
Title: Elution from: 62.442 to 62.442 scan no 9126 cid35.00 polarity:+
Data file 0-2_1.mgf

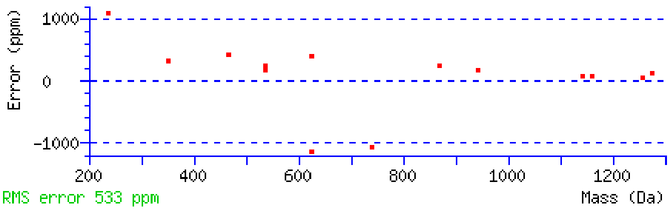
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1510.7022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 **Expect:** 0.0014
Matches : 15/182 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235			M							15
2	**237.0688**	119.0380	219.0582	110.0327	S	1363.6770	682.3421	1345.6534	673.3304	1345.6664	673.3369	14
3	337.1342	169.0707	319.1237	160.0655	V	***1275.6480***	638.3276	1257.6244	629.3158	1257.6374	629.3223	13
4	439.1789	220.0931	421.1684	211.0878	T	1175.5825	588.2949	1157.5589	579.2831	1157.5719	579.2896	12
5	511.2131	256.1102	493.2025	247.1049	A	1073.5378	537.2725	1055.5142	528.2607	1055.5272	528.2673	11
6	569.2316	285.1194	551.2210	276.1141	G	1001.5036	501.2555	983.4801	492.2437	983.4931	492.2502	10
7	669.2970	335.1522	651.2865	326.1469	V	***943.4851***	472.2462	925.4616	463.2344	925.4746	463.2409	9
8	757.3261	379.1667	739.3155	370.1614	S	843.4197	422.2135	825.3961	413.2017	825.4091	413.2082	8
9	887.3657	444.1865	869.3552	435.1812	E	755.3906	378.1990	737.3670	369.1872	737.3801	369.1937	7
10	975.3948	488.2010	957.3842	479.1957	S	***625.3510***	313.1791	607.3274	304.1673	607.3404	304.1739	6
11	1047.4289	524.2181	1029.4184	515.2128	A	***537.3219***	269.1646	519.2984	260.1528			5
12	**1161.5100**	581.2587	1143.4995	572.2534	I	***465.2878***	233.1475	447.2642	224.1357			4
13	1233.5442	617.2757	1215.5336	608.2704	A	***351.2067***	176.1070	333.1831	167.0952			3
14	1333.6096	667.3085	1315.5991	658.3032	V	279.1725	140.0899	261.1490	131.0781			2
15					R	179.1071	90.0572	161.0835	81.0454			1





AT4G08580.1

NCBI **BLAST** search of MSVTAGVSESAIAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.3	1510.7022	0.0040	MSVTAGVSESAIAVR
19.3	1510.7044	0.0017	MLGFKEHTSTLSK
10.9	1510.7092	-0.0030	VDFSNSLELIGSSK
7.6	1510.7066	-0.0005	HYMVFDEKVLSK
4.0	1510.7022	0.0040	IKMELSTDQSGLR
2.0	1510.7071	-0.0009	HMRAKVSDFGLSK
1.9	1510.7022	0.0040	MAANTISLSNVAASK
1.3	1510.7022	0.0040	LVMTATDLNSERK
1.0	1510.7100	-0.0039	LREMSPLYEMVK
0.1	1510.7022	0.0040	MTKSSNVEVIVDR

AT4G09000.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDTILVPAAASGDSK**
Found in **AT4G09000.1** in **TAIR_Arabidopsis**, Symbols: GF14 CHI | GRF1 (GENERAL REGULATORY FACTOR 1); protein phosphorylated amino acid binding | chr4:5775384-5777154 FORWARD

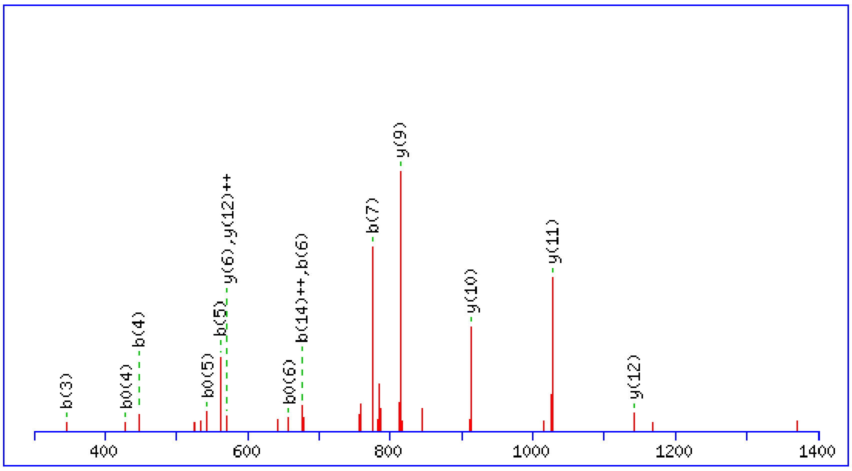
Match to Query 7192: 1586.807378 from(794.410965,2+) index(7486)
Title: Elution from: 65.405 to 65.405 scan no 9679 cid35.00 polarity:+
Data file C7-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1400 Da Full range

Label all possible matches ○ Label matches used for scoring ●

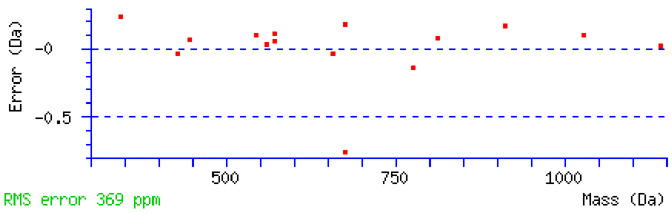
Show Y-axis ☐

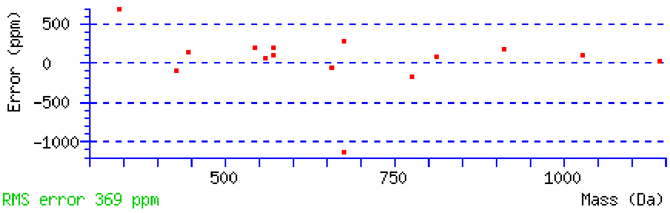


Monoisotopic mass of neutral peptide Mr(calc): 1586.8110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00042
Matches : 15/144 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							16
2	229.1695	115.0884			L	1473.7372	737.3722	1455.7136	728.3604	1455.7266	728.3669	15
3	***345.1935***	173.1004	327.1829	164.0951	D	1359.6561	680.3317	1341.6325	671.3199	1341.6455	671.3264	14
4	***447.2382***	224.1227	429.2276	215.1174	T	1243.6321	622.3197	1225.6085	613.3079	1225.6215	613.3144	13
5	***561.3193***	281.1633	543.3087	272.1580	I	***1141.5874***	571.2973	1123.5638	562.2855	1123.5768	562.2920	12
6	***675.4004***	338.2038	657.3898	329.1985	L	***1027.5063***	514.2568	1009.4827	505.2450	1009.4957	505.2515	11
7	***775.4658***	388.2365	757.4552	379.2313	V	***913.4252***	457.2162	895.4016	448.2044	895.4146	448.2109	10
8	873.5156	437.2614	855.5050	428.2562	P	***813.3597***	407.1835	795.3361	398.1717	795.3492	398.1782	9
9	945.5498	473.2785	927.5392	464.2732	A	715.3099	358.1586	697.2863	349.1468	697.2994	349.1533	8
10	1017.5839	509.2956	999.5733	500.2903	A	643.2758	322.1415	625.2522	313.1297	625.2652	313.1362	7
11	1089.6181	545.3127	1071.6075	536.3074	A	***571.2416***	286.1245	553.2180	277.1127	553.2311	277.1192	6
12	1177.6471	589.3272	1159.6366	580.3219	S	499.2075	250.1074	481.1839	241.0956	481.1969	241.1021	5
13	1235.6656	618.3364	1217.6551	609.3312	G	411.1784	206.0928	393.1548	197.0811	393.1678	197.0876	4
14	1351.6896	676.3484	1333.6790	667.3432	D	353.1599	177.0836	335.1363	168.0718	335.1493	168.0783	3
15	1439.7187	720.3630	1421.7081	711.3577	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
16					K	149.1069	75.0571	131.0833	66.0453			1

AT4G09000.1





NCBI **BLAST** search of LLDTILVPAAASGDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.4	1586.8110	-0.0036	LLDTILVPAAASGDSK
5.4	1586.8033	0.0041	QSEPLAGLRPTLQR

Mascot: http://www.matrixscience.com/

AT4G09010.1

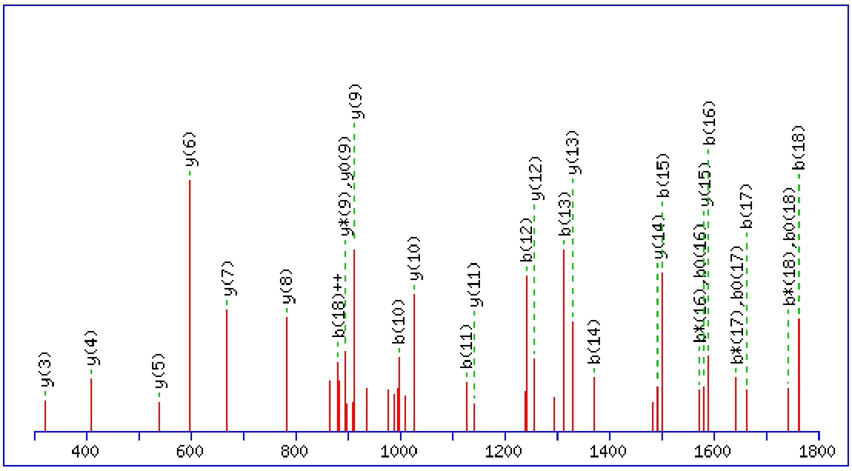
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGPISYADIIQLAGQSAVK**
Found in **AT4G09010.1** in **TAIR_Arabidopsis**, Symbols: APX4 | APX4 (ASCORBATE PEROXIDASE 4); peroxidase | chr4:5777499-5779335 REVERSE

Match to Query 8986: 1908.945966 from(955.480259,2+) index(9879)
Title: Elution from: 91.655 to 91.655 scan no 13752 cid35.00 polarity:+
Data file 0-1_2.mgf

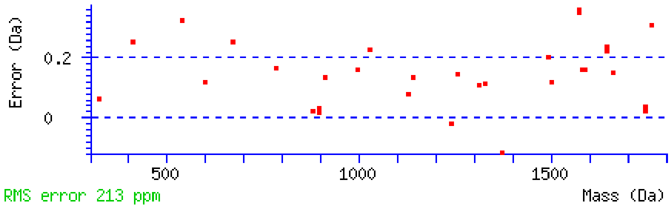
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

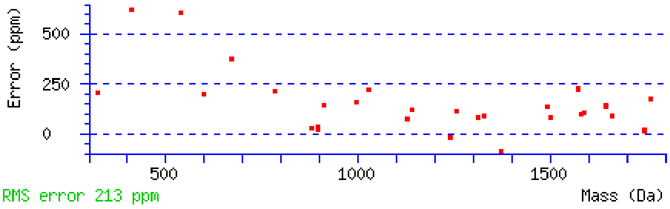


Monoisotopic mass of neutral peptide Mr(calc): 1908.9449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 138 **Expect:** 9.1e-014
Matches : 31/182 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							19
2	117.0443	59.0258					G	1851.9337	926.4705	1833.9101	917.4587	1833.9232	917.4652	18
3	215.0941	108.0507					P	1793.9152	897.4613	1775.8916	888.4495	1775.9047	888.4560	17
4	329.1752	165.0912					I	1695.8654	848.4364	1677.8418	839.4246	1677.8549	839.4311	16
5	417.2042	209.1058			399.1937	200.1005	S	***1581.7843***	791.3958	1563.7607	782.3840	1563.7738	782.3905	15
6	581.2646	291.1359			563.2540	282.1307	Y	***1493.7553***	747.3813	1475.7317	738.3695	1475.7447	738.3760	14
7	653.2987	327.1530			635.2882	318.1477	A	***1329.6949***	665.3511	1311.6713	656.3393	1311.6843	656.3458	13
8	769.3227	385.1650			751.3122	376.1597	D	***1257.6608***	629.3340	1239.6372	620.3222	1239.6502	620.3287	12
9	883.4038	442.2056			865.3933	433.2003	I	***1141.6368***	571.3220	1123.6132	562.3102	1123.6262	562.3167	11
10	***997.4849***	499.2461			979.4744	490.2408	I	***1027.5557***	514.2815	1009.5321	505.2697	1009.5451	505.2762	10
11	***1127.5376***	564.2724	1109.5140	555.2606	1109.5270	555.2671	Q	***913.4746***	457.2409	895.4510	448.2291	895.4640	448.2356	9
12	***1241.6187***	621.3130	1223.5951	612.3012	1223.6081	612.3077	L	***783.4219***	392.2146	765.3983	383.2028	765.4114	383.2093	8
13	***1313.6528***	657.3300	1295.6292	648.3183	1295.6423	648.3248	A	***669.3408***	335.1741	651.3172	326.1623	651.3303	326.1688	7
14	***1371.6713***	686.3393	1353.6477	677.3275	1353.6608	677.3340	G	***597.3067***	299.1570	579.2831	290.1452	579.2961	290.1517	6
15	***1501.7240***	751.3656	1483.7004	742.3538	1483.7134	742.3603	Q	***539.2882***	270.1477	521.2646	261.1359	521.2776	261.1424	5
16	***1589.7530***	795.3802	1571.7294	786.3684	1571.7425	786.3749	S	***409.2355***	205.1214	391.2120	196.1096	391.2250	196.1161	4
17	***1661.7872***	831.3972	1643.7636	822.3854	1643.7766	822.3919	A	***321.2065***	161.1069	303.1829	152.0951			3
18	***1761.8526***	881.4300	1743.8290	872.4182	1743.8421	872.4247	V	249.1723	125.0898	231.1487	116.0780			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT4G09010.1





NCBI **BLAST** search of GGPISYADIIQLAGQSAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
138.3	1908.9449	0.0010	GGPISYADIIQLAGQSAVK
11.7	1908.9450	0.0010	NSPTSVSISKVPTWEKK
10.6	1908.9454	0.0006	GRPPKAKSDSSQIGAVSAK
8.6	1908.9417	0.0042	FLPFARFGPIAHEINR
0.5	1908.9483	-0.0024	IMKGSDSIGLAPGAVEKSK

Mascot: http://www.matrixscience.com/

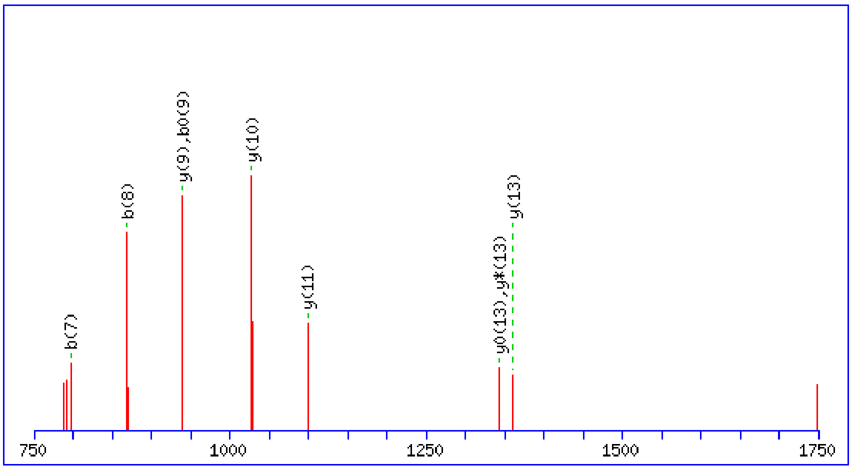
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLVFIEMASPEEAATALK**
Found in **AT4G09040.1** in **TAIR_Arabidopsis**, Symbols: | RNA recognition motif (RRM)-containing protein | chr4:5795072-5797312 REVERSE

Match to Query 8859: 1894.906836 from(948.460694,2+) index(9647)
Title: Elution from: 88.691 to 88.691 scan no 13370 cid35.00 polarity:+
Data file 0-1_3.mgf

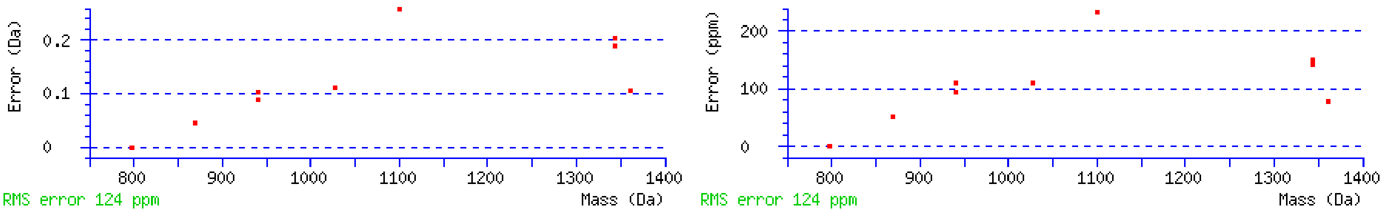
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 750 to 1750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1894.9089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.017
Matches : 9/154 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			G							18
2	173.1069	87.0571			L	1837.8976	919.4525	1819.8741	910.4407	1819.8871	910.4472	17
3	273.1723	137.0898			V	1723.8165	862.4119	1705.7930	853.4001	1705.8060	853.4066	16
4	421.2378	211.1225			F	1623.7511	812.3792	1605.7275	803.3674	1605.7405	803.3739	15
5	535.3189	268.1631			I	1475.6856	738.3465	1457.6621	729.3347	1457.6751	729.3412	14
6	665.3585	333.1829	647.3479	324.1776	E	***1361.6045***	681.3059	1343.5810	672.2941	1343.5940	672.3006	13
7	**797.3960**	399.2016	779.3855	390.1964	M	1231.5649	616.2861	1213.5413	607.2743	1213.5544	607.2808	12
8	**869.4302**	435.2187	851.4196	426.2134	A	***1099.5274***	550.2673	1081.5038	541.2555	1081.5168	541.2621	11
9	957.4592	479.2333	939.4487	470.2280	S	***1027.4933***	514.2503	1009.4697	505.2385	1009.4827	505.2450	10
10	1055.5090	528.2582	1037.4985	519.2529	P	***939.4642***	470.2357	921.4406	461.2239	921.4536	461.2304	9
11	1185.5487	593.2780	1167.5381	584.2727	E	841.4144	421.2108	823.3908	412.1990	823.4038	412.2056	8
12	1315.5883	658.2978	1297.5777	649.2925	E	711.3748	356.1910	693.3512	347.1792	693.3642	347.1857	7
13	1387.6224	694.3149	1369.6119	685.3096	A	581.3351	291.1712	563.3115	282.1594	563.3246	282.1659	6
14	1459.6566	730.3319	1441.6460	721.3266	A	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	5
15	1561.7013	781.3543	1543.6907	772.3490	T	437.2668	219.1371	419.2433	210.1253	419.2563	210.1318	4
16	1633.7354	817.3714	1615.7249	808.3661	A	335.2221	168.1147	317.1985	159.1029			3
17	1747.8165	874.4119	1729.8060	865.4066	L	263.1880	132.0976	245.1644	123.0858			2
18					K	149.1069	75.0571	131.0833	66.0453			1

AT4G09040.1



NCBI **BLAST** search of GLVFIEMASPEEAATALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.1	1894.9089	-0.0020	GLVFIEMASPEEAATALK
14.1	1894.9081	-0.0013	WVFPDTNSGIIVLAEGR
5.2	1894.9113	-0.0044	NPYQAIVAARDSLRHR
4.8	1894.9019	0.0050	ISHQMVMSLSGEVVVVK
4.8	1894.9033	0.0036	SYGITEPLSIAGPSAADVK
4.3	1894.9012	0.0057	SHEKVTIHGMAIKYGGK

Mascot: http://www.matrixscience.com/

AT4G09320.1

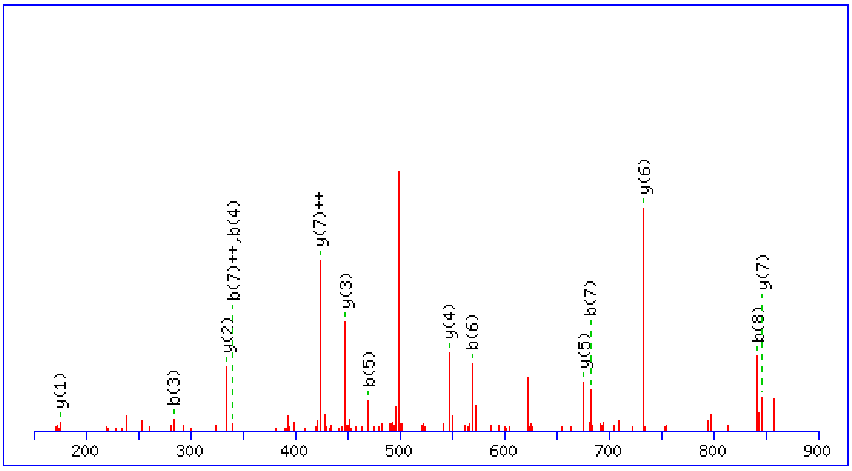
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLIGEVICR**
Found in **AT4G09320.1** in **TAIR_Arabidopsis**, Symbols: NDPK1 | NDPK1 (nucleoside diphosphate kinase 1); ATP binding / nucleoside diphosphate kinase | chr4:5923421-5924363 FORWARD

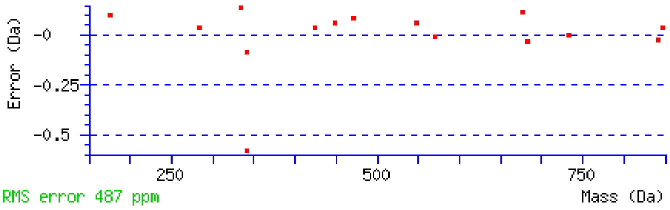
Match to Query 2600: 1015.547578 from(508.781065,2+) index(5359)
Title: Elution from: 47.708 to 47.708 scan no 6745 cid35.00 polarity:+
Data file 0-1_3.mgf

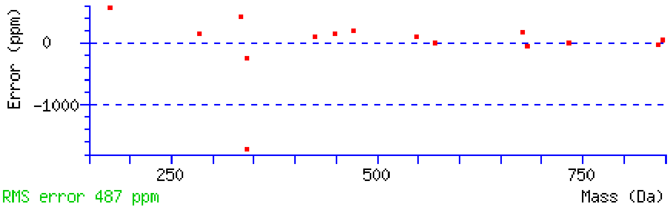
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1015.5484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.5e-005
Matches : 15/64 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							9
2	171.1128	86.0600			L	959.5343	480.2708	942.5077	471.7575	941.5237	471.2655	8
3	**284.1969**	142.6021			I	***846.4502***	423.7287	829.4237	415.2155	828.4396	414.7235	7
4	**341.2183**	171.1128			G	***733.3661***	367.1867	716.3396	358.6734	715.3556	358.1814	6
5	**470.2609**	235.6341	452.2504	226.6288	E	***676.3447***	338.6760	659.3181	330.1627	658.3341	329.6707	5
6	**569.3293**	285.1683	551.3188	276.1630	V	***547.3021***	274.1547	530.2755	265.6414			4
7	**682.4134**	341.7103	664.4028	332.7051	I	***448.2337***	224.6205	431.2071	216.1072			3
8	**842.4441**	421.7257	824.4335	412.7204	C	***335.1496***	168.0784	318.1231	159.5652			2
9					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GLIGEVICR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G09320.1

55.4	1015.5484	-0.0009	GLIGEVICR

Mascot: http://www.matrixscience.com/

AT4G09650.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVIDDIVK**
Found in **AT4G09650.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase delta chain, chloroplast, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative | chr4:6100796-6101500 FORWARD

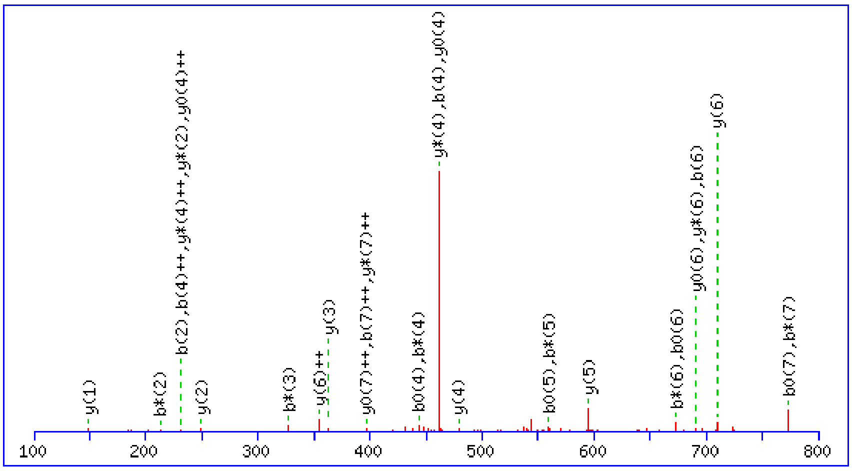
Match to Query 1888: 938.491868 from(470.253210,2+) index(3551)
Title: Elution from: 34.033 to 34.033 scan no 4435 cid35.00 polarity:+
Data file D6h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

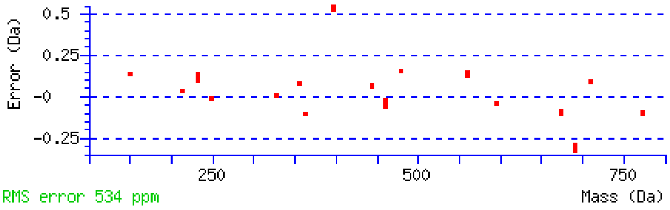
Label all possible matches ○ Label matches used for scoring ●

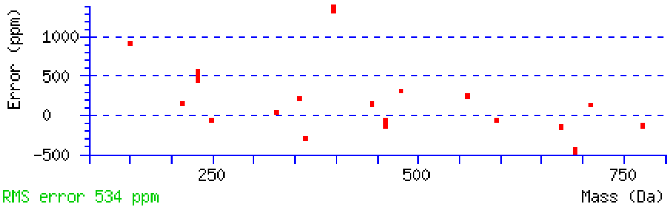
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 938.4933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00048
Matches : 31/72 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							8
2	**231.1254**	116.0663	213.1018	107.0545			V	809.4479	405.2276	791.4243	396.2158	791.4374	396.2223	7
3	345.2065	173.1069	327.1829	164.0951			I	***709.3825***	355.1949	691.3589	346.1831	691.3719	346.1896	6
4	**461.2304**	231.1189	443.2069	222.1071	443.2199	222.1136	D	***595.3014***	298.1543	577.2778	289.1425	577.2908	289.1490	5
5	577.2544	289.1309	559.2308	280.1191	559.2439	280.1256	D	***479.2774***	240.1423	461.2538	231.1305	461.2668	231.1371	4
6	**691.3355**	346.1714	673.3119	337.1596	673.3250	337.1661	I	***363.2534***	182.1303	345.2298	173.1186			3
7	791.4010	396.2041	773.3774	387.1923	773.3904	387.1988	V	***249.1723***	125.0898	231.1487	116.0780			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QVIDDIVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.5	938.4933	-0.0014	EVLDNLVK

AT4G09650.1

38.5	938.4933	-0.0014	QVIDDIVK
19.1	938.4933	-0.0014	LDLAEVAAK
19.0	938.4933	-0.0014	DLEQVVVK
18.8	938.4933	-0.0014	EVIVVDQK
18.8	938.4933	-0.0014	EVLQAIEK
10.6	938.4933	-0.0014	EAGVEVVVK
5.5	938.4933	-0.0014	VLEVNVEK
5.5	938.4933	-0.0014	EVAQEIIK
5.5	938.4933	-0.0014	QVVDDLIK

AT4G09670.1

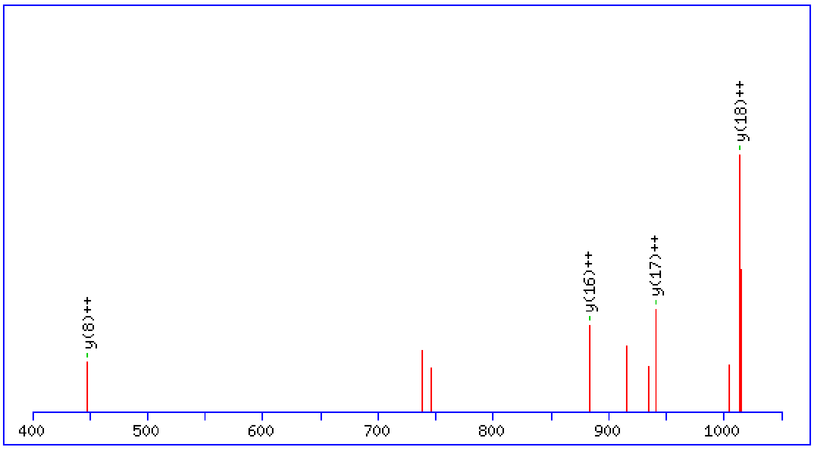
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AWFNDLVTAWVSPPSEHTVK**
Found in **AT4G09670.1** in **TAIR_Arabidopsis**, Symbols: | oxidoreductase family protein | chr4:6107379-6109046 REVERSE

Match to Query 9771: 2283.130092 from(762.050640,3+) index(10457)
Title: Elution from: 105.852 to 105.852 scan no 15437 cid35.00 polarity:+
Data file D1d-2_2.mgf

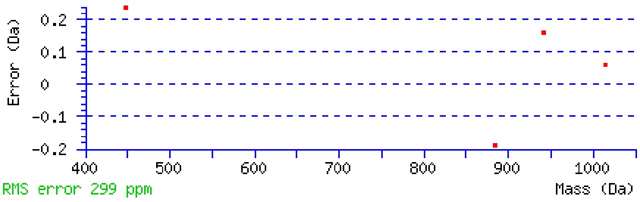
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

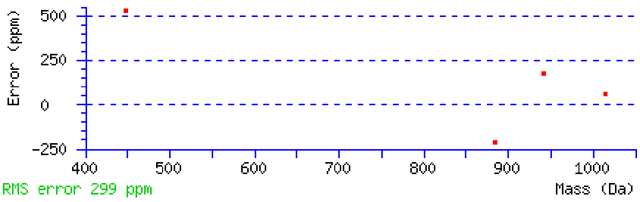


Monoisotopic mass of neutral peptide Mr(calc): 2283.1324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.014
Matches : 4/210 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							20
2	258.1237	129.5655					W	2213.1026	1107.0549	2196.0760	1098.5417	2195.0920	1098.0496	19
3	405.1921	203.0997					F	2027.0233	1014.0153	2009.9967	1005.5020	2009.0127	1005.0100	18
4	519.2350	260.1212	502.2085	251.6079			N	1879.9549	940.4811	1862.9283	931.9678	1861.9443	931.4758	17
5	634.2620	317.6346	617.2354	309.1214	616.2514	308.6293	D	1765.9119	883.4596	1748.8854	874.9463	1747.9014	874.4543	16
6	747.3461	374.1767	730.3195	365.6634	729.3355	365.1714	L	1650.8850	825.9461	1633.8584	817.4329	1632.8744	816.9408	15
7	846.4145	423.7109	829.3879	415.1976	828.4039	414.7056	V	1537.8009	769.4041	1520.7744	760.8908	1519.7904	760.3988	14
8	947.4621	474.2347	930.4356	465.7214	929.4516	465.2294	T	1438.7325	719.8699	1421.7060	711.3566	1420.7219	710.8646	13
9	1018.4993	509.7533	1001.4727	501.2400	1000.4887	500.7480	A	1337.6848	669.3461	1320.6583	660.8328	1319.6743	660.3408	12
10	1204.5786	602.7929	1187.5520	594.2796	1186.5680	593.7876	W	1266.6477	633.8275	1249.6212	625.3142	1248.6371	624.8222	11
11	1303.6470	652.3271	1286.6204	643.8139	1285.6364	643.3218	V	1080.5684	540.7878	1063.5419	532.2746	1062.5578	531.7826	10
12	1390.6790	695.8431	1373.6525	687.3299	1372.6684	686.8379	S	981.5000	491.2536	964.4734	482.7404	963.4894	482.2483	9
13	1487.7318	744.3695	1470.7052	735.8563	1469.7212	735.3642	P	894.4680	447.7376	877.4414	439.2243	876.4574	438.7323	8
14	1584.7845	792.8959	1567.7580	784.3826	1566.7740	783.8906	P	797.4152	399.2112	780.3886	390.6980	779.4046	390.2060	7
15	1671.8166	836.4119	1654.7900	827.8986	1653.8060	827.4066	S	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	6
16	1800.8592	900.9332	1783.8326	892.4199	1782.8486	891.9279	E	613.3304	307.1688	596.3039	298.6556	595.3198	298.1636	5
17	1937.9181	969.4627	1920.8915	960.9494	1919.9075	960.4574	H	484.2878	242.6475	467.2613	234.1343	466.2772	233.6423	4
18	2038.9658	1019.9865	2021.9392	1011.4732	2020.9552	1010.9812	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
19	2138.0342	1069.5207	2121.0076	1061.0074	2120.0236	1060.5154	V	246.1812	123.5942	229.1547	115.0810			2
20							K	147.1128	74.0600	130.0863	65.5468			1

AT4G09670.1





NCBI **BLAST** search of AWFNDLVTAWVSPPSEHTVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	2283.1324	-0.0023	AWFNDLVTAWVSPPSEHTVK
6.7	2283.1312	-0.0011	DSMALLIKGFMNGLEEKMEK
5.3	2283.1358	-0.0057	FQELESLVHHPIDYACVVK
5.0	2283.1310	-0.0010	EEFEDPLTYLQKIFPEASK

AT4G09940.1

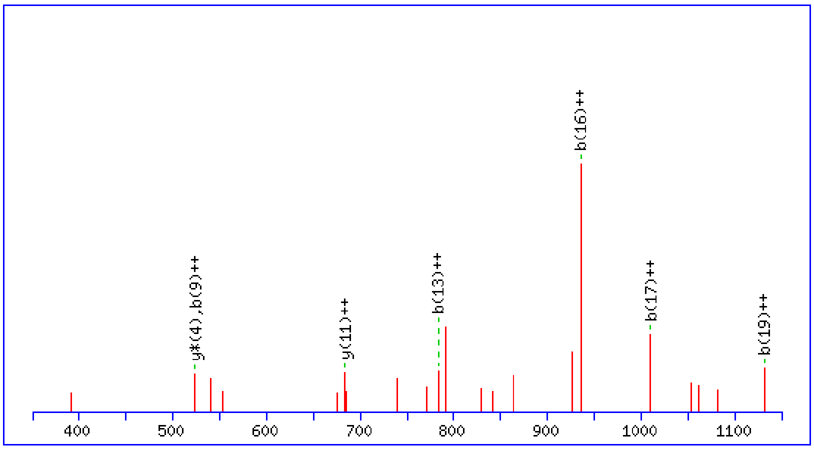
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYMADLSHEIRENETAFQIK**
Found in **AT4G09940.1** in **TAIR_Arabidopsis**, Symbols: | avirulence-responsive family protein / avirulence induced gene (AIG1) family protein | chr4:6231783-6233394 FORWARD

Match to Query 10574: 2409.048705 from(804.023511,3+) index(11195)
Title: Elution from: 116.828 to 116.828 scan no 16468 cid35.00 polarity:+
Data file 0-3_1.mgf

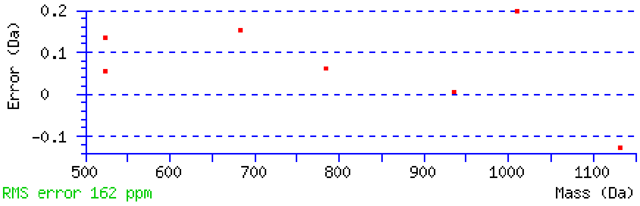
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

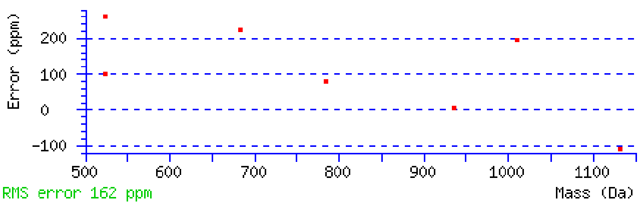


Monoisotopic mass of neutral peptide Mr(calc): 2409.0491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0092
Matches : 7/198 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							20
2	253.0967	127.0520			235.0861	118.0467	Y	2322.0274	1161.5173	2304.0038	1152.5055	2304.0168	1152.5120	19
3	385.1342	193.0707			367.1237	184.0655	M	2157.9670	1079.4871	2139.9434	1070.4753	2139.9564	1070.4818	18
4	457.1684	229.0878			439.1578	220.0825	A	2025.9295	1013.4684	2007.9059	1004.4566	2007.9189	1004.4631	17
5	573.1924	287.0998			555.1818	278.0945	D	1953.8953	977.4513	1935.8717	968.4395	1935.8848	968.4460	16
6	687.2734	344.1404			669.2629	335.1351	L	1837.8713	919.4393	1819.8478	910.4275	1819.8608	910.4340	15
7	775.3025	388.1549			757.2919	379.1496	S	1723.7902	862.3988	1705.7667	853.3870	1705.7797	853.3935	14
8	915.3525	458.1799			897.3420	449.1746	H	1635.7612	818.3842	1617.7376	809.3724	1617.7506	809.3789	13
9	1045.3922	***523.1997***			1027.3816	514.1944	E	1495.7112	748.3592	1477.6876	739.3474	1477.7006	739.3539	12
10	1159.4733	580.2403			1141.4627	571.2350	I	1365.6715	683.3394	1347.6480	674.3276	1347.6610	674.3341	11
11	1319.5625	660.2849	1301.5389	651.2731	1301.5519	651.2796	R	1251.5904	626.2989	1233.5669	617.2871	1233.5799	617.2936	10
12	1449.6021	725.3047	1431.5786	716.2929	1431.5916	716.2994	E	1091.5012	546.2542	1073.4776	537.2424	1073.4906	537.2489	9
13	1565.6391	***783.3232***	1547.6155	774.3114	1547.6286	774.3179	N	961.4616	481.2344	943.4380	472.2226	943.4510	472.2291	8
14	1695.6788	848.3430	1677.6552	839.3312	1677.6682	839.3377	E	845.4246	423.2159	827.4010	414.2041	827.4140	414.2106	7
15	1797.7235	899.3654	1779.6999	890.3536	1779.7129	890.3601	T	715.3849	358.1961	697.3613	349.1843	697.3744	349.1908	6
16	1869.7576	***935.3824***	1851.7340	926.3707	1851.7471	926.3772	A	613.3402	307.1737	595.3166	298.1620			5
17	2017.8231	***1009.4152***	1999.7995	1000.4034	1999.8125	1000.4099	F	541.3061	271.1567	523.2825	262.1449			4
18	2147.8757	1074.4415	2129.8521	1065.4297	2129.8652	1065.4362	Q	393.2406	197.1239	375.2170	188.1122			3
19	2261.9568	***1131.4820***	2243.9332	1122.4703	2243.9463	1122.4768	I	263.1880	132.0976	245.1644	123.0858			2
20							K	149.1069	75.0571	131.0833	66.0453			1

AT4G09940.1





NCBI **BLAST** search of SYMADLSHEIRENETAFQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.4	2409.0491	-0.0004	SYMADLSHEIRENETAFQIK
14.6	2409.0525	-0.0038	TLSETLENMHALNRMYGLEK
11.3	2409.0446	0.0041	GEEEDGETTSNSVMTKLLRGAR
6.9	2409.0422	0.0065	IDCFPCIKVPSSSRESVEGGR
5.7	2409.0512	-0.0025	VIDLDDYAADDDQYEEKLKK
2.5	2409.0444	0.0043	CSICRQLFTGFSYESKELR
1.7	2409.0547	-0.0060	QMDYSTRVQHYPIEVLEMK
1.7	2409.0536	-0.0049	NHVGDWGTQFGMLIEFLFEK
1.7	2409.0536	-0.0049	NHVGDWGTQFGMLIEYLFEK
1.2	2409.0480	0.0007	SLYYVTWRHGDQFPDEIEK

Mascot: http://www.matrixscience.com/

AT4G10060.1

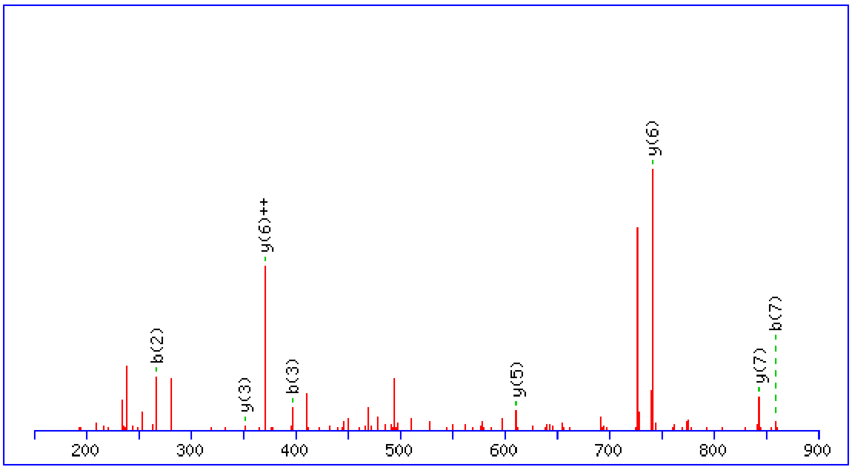
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTKEEAKK**
Found in **AT4G10060.1** in **TAIR_Arabidopsis**, Symbols: | catalytic | chr4:6289352-6295254 FORWARD

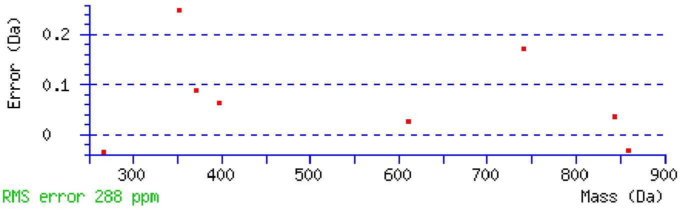
Match to Query 2462: 1006.499086 from(504.256819,2+) index(5432)
Title: Elution from: 48.480 to 48.480 scan no 6998 cid35.00 polarity:+
Data file D12h-3_3.mgf

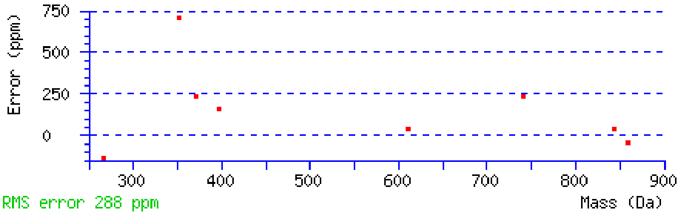
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1006.4961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.026
Matches : 8/72 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	165.0676	83.0375					Y							8
2	*267.1124*	134.0598			249.1018	125.0545	T	*843.4431*	422.2252	825.4195	413.2134	825.4325	413.2199	7
3	*397.2014*	199.1043	379.1778	190.0925	379.1908	190.0990	K	*741.3983*	371.2028	723.3748	362.1910	723.3878	362.1975	6
4	527.2410	264.1241	509.2174	255.1124	509.2304	255.1189	E	*611.3093*	306.1583	593.2857	297.1465	593.2987	297.1530	5
5	657.2806	329.1440	639.2571	320.1322	639.2701	320.1387	E	481.2697	241.1385	463.2461	232.1267	463.2591	232.1332	4
6	729.3148	365.1610	711.2912	356.1492	711.3042	356.1558	A	*351.2301*	176.1187	333.2065	167.1069			3
7	*859.4038*	430.2056	841.3802	421.1938	841.3933	421.2003	K	279.1959	140.1016	261.1723	131.0898			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YTKEEAKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.3	1006.4961	0.0029	YTKEEAKK
22.5	1006.4988	0.0003	LFSRVESR

AT4G10060.1

16.1	1006.5017	-0.0027	TYEVMVKK
6.3	1006.4988	0.0003	ASAYNRAIK
6.2	1006.4974	0.0016	MKTMRGLR
5.8	1006.5017	-0.0027	KFTDLMVK
5.5	1006.4988	0.0003	TNRATGFVK
4.3	1006.4984	0.0007	FINTDIFK
3.8	1006.4984	0.0007	FVFESLQK
3.7	1006.5018	-0.0027	YLQSVLMK

AT4G10300.1

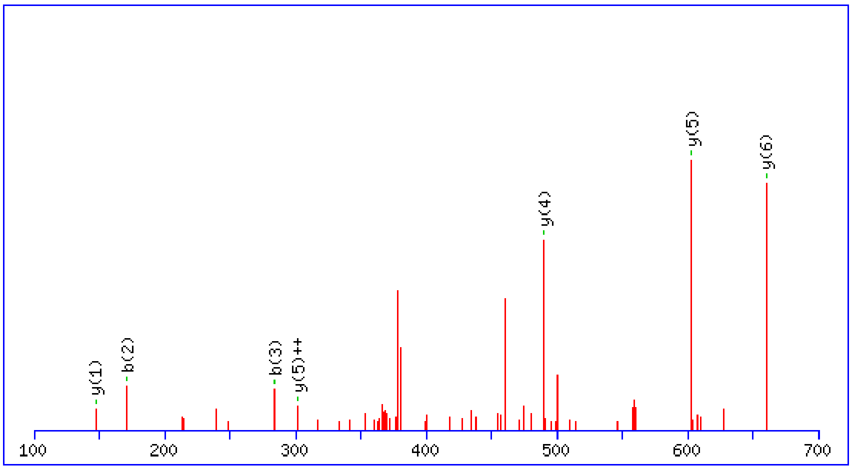
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGITIEK**
Found in **AT4G10300.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04300.1); similar to unknown [Populus trichocarpa] (GB:ABK95374.1); contains InterPro domain RmlC-like jelly roll fold (InterPro:IPR014710); contains InterPro domain Protein of

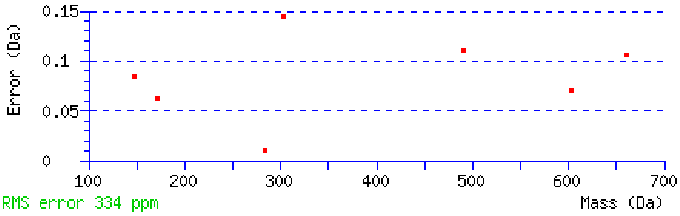
Match to Query 921: 772.469356 from(387.241954,2+) index(3319)
Title: Elution from: 32.206 to 32.206 scan no 4104 cid35.00 polarity:+
Data file D6h-1_1.mgf

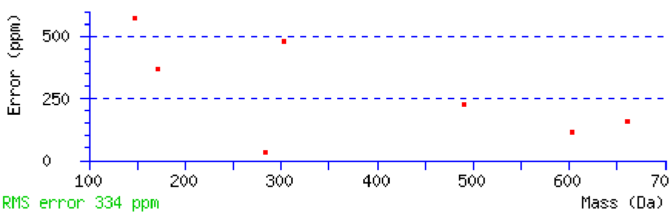
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 772.4694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0034
Matches : 7/52 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							7
2	**171.1128**	86.0600			G	***660.3927***	330.7000	643.3661	322.1867	642.3821	321.6947	6
3	**284.1969**	142.6021			I	***603.3712***	302.1892	586.3447	293.6760	585.3606	293.1840	5
4	385.2445	193.1259	367.2340	184.1206	T	***490.2871***	245.6472	473.2606	237.1339	472.2766	236.6419	4
5	498.3286	249.6679	480.3180	240.6627	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
6	627.3712	314.1892	609.3606	305.1840	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
7					K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LGITIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.0	772.4694	-0.0001	LGITIEK

AT4G10300.1

21.8	772.4695	-0.0001	ITVVDVK
11.6	772.4694	-0.0001	IAVETLK
10.9	772.4694	-0.0001	IVTELAK
10.9	772.4694	-0.0001	LSLAEIK
10.7	772.4694	-0.0001	LTALLDK
9.9	772.4694	-0.0001	LTGELLK
3.2	772.4694	-0.0001	LLETAVK
0.3	772.4695	-0.0001	SDVVLLK

AT4G10340.1

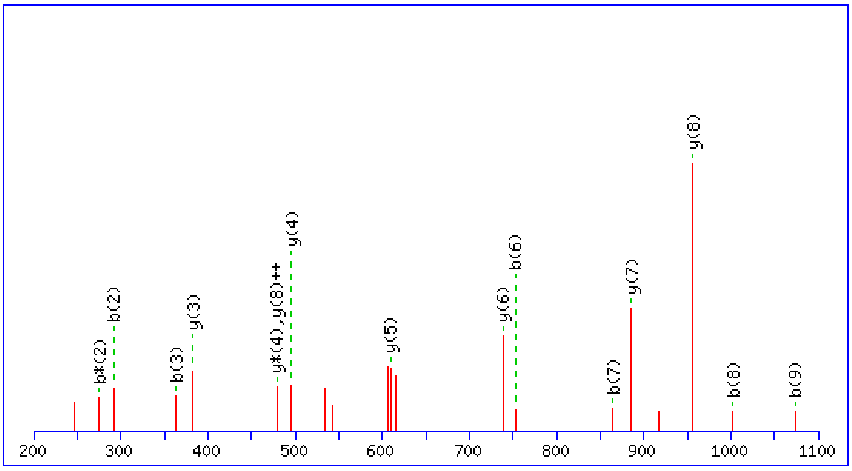
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQAFELIHAR**
Found in **AT4G10340.1** in **TAIR_Arabidopsis**, Symbols: LHCB5 | LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding | chr4:6408196-6409492 FORWARD

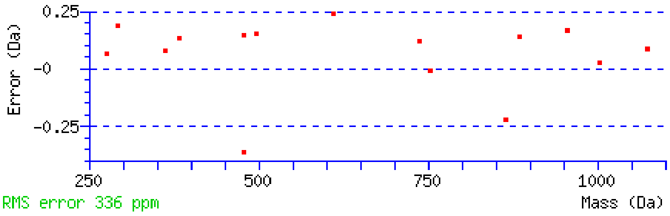
Match to Query 4449: 1246.645212 from(624.329882,2+) index(5105)
Title: Elution from: 47.317 to 47.317 scan no 6448 cid35.00 polarity:+
Data file D6h-2_1.mgf

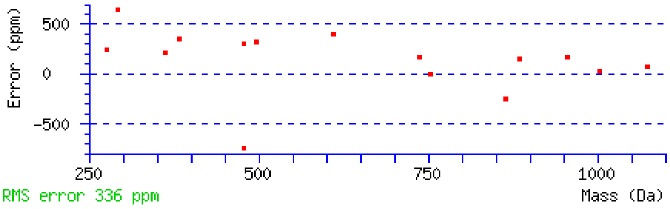
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.6458
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.1e-007
Matches : 15/88 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							10
2	***292.1292***	146.5682	275.1026	138.0550			Q	1084.5898	542.7985	1067.5633	534.2853	1066.5792	533.7933	9
3	***363.1663***	182.0868	346.1397	173.5735			A	***956.5312***	478.7693	939.5047	470.2560	938.5207	469.7640	8
4	510.2347	255.6210	493.2082	247.1077			F	***885.4941***	443.2507	868.4676	434.7374	867.4835	434.2454	7
5	639.2773	320.1423	622.2508	311.6290	621.2667	311.1370	E	***738.4257***	369.7165	721.3992	361.2032	720.4151	360.7112	6
6	***752.3614***	376.6843	735.3348	368.1710	734.3508	367.6790	L	***609.3831***	305.1952	592.3566	296.6819			5
7	***865.4454***	433.2264	848.4189	424.7131	847.4349	424.2211	I	***496.2990***	248.6532	479.2725	240.1399			4
8	***1002.5043***	501.7558	985.4778	493.2425	984.4938	492.7505	H	***383.2150***	192.1111	366.1884	183.5979			3
9	***1073.5415***	537.2744	1056.5149	528.7611	1055.5309	528.2691	A	246.1561	123.5817	229.1295	115.0684			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YQAFELIHAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G10340.1

Score	Mr(calc)	Delta	Sequence
76.2	1246.6458	-0.0006	YQAFELIHAR
2.0	1246.6458	-0.0006	WIPNKSFEAR
1.3	1246.6452	0.0000	LNAIQERTMR
1.1	1246.6452	0.0000	AKARETVEMGR

AT4G10390.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LELDILLR**
Found in **AT4G10390.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr4:6441945-6443157 REVERSE

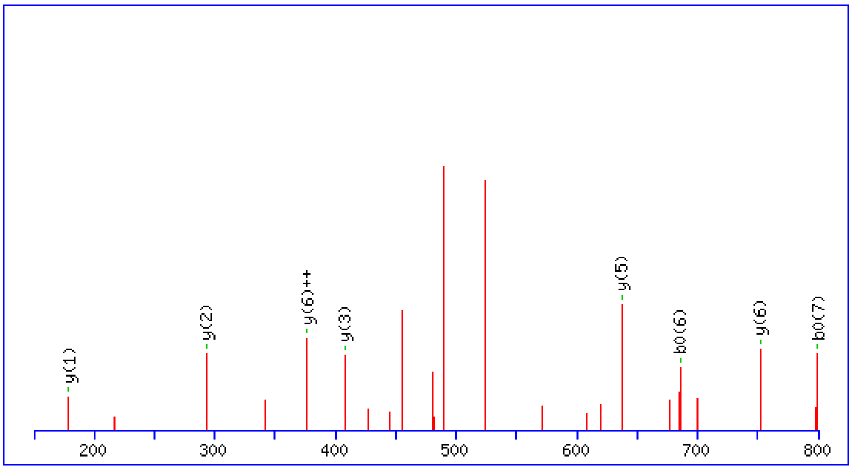
Match to Query 2560: 994.567022 from(498.290787,2+) index(9125)
Title: Elution from: 80.396 to 80.396 scan no 12152 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 800 Da Full range

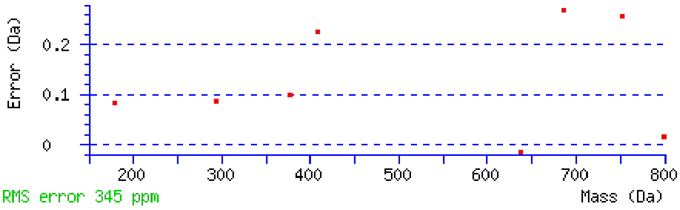
Label all possible matches ○ Label matches used for scoring ●

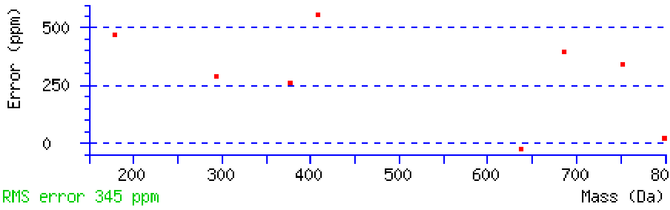
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.5689
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0024
Matches : 8/60 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	245.1280	123.0676	227.1174	114.0624	E	881.4951	441.2512	863.4715	432.2394	863.4845	432.2459	7
3	359.2091	180.1082	341.1985	171.1029	L	***751.4555***	376.2314	733.4319	367.2196	733.4449	367.2261	6
4	475.2331	238.1202	457.2225	229.1149	D	***637.3744***	319.1908	619.3508	310.1790	619.3638	310.1855	5
5	589.3142	295.1607	571.3036	286.1554	I	521.3504	261.1788	503.3268	252.1670			4
6	703.3953	352.2013	685.3847	343.1960	L	***407.2693***	204.1383	389.2457	195.1265			3
7	817.4764	409.2418	799.4658	400.2365	L	***293.1882***	147.0977	275.1646	138.0859			2
8					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LELDILLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.7	994.5689	-0.0019	LELDILLR
16.8	994.5689	-0.0019	IILEDLIR

AT4G10390.1

Mascot: http://www.matrixscience.com/

AT4G10480.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGPVIEEVNEEALMDAIK**
Found in **AT4G10480.1** in **TAIR_Arabidopsis**, Symbols: | nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative | chr4:6478085-6479075 REVERSE

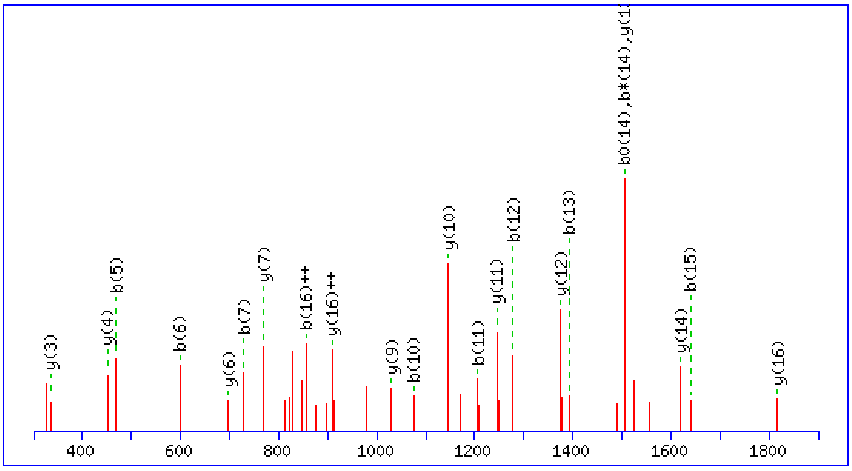
Match to Query 9264: 1972.918926 from(987.466739,2+) index(9468)
Title: Elution from: 88.797 to 88.797 scan no 13067 cid35.00 polarity:+
Data file D1d-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

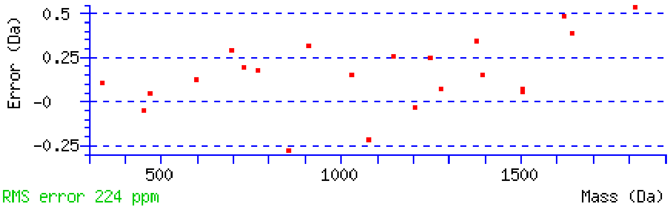
Show Y-axis ☐

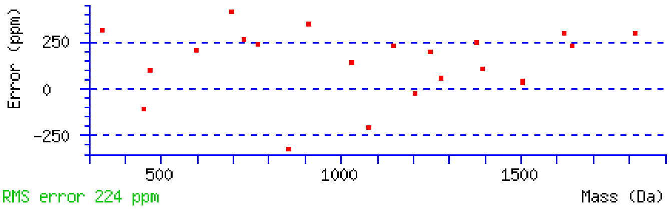


Monoisotopic mass of neutral peptide Mr(calc): 1972.9172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 93 **Expect:** 4.1e-009
Matches : 23/172 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	99.0571	50.0322					**P**							**18**
2	157.0756	79.0414					**G**	1875.8747	938.4410	1857.8511	929.4292	1857.8641	929.4357	**17**
3	255.1254	128.0663					**P**	***1817.8562***	909.4317	1799.8326	900.4199	1799.8456	900.4264	**16**
4	355.1908	178.0990					**V**	1719.8064	860.4068	1701.7828	851.3950	1701.7958	851.4015	**15**
5	***469.2719***	235.1396					**I**	***1619.7409***	810.3741	1601.7173	801.3623	1601.7304	801.3688	**14**
6	***599.3115***	300.1594			581.3010	291.1541	**E**	***1505.6598***	753.3336	1487.6362	744.3218	1487.6493	744.3283	**13**
7	***729.3512***	365.1792			711.3406	356.1739	**E**	***1375.6202***	688.3137	1357.5966	679.3019	1357.6096	679.3085	**12**
8	829.4166	415.2120			811.4061	406.2067	**V**	***1245.5806***	623.2939	1227.5570	614.2821	1227.5700	614.2886	**11**
9	945.4536	473.2304	927.4300	464.2187	927.4431	464.2252	**N**	***1145.5151***	573.2612	1127.4915	564.2494	1127.5046	564.2559	**10**
10	***1075.4933***	538.2503	1057.4697	529.2385	1057.4827	529.2450	**E**	***1029.4781***	515.2427	1011.4545	506.2309	1011.4676	506.2374	**9**
11	***1205.5329***	603.2701	1187.5093	594.2583	1187.5223	594.2648	**E**	899.4385	450.2229	881.4149	441.2111	881.4279	441.2176	**8**
12	***1277.5670***	639.2872	1259.5434	630.2754	1259.5565	630.2819	**A**	***769.3989***	385.2031	751.3753	376.1913	751.3883	376.1978	**7**
13	***1391.6481***	696.3277	1373.6245	687.3159	1373.6376	687.3224	**L**	***697.3647***	349.1860	679.3411	340.1742	679.3542	340.1807	**6**
14	1523.6856	762.3465	1505.6621	753.3347	1505.6751	753.3412	**M**	583.2836	292.1454	565.2600	283.1337	565.2731	283.1402	**5**
15	***1639.7096***	820.3585	1621.6860	811.3467	1621.6991	811.3532	**D**	***451.2461***	226.1267	433.2225	217.1149	433.2355	217.1214	**4**
16	1711.7438	856.3755	1693.7202	847.3637	1693.7332	847.3702	**A**	***335.2221***	168.1147	317.1985	159.1029			**3**
17	1825.8249	913.4161	1807.8013	904.4043	1807.8143	904.4108	**I**	263.1880	132.0976	245.1644	123.0858			**2**
18							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT4G10480.1





NCBI **BLAST** search of PGPVIEEVNEEALMDAIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.2	1972.9172	0.0017	PGPVIEEVNEEALMDAIK
7.8	1972.9142	0.0047	AFSNIEKVDEDLQRTGK
6.6	1972.9221	-0.0032	FPSALNMFDEIVNAAKGK
2.5	1972.9142	0.0047	GSGQGDIEFKNEVSLLTR
2.0	1972.9198	-0.0009	YAGDGGVTDMVVVGVVREK
1.3	1972.9138	0.0051	ENSDFIILDDNFATIVK

Mascot: http://www.matrixscience.com/

AT4G11010.1

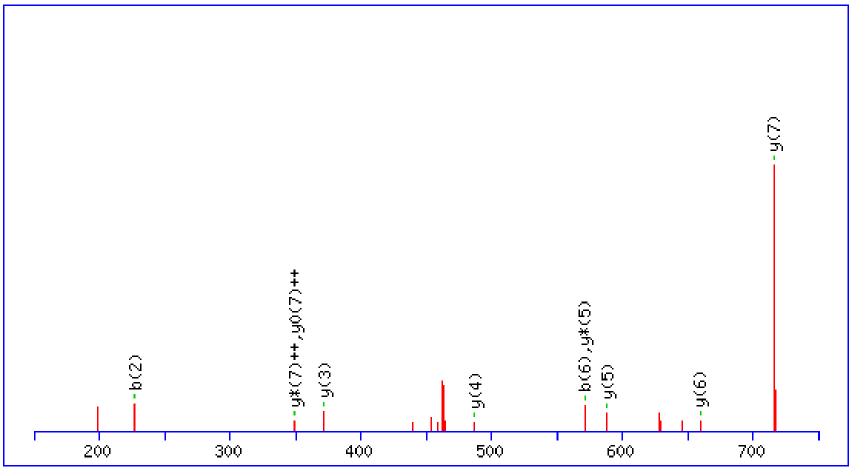
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIGATDPQK**
Found in **AT4G11010.1** in **TAIR_Arabidopsis**, Symbols: NDPK3 | NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3); ATP binding / nucleoside diphosphate kinase | chr4:6732776-6734294 REVERSE

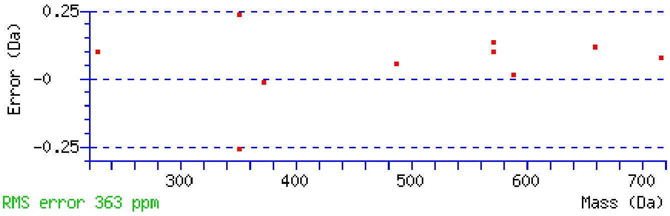
Match to Query 1959: 941.519202 from(471.766877,2+) index(719)
Title: Elution from: 12.804 to 12.804 scan no 1051 cid35.00 polarity:+
Data file 0-2_2.mgf

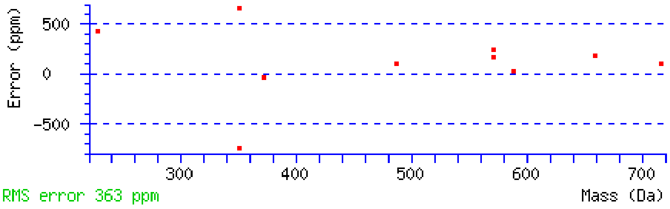
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 941.5182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00071
Matches : 10/68 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							9
2	**227.1754**	114.0913					I	829.4414	415.2243	812.4149	406.7111	811.4308	406.2191	8
3	284.1969	142.6021					G	***716.3573***	358.6823	699.3308	350.1690	698.3468	349.6770	7
4	355.2340	178.1206					A	***659.3359***	330.1716	642.3093	321.6583	641.3253	321.1663	6
5	456.2817	228.6445			438.2711	219.6392	T	***588.2988***	294.6530	571.2722	286.1397	570.2882	285.6477	5
6	**571.3086**	286.1579			553.2980	277.1527	D	***487.2511***	244.1292	470.2245	235.6159	469.2405	235.1239	4
7	668.3614	334.6843			650.3508	325.6790	P	***372.2241***	186.6157	355.1976	178.1024			3
8	796.4199	398.7136	779.3934	390.2003	778.4094	389.7083	Q	275.1714	138.0893	258.1448	129.5761			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LIGATDPQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G11010.1

36.0	941.5182	0.0010	LIGATDPQK

Mascot: http://www.matrixscience.com/

AT4G11110.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCEGSSMAIVGRPSSR**
Found in **AT4G11110.1** in **TAIR_Arabidopsis**, Symbols: SPA2 | SPA2 (SPA1-RELATED 2); signal transducer | chr4:6772159-6776671 FORWARD

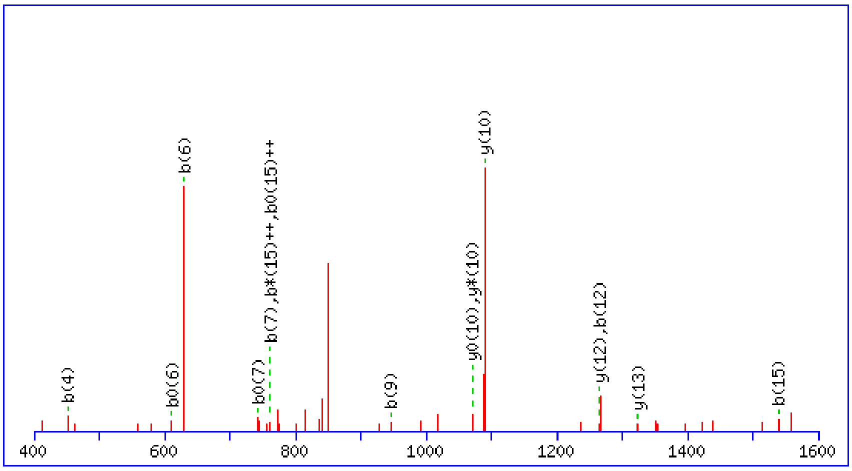
Match to Query 8583: 1716.717402 from(859.365977,2+) index(5458)
Title: Elution from: 48.347 to 48.347 scan no 6777 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

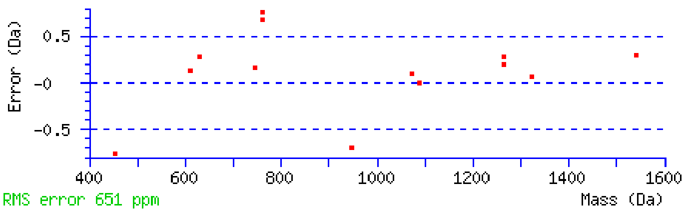
Show Y-axis ☐

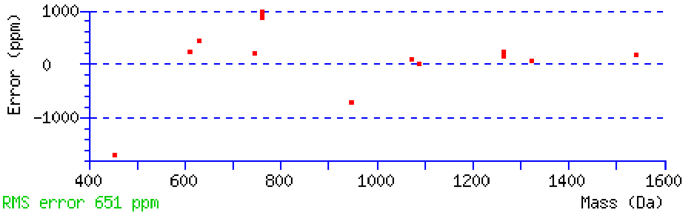


Monoisotopic mass of neutral peptide Mr(calc): 1716.7194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.029
Matches : 15/156 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							16
2	265.0767	133.0420			247.0661	124.0367	C	1615.6820	808.3446	1597.6584	799.3328	1597.6714	799.3393	15
3	395.1163	198.0618			377.1058	189.0565	E	1453.6572	727.3323	1435.6337	718.3205	1435.6467	718.3270	14
4	***453.1348***	227.0711			435.1243	218.0658	G	**1323.6176**	662.3124	1305.5940	653.3007	1305.6070	653.3072	13
5	541.1639	271.0856			523.1533	262.0803	S	**1265.5991**	633.3032	1247.5755	624.2914	1247.5885	624.2979	12
6	***629.1930***	315.1001			611.1824	306.0948	S	1177.5700	589.2887	1159.5465	580.2769	1159.5595	580.2834	11
7	***761.2305***	381.1189			743.2199	372.1136	M	**1089.5410**	545.2741	1071.5174	536.2623	1071.5304	536.2688	10
8	833.2646	417.1360			815.2541	408.1307	A	957.5035	479.2554	939.4799	470.2436	939.4929	470.2501	9
9	***947.3457***	474.1765			929.3352	465.1712	I	885.4693	443.2383	867.4457	434.2265	867.4587	434.2330	8
10	1047.4112	524.2092			1029.4006	515.2039	V	771.3882	386.1977	753.3646	377.1860	753.3777	377.1925	7
11	1105.4297	553.2185			1087.4191	544.2132	G	671.3228	336.1650	653.2992	327.1532	653.3122	327.1597	6
12	***1265.5189***	633.2631	1247.4953	624.2513	1247.5084	624.2578	R	613.3043	307.1558	595.2807	298.1440	595.2937	298.1505	5
13	1363.5687	682.2880	1345.5451	673.2762	1345.5582	673.2827	P	453.2150	227.1111	435.1914	218.0994	435.2045	218.1059	4
14	1451.5978	726.3025	1433.5742	717.2907	1433.5872	717.2972	S	355.1652	178.0862	337.1416	169.0745	337.1547	169.0810	3
15	***1539.6269***	770.3171	1521.6033	761.3053	1521.6163	761.3118	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
16							R	179.1071	90.0572	161.0835	81.0454			1

AT4G11110.1





NCBI **BLAST** search of TCEGSSMAIVGRPSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1716.7194	-0.0020	TCEGSSMAIVGRPSSR
15.2	1716.7225	-0.0051	SDEEYFLVPSFPDR
6.7	1716.7160	0.0014	RQRDLFGSMDIENN
2.7	1716.7169	0.0005	ADRMFVMDKCLHR
1.5	1716.7224	-0.0050	KNEMMMIPAAAASSSK
1.5	1716.7224	-0.0050	KNEMMMIPAAAASSSK
1.5	1716.7224	-0.0050	KNEMMMIPAAAASSSK

AT4G11150.1

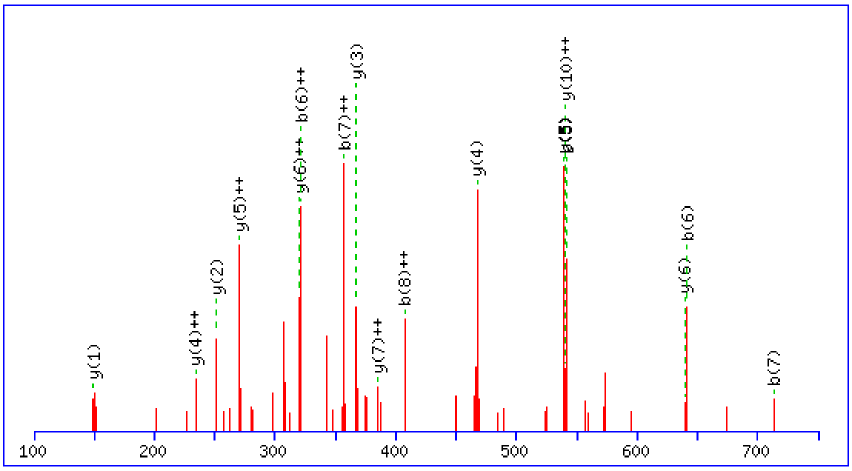
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VHAPEVAVDTK**
Found in **AT4G11150.1** in **TAIR_Arabidopsis**, Symbols: EMB2448, TUFF, VHA-E1, TUF | TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1) | chr4:6800087-6801692 FORWARD

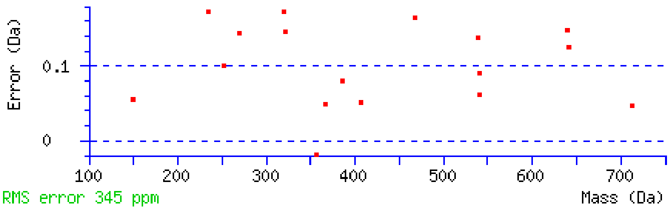
Match to Query 4254: 1178.571588 from(393.864472,3+) index(1424)
Title: Elution from: 20.457 to 20.457 scan no 1969 cid35.00 polarity:+
Data file 0-1_1.mgf

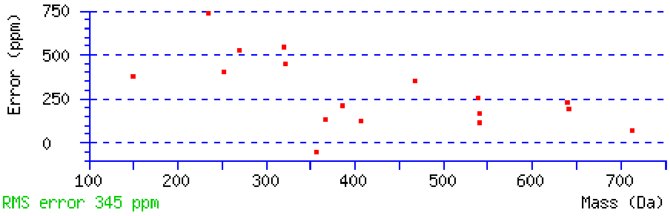
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1178.5724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00036
Matches : 17/90 fragment ions using 32 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400			V							11
2	241.1227	121.0650			H	1079.5142	540.2607	1061.4906	531.2489	1061.5036	531.2555	10
3	313.1569	157.0821			A	939.4642	470.2357	921.4406	461.2239	921.4536	461.2304	9
4	411.2067	206.1070			P	867.4300	434.2187	849.4065	425.2069	849.4195	425.2134	8
5	**541.2463**	271.1268	523.2358	262.1215	E	769.3802	385.1938	751.3567	376.1820	751.3697	376.1885	7
6	**641.3118**	**321.1595**	623.3012	312.1542	V	***639.3406***	320.1739	621.3170	311.1622	621.3300	311.1687	6
7	**713.3459**	**357.1766**	695.3354	348.1713	A	***539.2752***	270.1412	521.2516	261.1294	521.2646	261.1359	5
8	813.4114	**407.2093**	795.4008	398.2040	V	***467.2410***	234.1241	449.2174	225.1124	449.2304	225.1189	4
9	929.4353	465.2213	911.4248	456.2160	D	***367.1756***	184.0914	349.1520	175.0796	349.1650	175.0861	3
10	1031.4801	516.2437	1013.4695	507.2384	T	***251.1516***	126.0794	233.1280	117.0676	233.1410	117.0741	2
11					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VHAPEVAVDTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G11150.1

Score	Mr(calc)	Delta	Sequence
43.9	1178.5724	-0.0008	VHAPEVAVDTK
11.3	1178.5728	-0.0012	RASSKTNLER
6.3	1178.5683	0.0032	MIKMLGEVSK
6.0	1178.5699	0.0017	MFAPTKIWR
5.4	1178.5724	-0.0008	SDRTLGFLEK

AT4G11210.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLDLAKPCK**
Found in **AT4G11210.1** in **TAIR_Arabidopsis**, Symbols: | disease resistance-responsive family protein / dirigent family protein | chr4:6832687-6833241 FORWARD

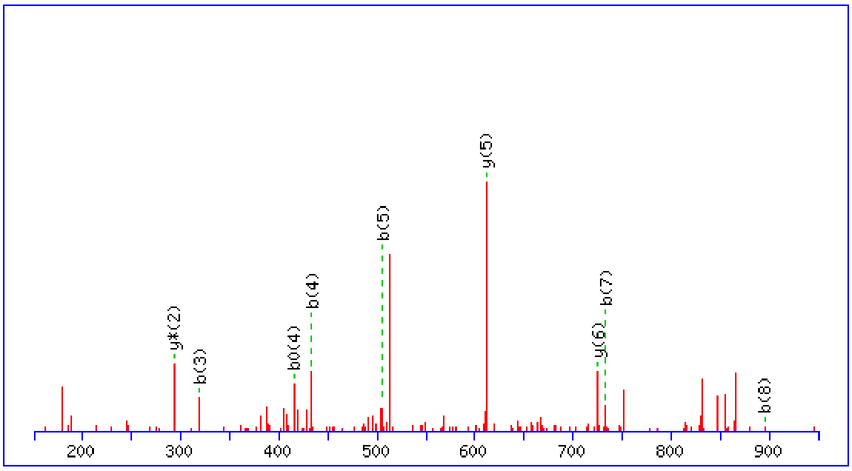
Match to Query 2762: 1042.514158 from(522.264355,2+) index(4199)
Title: Elution from: 38.987 to 38.987 scan no 5287 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

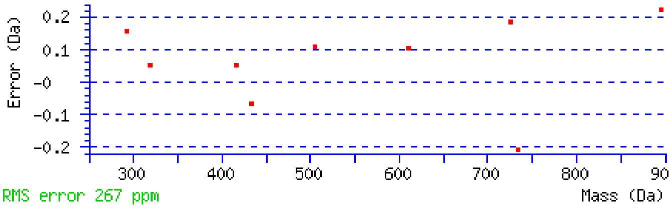
Label all possible matches ○ Label matches used for scoring ●

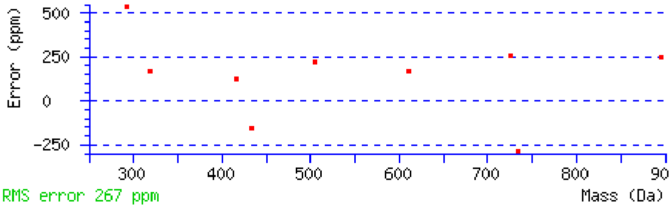
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1042.5125
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.035
Matches : 9/74 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218			71.0258	36.0165	S							9
2	203.1174	102.0624			185.1069	93.0571	L	955.4907	478.2490	937.4672	469.2372	937.4802	469.2437	8
3	***319.1414***	160.0743			301.1309	151.0691	D	841.4097	421.2085	823.3861	412.1967	823.3991	412.2032	7
4	***433.2225***	217.1149			415.2120	208.1096	L	**725.3857**	363.1965	707.3621	354.1847			6
5	***505.2567***	253.1320			487.2461	244.1267	A	**611.3046**	306.1559	593.2810	297.1441			5
6	635.3457	318.1765	617.3221	309.1647	617.3351	309.1712	K	539.2704	270.1389	521.2468	261.1271			4
7	***733.3955***	367.2014	715.3719	358.1896	715.3849	358.1961	P	409.1814	205.0943	391.1578	196.0825			3
8	***895.4202***	448.2137	877.3966	439.2020	877.4096	439.2085	C	311.1316	156.0694	293.1080	147.0576			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SLDLAKPCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G11210.1

23.9	1042.5125	0.0016	SLDLAKPCK
11.5	1042.5125	0.0016	VSISPMEIR
11.4	1042.5118	0.0023	FTQHNLLR
11.3	1042.5152	-0.0011	LPNGCAIKR
6.5	1042.5125	0.0016	EMELQILR
6.5	1042.5152	-0.0010	MKQLVTHR
5.6	1042.5125	0.0016	ELGLALEMR
5.5	1042.5118	0.0023	FGTVVVNHR
5.2	1042.5125	0.0016	GPLESLMIR
5.0	1042.5125	0.0016	LEELQLMR

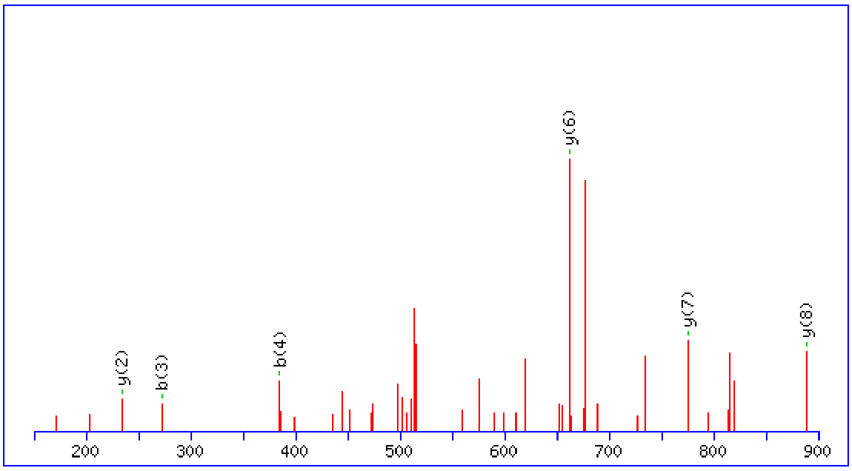
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SALLSELVSK**
Found in **AT4G11420.1** in **TAIR_Arabidopsis**, Symbols: ATEIF3A-1, EIF3A-1, ATTIF3A1, TIF3A1, EIF3A | EIF3A (eukaryotic translation initiation factor 3A) | chr4:6947829-6952048 REVERSE

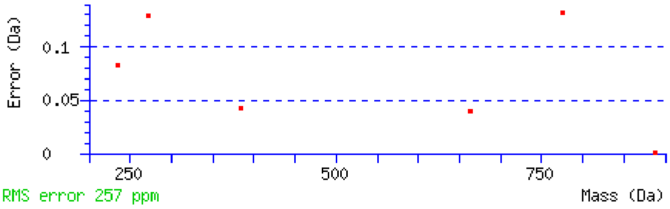
Match to Query 2458: 1045.600574 from(523.807563,2+) index(5894)
Title: Elution from: 55.595 to 55.595 scan no 7686 cid35.00 polarity:+
Data file D1d-2_2.mgf

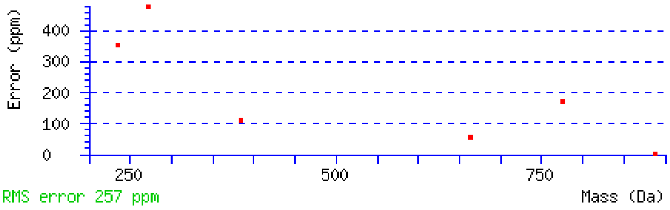
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1045.6019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0024
Matches : 6/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							10
2	159.0764	80.0418	141.0659	71.0366	A	959.5772	480.2922	942.5506	471.7790	941.5666	471.2869	9
3	**272.1605**	136.5839	254.1499	127.5786	L	***888.5401***	444.7737	871.5135	436.2604	870.5295	435.7684	8
4	**385.2445**	193.1259	367.2340	184.1206	L	***775.4560***	388.2316	758.4294	379.7184	757.4454	379.2264	7
5	472.2766	236.6419	454.2660	227.6366	S	***662.3719***	331.6896	645.3454	323.1763	644.3614	322.6843	6
6	601.3192	301.1632	583.3086	292.1579	E	575.3399	288.1736	558.3134	279.6603	557.3293	279.1683	5
7	714.4032	357.7053	696.3927	348.7000	L	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
8	813.4716	407.2395	795.4611	398.2342	V	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
9	900.5037	450.7555	882.4931	441.7502	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SALLSELVSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G11420.1

Score	Mr(calc)	Delta	Sequence
31.3	1045.6019	-0.0013	SALLSELVSK
6.4	1045.6019	-0.0013	ELKTIDLSK

AT4G11600.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAPTTSPLSIEK**
Found in **AT4G11600.1** in **TAIR_Arabidopsis**, Symbols: PHGPX, LSC803, ATGPX6 | ATGPX6 (GLUTATHIONE PEROXIDASE 6); glutathione peroxidase | chr4:7010015-7011324 REVERSE

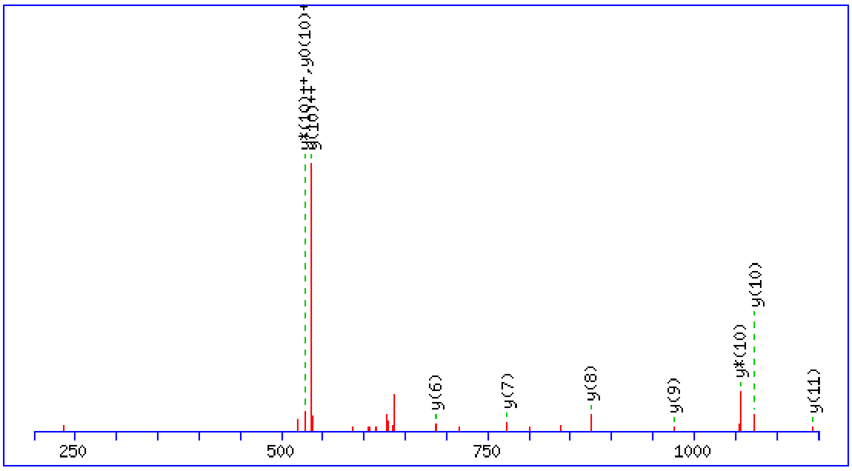
Match to Query 4928: 1289.685054 from(645.849803,2+) index(5256)
Title: Elution from: 46.399 to 46.399 scan no 6558 cid35.00 polarity:+
Data file C7-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1150 Da Full range

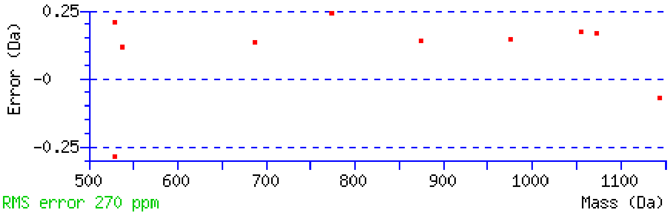
Label all possible matches ○ Label matches used for scoring ●

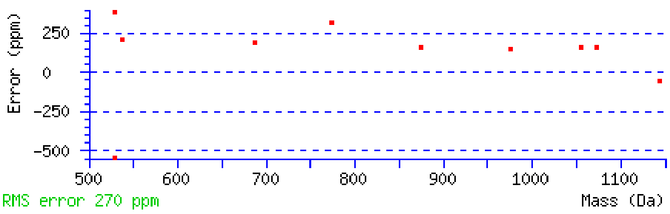
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1289.6867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.0002
Matches : 10/102 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							12
2	219.1128	110.0600			A	***1143.6256***	572.3164	1126.5990	563.8032	1125.6150	563.3111	11
3	316.1656	158.5864			P	***1072.5885***	536.7979	1055.5619	528.2846	1054.5779	527.7926	10
4	417.2132	209.1103	399.2027	200.1050	T	***975.5357***	488.2715	958.5092	479.7582	957.5251	479.2662	9
5	518.2609	259.6341	500.2504	250.6288	T	***874.4880***	437.7477	857.4615	429.2344	856.4775	428.7424	8
6	605.2930	303.1501	587.2824	294.1448	S	***773.4403***	387.2238	756.4138	378.7105	755.4298	378.2185	7
7	702.3457	351.6765	684.3352	342.6712	P	***686.4083***	343.7078	669.3818	335.1945	668.3978	334.7025	6
8	815.4298	408.2185	797.4192	399.2132	L	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
9	902.4618	451.7345	884.4512	442.7293	S	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
10	1015.5459	508.2766	997.5353	499.2713	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	1144.5885	572.7979	1126.5779	563.7926	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FAPTTSPLSIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G11600.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.5	1289.6867	-0.0017	FAPTTSPLSIEK
4.6	1289.6874	-0.0023	MAGRGKTLGSGGAK
3.9	1289.6874	-0.0023	MADLVKTNARR
3.8	1289.6874	-0.0023	MARVGAKSSGAGAK
2.5	1289.6840	0.0010	SGGKVFSRAEPR
2.3	1289.6827	0.0024	KLDTEVSDQKK

AT4G11880.1

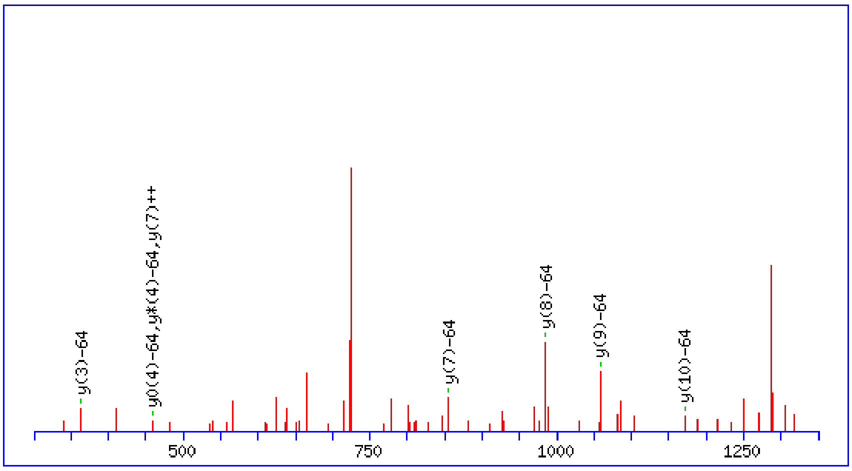
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLIAENKMLMEK**
Found in **AT4G11880.1** in **TAIR_Arabidopsis**, Symbols: | AGL14 (AGAMOUS-LIKE 14); DNA binding / transcription factor | chr4:7143506-7147102 FORWARD

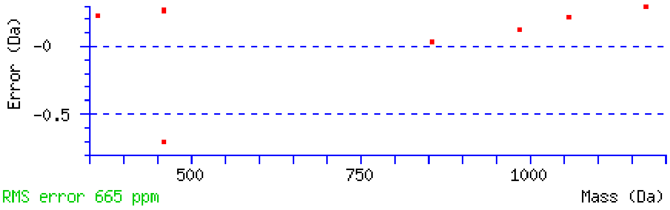
Match to Query 6375: 1464.692748 from(733.353650,2+) index(7137)
Title: Elution from: 61.963 to 61.963 scan no 9064 cid35.00 polarity:+
Data file D12h-1_1.mgf

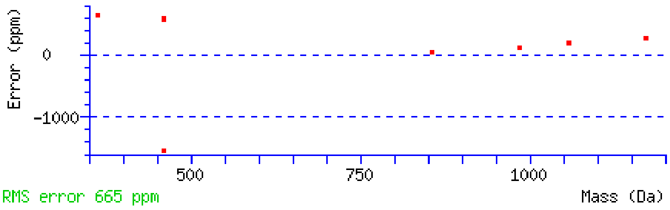
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1464.6893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.033
Matches : 8/188 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							12
2	231.1254	116.0663	213.1018	107.0545			L	1285.6613	643.3343	1267.6377	634.3225	1267.6507	634.3290	11
3	345.2065	173.1069	327.1829	164.0951			I	***1171.5802***	586.2937	1153.5566	577.2819	1153.5696	577.2884	10
4	417.2406	209.1239	399.2170	200.1122			A	***1057.4991***	529.2532	1039.4755	520.2414	1039.4885	520.2479	9
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	E	***985.4649***	493.2361	967.4413	484.2243	967.4544	484.2308	8
6	663.3172	332.1623	645.2937	323.1505	645.3067	323.1570	N	***855.4253***	428.2163	837.4017	419.2045	837.4147	419.2110	7
7	793.4063	397.2068	775.3827	388.1950	775.3957	388.2015	K	739.3883	370.1978	721.3647	361.1860	721.3777	361.1925	6
8	925.4438	463.2255	907.4202	454.2137	907.4332	454.2203	M	609.2993	305.1533	591.2757	296.1415	591.2887	296.1480	5
9	1039.5249	520.2661	1021.5013	511.2543	1021.5143	511.2608	L	477.2618	239.1345	459.2382	230.1227	459.2512	230.1292	4
10	1123.5590	562.2832	1105.5355	553.2714	1105.5485	553.2779	M	***363.1807***	182.0940	345.1571	173.0822	345.1701	173.0887	3
11	1253.5987	627.3030	1235.5751	618.2912	1235.5881	618.2977	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NLIAENKMLMEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G11880.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
25.4	1464.6893	0.0034	NLIAENKMLMEK	Oxidation M10 96.21%
15.7	1464.6933	-0.0006	RAFVEDILNENK	
13.1	1464.6911	0.0017	NSKDDLTVTANLR	
12.0	1464.6933	-0.0006	RVFGAEAPKESEK	
11.4	1464.6893	0.0034	NLIAENKMLMEK	Oxidation M8 3.79%
10.2	1464.6911	0.0017	QSSTDVSQVLNLR	
9.7	1464.6933	-0.0005	DQDIRLGDFGLAK	
9.2	1464.6906	0.0021	TEEVLSGFSKPEK	
8.8	1464.6967	-0.0039	RIMVTPEETISR	
8.5	1464.6967	-0.0039	IGSPAMTTRGLSEK	

AT4G12020.1

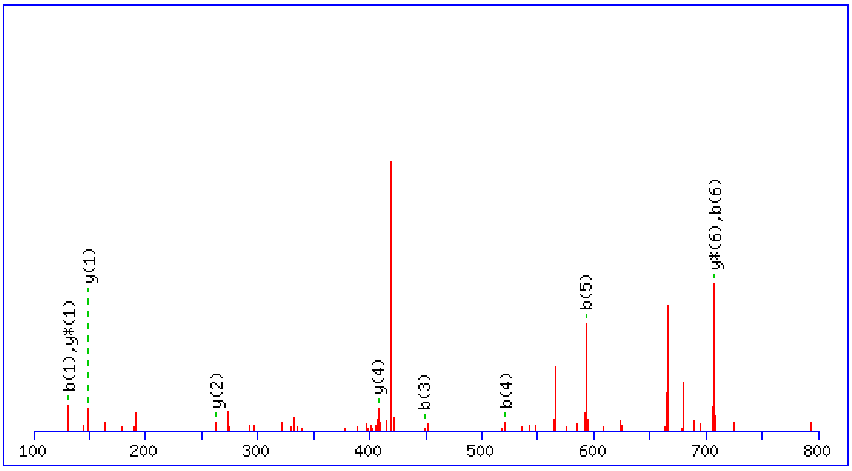
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KWQAALK**
Found in **AT4G12020.1** in **TAIR_Arabidopsis**, Symbols: ATWRKY19, MAPKKK11, WRKY19 | WRKY19 (WRKY DNA-binding protein 19); transcription factor | chr4:7201650-7208590 FORWARD

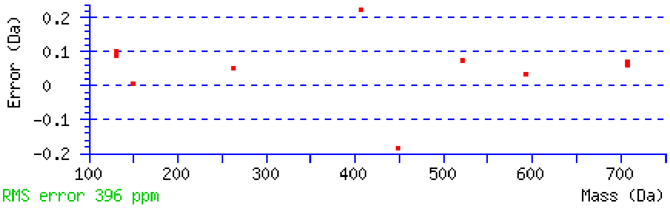
Match to Query 1239: 854.463592 from(428.239072,2+) index(2862)
Title: Elution from: 28.604 to 28.604 scan no 3569 cid35.00 polarity:+
Data file 0-3_3.mgf

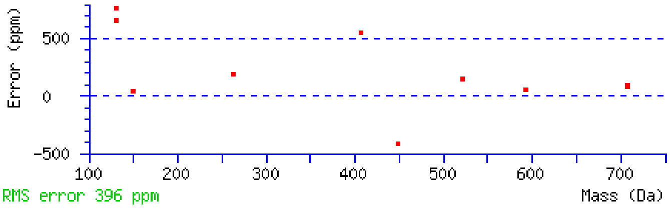
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 854.4641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.009
Matches : 10/48 fragment ions using 19 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	#
1	***131.0963***	66.0518	113.0727	57.0400	K					7
2	319.1697	160.0885	301.1461	151.0767	W	725.3823	363.1948	707.3587	354.1830	6
3	***449.2223***	225.1148	431.1988	216.1030	Q	537.3089	269.1581	519.2853	260.1463	5
4	***521.2565***	261.1319	503.2329	252.1201	A	**407.2563**	204.1318	389.2327	195.1200	4
5	***593.2906***	297.1490	575.2671	288.1372	A	335.2221	168.1147	317.1985	159.1029	3
6	***707.3717***	354.1895	689.3482	345.1777	L	**263.1880**	132.0976	245.1644	123.0858	2
7					K	**149.1069**	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of KWQAALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.4	854.4641	-0.0005	KWQAALK
28.3	854.4618	0.0018	QRLELGK

AT4G12020.1

24.0	854.4618	0.0018	REIQAVK
16.6	854.4641	-0.0005	ELRWLK
15.6	854.4618	0.0018	ERGVVVGK
14.3	854.4618	0.0018	DQIRALK
14.3	854.4618	0.0018	NLREAIK
14.3	854.4618	0.0018	RVAEGALK
14.3	854.4618	0.0018	EANRLLK
14.3	854.4618	0.0018	EARNILK

AT4G12400.1

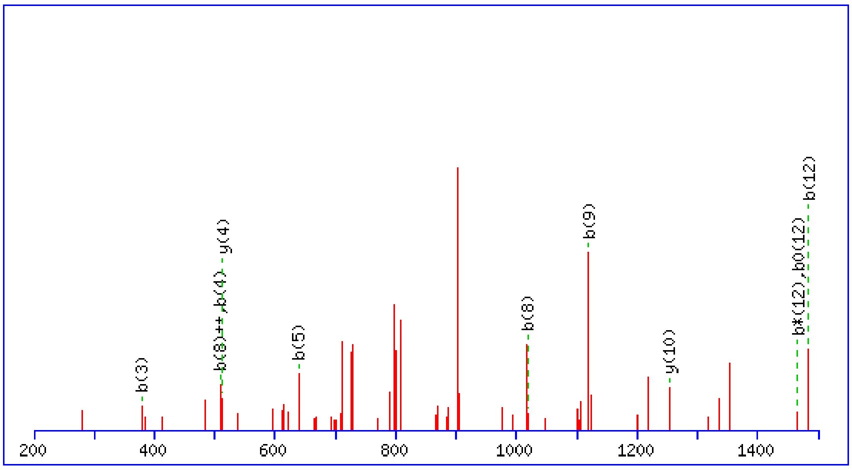
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYLEQDDFVKTMK**
Found in **AT4G12400.1** in **TAIR_Arabidopsis**, Symbols: | stress-inducible protein, putative | chr4:7339021-7341236 REVERSE

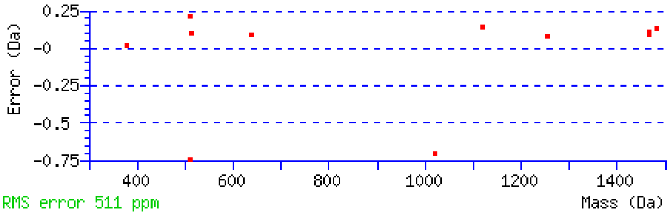
Match to Query 7522: 1630.751258 from(816.382905,2+) index(6878)
Title: Elution from: 59.983 to 59.983 scan no 8795 cid35.00 polarity:+
Data file C7-2_2.mgf

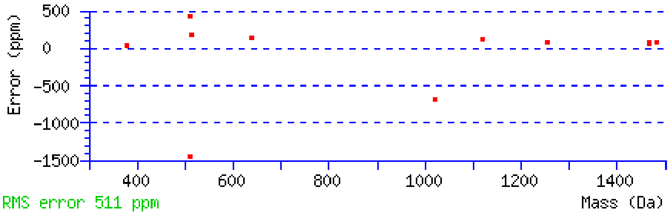
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1630.7489
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.013
Matches : 11/126 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							13
2	265.1331	133.0702					Y	1531.6907	766.3490	1513.6671	757.3372	1513.6802	757.3437	12
3	***379.2142***	190.1107					L	1367.6304	684.3188	1349.6068	675.3070	1349.6198	675.3135	11
4	***509.2538***	255.1305			491.2433	246.1253	E	**1253.5493**	627.2783	1235.5257	618.2665	1235.5387	618.2730	10
5	***639.3065***	320.1569	621.2829	311.1451	621.2959	311.1516	Q	1123.5096	562.2585	1105.4861	553.2467	1105.4991	553.2532	9
6	755.3304	378.1689	737.3069	369.1571	737.3199	369.1636	D	993.4570	497.2321	975.4334	488.2203	975.4464	488.2269	8
7	871.3544	436.1808	853.3308	427.1691	853.3439	427.1756	D	877.4330	439.2201	859.4094	430.2084	859.4225	430.2149	7
8	***1019.4199***	510.2136	1001.3963	501.2018	1001.4093	501.2083	F	761.4090	381.2082	743.3855	372.1964	743.3985	372.2029	6
9	***1119.4853***	560.2463	1101.4617	551.2345	1101.4748	551.2410	V	613.3436	307.1754	595.3200	298.1636	595.3330	298.1702	5
10	1249.5743	625.2908	1231.5508	616.2790	1231.5638	616.2855	K	**513.2781**	257.1427	495.2546	248.1309	495.2676	248.1374	4
11	1351.6191	676.3132	1333.5955	667.3014	1333.6085	667.3079	T	383.1891	192.0982	365.1655	183.0864	365.1785	183.0929	3
12	***1483.6566***	742.3319	1465.6330	733.3201	1465.6460	733.3266	M	281.1444	141.0758	263.1208	132.0640			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VYLEQDDFVKTMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G12400.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.9	1630.7489	0.0024	VYLEQDDFVKTMK
19.3	1630.7493	0.0019	DMYNATRGESLVKK
12.5	1630.7549	-0.0037	GGCYGGMKLSVKVEK
9.3	1630.7538	-0.0025	FEDVLKYFHLMR
8.2	1630.7511	0.0001	TFETLMWGYLEVK
6.0	1630.7493	0.0019	GQEIQAHEGAILAMK
4.5	1630.7516	-0.0003	DQRTVFAYQMPLK
4.4	1630.7545	-0.0032	LCIVSYDIMFVEK
0.4	1630.7523	-0.0010	MLKMGLTSFEDAIK
0.3	1630.7538	-0.0025	EMKFRLWFDPTK

AT4G12640.1

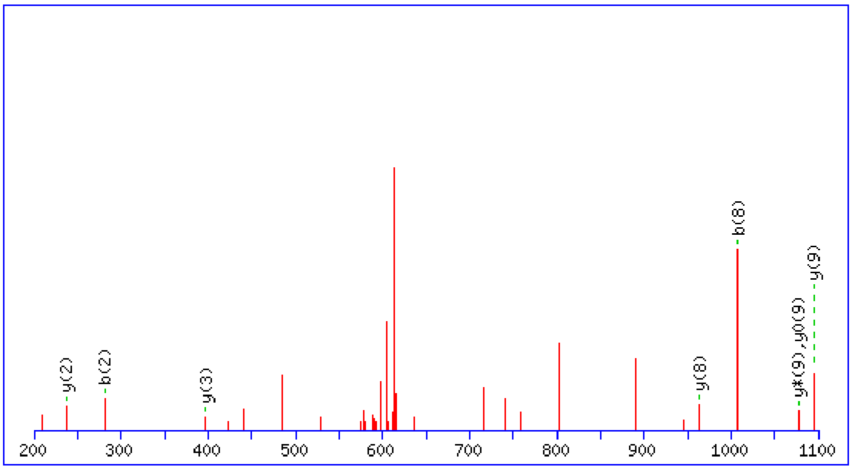
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MMMKEDGRGR**
Found in **AT4G12640.1** in **TAIR_Arabidopsis**, Symbols: | RNA recognition motif (RRM)-containing protein | chr4:7462694-7467627 FORWARD

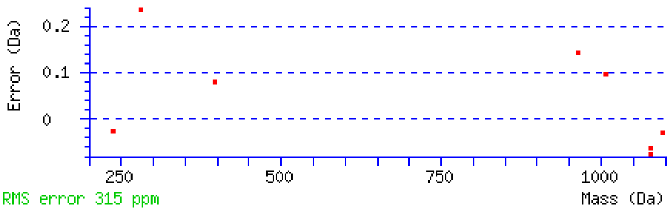
Match to Query 3827: 1242.489058 from(622.251805,2+) index(1474)
Title: Elution from: 23.049 to 23.049 scan no 2078 cid35.00 polarity:+
Data file D1d-1-2.mgf

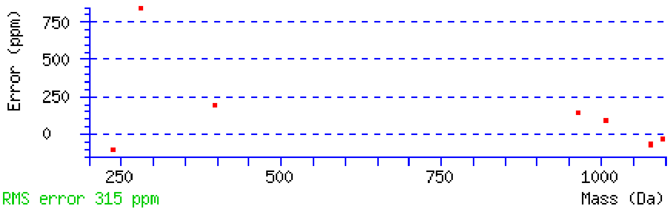
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1242.4862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 17 **Expect:** 0.045
Matches : 8/126 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235					M							10
2	**281.0772**	141.0423					M	***1095.4610***	548.2341	1077.4374	539.2224	1077.4505	539.2289	9
3	413.1148	207.0610					M	***963.4235***	482.2154	945.3999	473.2036	945.4129	473.2101	8
4	543.2038	272.1055	525.1802	263.0937			K	831.3860	416.1966	813.3624	407.1848	813.3754	407.1913	7
5	673.2434	337.1253	655.2198	328.1136	655.2328	328.1201	E	701.2969	351.1521	683.2734	342.1403	683.2864	342.1468	6
6	789.2674	395.1373	771.2438	386.1255	771.2568	386.1321	D	571.2573	286.1323	553.2337	277.1205	553.2468	277.1270	5
7	847.2859	424.1466	829.2623	415.1348	829.2753	415.1413	G	455.2333	228.1203	437.2098	219.1085			4
8	**1007.3751**	504.1912	989.3516	495.1794	989.3646	495.1859	R	***397.2148***	199.1111	379.1913	190.0993			3
9	1065.3936	533.2005	1047.3701	524.1887	1047.3831	524.1952	G	***237.1256***	119.0664	219.1020	110.0546			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MMMKEDGRGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G12640.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
16.9	1242.4862	0.0029	MMMKEDGRGR	Oxidation M1 85.90%
8.6	1242.4862	0.0029	MMMKEDGRGR	Oxidation M2 12.42%
6.3	1242.4896	-0.0006	ELESDPDSDPK	
2.8	1242.4905	-0.0014	MASMYADAVEK	
2.1	1242.4857	0.0033	ASMVFQMCEK	
2.1	1242.4875	0.0015	AFTCLSDGNSR	
1.4	1242.4905	-0.0014	MTVVCSEFDK	
1.3	1242.4905	-0.0014	EAFEMMDSKK	
1.3	1242.4905	-0.0014	QSDMEMALFK	
0.9	1242.4905	-0.0014	MASMYADAVEK	

Mascot: http://www.matrixscience.com/

AT4G12670.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGVQKFPGERNIPWR**
Found in **AT4G12670.1** in **TAIR_Arabidopsis**, Symbols: | DNA binding | chr4:7472527-7474516 FORWARD

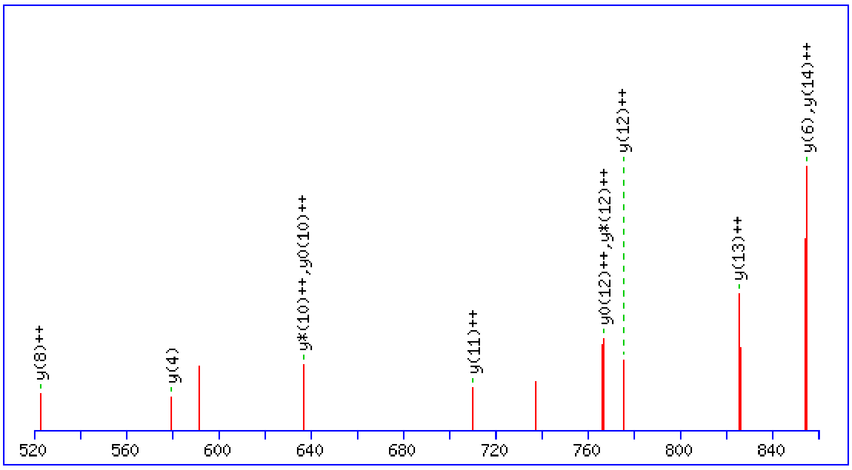
Match to Query 8629: 1806.890373 from(603.304067,3+) index(10741)
Title: Elution from: 107.314 to 107.314 scan no 15599 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 520 to 860 Da Full range

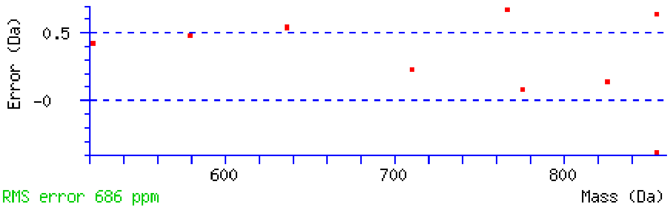
Label all possible matches ○ Label matches used for scoring ●

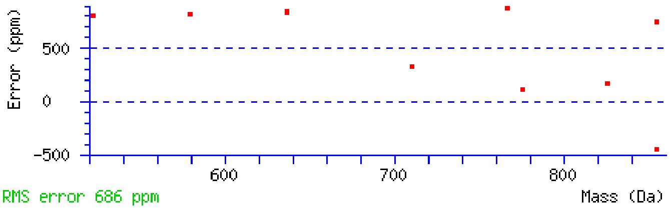
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1806.8948
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00064
Matches : 11/134 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							15
2	159.0912	80.0492					G	1707.8366	854.4220	1689.8130	845.4102	1689.8261	845.4167	14
3	259.1567	130.0820					V	1649.8181	825.4127	1631.7945	816.4009	1631.8076	816.4074	13
4	389.2093	195.1083	371.1857	186.0965			Q	1549.7527	775.3800	1531.7291	766.3682	1531.7421	766.3747	12
5	519.2984	260.1528	501.2748	251.1410			K	1419.7000	710.3537	1401.6764	701.3419	1401.6895	701.3484	11
6	667.3638	334.1855	649.3402	325.1737			F	1289.6110	645.3091	1271.5874	636.2973	1271.6004	636.3039	10
7	765.4136	383.2104	747.3900	374.1986			P	1141.5455	571.2764	1123.5220	562.2646	1123.5350	562.2711	9
8	823.4321	412.2197	805.4085	403.2079			G	1043.4957	522.2515	1025.4722	513.2397	1025.4852	513.2462	8
9	953.4717	477.2395	935.4481	468.2277	935.4612	468.2342	E	985.4772	493.2423	967.4537	484.2305	967.4667	484.2370	7
10	1113.5610	557.2841	1095.5374	548.2723	1095.5504	548.2788	R	**855.4376**	428.2224	837.4140	419.2107			6
11	1229.5980	615.3026	1211.5744	606.2908	1211.5874	606.2973	N	695.3484	348.1778	677.3248	339.1660			5
12	1343.6791	672.3432	1325.6555	663.3314	1325.6685	663.3379	I	**579.3114**	290.1593	561.2878	281.1475			4
13	1441.7289	721.3681	1423.7053	712.3563	1423.7183	712.3628	P	465.2303	233.1188	447.2067	224.1070			3
14	1629.8023	815.4048	1611.7787	806.3930	1611.7917	806.3995	W	367.1805	184.0939	349.1569	175.0821			2
15							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VGVQKFPGERNIPWR

AT4G12670.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	1806.8948	-0.0044	VGVQKFPGERNIPWR
27.9	1806.8894	0.0010	VGVQFYHDLIDELLK
6.4	1806.8898	0.0005	VVGEGLVIDEWKERR
6.0	1806.8928	-0.0024	SKTMKTQFLLDLGYK
3.1	1806.8955	-0.0051	LFGLSLERVCVDIHK
2.6	1806.8899	0.0005	VGREPSTGHLSFATVVK
1.1	1806.8858	0.0046	GLCQIGEIDAVMLLVR
0.3	1806.8955	-0.0051	SISRFEMYQVLKLR

AT4G12740.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLLEGAK**
Found in **AT4G12740.1** in **TAIR_Arabidopsis**, Symbols: | adenine-DNA glycosylase-related / MYH-related | chr4:7494575-7497593 REVERSE

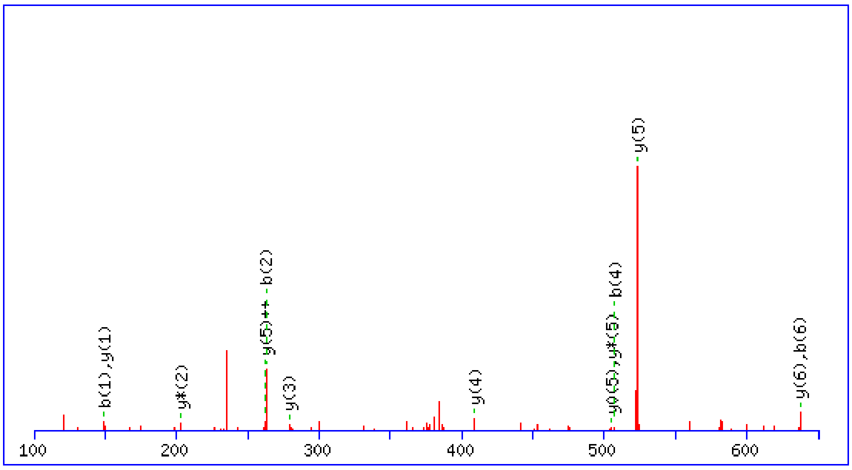
Match to Query 878: 784.418280 from(393.216416,2+) index(2793)
Title: Elution from: 27.754 to 27.754 scan no 3480 cid35.00 polarity:+
Data file 0-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 650 Da Full range

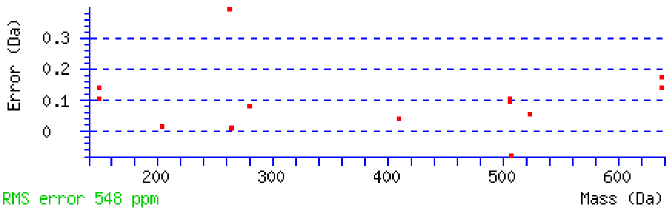
Label all possible matches ○ Label matches used for scoring ●

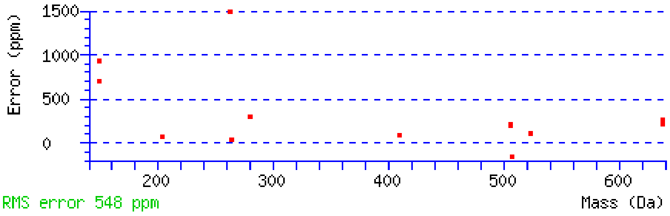
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 784.4195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.037
Matches : 13/48 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	**149.0727**	75.0400			F							7
2	**263.1538**	132.0805			L	***637.3613***	319.1843	619.3378	310.1725	619.3508	310.1790	6
3	377.2349	189.1211			L	***523.2802***	262.1438	505.2567	253.1320	505.2697	253.1385	5
4	**507.2746**	254.1409	489.2640	245.1356	E	***409.1991***	205.1032	391.1756	196.0914	391.1886	196.0979	4
5	565.2930	283.1502	547.2825	274.1449	G	***279.1595***	140.0834	261.1359	131.0716			3
6	**637.3272**	319.1672	619.3166	310.1620	A	221.1410	111.0741	203.1174	102.0624			2
7					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FLLEGAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.7	784.4195	-0.0012	FLLEGAK
26.4	784.4195	-0.0012	FLLQEK
17.3	784.4173	0.0010	EISATKK

16.9	784.4195	-0.0012	FLEIQK
16.9	784.4195	-0.0012	FLELQK
16.4	784.4173	0.0010	EISAKTK
16.3	784.4195	-0.0012	FLAGEKI
16.3	784.4195	-0.0012	YPEKIK
16.0	784.4195	-0.0012	QFLELK
15.9	784.4195	-0.0012	EAAVFLK

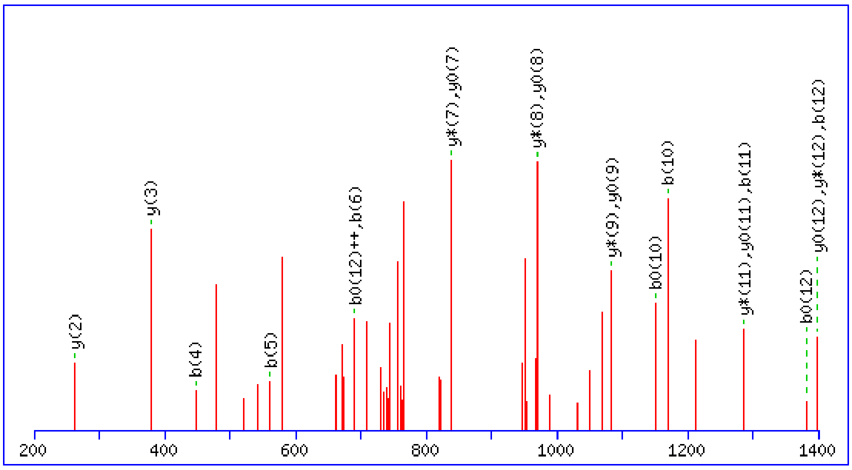
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELISLEDVMEDLK**
Found in **AT4G12790.1** in **TAIR_Arabidopsis**, Symbols: | ATP-binding family protein | chr4:7517277-7518889 REVERSE

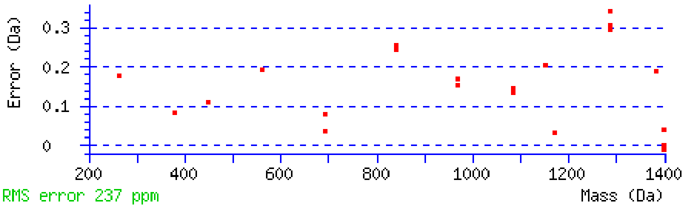
Match to Query 6598: 1546.723900 from(774.369226,2+) index(5566)
Title: Elution from: 48.624 to 48.624 scan no 7035 cid35.00 polarity:+
Data file C7-2_3.mgf

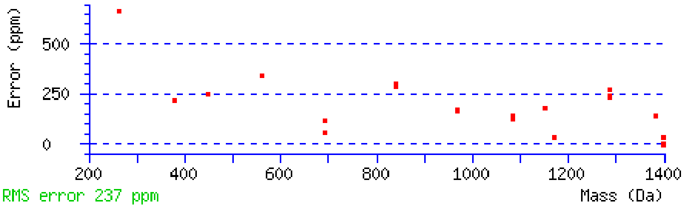
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1546.7229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0012
Matches : 21/116 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							13
2	245.1280	123.0676	227.1174	114.0624	L	1417.6905	709.3489	1399.6669	700.3371	1399.6799	700.3436	12
3	359.2091	180.1082	341.1985	171.1029	I	1303.6094	652.3083	1285.5858	643.2966	1285.5988	643.3031	11
4	***447.2382***	224.1227	429.2276	215.1174	S	1189.5283	595.2678	1171.5047	586.2560	1171.5178	586.2625	10
5	***561.3193***	281.1633	543.3087	272.1580	L	1101.4993	551.2533	1083.4757	542.2415	1083.4887	542.2480	9
6	***691.3589***	346.1831	673.3483	337.1778	E	987.4182	494.2127	969.3946	485.2009	969.4076	485.2074	8
7	807.3829	404.1951	789.3723	395.1898	D	857.3785	429.1929	839.3549	420.1811	839.3680	420.1876	7
8	907.4483	454.2278	889.4378	445.2225	V	741.3545	371.1809	723.3310	362.1691	723.3440	362.1756	6
9	1039.4858	520.2466	1021.4753	511.2413	M	641.2891	321.1482	623.2655	312.1364	623.2785	312.1429	5
10	***1169.5255***	585.2664	1151.5149	576.2611	E	509.2516	255.1294	491.2280	246.1176	491.2410	246.1241	4
11	***1285.5494***	643.2784	1267.5389	634.2731	D	**379.2120**	190.1096	361.1884	181.0978	361.2014	181.1043	3
12	***1399.6305***	700.3189	1381.6200	691.3136	L	**263.1880**	132.0976	245.1644	123.0858			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ELISLEDVMEDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G12790.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.0	1546.7229	0.0010	ELISLEDVMEDLK
23.8	1546.7199	0.0040	ELNDDDKAGLVNVK
11.4	1546.7282	-0.0043	MKEQHRLEEIAK
7.8	1546.7282	-0.0043	AKASHLPSSMQNLK
7.3	1546.7278	-0.0039	MIATNYVGAFSLTK
6.0	1546.7278	-0.0039	WEIVSEISPACIK
5.4	1546.7255	-0.0016	MELQQSNLETPLK
2.9	1546.7226	0.0013	NVSSPSPEISRTPR
0.7	1546.7255	-0.0016	ITVKNEMNPEEVK

AT4G12800.1

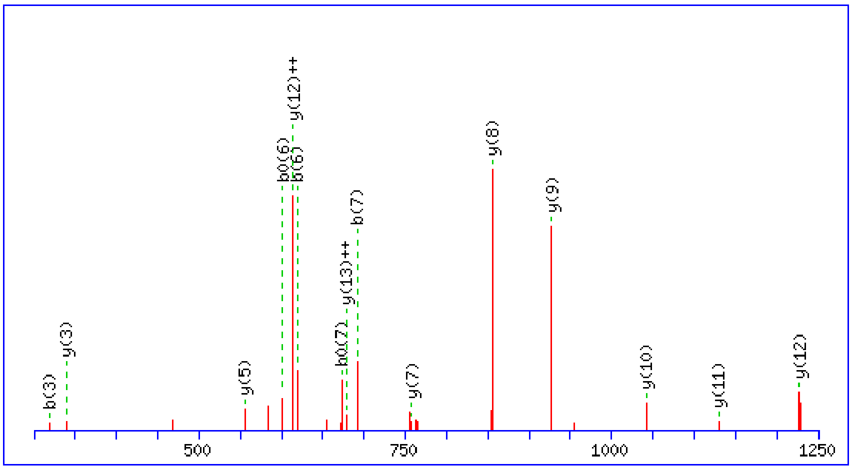
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGEPSIAPSLTLTGR**
Found in **AT4G12800.1** in **TAIR_Arabidopsis**, Symbols: PSAL | PSAL (photosystem I subunit L) | chr4:7521466-7522490 FORWARD

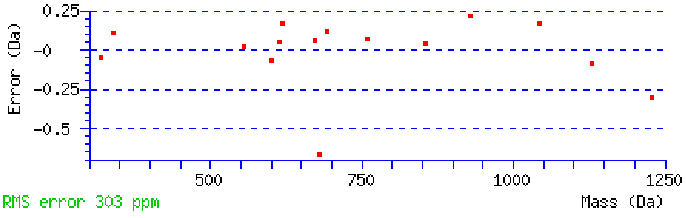
Match to Query 6593: 1544.739462 from(773.377007,2+) index(6127)
Title: Elution from: 54.295 to 54.295 scan no 7841 cid35.00 polarity:+
Data file 0-3_2.mgf

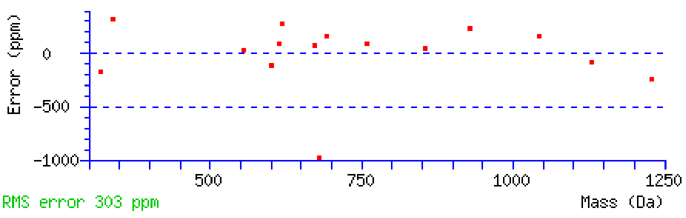
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



`Monoisotopic mass of neutral peptide Mr(calc): 1544.7407`
`Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)`
`Ions Score: 65 Expect: 1.7e-006`
`Matches : 15/136 fragment ions using 25 most intense peaks (help)`

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							15
2	189.0654	95.0363	171.0548	86.0311	G	1415.7083	708.3578	1397.6847	699.3460	1397.6977	699.3525	14
3	**319.1050**	160.0562	301.0945	151.0509	E	1357.6898	679.3485	1339.6662	670.3368	1339.6793	670.3433	13
4	417.1548	209.0811	399.1443	200.0758	P	***1227.6502***	614.3287	1209.6266	605.3169	1209.6396	605.3234	12
5	505.1839	253.0956	487.1733	244.0903	S	***1129.6004***	565.3038	1111.5768	556.2920	1111.5898	556.2985	11
6	**619.2650**	310.1361	601.2544	301.1309	I	***1041.5713***	521.2893	1023.5477	512.2775	1023.5608	512.2840	10
7	**691.2991**	346.1532	673.2886	337.1479	A	***927.4902***	464.2488	909.4666	455.2370	909.4797	455.2435	9
8	789.3489	395.1781	771.3384	386.1728	P	***855.4561***	428.2317	837.4325	419.2199	837.4455	419.2264	8
9	877.3780	439.1926	859.3674	430.1874	S	***757.4063***	379.2068	739.3827	370.1950	739.3957	370.2015	7
10	991.4591	496.2332	973.4485	487.2279	L	669.3772	335.1922	651.3536	326.1805	651.3667	326.1870	6
11	1093.5038	547.2555	1075.4933	538.2503	T	***555.2961***	278.1517	537.2725	269.1399	537.2856	269.1464	5
12	1207.5849	604.2961	1189.5743	595.2908	L	453.2514	227.1293	435.2278	218.1175	435.2408	218.1241	4
13	1309.6296	655.3185	1291.6191	646.3132	T	***339.1703***	170.0888	321.1467	161.0770	321.1597	161.0835	3
14	1367.6481	684.3277	1349.6376	675.3224	G	237.1256	119.0664	219.1020	110.0546			2
15					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EGEPSIAPSLTLTGR

AT4G12800.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.5	1544.7407	-0.0012	EGEPSIAPSLTLTGR

Mascot: http://www.matrixscience.com/

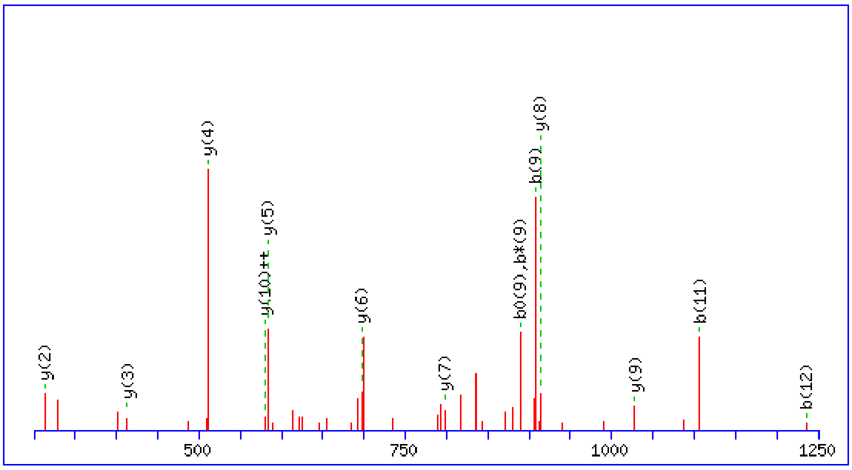
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGSQLDVLAPVKY**
Found in **AT4G13170.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L13A (RPL13aC) | chr4:7655129-7656538 REVERSE

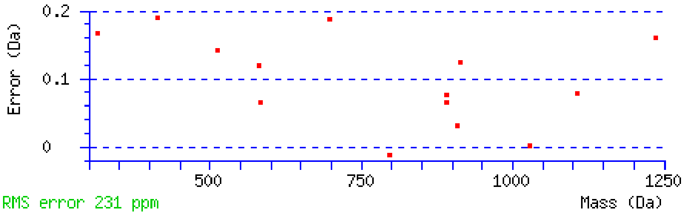
Match to Query 5605: 1416.743212 from(709.378882,2+) index(7717)
Title: Elution from: 68.332 to 68.332 scan no 10127 cid35.00 polarity:+
Data file D6h-3_1.mgf

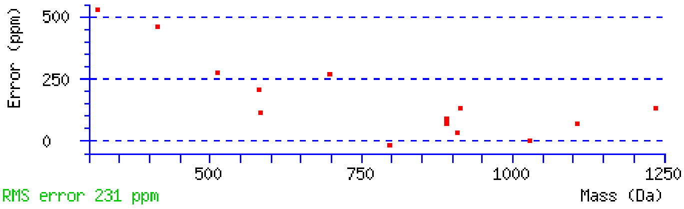
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1416.7423
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 9.8e-007
Matches : 14/118 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							13
2	173.1069	87.0571					G	1303.6685	652.3379	1285.6449	643.3261	1285.6579	643.3326	12
3	261.1359	131.0716			243.1254	122.0663	S	1245.6500	623.3286	1227.6264	614.3168	1227.6394	614.3233	11
4	391.1886	196.0979	373.1650	187.0861	373.1780	187.0926	Q	1157.6209	579.3141	1139.5973	570.3023	1139.6103	570.3088	10
5	505.2697	253.1385	487.2461	244.1267	487.2591	244.1332	L	***1027.5683***	514.2878	1009.5447	505.2760	1009.5577	505.2825	9
6	621.2937	311.1505	603.2701	302.1387	603.2831	302.1452	D	***913.4872***	457.2472	895.4636	448.2354	895.4766	448.2419	8
7	721.3591	361.1832	703.3355	352.1714	703.3485	352.1779	V	***797.4632***	399.2352	779.4396	390.2234			7
8	835.4402	418.2237	817.4166	409.2120	817.4296	409.2185	L	***697.3977***	349.2025	679.3741	340.1907			6
9	**907.4744**	454.2408	889.4508	445.2290	889.4638	445.2355	A	***583.3166***	292.1620	565.2931	283.1502			5
10	1005.5242	503.2657	987.5006	494.2539	987.5136	494.2604	P	***511.2825***	256.1449	493.2589	247.1331			4
11	**1105.5896**	553.2984	1087.5660	544.2866	1087.5790	544.2932	V	***413.2327***	207.1200	395.2091	198.1082			3
12	**1235.6786**	618.3430	1217.6551	609.3312	1217.6681	609.3377	K	***313.1672***	157.0873	295.1437	148.0755			2
13							Y	183.0782	92.0427					1





NCBI **BLAST** search of LGSQLDVLAPVKY
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G13170.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.7	1416.7423	0.0009	LGSQLDVLAPVKY
10.2	1416.7450	-0.0018	ALSDLFHLSKIR

AT4G13360.1

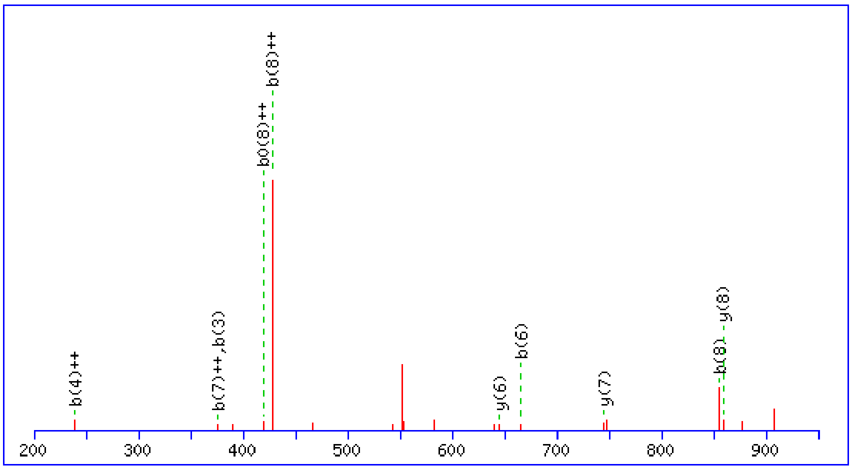
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CVIVEGSTSR**
Found in **AT4G13360.1** in **TAIR_Arabidopsis**, Symbols: | catalytic | chr4:7775129-7777697 FORWARD

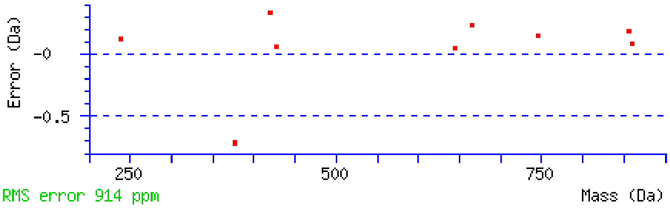
Match to Query 3525: 1120.498868 from(561.256710,2+) index(901)
Title: Elution from: 14.369 to 14.369 scan no 1270 cid35.00 polarity:+
Data file 0-2_2.mgf

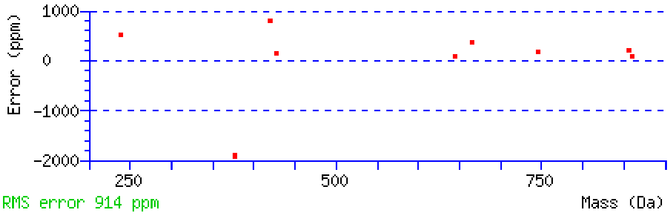
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1120.4975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.022
Matches : 10/80 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	163.0320	82.0196			C							10
2	263.0974	132.0524			V	959.4801	480.2437	941.4565	471.2319	941.4695	471.2384	9
3	***377.1785***	189.0929			I	***859.4146***	430.2109	841.3910	421.1991	841.4040	421.2057	8
4	477.2440	***239.1256***			V	***745.3335***	373.1704	727.3099	364.1586	727.3229	364.1651	7
5	607.2836	304.1454	589.2731	295.1402	E	***645.2681***	323.1377	627.2445	314.1259	627.2575	314.1324	6
6	***665.3021***	333.1547	647.2916	324.1494	G	515.2284	258.1179	497.2048	249.1061	497.2179	249.1126	5
7	753.3312	***377.1692***	735.3206	368.1639	S	457.2099	229.1086	439.1863	220.0968	439.1994	220.1033	4
8	***855.3759***	***428.1916***	837.3653	419.1863	T	369.1809	185.0941	351.1573	176.0823	351.1703	176.0888	3
9	943.4050	472.2061	925.3944	463.2008	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
10					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of CVIVEGSTSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G13360.1

25.3	1120.4975	0.0014	CVIVEGSTSR
5.6	1120.4975	0.0014	AKSMEELQR
2.1	1120.4975	0.0014	AKEESIQMR

AT4G13430.1

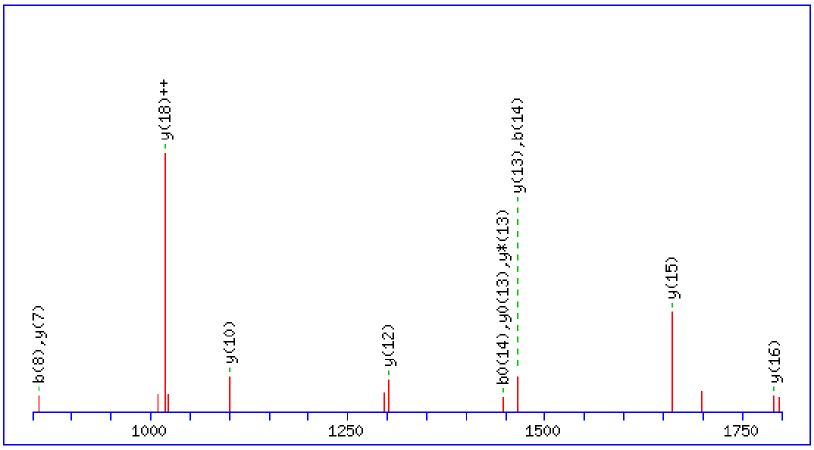
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSVPFEPVYSDGNASFVADYR**
Found in **AT4G13430.1** in **TAIR_Arabidopsis**, Symbols: | aconitase family protein / aconitate hydratase family protein | chr4:7804190-7807785 REVERSE

Match to Query 9999: 2320.063634 from(1161.039093,2+) index(8425)
Title: Elution from: 75.623 to 75.623 scan no 11311 cid35.00 polarity:+
Data file 0-2_2.mgf

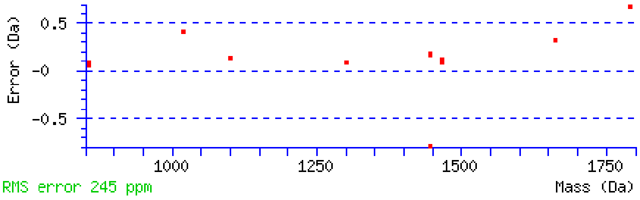
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 850 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

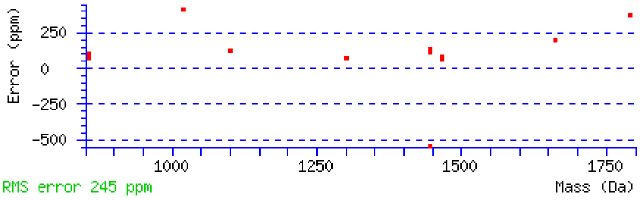


Monoisotopic mass of neutral peptide Mr(calc): 2320.0648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 2.9e-005
Matches : 12/212 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							21
2	189.0870	95.0471			171.0764	86.0418	S	2220.0244	1110.5158	2202.9978	1102.0026	2202.0138	1101.5106	20
3	288.1554	144.5813			270.1448	135.5761	V	2132.9924	1066.9998	2115.9658	1058.4865	2114.9818	1057.9945	19
4	385.2082	193.1077			367.1976	184.1024	P	2033.9239	1017.4656	2016.8974	1008.9523	2015.9134	1008.4603	18
5	532.2766	266.6419			514.2660	257.6366	F	1936.8712	968.9392	1919.8446	960.4260	1918.8606	959.9339	17
6	661.3192	331.1632			643.3086	322.1579	E	***1789.8028***	895.4050	1772.7762	886.8917	1771.7922	886.3997	16
7	758.3719	379.6896			740.3614	370.6843	P	***1660.7602***	830.8837	1643.7336	822.3705	1642.7496	821.8784	15
8	**857.4403**	429.2238			839.4298	420.2185	V	1563.7074	782.3573	1546.6809	773.8441	1545.6968	773.3521	14
9	1020.5037	510.7555			1002.4931	501.7502	Y	***1464.6390***	732.8231	1447.6125	724.3099	1446.6284	723.8179	13
10	1107.5357	554.2715			1089.5251	545.2662	S	***1301.5757***	651.2915	1284.5491	642.7782	1283.5651	642.2862	12
11	1222.5626	611.7850			1204.5521	602.7797	D	1214.5436	607.7755	1197.5171	599.2622	1196.5331	598.7702	11
12	1279.5841	640.2957			1261.5735	631.2904	G	***1099.5167***	550.2620	1082.4902	541.7487	1081.5061	541.2567	10
13	1393.6270	697.3172	1376.6005	688.8039	1375.6165	688.3119	N	1042.4952	521.7513	1025.4687	513.2380	1024.4847	512.7460	9
14	**1464.6642**	732.8357	1447.6376	724.3224	1446.6536	723.8304	A	928.4523	464.7298	911.4258	456.2165	910.4417	455.7245	8
15	1551.6962	776.3517	1534.6696	767.8385	1533.6856	767.3464	S	***857.4152***	429.2112	840.3886	420.6980	839.4046	420.2060	7
16	1698.7646	849.8859	1681.7380	841.3727	1680.7540	840.8807	F	770.3832	385.6952	753.3566	377.1819	752.3726	376.6899	6
17	1797.8330	899.4201	1780.8065	890.9069	1779.8224	890.4149	V	623.3148	312.1610	606.2882	303.6477	605.3042	303.1557	5
18	1868.8701	934.9387	1851.8436	926.4254	1850.8596	925.9334	A	524.2463	262.6268	507.2198	254.1135	506.2358	253.6215	4
19	1983.8971	992.4522	1966.8705	983.9389	1965.8865	983.4469	D	453.2092	227.1082	436.1827	218.5950	435.1987	218.1030	3
20	2146.9604	1073.9838	2129.9338	1065.4706	2128.9498	1064.9786	Y	338.1823	169.5948	321.1557	161.0815			2
21							R	175.1190	88.0631	158.0924	79.5498			1

AT4G13430.1





NCBI **BLAST** search of TSVPFEPVYSDGNASFVADYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.6	2320.0648	-0.0012	TSVPFEPVYSDGNASFVADYR

Mascot: http://www.matrixscience.com/

AT4G13850.1

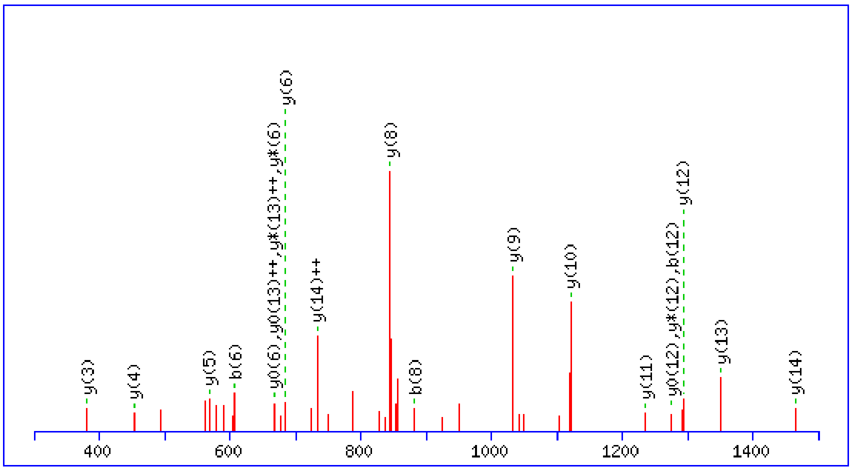
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFIGGLSWGTDDASLR**
Found in **AT4G13850.1** in **TAIR_Arabidopsis**, Symbols: GR-RBP2, GRP2, ATGRP2 | ATGRP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding | chr4:8021310-8022061 FORWARD

Match to Query 8422: 1726.804128 from(864.409340,2+) index(9862)
Title: Elution from: 89.735 to 89.735 scan no 13471 cid35.00 polarity:+
Data file C7-3_1.mgf

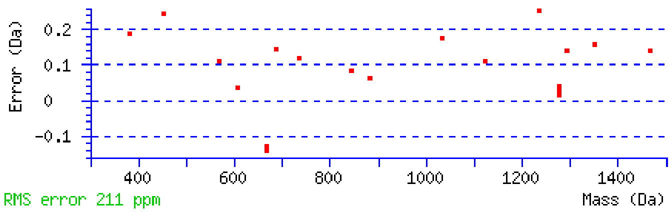
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

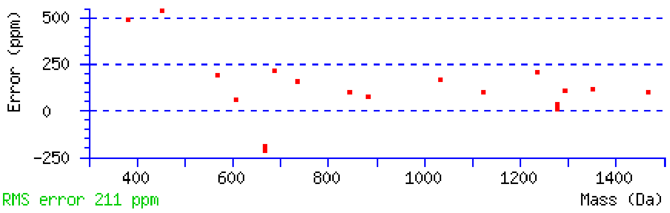


Monoisotopic mass of neutral peptide Mr(calc): 1726.8035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 106 **Expect:** 2.7e-010
Matches : 21/134 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							16
2	263.1538	132.0805			F	1613.7297	807.3685	1595.7061	798.3567	1595.7191	798.3632	15
3	377.2349	189.1211			I	***1465.6642***	733.3357	1447.6406	724.3240	1447.6536	724.3305	14
4	435.2534	218.1303			G	***1351.5831***	676.2952	1333.5595	667.2834	1333.5725	667.2899	13
5	493.2719	247.1396			G	***1293.5646***	647.2859	1275.5410	638.2742	1275.5541	638.2807	12
6	**607.3530**	304.1801			L	***1235.5461***	618.2767	1217.5225	609.2649	1217.5356	609.2714	11
7	695.3821	348.1947	677.3715	339.1894	S	***1121.4650***	561.2361	1103.4414	552.2244	1103.4545	552.2309	10
8	**883.4555**	442.2314	865.4449	433.2261	W	***1033.4360***	517.2216	1015.4124	508.2098	1015.4254	508.2163	9
9	941.4740	471.2406	923.4634	462.2353	G	***845.3626***	423.1849	827.3390	414.1731	827.3520	414.1796	8
10	1043.5187	522.2630	1025.5081	513.2577	T	787.3441	394.1757	769.3205	385.1639	769.3335	385.1704	7
11	1159.5427	580.2750	1141.5321	571.2697	D	***685.2994***	343.1533	667.2758	334.1415	667.2888	334.1480	6
12	**1275.5666**	638.2870	1257.5561	629.2817	D	***569.2754***	285.1413	551.2518	276.1295	551.2648	276.1360	5
13	1347.6008	674.3040	1329.5902	665.2987	A	***453.2514***	227.1293	435.2278	218.1175	435.2408	218.1241	4
14	1435.6298	718.3186	1417.6193	709.3133	S	***381.2173***	191.1123	363.1937	182.1005	363.2067	182.1070	3
15	1549.7109	775.3591	1531.7004	766.3538	L	293.1882	147.0977	275.1646	138.0859			2
16					R	179.1071	90.0572	161.0835	81.0454			1

AT4G13850.1





NCBI **BLAST** search of LFIGGLSWGTDDASLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
105.7	1726.8035	0.0007	LFIGGLSWGTDDASLR
10.5	1726.8073	-0.0032	LTEEQNRRLLMER

Mascot: http://www.matrixscience.com/

AT4G13930.1

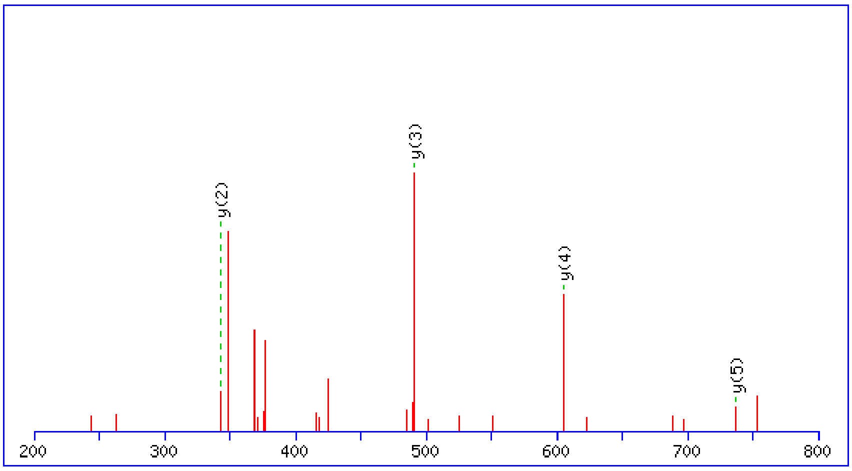
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGMIFYR**
Found in **AT4G13930.1** in **TAIR_Arabidopsis**, Symbols: SHM4 | SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4); glycine hydroxymethyltransferase | chr4:8048008-8050016 REVERSE

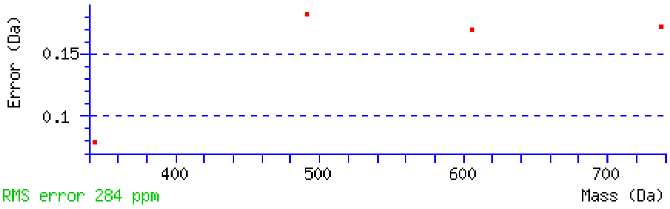
Match to Query 1345: 866.396444 from(434.205498,2+) index(3968)
Title: Elution from: 36.861 to 36.861 scan no 5032 cid35.00 polarity:+
Data file D12h-3_3.mgf

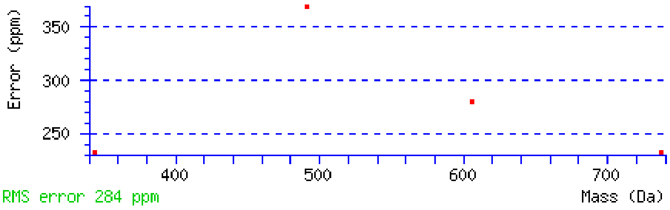
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 866.3969
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0029
Matches : 4/36 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	73.0414	37.0244	A					7
2	131.0599	66.0336	G	795.3700	398.1886	777.3464	389.1769	6
3	263.0974	132.0524	M	***737.3515***	369.1794	719.3279	360.1676	5
4	377.1785	189.0929	I	***605.3140***	303.1606	587.2904	294.1488	4
5	525.2440	263.1256	F	***491.2329***	246.1201	473.2093	237.1083	3
6	689.3044	345.1558	Y	***343.1675***	172.0874	325.1439	163.0756	2
7			R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of AGMIFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.3	866.3969	-0.0004	AGMIFYR
12.6	866.3969	-0.0004	IFMQYR

AT4G13930.1

Mascot: http://www.matrixscience.com/

AT4G13940.1

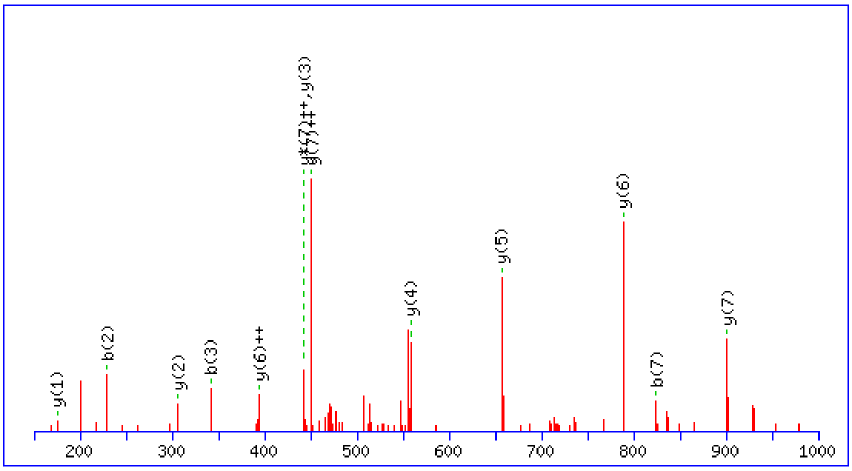
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIIMVDHMR**
Found in **AT4G13940.1** in **TAIR_Arabidopsis**, Symbols: EMB1395, MEE58, SAHH, SAHH1, HOG1 | HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosylhomocysteinase | chr4:8054926-8056671 FORWARD

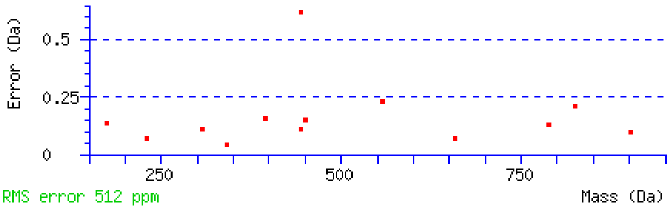
Match to Query 3326: 1128.539006 from(565.276779,2+) index(4154)
Title: Elution from: 41.805 to 41.805 scan no 5365 cid35.00 polarity:+
Data file D12h-2_1.mgf

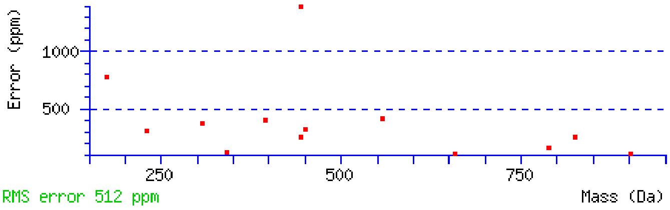
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1128.5420
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 5.9e-005
Matches : 13/74 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	**229.1183**	115.0628	211.1077	106.0575	I	1014.5223	507.7648	997.4958	499.2515	996.5118	498.7595	8
3	**342.2023**	171.6048	324.1918	162.5995	I	***901.4383***	451.2228	884.4117	442.7095	883.4277	442.2175	7
4	473.2428	237.1251	455.2323	228.1198	M	***788.3542***	394.6807	771.3276	386.1675	770.3436	385.6755	6
5	572.3112	286.6593	554.3007	277.6540	V	***657.3137***	329.1605	640.2872	320.6472	639.3031	320.1552	5
6	687.3382	344.1727	669.3276	335.1674	D	***558.2453***	279.6263	541.2187	271.1130	540.2347	270.6210	4
7	**824.3971**	412.7022	806.3865	403.6969	H	***443.2183***	222.1128	426.1918	213.5995			3
8	955.4376	478.2224	937.4270	469.2171	M	***306.1594***	153.5834	289.1329	145.0701			2
9					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DIIMVDHMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G13940.1

46.1	1128.5420	-0.0030	DIIMVDHMR
3.1	1128.5411	-0.0021	AEPPSEGSSLR
2.1	1128.5411	-0.0021	LSPEEEAQAR

AT4G14040.1

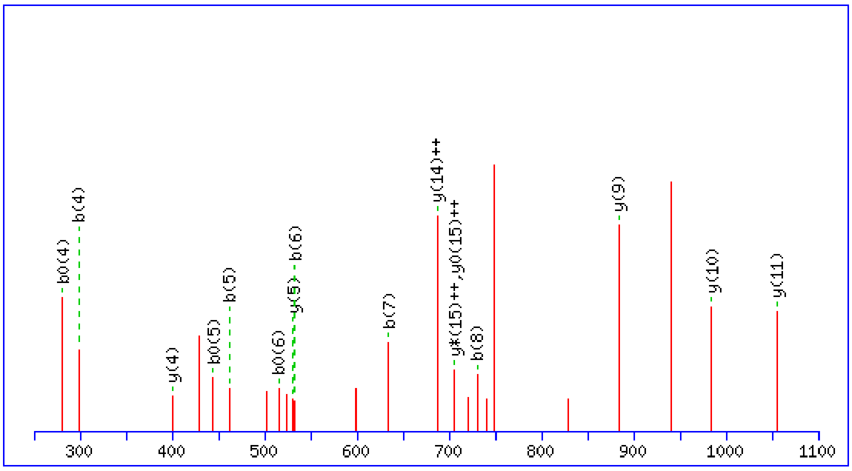
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGPGYATPLAAMAGPR**
Found in **AT4G14040.1** in **TAIR_Arabidopsis**, Symbols: EDA38, SBP2 | EDA38 (embryo sac development arrest 38); selenium binding | chr4:8100686-8102823 REVERSE

Match to Query 6549: 1515.748590 from(758.881571,2+) index(6177)
Title: Elution from: 55.389 to 55.389 scan no 7864 cid35.00 polarity:+
Data file 0-3_1.mgf

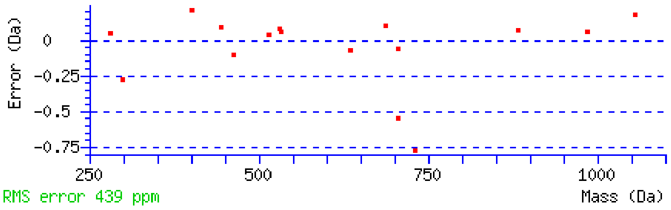
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

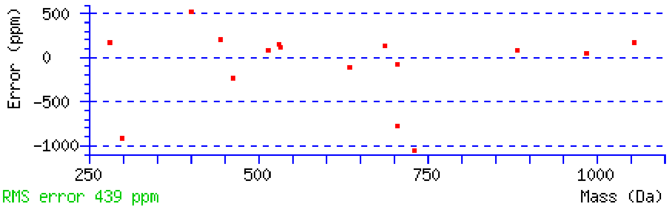


Monoisotopic mass of neutral peptide Mr(calc): 1515.7504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0015
Matches : 16/132 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							16
2	145.0608	73.0340	127.0502	64.0287	G	1429.7256	715.3665	1412.6991	706.8532	1411.7151	706.3612	15
3	242.1135	121.5604	224.1030	112.5551	P	1372.7042	686.8557	1355.6776	678.3425	1354.6936	677.8504	14
4	***299.1350***	150.0711	281.1244	141.0659	G	1275.6514	638.3293	1258.6249	629.8161	1257.6409	629.3241	13
5	***462.1983***	231.6028	444.1878	222.5975	Y	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	12
6	***533.2354***	267.1214	515.2249	258.1161	A	***1055.5666***	528.2870	1038.5401	519.7737	1037.5561	519.2817	11
7	***634.2831***	317.6452	616.2726	308.6399	T	***984.5295***	492.7684	967.5030	484.2551	966.5189	483.7631	10
8	***731.3359***	366.1716	713.3253	357.1663	P	***883.4818***	442.2446	866.4553	433.7313			9
9	844.4199	422.7136	826.4094	413.7083	L	786.4291	393.7182	769.4025	385.2049			8
10	915.4571	458.2322	897.4465	449.2269	A	673.3450	337.1761	656.3185	328.6629			7
11	986.4942	493.7507	968.4836	484.7454	A	602.3079	301.6576	585.2813	293.1443			6
12	1117.5347	559.2710	1099.5241	550.2657	M	***531.2708***	266.1390	514.2442	257.6258			5
13	1188.5718	594.7895	1170.5612	585.7842	A	***400.2303***	200.6188	383.2037	192.1055			4
14	1245.5932	623.3003	1227.5827	614.2950	G	329.1932	165.1002	312.1666	156.5870			3
15	1342.6460	671.8266	1324.6354	662.8214	P	272.1717	136.5895	255.1452	128.0762			2
16					R	175.1190	88.0631	158.0924	79.5498			1

AT4G14040.1





NCBI **BLAST** search of SGPGYATPLAAMAGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.2	1515.7504	-0.0018	SGPGYATPLAAMAGPR
6.0	1515.7529	-0.0043	DITAAVANDLAASER

Mascot: http://www.matrixscience.com/

AT4G14360.1

MATRIX SCIENCE

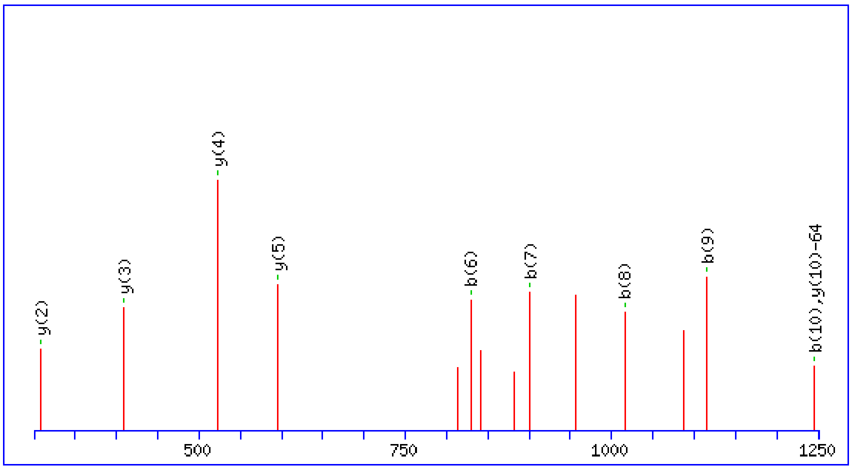
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IWREMSALVER**
Found in **AT4G14360.1** in **TAIR_Arabidopsis**, Symbols: | dehydration-responsive protein-related | chr4:8267865-8270187 REVERSE

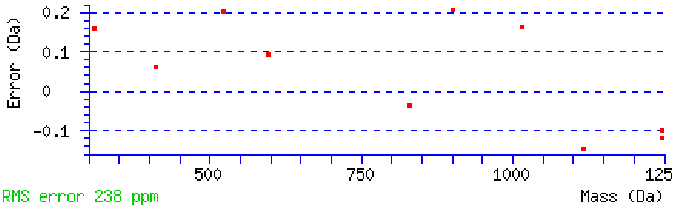
Match to Query 5405: 1422.663310 from(712.338931,2+) index(10563)
Title: Elution from: 106.500 to 106.500 scan no 15474 cid35.00 polarity:+
Data file D12h-1_3.mgf

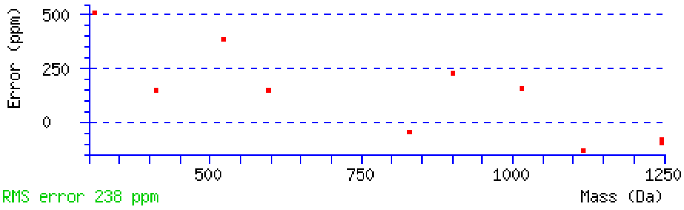
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1422.6650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 **Expect:** 0.00096
Matches : 10/168 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							11
2	303.1618	152.0845					W	1309.5912	655.2992	1291.5676	646.2874	1291.5806	646.2939	10
3	463.2510	232.1291	445.2274	223.1174			R	1121.5178	561.2625	1103.4942	552.2507	1103.5072	552.2573	9
4	593.2906	297.1490	575.2671	288.1372	575.2801	288.1437	E	961.4285	481.2179	943.4050	472.2061	943.4180	472.2126	8
5	741.3231	371.1652	723.2995	362.1534	723.3125	362.1599	M	831.3889	416.1981	813.3653	407.1863	813.3783	407.1928	7
6	***829.3521***	415.1797	811.3286	406.1679	811.3416	406.1744	S	683.3565	342.1819	665.3329	333.1701	665.3459	333.1766	6
7	***901.3863***	451.1968	883.3627	442.1850	883.3757	442.1915	A	**595.3274**	298.1673	577.3038	289.1556	577.3169	289.1621	5
8	***1015.4674***	508.2373	997.4438	499.2255	997.4568	499.2320	L	**523.2933**	262.1503	505.2697	253.1385	505.2827	253.1450	4
9	***1115.5328***	558.2701	1097.5092	549.2583	1097.5223	549.2648	V	**409.2122**	205.1097	391.1886	196.0979	391.2016	196.1044	3
10	***1245.5725***	623.2899	1227.5489	614.2781	1227.5619	614.2846	E	**309.1467**	155.0770	291.1231	146.0652	291.1362	146.0717	2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IWREMSALVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G14360.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.8	1422.6650	-0.0017	IWREMSALVER
18.2	1422.6675	-0.0042	QASLSTDKALSER
17.1	1422.6616	0.0017	GVWERDFLLDR
11.8	1422.6620	0.0013	THHHKETDIKR
11.2	1422.6657	-0.0024	KMKIMDAELGEK
5.5	1422.6616	0.0017	GQNFELLPFGAGR
5.0	1422.6675	-0.0042	DLSSRASTAQLEK
4.3	1422.6628	0.0006	SLDCQKLSAQVR
2.5	1422.6657	-0.0024	MKIMDAELGEKK
2.4	1422.6628	0.0005	IKGNKVNMEEAR

AT4G14605.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELTTLEIR**
Found in **AT4G14605.1** in **TAIR_Arabidopsis**, Symbols: | mitochondrial transcription termination factor-related / mTERF-related | chr4:8378810-8380412 FORWARD

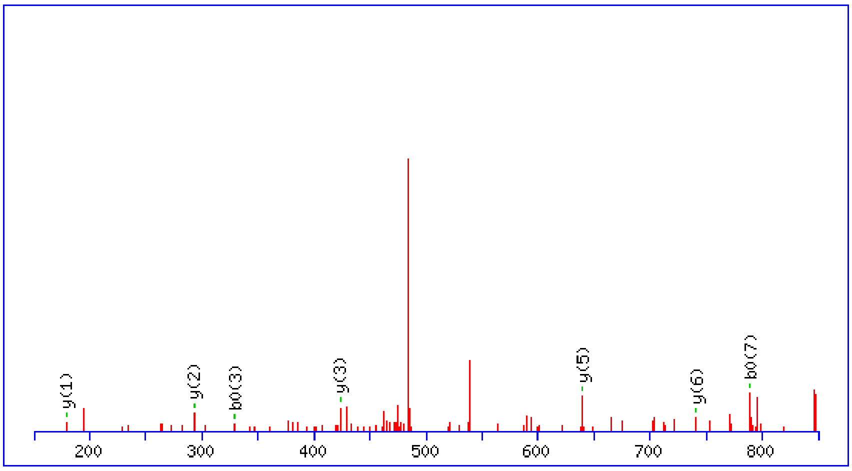
Match to Query 2196: 984.510234 from(493.262393,2+) index(3251)
Title: Elution from: 31.256 to 31.256 scan no 4022 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

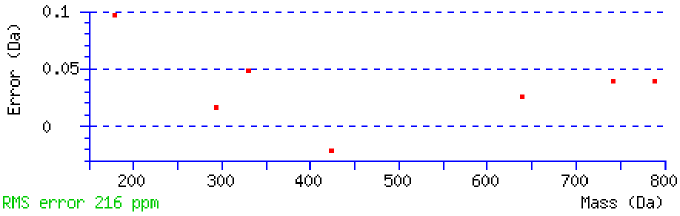
Label all possible matches ○ Label matches used for scoring ●

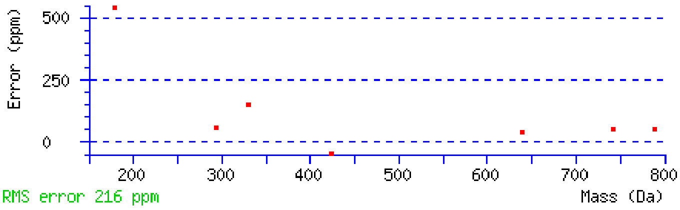
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.5118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.044
Matches : 7/66 fragment ions using 21 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0469	66.0271	113.0363	57.0218	E							8
2	245.1280	123.0676	227.1174	114.0624	L	855.4794	428.2434	837.4559	419.2316	837.4689	419.2381	7
3	347.1727	174.0900	329.1622	165.0847	T	*741.3983*	371.2028	723.3748	362.1910	723.3878	362.1975	6
4	449.2174	225.1124	431.2069	216.1071	T	*639.3536*	320.1805	621.3300	311.1687	621.3431	311.1752	5
5	563.2985	282.1529	545.2880	273.1476	L	537.3089	269.1581	519.2853	260.1463	519.2984	260.1528	4
6	693.3382	347.1727	675.3276	338.1674	E	*423.2278*	212.1175	405.2042	203.1058	405.2173	203.1123	3
7	807.4193	404.2133	789.4087	395.2080	I	*293.1882*	147.0977	275.1646	138.0859			2
8					R	*179.1071*	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ELTTLEIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.0	984.5118	-0.0015	ELTTLEIR

AT4G14605.1

1.1	984.5097	0.0005	KHMAKSIR
0.3	984.5118	-0.0015	LDDKLKDK
0.2	984.5118	-0.0015	TAVAVEKEK
0.0	984.5118	-0.0016	ELEAEKKK
0.0	984.5118	-0.0016	LEAEEKKK

AT4G14690.1

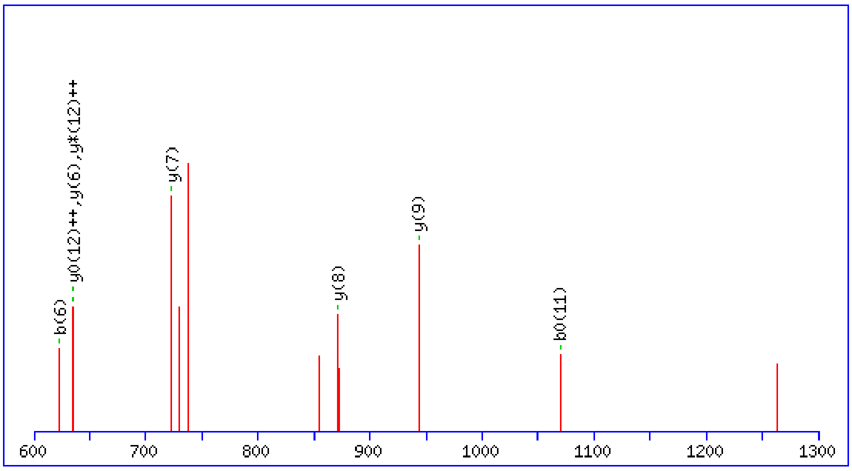
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGDLLAFSGPAPER**
Found in **AT4G14690.1** in **TAIR_Arabidopsis**, Symbols: ELIP2 | ELIP2 (EARLY LIGHT-INDUCIBLE PROTEIN 2); chlorophyll binding | chr4:8418368-8419124 FORWARD

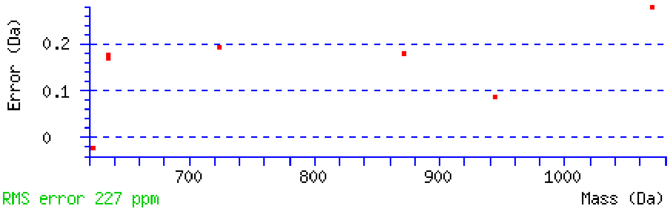
Match to Query 5812: 1492.691522 from(747.353037,2+) index(7679)
Title: Elution from: 68.861 to 68.861 scan no 10156 cid35.00 polarity:+
Data file D1d-2_3.mgf

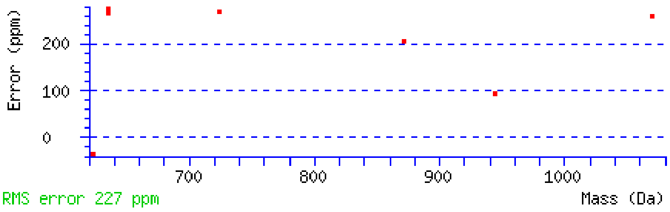
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1492.6905
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.042
Matches : 8/124 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400			**F**							**14**
2	207.0912	104.0492			**G**	1345.6323	673.3198	1327.6087	664.3080	1327.6217	664.3145	**13**
3	323.1152	162.0612	305.1046	153.0560	**D**	1287.6138	644.3105	1269.5902	635.2987	1269.6032	635.3053	**12**
4	437.1963	219.1018	419.1857	210.0965	**L**	1171.5898	586.2986	1153.5662	577.2868	1153.5793	577.2933	**11**
5	551.2774	276.1423	533.2668	267.1371	**L**	1057.5087	529.2580	1039.4851	520.2462	1039.4982	520.2527	**10**
6	623.3115	312.1594	605.3010	303.1541	**A**	***943.4276***	472.2175	925.4040	463.2057	925.4171	463.2122	**9**
7	771.3770	386.1921	753.3664	377.1869	**F**	***871.3935***	436.2004	853.3699	427.1886	853.3829	427.1951	**8**
8	859.4061	430.2067	841.3955	421.2014	**S**	***723.3280***	362.1677	705.3044	353.1559	705.3175	353.1624	**7**
9	917.4246	459.2159	899.4140	450.2106	**G**	***635.2990***	318.1531	617.2754	309.1413	617.2884	309.1478	**6**
10	1015.4744	508.2408	997.4638	499.2355	**P**	577.2805	289.1439	559.2569	280.1321	559.2699	280.1386	**5**
11	1087.5085	544.2579	1069.4979	535.2526	**A**	479.2307	240.1190	461.2071	231.1072	461.2201	231.1137	**4**
12	1185.5583	593.2828	1167.5477	584.2775	**P**	407.1965	204.1019	389.1729	195.0901	389.1860	195.0966	**3**
13	1315.5979	658.3026	1297.5874	649.2973	**E**	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	**2**
14					**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of FGDLLAFSGPAPER

AT4G14690.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	1492.6905	0.0011	FGDLLAFSGPAPER
4.8	1492.6882	0.0033	KGAWTAEEDSLLR
3.4	1492.6882	0.0033	KVEQDYLHTSQK
3.3	1492.6909	0.0006	LDTPADHVNVHVR
3.2	1492.6878	0.0037	IIDFEFLNPDEK
2.8	1492.6889	0.0026	QKLEESELVEMK

AT4G14880.1

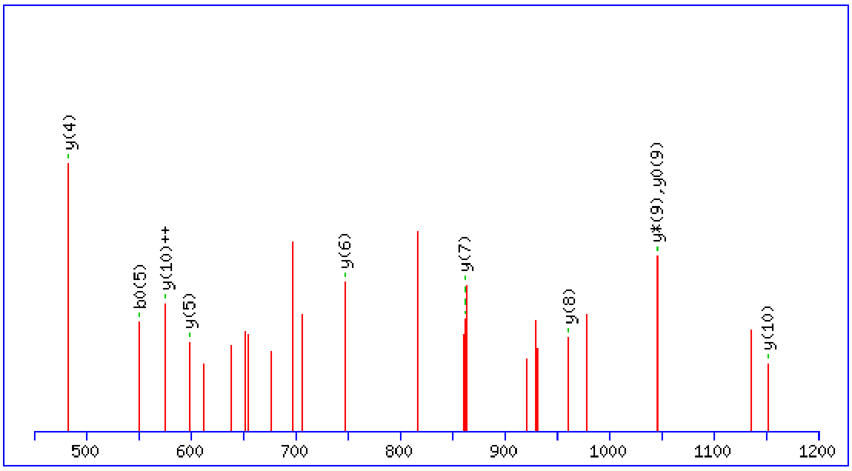
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLSTVLFDATRK**
Found in **AT4G14880.1** in **TAIR_Arabidopsis**, Symbols: CYTACS1, ATCYS-3A, OASA1 | OASA1 (O-ACETYLSERINE (THIOL) LYASE (OAS-TL) ISOFORM A1) | chr4:8518204-8520045 REVERSE

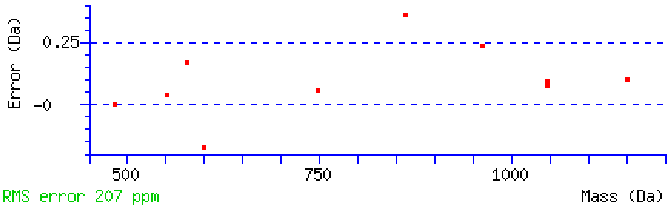
Match to Query 5588: 1428.721950 from(715.368251,2+) index(5873)
Title: Elution from: 52.087 to 52.087 scan no 7481 cid35.00 polarity:+
Data file 0-1_3.mgf

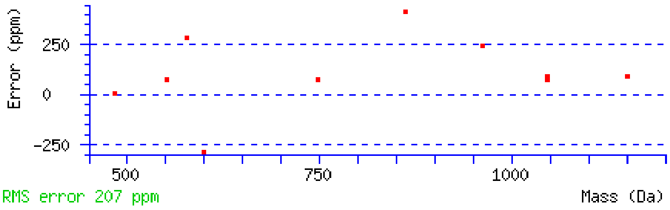
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1428.7189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0068
Matches : 10/104 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							12
2	279.1487	140.0780					L	1265.6658	633.3366	1247.6423	624.3248	1247.6553	624.3313	11
3	367.1778	184.0925			349.1672	175.0873	S	***1151.5847***	576.2960	1133.5612	567.2842	1133.5742	567.2907	10
4	469.2225	235.1149			451.2120	226.1096	T	1063.5557	532.2815	1045.5321	523.2697	1045.5451	523.2762	9
5	569.2880	285.1476			551.2774	276.1423	V	***961.5110***	481.2591	943.4874	472.2473	943.5004	472.2538	8
6	683.3691	342.1882			665.3585	333.1829	L	***861.4455***	431.2264	843.4219	422.2146	843.4349	422.2211	7
7	831.4345	416.2209			813.4239	407.2156	F	***747.3644***	374.1858	729.3408	365.1741	729.3538	365.1806	6
8	947.4585	474.2329			929.4479	465.2276	D	***599.2990***	300.1531	581.2754	291.1413	581.2884	291.1478	5
9	1019.4926	510.2500			1001.4821	501.2447	A	***483.2750***	242.1411	465.2514	233.1293	465.2644	233.1358	4
10	1121.5374	561.2723			1103.5268	552.2670	T	411.2408	206.1241	393.2173	197.1123	393.2303	197.1188	3
11	1281.6266	641.3169	1263.6030	632.3051	1263.6160	632.3117	R	309.1961	155.1017	291.1725	146.0899			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YLSTVLFDATRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G14880.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.4	1428.7189	0.0030	YLSTVLFDATRK
0.6	1428.7223	-0.0003	DNVLPLSIVQGMK

AT4G14960.2

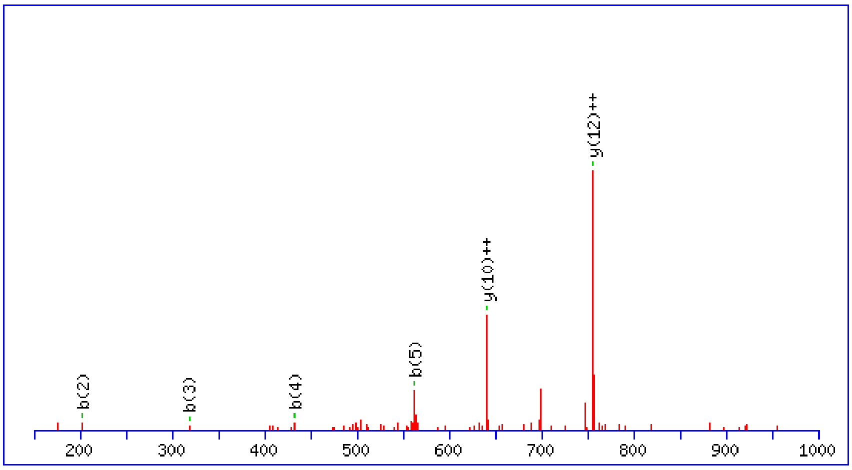
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLNIERPTYTNLNR**
Found in **AT4G14960.2** in **TAIR_Arabidopsis**, Symbols: TUA6 | TUA6 (tubulin alpha-6 chain) | chr4:8548765-8550315 REVERSE

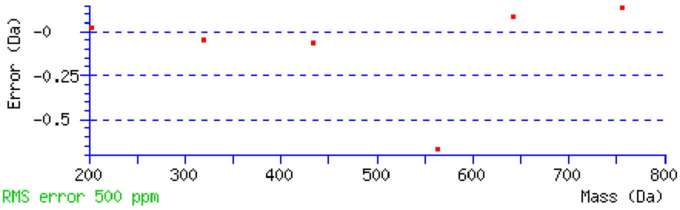
Match to Query 8479: 1712.811669 from(571.944499,3+) index(4350)
Title: Elution from: 39.550 to 39.550 scan no 5387 cid35.00 polarity:+
Data file C7-1_1.mgf

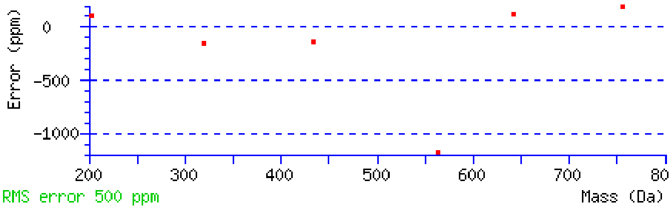
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1712.8116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.025
Matches : 6/144 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							14
2	***203.1174***	102.0624			185.1069	93.0571	L	1625.7898	813.3986	1607.7663	804.3868	1607.7793	804.3933	13
3	***319.1544***	160.0809	301.1309	151.0691	301.1439	151.0756	N	1511.7087	756.3580	1493.6852	747.3462	1493.6982	747.3527	12
4	***433.2355***	217.1214	415.2120	208.1096	415.2250	208.1161	I	1395.6718	698.3395	1377.6482	689.3277	1377.6612	689.3342	11
5	***563.2752***	282.1412	545.2516	273.1294	545.2646	273.1359	E	1281.5907	641.2990	1263.5671	632.2872	1263.5801	632.2937	10
6	723.3644	362.1858	705.3408	353.1741	705.3538	353.1806	R	1151.5510	576.2792	1133.5274	567.2674	1133.5405	567.2739	9
7	821.4142	411.2107	803.3906	402.1990	803.4036	402.2055	P	991.4618	496.2345	973.4382	487.2227	973.4512	487.2292	8
8	923.4589	462.2331	905.4353	453.2213	905.4484	453.2278	T	893.4120	447.2096	875.3884	438.1978	875.4014	438.2043	7
9	1087.5193	544.2633	1069.4957	535.2515	1069.5087	535.2580	Y	791.3673	396.1873	773.3437	387.1755	773.3567	387.1820	6
10	1189.5640	595.2856	1171.5404	586.2738	1171.5534	586.2804	T	627.3069	314.1571	609.2833	305.1453	609.2963	305.1518	5
11	1305.6010	653.3041	1287.5774	644.2923	1287.5904	644.2989	N	525.2622	263.1347	507.2386	254.1229			4
12	1419.6821	710.3447	1401.6585	701.3329	1401.6715	701.3394	L	409.2252	205.1162	391.2016	196.1044			3
13	1535.7191	768.3632	1517.6955	759.3514	1517.7085	759.3579	N	295.1441	148.0757	277.1205	139.0639			2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SLNIERPTYTNLNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G14960.2

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.3	1712.8116	0.0000	SLNIERPTYTNLNR
4.4	1712.8089	0.0027	DSLIEVAKSYVADQR
3.1	1712.8145	-0.0029	QAQIGMLFDTLEKGK
1.2	1712.8123	-0.0007	SLGMTSGEELEKIRK
0.1	1712.8129	-0.0013	ANQILMRGSCRPKR

AT4G15000.1

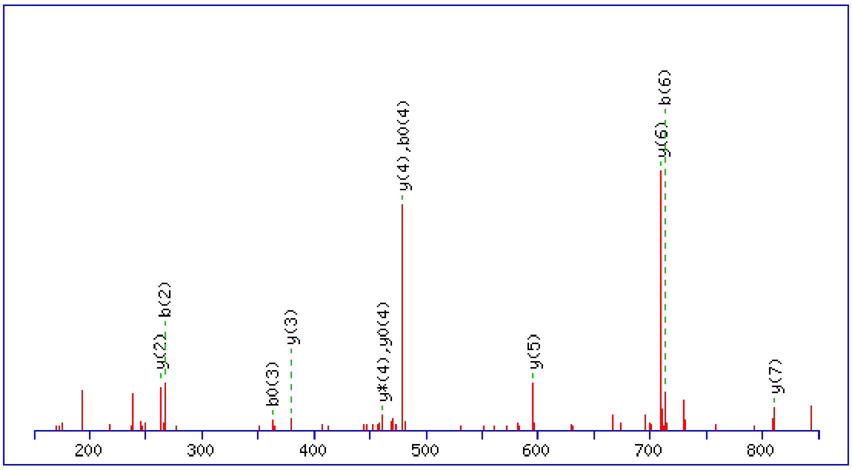
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTLDVDLK**
Found in **AT4G15000.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L27 (RPL27C) | chr4:8571892-8572299 FORWARD

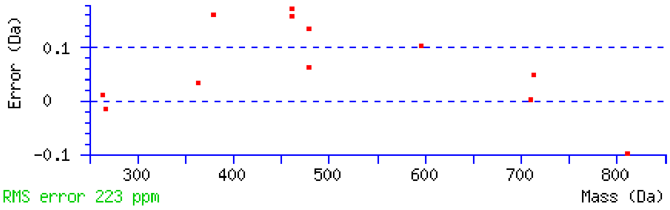
Match to Query 2193: 974.480344 from(488.247448,2+) index(5143)
Title: Elution from: 47.266 to 47.266 scan no 6455 cid35.00 polarity:+
Data file D6h-2_2.mgf

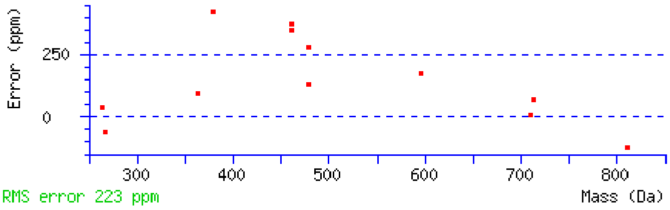
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 974.4803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 4.6e-005
Matches : 12/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375			Y							8
2	**267.1124**	134.0598	249.1018	125.0545	T	***811.4272***	406.2172	793.4036	397.2054	793.4166	397.2120	7
3	381.1935	191.1004	363.1829	182.0951	L	***709.3825***	355.1949	691.3589	346.1831	691.3719	346.1896	6
4	497.2174	249.1124	479.2069	240.1071	D	***595.3014***	298.1543	577.2778	289.1425	577.2908	289.1490	5
5	597.2829	299.1451	579.2723	290.1398	V	***479.2774***	240.1423	461.2538	231.1305	461.2668	231.1371	4
6	**713.3069**	357.1571	695.2963	348.1518	D	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	3
7	827.3880	414.1976	809.3774	405.1923	L	***263.1880***	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YTLDVDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.5	974.4803	0.0001	YTLDVDLK
23.7	974.4829	-0.0026	FLNVVESR

AT4G15000.1

17.8	974.4829	-0.0026	RFDAVDLK
14.2	974.4830	-0.0026	YPNITSLR
12.6	974.4829	-0.0026	NDFVLLSR
12.0	974.4789	0.0014	KMSEIMVK
7.5	974.4789	0.0014	EMVTMVKK
7.5	974.4782	0.0021	TICVWKR
7.3	974.4807	-0.0004	DRTVESKK
7.2	974.4807	-0.0004	TKGDVSLSR

AT4G15180.1

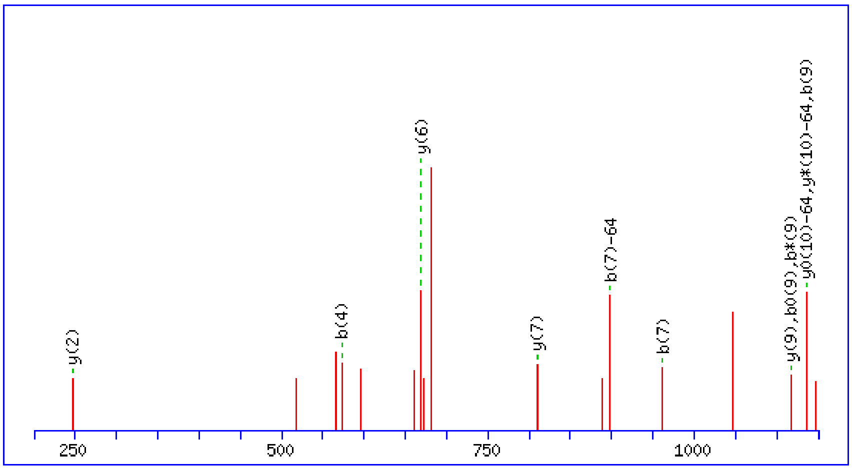
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMRHVFGDPK**
Found in **AT4G15180.1** in **TAIR_Arabidopsis**, Symbols: | SET domain-containing protein | chr4:8651999-8662178 FORWARD

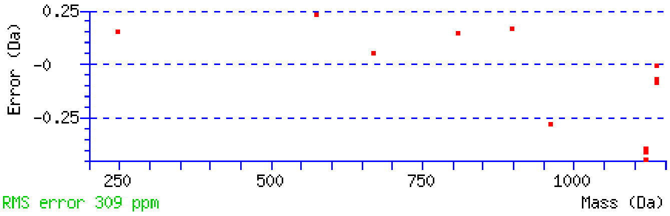
Match to Query 5132: 1380.619764 from(691.317158,2+) index(6655)
Title: Elution from: 61.639 to 61.639 scan no 8692 cid35.00 polarity:+
Data file D12h-2_1.mgf

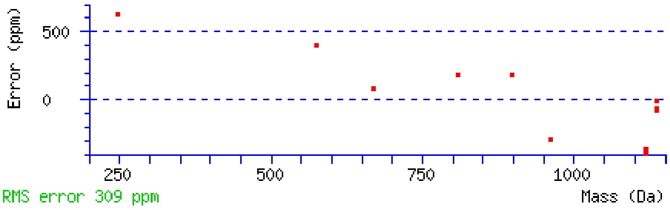
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1380.6203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.03
Matches : 12/140 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	165.0676	83.0375					Y							11
2	265.1331	133.0702					V	1217.5672	609.2872	1199.5436	600.2754	1199.5566	600.2820	10
3	413.1655	207.0864					M	***1117.5018***	559.2545	1099.4782	550.2427	1099.4912	550.2492	9
4	***573.2548***	287.1310	555.2312	278.1192			R	969.4693	485.2383	951.4457	476.2265	951.4588	476.2330	8
5	713.3048	357.1560	695.2812	348.1442			H	***809.3801***	405.1937	791.3565	396.1819	791.3695	396.1884	7
6	813.3702	407.1888	795.3467	398.1770			V	***669.3300***	335.1687	651.3065	326.1569	651.3195	326.1634	6
7	***961.4357***	481.2215	943.4121	472.2097			F	569.2646	285.1359	551.2410	276.1241	551.2540	276.1307	5
8	1019.4542	510.2307	1001.4306	501.2189			G	421.1991	211.1032	403.1756	202.0914	403.1886	202.0979	4
9	***1135.4782***	568.2427	1117.4546	559.2309	1117.4676	559.2374	D	363.1807	182.0940	345.1571	173.0822	345.1701	173.0887	3
10	1233.5280	617.2676	1215.5044	608.2558	1215.5174	608.2623	P	***247.1567***	124.0820	229.1331	115.0702			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YVMRHVFGDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G15180.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.9	1380.6203	-0.0005	YVMRHVFGDPK
2.0	1380.6180	0.0017	FDINGPGSCLKR
1.4	1380.6176	0.0021	FPWEKVSSMEK
1.3	1380.6188	0.0010	NSNIMLDVMSVK
0.9	1380.6232	-0.0035	ARAEENNVSSKR
0.8	1380.6206	-0.0008	SNLEIKDSSNTR
0.4	1380.6180	0.0017	MGGGPRTFPGGVSK
0.0	1380.6214	-0.0017	DMALLMKQQNR

AT4G16155.1

Mascot Search Results

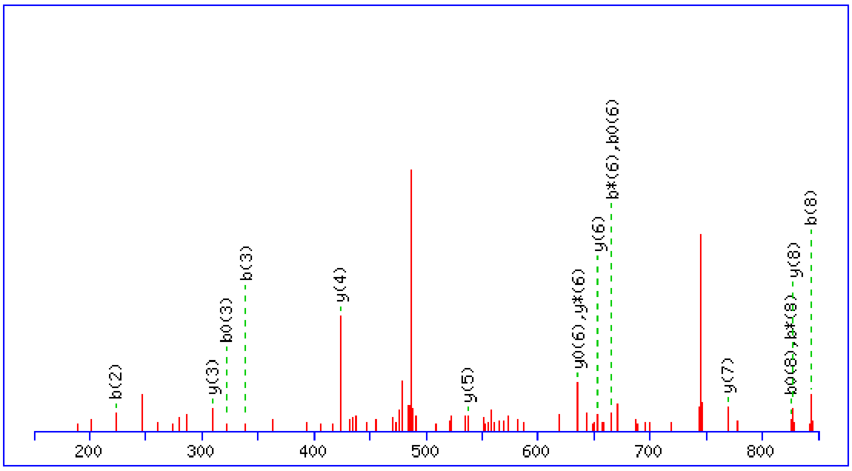
Peptide View

MS/MS Fragmentation of **YGDNIITGK**
Found in **AT4G16155.1** in **TAIR_Arabidopsis**, Symbols: | dihydrolipoamide dehydrogenase 2, plastidic / lipoamide dehydrogenase 2 (PTLPD2) | chr4:9153586-9157149 REVERSE

Match to Query 2221: 990.466652 from(496.240602,2+) index(2359)
Title: Elution from: 24.691 to 24.691 scan no 2935 cid35.00 polarity:+
Data file D6h-3_3.mgf

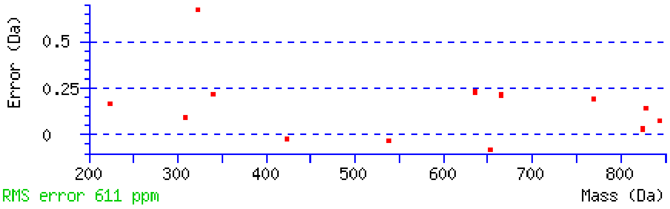
Click mouse within plot area to zoom in by factor of two about that point

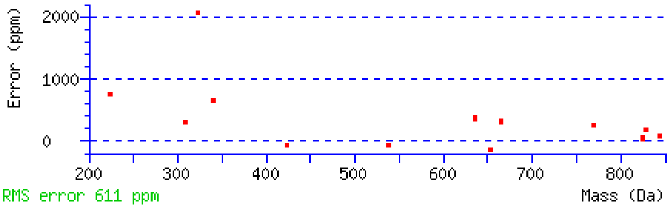
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 990.4648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.011
Matches : 16/82 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							9
2	**223.0861**	112.0467					G	***827.4118***	414.2095	809.3882	405.1977	809.4012	405.2042	8
3	**339.1101**	170.0587			321.0996	161.0534	D	***769.3933***	385.2003	751.3697	376.1885	751.3827	376.1950	7
4	455.1471	228.0772	437.1235	219.0654	437.1365	219.0719	N	***653.3693***	327.1883	635.3457	318.1765	635.3587	318.1830	6
5	569.2282	285.1177	551.2046	276.1060	551.2176	276.1125	I	***537.3323***	269.1698	519.3087	260.1580	519.3217	260.1645	5
6	683.3093	342.1583	665.2857	333.1465	665.2987	333.1530	I	***423.2512***	212.1292	405.2276	203.1174	405.2406	203.1239	4
7	785.3540	393.1807	767.3304	384.1689	767.3435	384.1754	T	***309.1701***	155.0887	291.1465	146.0769	291.1595	146.0834	3
8	**843.3725**	422.1899	825.3489	413.1781	825.3620	413.1846	G	207.1254	104.0663	189.1018	95.0545			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YGDNIITGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G16155.1

30.1	990.4648	0.0018	YGDNIITGK
13.6	990.4648	0.0018	DKDAIGFSK
13.6	990.4648	0.0018	ENGEKYIK
13.6	990.4648	0.0018	NEKGYIEK
13.6	990.4648	0.0018	SGVGQYLEK
7.1	990.4671	-0.0004	GTFLETWK
6.0	990.4675	-0.0008	FGIDGGKQR
5.9	990.4648	0.0018	SKYKDDPK
3.0	990.4648	0.0018	EGSDKFVAK
2.4	990.4671	-0.0004	EDYKWLK

AT4G16480.1

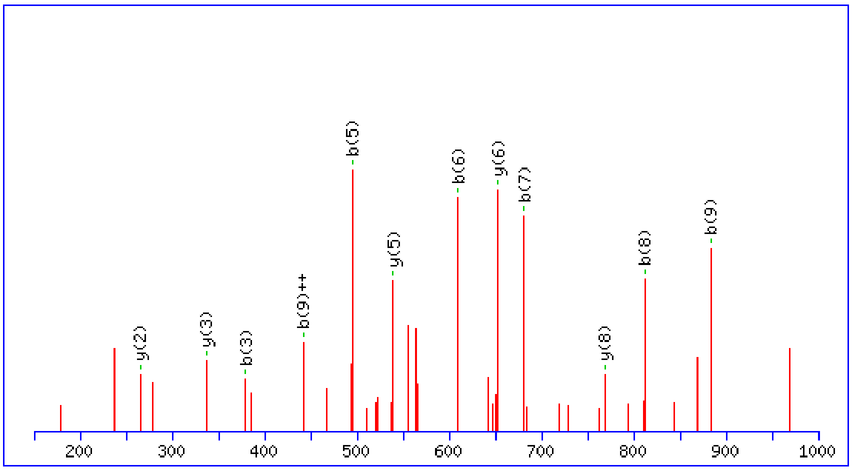
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVEGGIAKADK**
Found in **AT4G16480.1** in **TAIR_Arabidopsis**, Symbols: ATINT4 | ATINT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen ion symporter | chr4:9291268-9293105 FORWARD

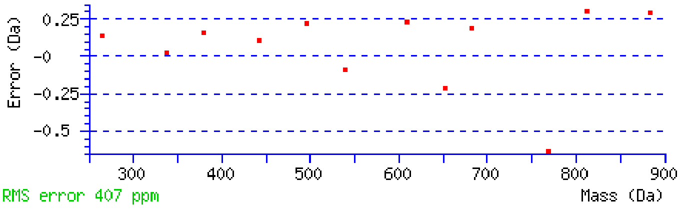
Match to Query 3826: 1146.534076 from(574.274314,2+) index(6788)
Title: Elution from: 59.699 to 59.699 scan no 8725 cid35.00 polarity:+
Data file D12h-1_2.mgf

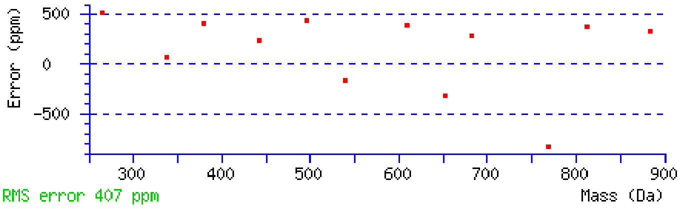
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1146.5365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 45 **Expect:** 0.0005
Matches : 12/142 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							11
2	249.1052	125.0562					V	999.5114	500.2593	981.4878	491.2475	981.5008	491.2540	10
3	*379.1448*	190.0760			361.1342	181.0707	E	899.4459	450.2266	881.4223	441.2148	881.4353	441.2213	9
4	437.1633	219.0853			419.1527	210.0800	G	**769.4063**	385.2068	751.3827	376.1950	751.3957	376.2015	8
5	*495.1818*	248.0945			477.1712	239.0892	G	711.3878	356.1975	693.3642	347.1857	693.3772	347.1922	7
6	*609.2629*	305.1351			591.2523	296.1298	I	**653.3693**	327.1883	635.3457	318.1765	635.3587	318.1830	6
7	*681.2970*	341.1522			663.2865	332.1469	A	**539.2882**	270.1477	521.2646	261.1359	521.2776	261.1424	5
8	*811.3861*	406.1967	793.3625	397.1849	793.3755	397.1914	K	467.2540	234.1307	449.2304	225.1189	449.2435	225.1254	4
9	*883.4202*	442.2137	865.3966	433.2020	865.4097	433.2085	A	**337.1650**	169.0861	319.1414	160.0743	319.1544	160.0809	3
10	999.4442	500.2257	981.4206	491.2139	981.4336	491.2205	D	**265.1309**	133.0691	247.1073	124.0573	247.1203	124.0638	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MVEGGIAKADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G16480.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.6	1146.5365	-0.0024	MVEGGIAKADK
15.9	1146.5365	-0.0024	MEKEIAELR
14.7	1146.5309	0.0032	SSLGESLEGVR
12.8	1146.5309	0.0032	KDASKDDVAGK
10.8	1146.5365	-0.0025	MKVPLNSSDK
9.4	1146.5358	-0.0017	LGSKSEAFHR
9.0	1146.5365	-0.0024	MRVLEDVEK
8.1	1146.5358	-0.0017	RFVDGPSPTR
7.5	1146.5365	-0.0025	LINEMVSANK
7.4	1146.5358	-0.0017	QNFAQAVPTR

AT4G16680.1

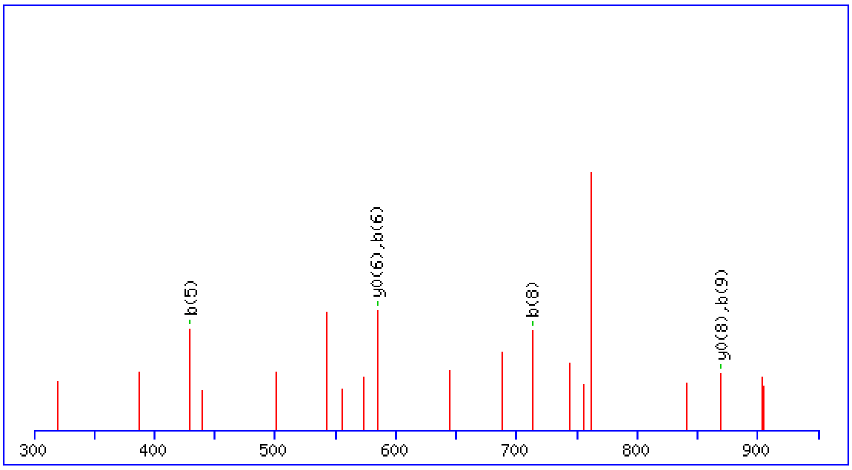
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAAQRAGRSGR**
Found in **AT4G16680.1** in **TAIR_Arabidopsis**, Symbols: | RNA helicase, putative | chr4:9388093-9390796 REVERSE

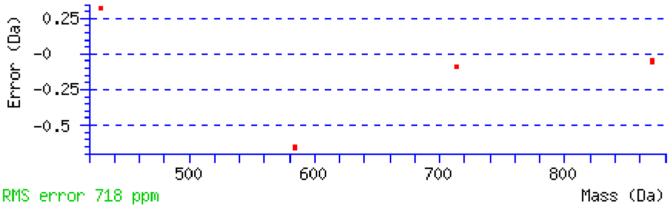
Match to Query 4078: 1186.628610 from(594.321581,2+) index(5113)
Title: Elution from: 45.789 to 45.789 scan no 6396 cid35.00 polarity:+
Data file D12h-1_2.mgf

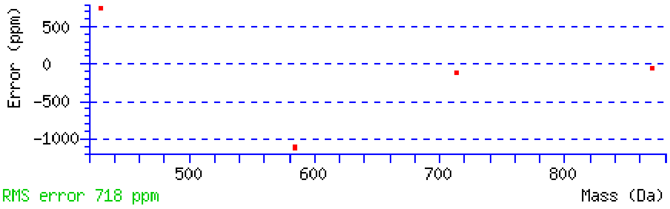
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1186.6279
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.021
Matches : 6/118 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	159.0764	80.0418			141.0659	71.0366	S	1116.5981	558.8027	1099.5715	550.2894	1098.5875	549.7974	11
3	230.1135	115.5604			212.1030	106.5551	A	1029.5661	515.2867	1012.5395	506.7734	1011.5555	506.2814	10
4	301.1506	151.0790			283.1401	142.0737	A	958.5289	479.7681	941.5024	471.2548	940.5184	470.7628	9
5	***429.2092***	215.1083	412.1827	206.5950	411.1987	206.1030	Q	887.4918	444.2495	870.4653	435.7363	869.4813	435.2443	8
6	***585.3103***	293.1588	568.2838	284.6455	567.2998	284.1535	R	759.4332	380.2203	742.4067	371.7070	741.4227	371.2150	7
7	656.3474	328.6774	639.3209	320.1641	638.3369	319.6721	A	603.3321	302.1697	586.3056	293.6564	585.3216	293.1644	6
8	***713.3689***	357.1881	696.3424	348.6748	695.3583	348.1828	G	532.2950	266.6511	515.2685	258.1379	514.2845	257.6459	5
9	***869.4700***	435.2387	852.4435	426.7254	851.4595	426.2334	R	475.2736	238.1404	458.2470	229.6271	457.2630	229.1351	4
10	956.5021	478.7547	939.4755	470.2414	938.4915	469.7494	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
11	1013.5235	507.2654	996.4970	498.7521	995.5130	498.2601	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ASAAQRAGRSGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G16680.1

Score	Mr(calc)	Delta	Sequence
24.0	1186.6279	0.0007	ASAAQRAGRSGR
1.4	1186.6306	-0.0019	EAVEQRKAEK
0.5	1186.6306	-0.0020	GSLEREEIVR
0.0	1186.6306	-0.0020	VQTSSGEKPVR

AT4G16720.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYEIILVDPAHNAVR**
Found in **AT4G16720.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L15 (RPL15A) | chr4:9400178-9401337 REVERSE

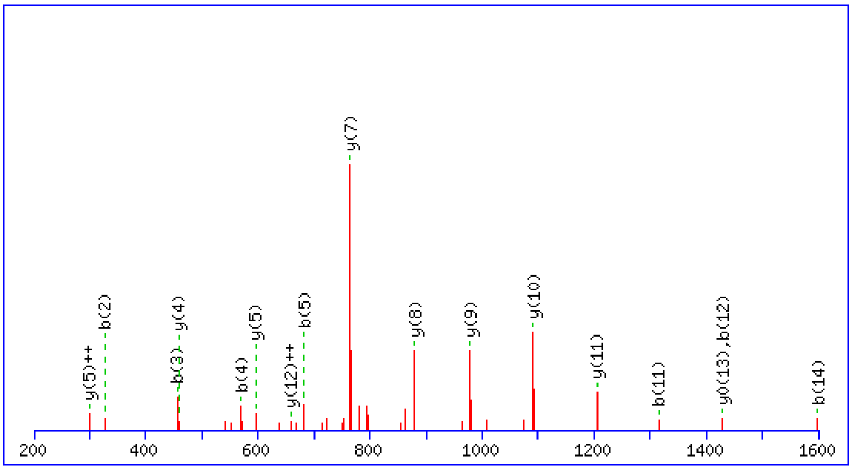
Match to Query 8769: 1771.926646 from(886.970599,2+) index(7436)
Title: Elution from: 65.319 to 65.319 scan no 9585 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1600 Da Full range

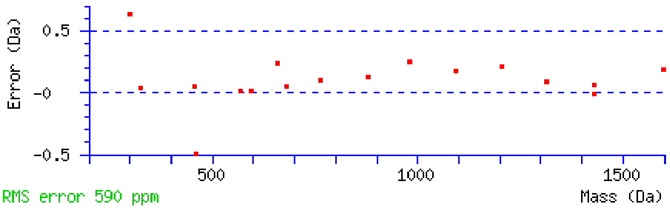
Label all possible matches ○ Label matches used for scoring ●

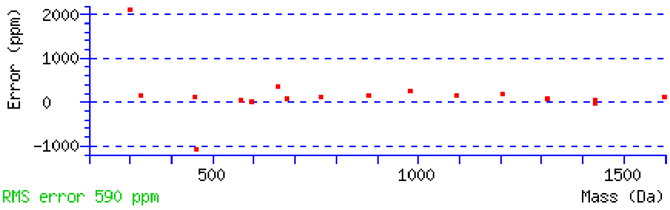
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1771.9257
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.1e-007
Matches : 17/128 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							15
2	***327.1339***	164.0706					Y	1609.8697	805.4385	1592.8431	796.9252	1591.8591	796.4332	14
3	***456.1765***	228.5919			438.1660	219.5866	E	1446.8063	723.9068	1429.7798	715.3935	1428.7958	714.9015	13
4	***569.2606***	285.1339			551.2500	276.1287	I	1317.7637	659.3855	1300.7372	650.8722	1299.7532	650.3802	12
5	***682.3447***	341.6760			664.3341	332.6707	I	***1204.6797***	602.8435	1187.6531	594.3302	1186.6691	593.8382	11
6	795.4287	398.2180			777.4182	389.2127	L	***1091.5956***	546.3014	1074.5691	537.7882	1073.5851	537.2962	10
7	894.4971	447.7522			876.4866	438.7469	V	***978.5116***	489.7594	961.4850	481.2461	960.5010	480.7541	9
8	1009.5241	505.2657			991.5135	496.2604	D	***879.4431***	440.2252	862.4166	431.7119	861.4326	431.2199	8
9	1106.5768	553.7921			1088.5663	544.7868	P	***764.4162***	382.7117	747.3896	374.1985			7
10	1177.6140	589.3106			1159.6034	580.3053	A	667.3634	334.1854	650.3369	325.6721			6
11	***1314.6729***	657.8401			1296.6623	648.8348	H	***596.3263***	298.6668	579.2998	290.1535			5
12	***1428.7158***	714.8615	1411.6892	706.3483	1410.7052	705.8563	N	***459.2674***	230.1373	442.2409	221.6241			4
13	1499.7529	750.3801	1482.7264	741.8668	1481.7423	741.3748	A	345.2245	173.1159	328.1979	164.6026			3
14	***1598.8213***	799.9143	1581.7948	791.4010	1580.8108	790.9090	V	274.1874	137.5973	257.1608	129.0840			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YYEIILVDPAHNAVR

AT4G16720.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.0	1771.9257	0.0010	YYEIILVDPAHNAVR
1.4	1771.9217	0.0050	SRLQDPPTPTHPAIDK

AT4G17040.1

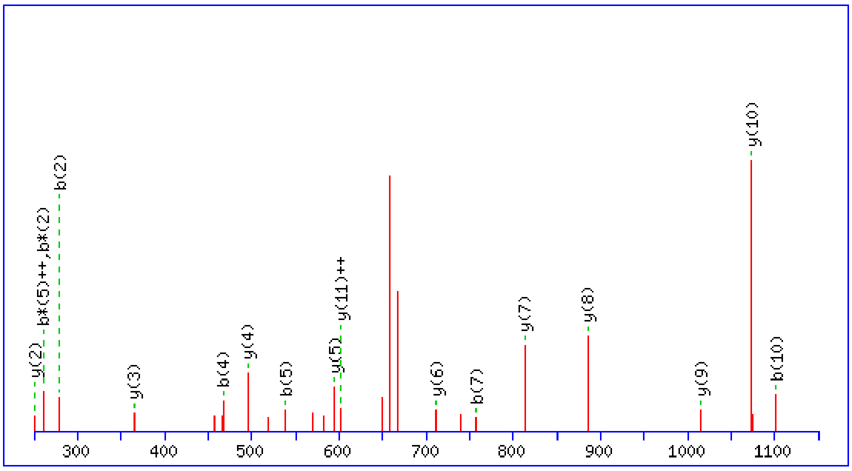
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQGQATDVEIAR**
Found in **AT4G17040.1** in **TAIR_Arabidopsis**, Symbols: | ATP-dependent Clp protease proteolytic subunit, putative | chr4:9586759-9589316 REVERSE

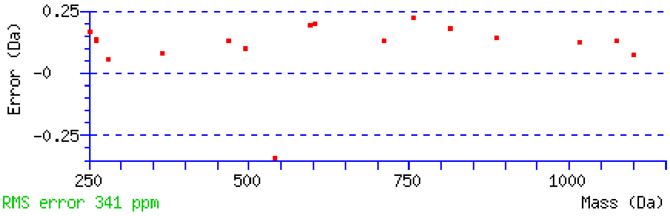
Match to Query 5029: 1350.614004 from(676.314278,2+) index(2743)
Title: Elution from: 28.700 to 28.700 scan no 3473 cid35.00 polarity:+
Data file 0-2_2.mgf

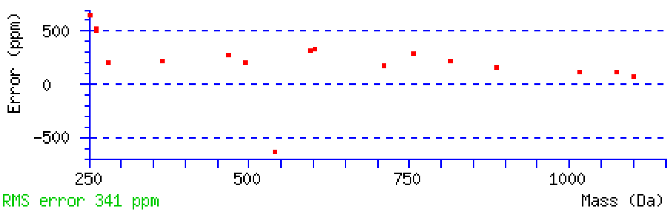
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1350.6122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 9.5e-009
Matches : 17/114 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400					F							12
2	**279.1254**	140.0663	261.1018	131.0545			Q	1203.5541	602.2807	1185.5305	593.2689	1185.5435	593.2754	11
3	337.1439	169.0756	319.1203	160.0638			G	***1073.5014***	537.2543	1055.4778	528.2425	1055.4908	528.2491	10
4	**467.1965**	234.1019	449.1729	225.0901			Q	***1015.4829***	508.2451	997.4593	499.2333	997.4723	499.2398	9
5	**539.2307**	270.1190	521.2071	261.1072			A	***885.4303***	443.2188	867.4067	434.2070	867.4197	434.2135	8
6	641.2754	321.1413	623.2518	312.1295	623.2648	312.1360	T	***813.3961***	407.2017	795.3725	398.1899	795.3855	398.1964	7
7	**757.2994**	379.1533	739.2758	370.1415	739.2888	370.1480	D	***711.3514***	356.1793	693.3278	347.1675	693.3408	347.1741	6
8	857.3648	429.1860	839.3412	420.1742	839.3542	420.1808	V	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	5
9	987.4044	494.2059	969.3809	485.1941	969.3939	485.2006	E	***495.2620***	248.1346	477.2384	239.1228	477.2514	239.1293	4
10	**1101.4855**	551.2464	1083.4619	542.2346	1083.4750	542.2411	I	***365.2223***	183.1148	347.1988	174.1030			3
11	1173.5197	587.2635	1155.4961	578.2517	1155.5091	578.2582	A	***251.1412***	126.0743	233.1177	117.0625			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FQGQATDVEIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G17040.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.8	1350.6122	0.0018	FQGQATDVEIAR
19.7	1350.6164	-0.0024	MCGIAIVVCGVR
14.2	1350.6156	-0.0016	TRNLLEMEGQK
14.2	1350.6156	-0.0016	MKSGKQSSQPEK
12.3	1350.6156	-0.0016	EQECSQLKKGK
11.6	1350.6178	-0.0038	SNFLAHLMTGTK
10.5	1350.6122	0.0018	YHDATSKLSQGK
10.3	1350.6156	-0.0016	DMAGIKGDSVAVR
10.2	1350.6156	-0.0016	RKSVDNVMEEK
9.2	1350.6167	-0.0027	FNPYLWPSGQK

AT4G17520.1

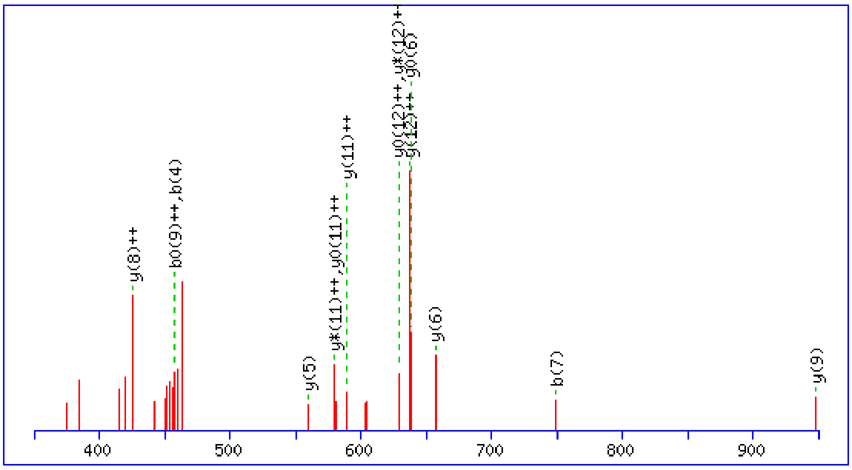
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPTKPPPPSQAVR**
Found in **AT4G17520.1** in **TAIR_Arabidopsis**, Symbols: | nuclear RNA-binding protein, putative | chr4:9771509-9773326 FORWARD

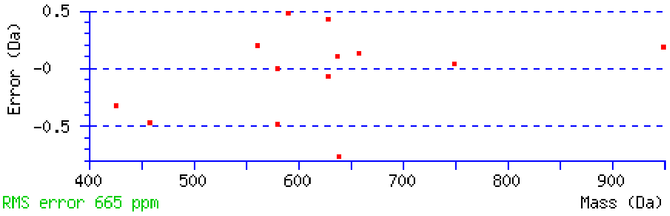
Match to Query 4924: 1404.754371 from(469.258733,3+) index(613)
Title: Elution from: 14.184 to 14.184 scan no 1000 cid35.00 polarity:+
Data file D1d-1-2.mgf

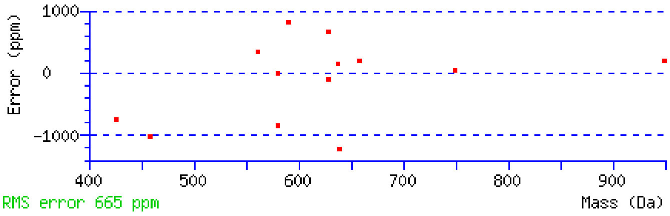
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1404.7547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0082
Matches : 14/126 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					M							13
2	229.1005	115.0539					P	1274.7215	637.8644	1257.6950	629.3511	1256.7110	628.8591	12
3	330.1482	165.5777			312.1376	156.5725	T	1177.6688	589.3380	1160.6422	580.8248	1159.6582	580.3327	11
4	**458.2432**	229.6252	441.2166	221.1119	440.2326	220.6199	K	1076.6211	538.8142	1059.5946	530.3009	1058.6105	529.8089	10
5	555.2959	278.1516	538.2694	269.6383	537.2854	269.1463	P	***948.5261***	474.7667	931.4996	466.2534	930.5156	465.7614	9
6	652.3487	326.6780	635.3221	318.1647	634.3381	317.6727	P	851.4734	426.2403	834.4468	417.7271	833.4628	417.2350	8
7	**749.4015**	375.2044	732.3749	366.6911	731.3909	366.1991	P	754.4206	377.7139	737.3941	369.2007	736.4100	368.7087	7
8	846.4542	423.7307	829.4277	415.2175	828.4437	414.7255	P	***657.3679***	329.1876	640.3413	320.6743	639.3573	320.1823	6
9	933.4863	467.2468	916.4597	458.7335	915.4757	458.2415	S	***560.3151***	280.6612	543.2885	272.1479	542.3045	271.6559	5
10	1061.5448	531.2761	1044.5183	522.7628	1043.5343	522.2708	Q	473.2831	237.1452	456.2565	228.6319			4
11	1132.5819	566.7946	1115.5554	558.2813	1114.5714	557.7893	A	345.2245	173.1159	328.1979	164.6026			3
12	1231.6504	616.3288	1214.6238	607.8155	1213.6398	607.3235	V	274.1874	137.5973	257.1608	129.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MPTKPPPPSQAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G17520.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.8	1404.7547	-0.0004	MPTKPPPPSQAVR
2.8	1404.7572	-0.0029	LTSRSSDVSVNLK
2.0	1404.7581	-0.0037	MLKMAARDTGALK
1.9	1404.7547	-0.0004	MIFVDRIDALGR

AT4G17530.1

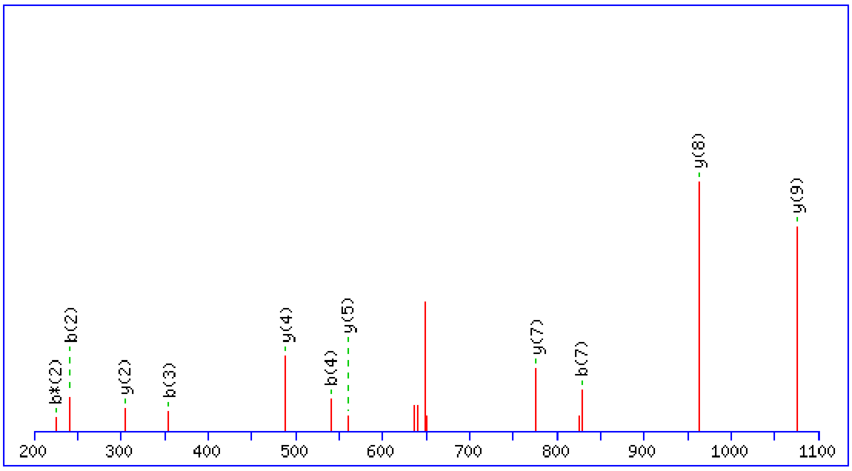
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQIWDTAGQER**
Found in **AT4G17530.1** in **TAIR_Arabidopsis**, Symbols: ATRAB1C, ATRABD2C, RAB1C | RAB1C; GTP binding | chr4:9773734-9775437 REVERSE

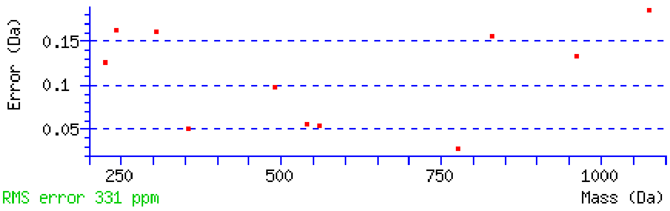
Match to Query 4784: 1315.651738 from(658.833145,2+) index(4923)
Title: Elution from: 43.427 to 43.427 scan no 6160 cid35.00 polarity:+
Data file C7-2_3.mgf

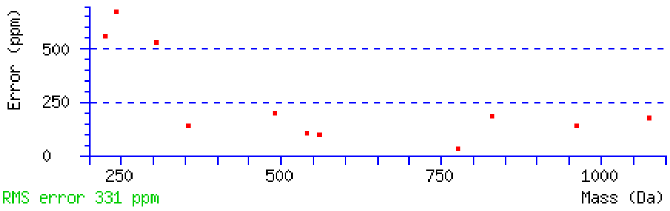
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1315.6521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 2.3e-005
Matches : 11/108 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	**242.1499**	121.5786	225.1234	113.0653			Q	1203.5753	602.2913	1186.5487	593.7780	1185.5647	593.2860	10
3	**355.2340**	178.1206	338.2074	169.6074			I	***1075.5167***	538.2620	1058.4902	529.7487	1057.5061	529.2567	9
4	**541.3133**	271.1603	524.2867	262.6470			W	***962.4326***	481.7200	945.4061	473.2067	944.4221	472.7147	8
5	656.3402	328.6738	639.3137	320.1605	638.3297	319.6685	D	***776.3533***	388.6803	759.3268	380.1670	758.3428	379.6750	7
6	757.3879	379.1976	740.3614	370.6843	739.3774	370.1923	T	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	6
7	**828.4250**	414.7162	811.3985	406.2029	810.4145	405.7109	A	***560.2787***	280.6430	543.2522	272.1297	542.2681	271.6377	5
8	885.4465	443.2269	868.4199	434.7136	867.4359	434.2216	G	***489.2416***	245.1244	472.2150	236.6112	471.2310	236.1191	4
9	1013.5051	507.2562	996.4785	498.7429	995.4945	498.2509	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
10	1142.5477	571.7775	1125.5211	563.2642	1124.5371	562.7722	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LQIWDTAGQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G17530.1

Score	Mr(calc)	Delta	Sequence
54.1	1315.6521	-0.0003	LQIWDTAGQER
54.1	1315.6521	-0.0003	LQLWDTAGQER
8.0	1315.6482	0.0035	QILYATMADFK

AT4G17830.1

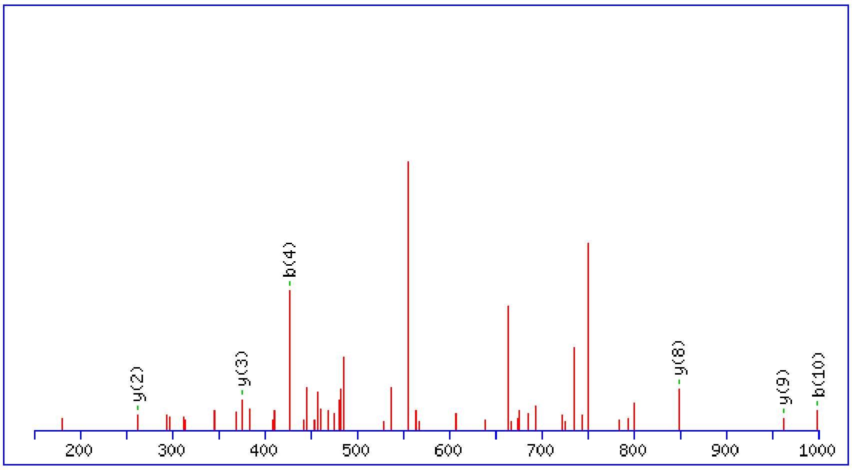
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALIESIGSLDK**
Found in **AT4G17830.1** in **TAIR_Arabidopsis**, Symbols: | peptidase M20/M25/M40 family protein | chr4:9915929-9918062 FORWARD

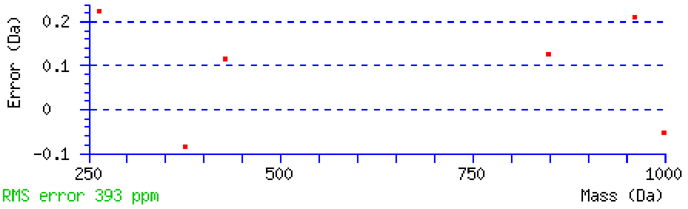
Match to Query 3314: 1144.631510 from(573.323031,2+) index(8016)
Title: Elution from: 71.945 to 71.945 scan no 10658 cid35.00 polarity:+
Data file D1d-2_3.mgf

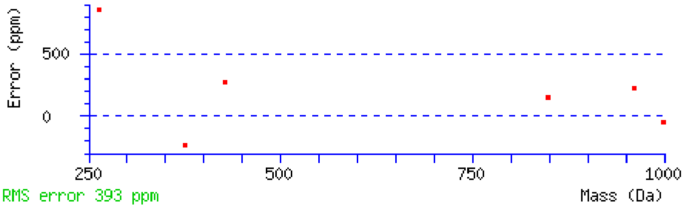
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.6339
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0022
Matches : 6/92 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			**A**							**11**
2	185.1285	93.0679			**L**	1074.6041	537.8057	1057.5776	529.2924	1056.5936	528.8004	**10**
3	298.2125	149.6099			**I**	***961.5201***	481.2637	944.4935	472.7504	943.5095	472.2584	**9**
4	***427.2551***	214.1312	409.2445	205.1259	**E**	***848.4360***	424.7216	831.4094	416.2084	830.4254	415.7163	**8**
5	514.2871	257.6472	496.2766	248.6419	**S**	719.3934	360.2003	702.3668	351.6871	701.3828	351.1951	**7**
6	627.3712	314.1892	609.3606	305.1840	**I**	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	**6**
7	684.3927	342.7000	666.3821	333.6947	**G**	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	**5**
8	771.4247	386.2160	753.4141	377.2107	**S**	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	**4**
9	884.5088	442.7580	866.4982	433.7527	**L**	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
10	***999.5357***	500.2715	981.5251	491.2662	**D**	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
11					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ALIESIGSLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G17830.1

Score	Mr(calc)	Delta	Sequence
29.6	1144.6339	-0.0024	ALIESIGSLDK
3.0	1144.6339	-0.0024	GAESTDVILLK

AT4G18100.1

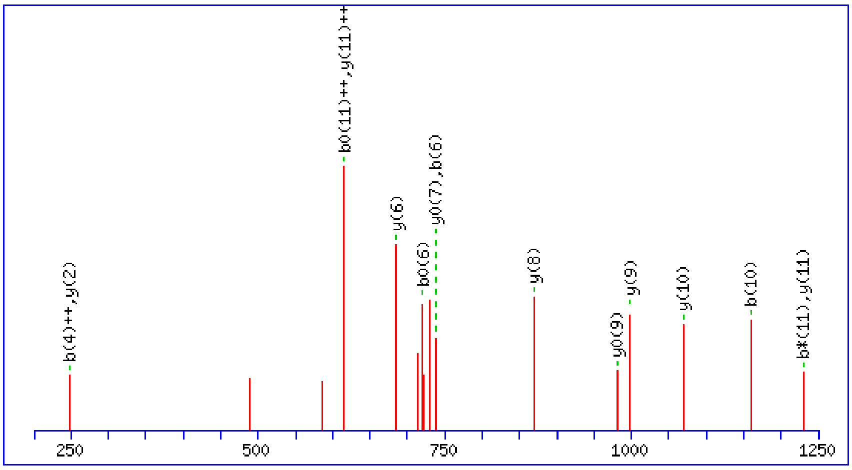
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYCAEIAHNVSTK**
Found in **AT4G18100.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L32 (RPL32A) | chr4:10035727-10036487 REVERSE

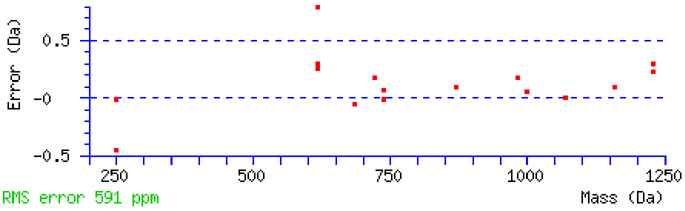
Match to Query 6173: 1492.697256 from(747.355904,2+) index(1899)
Title: Elution from: 24.840 to 24.840 scan no 2543 cid35.00 polarity:+
Data file D1d-2_1.mgf

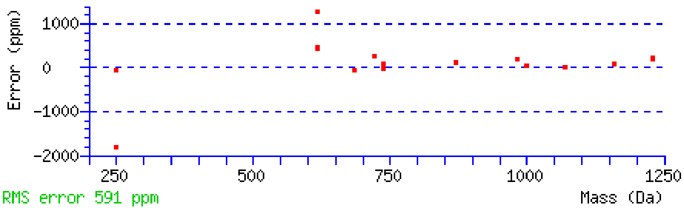
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1492.6980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 2.7e-005
Matches : 16/126 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							13
2	265.1183	133.0628			247.1077	124.0575	Y	1392.6576	696.8325	1375.6311	688.3192	1374.6471	687.8272	12
3	425.1489	213.0781			407.1384	204.0728	C	***1229.5943***	615.3008	1212.5677	606.7875	1211.5837	606.2955	11
4	496.1860	248.5967			478.1755	239.5914	A	***1069.5636***	535.2855	1052.5371	526.7722	1051.5531	526.2802	10
5	625.2286	313.1180			607.2181	304.1127	E	***998.5265***	499.7669	981.5000	491.2536	980.5160	490.7616	9
6	**738.3127**	369.6600			720.3021	360.6547	I	***869.4839***	435.2456	852.4574	426.7323	851.4734	426.2403	8
7	809.3498	405.1785			791.3393	396.1733	A	756.3999	378.7036	739.3733	370.1903	738.3893	369.6983	7
8	946.4087	473.7080			928.3982	464.7027	H	***685.3628***	343.1850	668.3362	334.6717	667.3522	334.1797	6
9	1060.4517	530.7295	1043.4251	522.2162	1042.4411	521.7242	N	548.3039	274.6556	531.2773	266.1423	530.2933	265.6503	5
10	**1159.5201**	580.2637	1142.4935	571.7504	1141.5095	571.2584	V	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
11	1246.5521	623.7797	1229.5256	615.2664	1228.5415	614.7744	S	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
12	1347.5998	674.3035	1330.5732	665.7903	1329.5892	665.2982	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TYCAEIAHNVSTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G18100.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.6	1492.6980	-0.0008	TYCAEIAHNVSTK

AT4G18300.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIMTMVFK**
Found in **AT4G18300.1** in **TAIR_Arabidopsis**, Symbols: | eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein | chr4:10118863-10120992 FORWARD

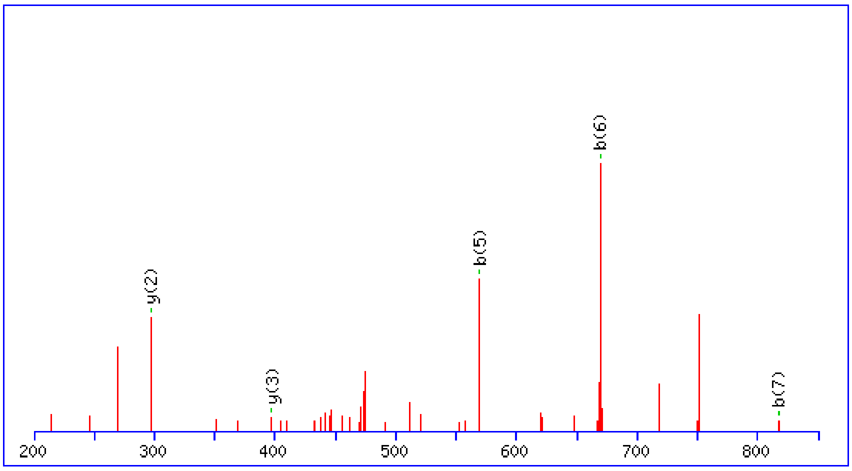
Match to Query 2145: 964.458770 from(483.236661,2+) index(5767)
Title: Elution from: 52.492 to 52.492 scan no 7325 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 850 Da Full range

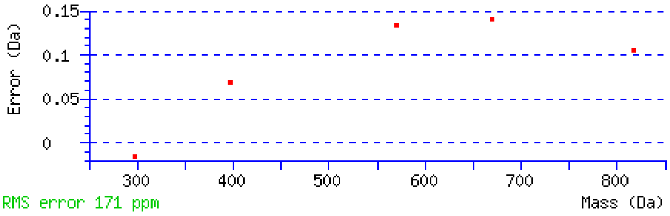
Label all possible matches ○ Label matches used for scoring ●

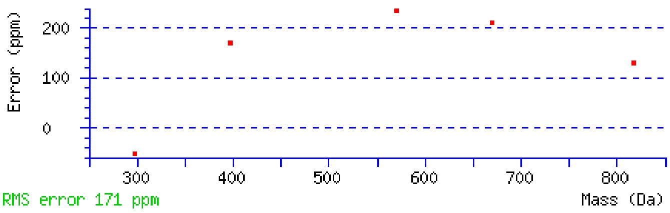
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 964.4604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.027
Matches : 5/90 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							8
2	187.1225	94.0649			I	893.4335	447.2204	875.4100	438.2086	875.4230	438.2151	7
3	319.1600	160.0837			M	779.3524	390.1799	761.3289	381.1681	761.3419	381.1746	6
4	421.2048	211.1060	403.1942	202.1007	T	647.3149	324.1611	629.2913	315.1493	629.3044	315.1558	5
5	***569.2372***	285.1222	551.2266	276.1170	M	545.2702	273.1387	527.2466	264.1269			4
6	***669.3026***	335.1550	651.2921	326.1497	V	**397.2378**	199.1225	379.2142	190.1107			3
7	***817.3681***	409.1877	799.3575	400.1824	F	**297.1723**	149.0898	279.1487	140.0780			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AIMTMVFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis

22.5	964.4604	-0.0016	AIMTMVFK	Oxidation M5 50.00%
22.5	964.4604	-0.0016	AIMTMVFK	Oxidation M3 50.00%
9.2	964.4575	0.0013	NLRQMFK	
9.2	964.4579	0.0009	MSRRQVR	
9.0	964.4575	0.0013	MIGARNFK	
9.0	964.4597	-0.0009	MWGLRFK	
6.8	964.4600	-0.0012	STSSSLSRK	
5.6	964.4597	-0.0009	FKMWGLR	
2.2	964.4575	0.0013	MGSRLNFK	

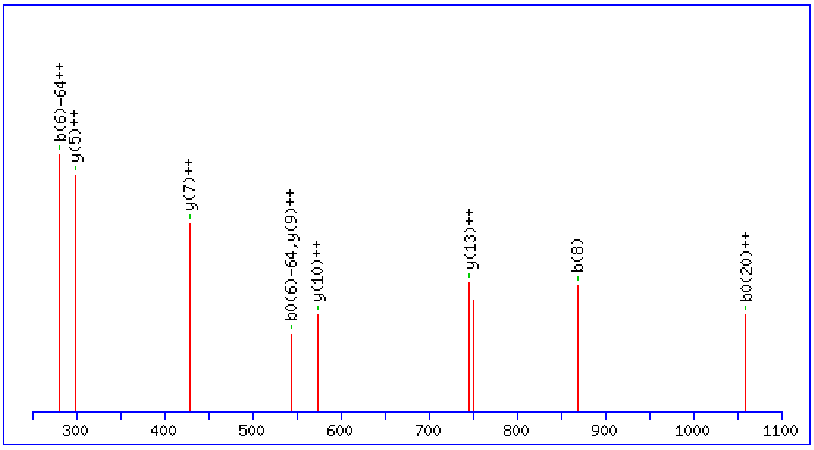
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MILASSELGCSHEIITIAAVLSVQSVWIIARGVQKEQDEAK**
Found in **AT4G18465.1** in **TAIR_Arabidopsis**, Symbols: | RNA helicase, putative | chr4:10197067-10201622 FORWARD

Match to Query 10782: 4548.175926 from(759.036597,6+) index(10285)
Title: Elution from: 98.784 to 98.784 scan no 14808 cid35.00 polarity:+
Data file D12h-1_3.mgf

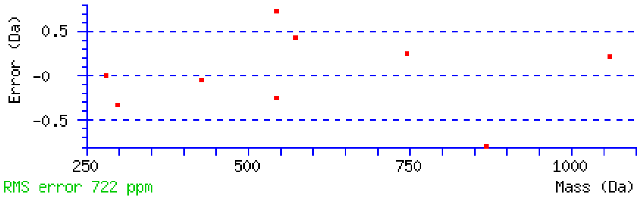
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

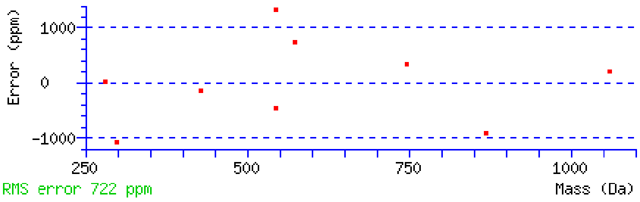


Monoisotopic mass of neutral peptide Mr(calc): 4548.1883
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.027
Matches : 9/608 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	85.0414	43.0244					M							41
2	199.1225	100.0649					I	4401.1632	2201.0852	4383.1396	2192.0734	4383.1526	2192.0799	40
3	313.2036	157.1054					L	4287.0821	2144.0447	4269.0585	2135.0329	4269.0715	2135.0394	39
4	385.2378	193.1225					A	4173.0010	2087.0041	4154.9774	2077.9923	4154.9904	2077.9988	38
5	473.2668	237.1371			455.2563	228.1318	S	4100.9668	2050.9870	4082.9432	2041.9753	4082.9563	2041.9818	37
6	561.2959	281.1516			543.2853	272.1463	S	4012.9378	2006.9725	3994.9142	1997.9607	3994.9272	1997.9672	36
7	691.3355	346.1714			673.3250	337.1661	E	3924.9087	1962.9580	3906.8851	1953.9462	3906.8981	1953.9527	35
8	805.4166	403.2120			787.4061	394.2067	L	3794.8691	1897.9382	3776.8455	1888.9264	3776.8585	1888.9329	34
9	863.4351	432.2212			845.4246	423.2159	G	3680.7880	1840.8976	3662.7644	1831.8858	3662.7774	1831.8923	33
10	1025.4598	513.2336			1007.4493	504.2283	C	3622.7695	1811.8884	3604.7459	1802.8766	3604.7589	1802.8831	32
11	1113.4889	557.2481			1095.4783	548.2428	S	3460.7447	1730.8760	3442.7212	1721.8642	3442.7342	1721.8707	31
12	1253.5389	627.2731			1235.5284	618.2678	H	3372.7157	1686.8615	3354.6921	1677.8497	3354.7051	1677.8562	30
13	1383.5786	692.2929			1365.5680	683.2876	E	3232.6657	1616.8365	3214.6421	1607.8247	3214.6551	1607.8312	29
14	1497.6597	749.3335			1479.6491	740.3282	I	3102.6260	1551.8167	3084.6025	1542.8049	3084.6155	1542.8114	28
15	1611.7407	806.3740			1593.7302	797.3687	I	2988.5449	1494.7761	2970.5214	1485.7643	2970.5344	1485.7708	27
16	1713.7855	857.3964			1695.7749	848.3911	T	2874.4638	1437.7356	2856.4403	1428.7238	2856.4533	1428.7303	26
17	1827.8666	914.4369			1809.8560	905.4316	I	2772.4191	1386.7132	2754.3955	1377.7014	2754.4086	1377.7079	25
18	1899.9007	950.4540			1881.8901	941.4487	A	2658.3380	1329.6727	2640.3144	1320.6609	2640.3275	1320.6674	24
19	1971.9349	986.4711			1953.9243	977.4658	A	2586.3039	1293.6556	2568.2803	1284.6438	2568.2933	1284.6503	23
20	2072.0003	1036.5038			2053.9897	1027.4985	V	2514.2697	1257.6385	2496.2461	1248.6267	2496.2592	1248.6332	22
21	2186.0814	1093.5443			2168.0708	1084.5391	L	2414.2043	1207.6058	2396.1807	1198.5940	2396.1937	1198.6005	21
22	2274.1105	1137.5589			2256.0999	1128.5536	S	2300.1232	1150.5652	2282.0996	1141.5534	2282.1126	1141.5599	20
23	2374.1759	1187.5916			2356.1654	1178.5863	V	2212.0941	1106.5507	2194.0705	1097.5389	2194.0836	1097.5454	19
24	2504.2286	1252.6179	2486.2050	1243.6061	2486.2180	1243.6126	Q	2112.0287	1056.5180	2094.0051	1047.5062	2094.0181	1047.5127	18

25	2592.2576	1296.6325	2574.2340	1287.6207	2574.2471	1287.6272	**S**	1981.9760	991.4917	1963.9524	982.4799	1963.9655	982.4864	**17**
26	2692.3231	1346.6652	2674.2995	1337.6534	2674.3125	1337.6599	**V**	1893.9470	947.4771	1875.9234	938.4653	1875.9364	938.4718	**16**
27	2880.3965	1440.7019	2862.3729	1431.6901	2862.3859	1431.6966	**W**	1793.8815	897.4444	1775.8579	888.4326	1775.8709	888.4391	**15**
28	2994.4776	1497.7424	2976.4540	1488.7306	2976.4670	1488.7371	**I**	1605.8081	803.4077	1587.7845	794.3959	1587.7976	794.4024	**14**
29	3108.5587	1554.7830	3090.5351	1545.7712	3090.5481	1545.7777	**I**	1491.7270	746.3672	1473.7034	737.3554	1473.7165	737.3619	**13**
30	3180.5928	1590.8000	3162.5692	1581.7882	3162.5822	1581.7948	**A**	1377.6459	689.3266	1359.6223	680.3148	1359.6354	680.3213	**12**
31	3340.6821	1670.8447	3322.6585	1661.8329	3322.6715	1661.8394	**R**	1305.6118	653.3095	1287.5882	644.2977	1287.6012	644.3042	**11**
32	3398.7006	1699.8539	3380.6770	1690.8421	3380.6900	1690.8486	**G**	1145.5225	573.2649	1127.4989	564.2531	1127.5120	564.2596	**10**
33	3498.7660	1749.8866	3480.7424	1740.8748	3480.7554	1740.8814	**V**	1087.5040	544.2557	1069.4804	535.2439	1069.4935	535.2504	**9**
34	3628.8187	1814.9130	3610.7951	1805.9012	3610.8081	1805.9077	**Q**	987.4386	494.2229	969.4150	485.2111	969.4280	485.2176	**8**
35	3758.9077	1879.9575	3740.8841	1870.9457	3740.8971	1870.9522	**K**	857.3859	429.1966	839.3624	420.1848	839.3754	420.1913	**7**
36	3888.9473	1944.9773	3870.9237	1935.9655	3870.9367	1935.9720	**E**	727.2969	364.1521	709.2733	355.1403	709.2863	355.1468	**6**
37	4019.0000	2010.0036	4000.9764	2000.9918	4000.9894	2000.9983	**Q**	597.2573	299.1323	579.2337	290.1205	579.2467	290.1270	**5**
38	4135.0239	2068.0156	4117.0004	2059.0038	4117.0134	2059.0103	**D**	467.2046	234.1060	449.1810	225.0942	449.1941	225.1007	**4**
39	4265.0636	2133.0354	4247.0400	2124.0236	4247.0530	2124.0301	**E**	351.1807	176.0940	333.1571	167.0822	333.1701	167.0887	**3**
40	4337.0977	2169.0525	4319.0741	2160.0407	4319.0872	2160.0472	**A**	221.1410	111.0741	203.1174	102.0624			**2**
41							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MILASSELGCSHEIITIAAVLSVQSVWIIARGVQKEQDEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.1	4548.1883	-0.0124	MILASSELGCSHEIITIAAVLSVQSVWIIARGVQKEQDEAK

Mascot: http://www.matrixscience.com/

AT4G18480.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQVPVIATK**
Found in **AT4G18480.1** in **TAIR_Arabidopsis**, Symbols: CH42, CH-42, CHL11, CHLI-1, CHLI1 | CHLI1 (CHLORINA 42); magnesium chelatase | chr4:10201908-10203372 REVERSE

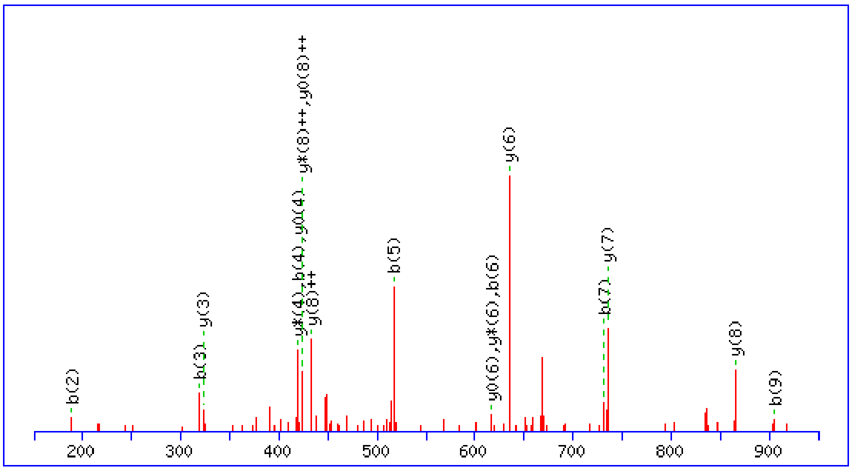
Match to Query 2736: 1052.550066 from(527.282309,2+) index(2324)
Title: Elution from: 24.445 to 24.445 scan no 2893 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

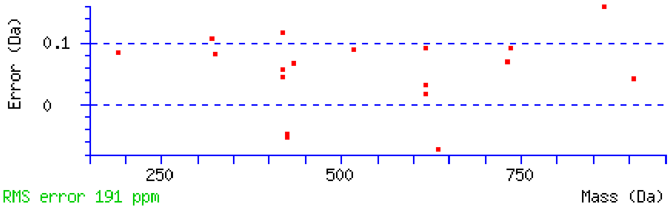
Label all possible matches ○ Label matches used for scoring ●

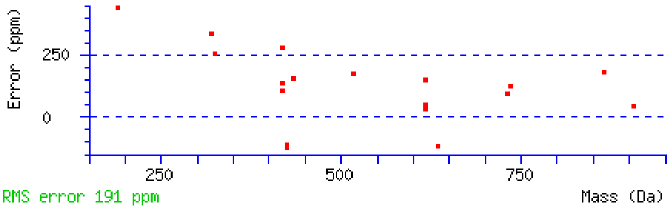
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1052.5510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 2.1e-005
Matches : 18/100 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							10
2	***189.0654***	95.0363			171.0548	86.0311	E	995.5398	498.2735	977.5162	489.2617	977.5292	489.2683	9
3	***319.1180***	160.0627	301.0945	151.0509	301.1075	151.0574	Q	**865.5002**	433.2537	847.4766	424.2419	847.4896	424.2484	8
4	***419.1835***	210.0954	401.1599	201.0836	401.1729	201.0901	V	**735.4475**	368.2274	717.4239	359.2156	717.4370	359.2221	7
5	***517.2333***	259.1203	499.2097	250.1085	499.2227	250.1150	P	**635.3821**	318.1947	617.3585	309.1829	617.3715	309.1894	6
6	***617.2987***	309.1530	599.2752	300.1412	599.2882	300.1477	V	537.3323	269.1698	519.3087	260.1580	519.3217	260.1645	5
7	***731.3798***	366.1936	713.3563	357.1818	713.3693	357.1883	I	437.2668	219.1371	419.2433	210.1253	419.2563	210.1318	4
8	803.4140	402.2106	785.3904	393.1988	785.4034	393.2054	A	**323.1857**	162.0965	305.1622	153.0847	305.1752	153.0912	3
9	***905.4587***	453.2330	887.4351	444.2212	887.4481	444.2277	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GEQVPVIATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G18480.1

Score	Mr(calc)	Delta	Sequence
47.3	1052.5510	-0.0009	GEQVPVIATK
4.7	1052.5510	-0.0010	SPLVNVLDGK
1.1	1052.5510	-0.0010	IGEKLPAADK

AT4G18670.1

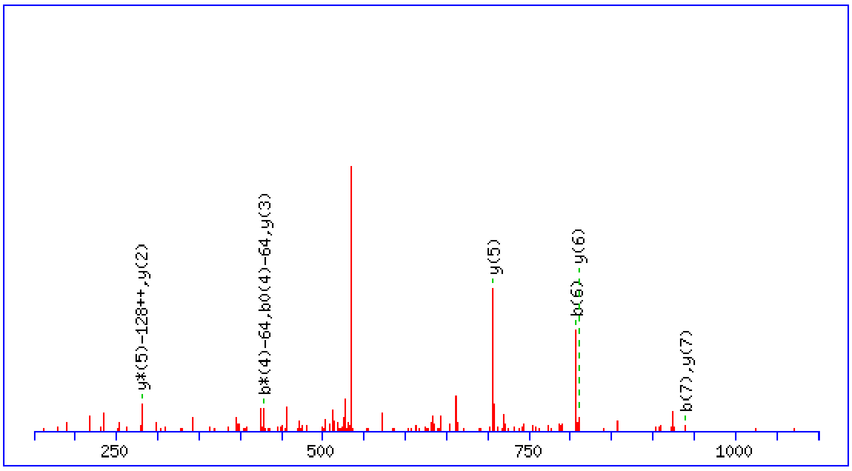
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKTKMMMK**
Found in **AT4G18670.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat family protein / extensin family protein | chr4:10275928-10278502 REVERSE

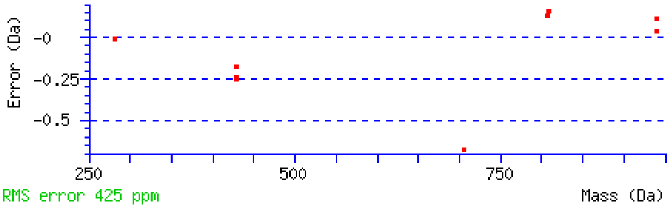
Match to Query 3187: 1086.458906 from(544.236729,2+) index(2989)
Title: Elution from: 29.284 to 29.284 scan no 3723 cid35.00 polarity:+
Data file D12h-3_3.mgf

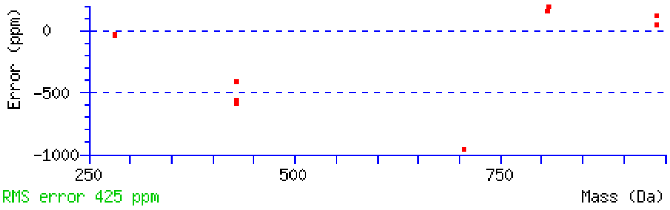
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1086.4572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.02
Matches : 10/128 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							8
2	279.1287	140.0680	261.1052	131.0562			K	*939.4320*	470.2197	921.4085	461.2079	921.4215	461.2144	7
3	381.1735	191.0904	363.1499	182.0786	363.1629	182.0851	T	*809.3430*	405.1751	791.3194	396.1634	791.3324	396.1699	6
4	511.2625	256.1349	493.2389	247.1231	493.2519	247.1296	K	*707.2983*	354.1528	689.2747	345.1410			5
5	659.2949	330.1511	641.2713	321.1393	641.2844	321.1458	M	577.2093	289.1083	559.1857	280.0965			4
6	**807.3274**	404.1673	789.3038	395.1555	789.3168	395.1620	M	*429.1768*	215.0921	411.1532	206.0803			3
7	**939.3649**	470.1861	921.3413	461.1743	921.3543	461.1808	M	*281.1444*	141.0758	263.1208	132.0640			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MKTKMMMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G18670.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
22.7	1086.4572	0.0017	MKTKMMMK	Oxidation M1, M5, M6 72.00%
17.3	1086.4572	0.0017	MKTKMMMK	Oxidation M1, M5, M7 20.96%
12.4	1086.4572	0.0017	MKTKMMMK	Oxidation M1, M6, M7 6.72%
6.0	1086.4574	0.0015	FVFEDYMK	
1.6	1086.4579	0.0010	FYNAKSCGK	
0.4	1086.4579	0.0011	FFRDQMSK	
0.1	1086.4612	-0.0023	MLHEEMIR	

AT4G18800.1

Mascot Search Results

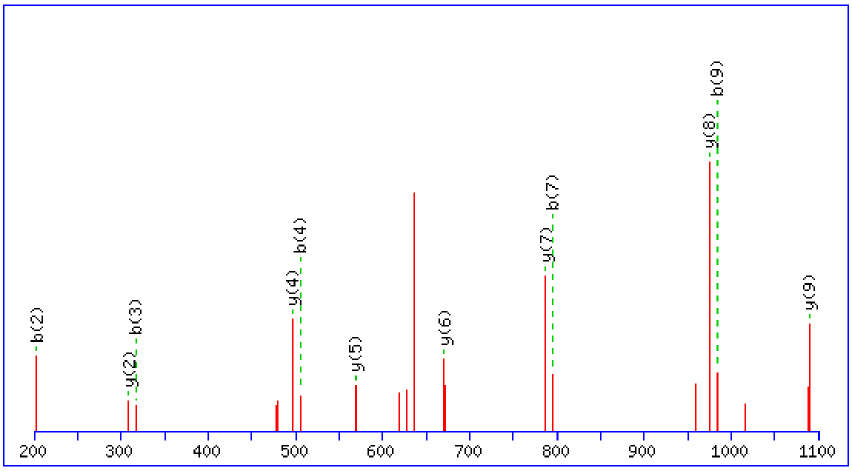
Peptide View

MS/MS Fragmentation of **AQIWDTAGQER**
Found in **AT4G18800.1** in **TAIR_Arabidopsis**, Symbols: AthSGBP, AtRab11B, AtRABA1d | AtRABA1d/AtRab11B/AthSGBP (Arabidopsis Rab GTPase homolog A1d); GTP binding | chr4:10320167-10321350 REVERSE

Match to Query 4799: 1290.552696 from(646.283624,2+) index(3376)
Title: Elution from: 32.491 to 32.491 scan no 4164 cid35.00 polarity:+
Data file C7-2_2.mgf

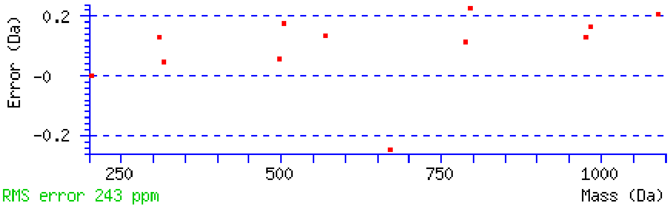
Click mouse within plot area to zoom in by factor of two about that point

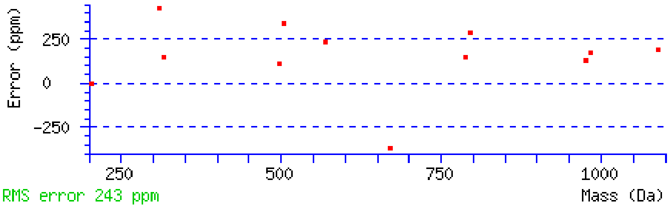
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1290.5547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 5.7e-007
Matches : 12/108 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							11
2	**203.0941**	102.0507	185.0705	93.0389			Q	1219.5278	610.2676	1201.5043	601.2558	1201.5173	601.2623	10
3	**317.1752**	159.0912	299.1516	150.0794			I	***1089.4752***	545.2412	1071.4516	536.2294	1071.4646	536.2359	9
4	**505.2486**	253.1279	487.2250	244.1161			W	***975.3941***	488.2007	957.3705	479.1889	957.3835	479.1954	8
5	621.2725	311.1399	603.2489	302.1281	603.2620	302.1346	D	***787.3207***	394.1640	769.2971	385.1522	769.3101	385.1587	7
6	723.3172	362.1623	705.2937	353.1505	705.3067	353.1570	T	***671.2967***	336.1520	653.2731	327.1402	653.2862	327.1467	6
7	**795.3514**	398.1793	777.3278	389.1675	777.3408	389.1741	A	***569.2520***	285.1296	551.2284	276.1179	551.2414	276.1244	5
8	853.3699	427.1886	835.3463	418.1768	835.3593	418.1833	G	***497.2179***	249.1126	479.1943	240.1008	479.2073	240.1073	4
9	**983.4225**	492.2149	965.3990	483.2031	965.4120	483.2096	Q	439.1994	220.1033	421.1758	211.0915	421.1888	211.0980	3
10	1113.4622	557.2347	1095.4386	548.2229	1095.4516	548.2294	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AQIWDTAGQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G18800.1

Score	Mr(calc)	Delta	Sequence
69.8	1290.5547	-0.0020	AQIWDTAGQER
69.8	1290.5547	-0.0020	AQLWDTAGQER
3.1	1290.5554	-0.0027	LDADGMAEGLASK
2.5	1290.5524	0.0003	LVTDENGQNQR
1.5	1290.5500	0.0027	TEMSAHQWRK

Mascot: http://www.matrixscience.com/

AT4G18830.1

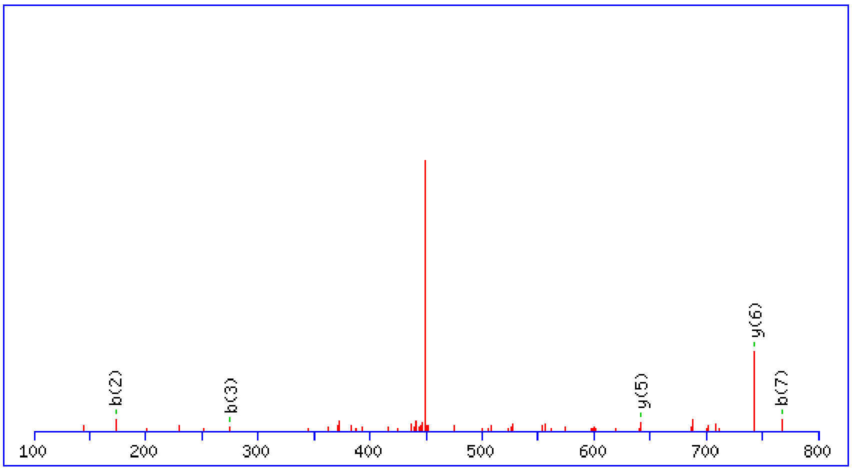
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGTKENNK**
Found in **AT4G18830.1** in **TAIR_Arabidopsis**, Symbols: ATOFP5, OFP5 | ATOFP5/OFP5 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 5) | chr4:10337460-10338509 FORWARD

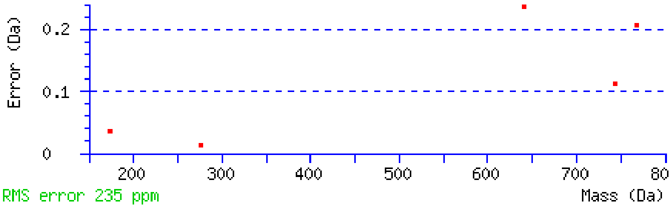
Match to Query 1782: 914.444512 from(458.229532,2+) index(2481)
Title: Elution from: 26.340 to 26.340 scan no 3111 cid35.00 polarity:+
Data file C7-2_2.mgf

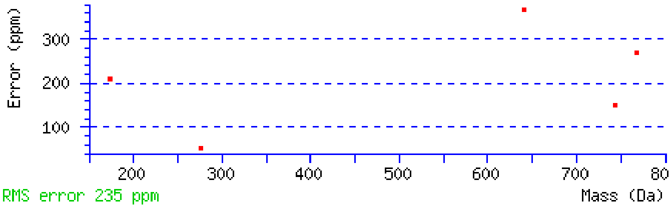
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 914.4466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.018
Matches : 5/68 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							8
2	*173.1069*	87.0571					G	801.3727	401.1900	783.3492	392.1782	783.3622	392.1847	7
3	*275.1516*	138.0794			257.1410	129.0741	T	**743.3542**	372.1808	725.3307	363.1690	725.3437	363.1755	6
4	405.2406	203.1239	387.2170	194.1122	387.2301	194.1187	K	**641.3095**	321.1584	623.2859	312.1466	623.2990	312.1531	5
5	535.2802	268.1438	517.2567	259.1320	517.2697	259.1385	E	511.2205	256.1139	493.1969	247.1021	493.2099	247.1086	4
6	651.3172	326.1623	633.2937	317.1505	633.3067	317.1570	N	381.1809	191.0941	363.1573	182.0823			3
7	*767.3542*	384.1808	749.3307	375.1690	749.3437	375.1755	N	265.1439	133.0756	247.1203	124.0638			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IGTKENNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.8	914.4466	-0.0021	IGTKENNK

AT4G18830.1

10.7	914.4439	0.0006	LLSESETK
6.0	914.4461	-0.0016	LLEEFEK
5.5	914.4465	-0.0020	AVAKQDGSK
4.5	914.4465	-0.0020	RLDDGSLK
4.5	914.4465	-0.0020	RLDKEDK
4.4	914.4465	-0.0020	TIDDVGRK
4.4	914.4466	-0.0021	TLNNVSAGK
4.3	914.4466	-0.0021	EISNGKAGK
4.3	914.4465	-0.0020	LDGREVSK

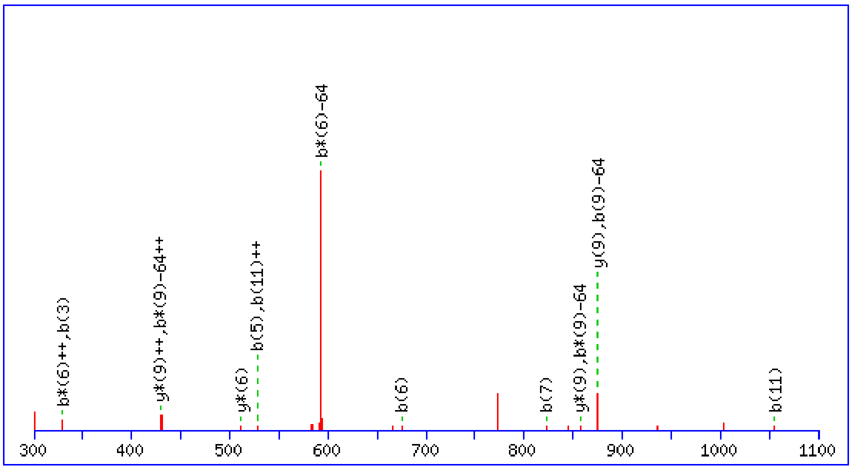
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGKHGMFGGGGK**
Found in **AT4G19200.1** in **TAIR_Arabidopsis**, Symbols: | proline-rich family protein | chr4:10499288-10500401 FORWARD

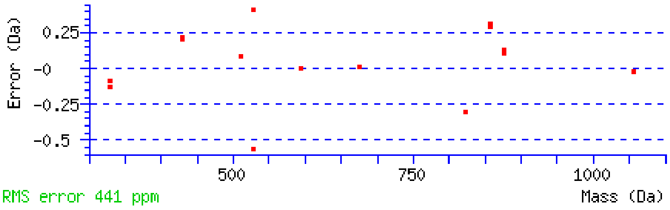
Match to Query 4217: 1202.500824 from(602.257688,2+) index(2295)
Title: Elution from: 25.127 to 25.127 scan no 2900 cid35.00 polarity:+
Data file C7-2_2.mgf

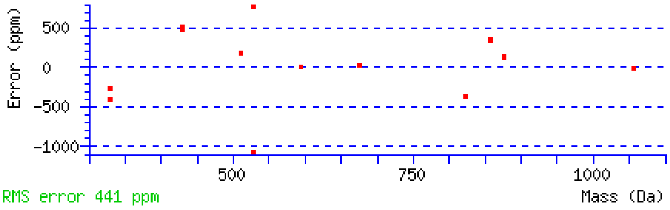
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1202.4975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.029
Matches : 15/128 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	141.0573	71.0323			H					12
2	199.0758	100.0415			G	1063.4548	532.2310	1045.4312	523.2192	11
3	***329.1648***	165.0861	311.1412	156.0743	K	1005.4363	503.2218	987.4127	494.2100	10
4	469.2148	235.1111	451.1913	226.0993	H	875.3473	438.1773	857.3237	429.1655	9
5	***527.2333***	264.1203	509.2098	255.1085	G	735.2973	368.1523	717.2737	359.1405	8
6	***675.2658***	338.1365	657.2422	329.1247	M	677.2788	339.1430	659.2552	330.1312	7
7	***823.3312***	412.1693	805.3076	403.1575	F	529.2463	265.1268	511.2227	256.1150	6
8	881.3497	441.1785	863.3261	432.1667	G	381.1809	191.0941	363.1573	182.0823	5
9	939.3682	470.1877	921.3446	461.1760	G	323.1624	162.0848	305.1388	153.0730	4
10	997.3867	499.1970	979.3631	490.1852	G	265.1439	133.0756	247.1203	124.0638	3
11	***1055.4052***	528.2062	1037.3816	519.1945	G	207.1254	104.0663	189.1018	95.0545	2
12					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of HGKHGMFGGGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G19200.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	1202.4975	0.0033	HGKHGMFGGGGK
5.1	1202.5001	0.0008	AEEPRNNNNK
4.2	1202.5038	-0.0030	MMVLYCGRK
3.2	1202.5030	-0.0021	GQMGLPGGEAEK
2.7	1202.5003	0.0005	MEEEDSVIPK
2.4	1202.5029	-0.0021	MGDIDGVVDPR
2.4	1202.5018	-0.0010	VYYANFNDGK
1.5	1202.4978	0.0030	FMITYVDCK

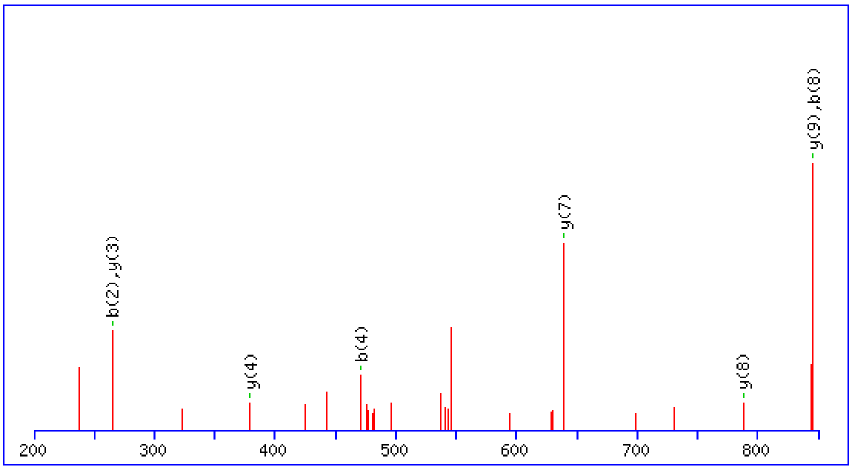
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFGFSGILGGK**
Found in **AT4G19410.1** in **TAIR_Arabidopsis**, Symbols: | pectinacetylesterase, putative | chr4:10582199-10584777 REVERSE

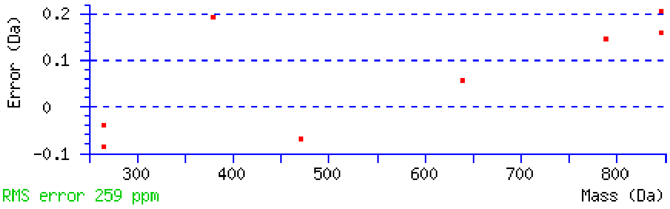
Match to Query 3611: 1108.518146 from(555.266349,2+) index(9008)
Title: Elution from: 80.108 to 80.108 scan no 11977 cid35.00 polarity:+
Data file C7-3_1.mgf

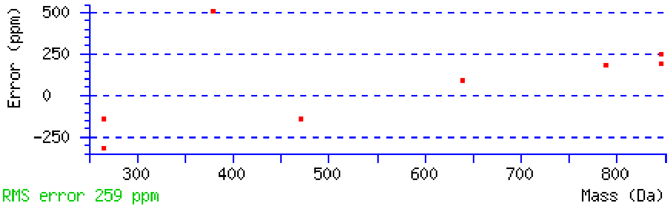
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1108.5197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 9.8e-005
Matches : 8/88 fragment ions using 7 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0313	59.0193	99.0207	50.0140	D							11
2	**265.0967**	133.0520	247.0861	124.0467	F	993.5030	497.2552	975.4794	488.2434	975.4925	488.2499	10
3	323.1152	162.0612	305.1046	153.0560	G	***845.4376***	423.2224	827.4140	414.2106	827.4270	414.2171	9
4	**471.1807**	236.0940	453.1701	227.0887	F	***787.4191***	394.2132	769.3955	385.2014	769.4085	385.2079	8
5	559.2097	280.1085	541.1991	271.1032	S	***639.3536***	320.1805	621.3300	311.1687	621.3431	311.1752	7
6	617.2282	309.1177	599.2176	300.1125	G	551.3246	276.1659	533.3010	267.1541			6
7	731.3093	366.1583	713.2987	357.1530	I	493.3061	247.1567	475.2825	238.1449			5
8	**845.3904**	423.1988	827.3798	414.1936	L	***379.2250***	190.1161	361.2014	181.1043			4
9	903.4089	452.2081	885.3983	443.2028	G	***265.1439***	133.0756	247.1203	124.0638			3
10	961.4274	481.2173	943.4168	472.2121	G	207.1254	104.0663	189.1018	95.0545			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DFGFSGILGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G19410.1

Score	Mr(calc)	Delta	Sequence
49.3	1108.5197	-0.0016	DFGFSGILGGK
10.0	1108.5197	-0.0016	NFDAILYNK
8.3	1108.5150	0.0032	WMTLFRDK
3.1	1108.5175	0.0007	KYSSQEQVK
0.4	1108.5197	-0.0016	FNFEVVSQK

AT4G19610.1

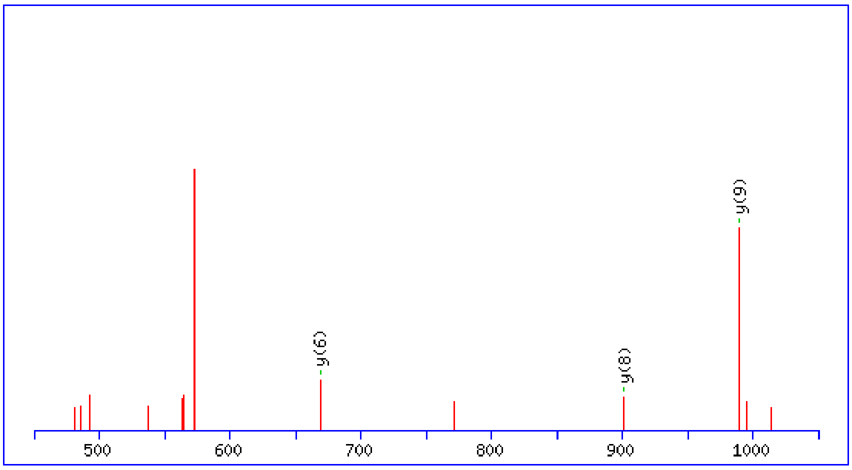
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVSDDVLDTGR**
Found in **AT4G19610.1** in **TAIR_Arabidopsis**, Symbols: | RNA binding | chr4:10677492-10681633 FORWARD

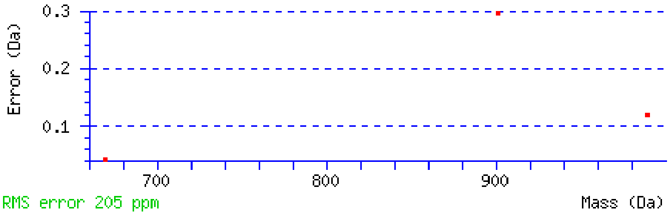
Match to Query 3355: 1160.509946 from(581.262249,2+) index(456)
Title: Elution from: 11.952 to 11.952 scan no 781 cid35.00 polarity:+
Data file D1d-1-2.mgf

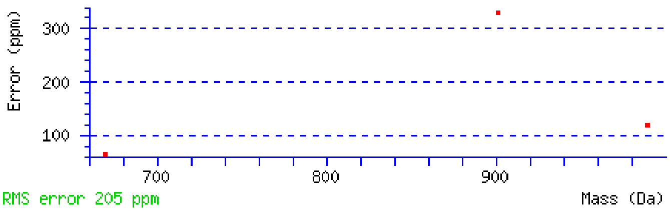
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [450] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1160.5101
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.034
Matches : 3/92 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244			A							11
2	173.1069	87.0571			V	1089.4833	545.2453	1071.4597	536.2335	1071.4727	536.2400	10
3	261.1359	131.0716	243.1254	122.0663	S	***989.4178***	495.2126	971.3943	486.2008	971.4073	486.2073	9
4	377.1599	189.0836	359.1494	180.0783	D	***901.3888***	451.1980	883.3652	442.1862	883.3782	442.1927	8
5	493.1839	247.0956	475.1733	238.0903	D	785.3648	393.1860	767.3412	384.1742	767.3542	384.1808	7
6	593.2493	297.1283	575.2388	288.1230	V	***669.3408***	335.1741	651.3172	326.1623	651.3303	326.1688	6
7	707.3304	354.1689	689.3199	345.1636	L	569.2754	285.1413	551.2518	276.1295	551.2648	276.1360	5
8	823.3544	412.1808	805.3439	403.1756	D	455.1943	228.1008	437.1707	219.0890	437.1837	219.0955	4
9	925.3991	463.2032	907.3886	454.1979	T	339.1703	170.0888	321.1467	161.0770	321.1597	161.0835	3
10	983.4176	492.2125	965.4071	483.2072	G	237.1256	119.0664	219.1020	110.0546			2
11					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AVSDDVLDTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G19610.1

Score	**Mr(calc)**	**Delta**	**Sequence**
22.6	1160.5101	-0.0002	AVSDDVLDTGR
17.9	1160.5077	0.0023	MNPEKFTHK
8.9	1160.5102	-0.0002	EEEKNGSLNK
8.9	1160.5102	-0.0002	EEENISGNKK
8.9	1160.5102	-0.0002	EKEAEEERK
8.9	1160.5102	-0.0002	KEEEEEAKR
3.6	1160.5102	-0.0002	NNEKEKEEK
3.1	1160.5110	-0.0011	EPAMMIGDRK
3.1	1160.5084	0.0016	ISEMVDPTMK
3.1	1160.5124	-0.0024	KDLSDWQEK

AT4G19650.1

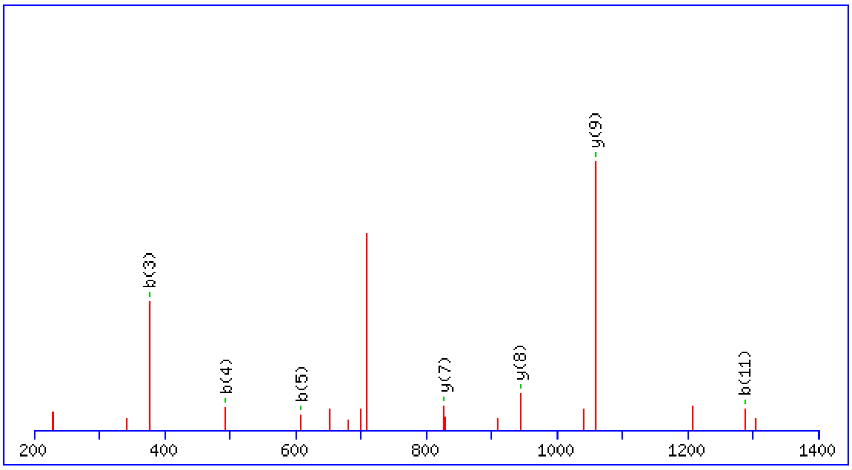
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFIDNPEMLSDK**
Found in **AT4G19650.1** in **TAIR_Arabidopsis**, Symbols: | similar to mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana] (TAIR:AT5G45113.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO44451.1); contains InterPro domain Mitochondrial tran

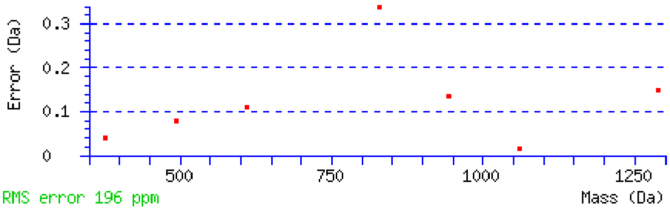
Match to Query 5601: 1434.647044 from(718.330798,2+) index(5644)
Title: Elution from: 50.686 to 50.686 scan no 7194 cid35.00 polarity:+
Data file D6h-1_3.mgf

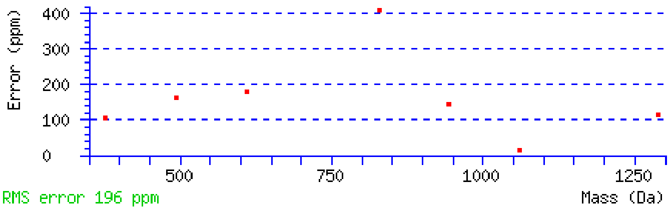
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1434.6493
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.013
Matches : 7/116 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**12**
2	263.1538	132.0805					**F**	1321.5755	661.2914	1303.5519	652.2796	1303.5649	652.2861	**11**
3	***377.2349***	189.1211					**I**	1173.5100	587.2587	1155.4865	578.2469	1155.4995	578.2534	**10**
4	***493.2589***	247.1331			475.2483	238.1278	**D**	**1059.4289**	530.2181	1041.4054	521.2063	1041.4184	521.2128	**9**
5	***609.2959***	305.1516	591.2723	296.1398	591.2853	296.1463	**N**	**943.4050**	472.2061	925.3814	463.1943	925.3944	463.2008	**8**
6	707.3457	354.1765	689.3221	345.1647	689.3351	345.1712	**P**	**827.3680**	414.1876	809.3444	405.1758	809.3574	405.1823	**7**
7	837.3853	419.1963	819.3617	410.1845	819.3748	410.1910	**E**	729.3182	365.1627	711.2946	356.1509	711.3076	356.1574	**6**
8	969.4228	485.2151	951.3993	476.2033	951.4123	476.2098	**M**	599.2785	300.1429	581.2549	291.1311	581.2680	291.1376	**5**
9	1083.5039	542.2556	1065.4804	533.2438	1065.4934	533.2503	**L**	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	**4**
10	1171.5330	586.2701	1153.5094	577.2583	1153.5224	577.2649	**S**	353.1599	177.0836	335.1363	168.0718	335.1493	168.0783	**3**
11	***1287.5570***	644.2821	1269.5334	635.2703	1269.5464	635.2768	**D**	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	**2**
12							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of LFIDNPEMLSDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G19650.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.3	1434.6493	-0.0023	LFIDNPEMLSDK
14.8	1434.6471	-0.0000	LECSEAQETLLK
14.8	1434.6498	-0.0027	VRNETSNPLEMK
14.7	1434.6497	-0.0027	RDLTNCALEPTK
12.8	1434.6470	-0.0000	KDKEEDMVGIEK
12.6	1434.6497	-0.0027	EMISQGRVEPQK
6.5	1434.6464	0.0007	QQQYAAENPLQK
6.0	1434.6471	-0.0000	MAPGTLTELAGESK
2.5	1434.6486	-0.0016	FKDLNPQWNEK
2.0	1434.6490	-0.0020	GISDRNSPLWNR

AT4G19660.1

Mascot Search Results

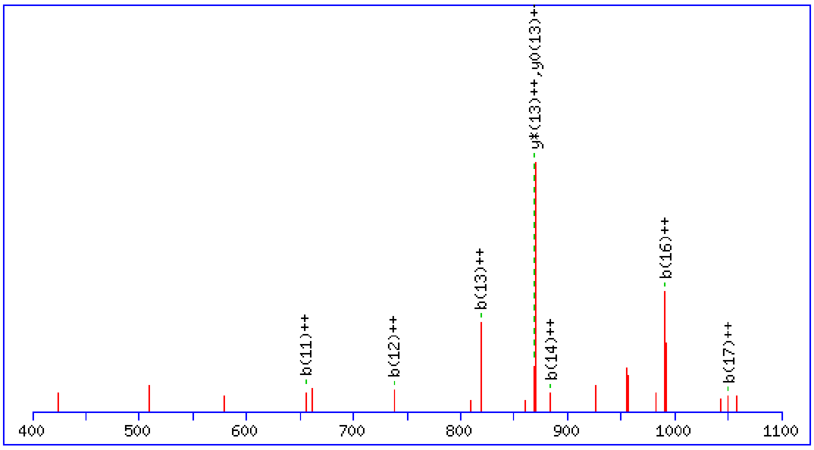
Peptide View

MS/MS Fragmentation of **TVETGRRYFPSCYEVLDK**
Found in **AT4G19660.1** in **TAIR_Arabidopsis**, Symbols: NPR4 | NPR4 (NPR1-LIKE PROTEIN 4); protein binding | chr4:10696276-10698253 REVERSE

Match to Query 10121: 2244.997140 from(749.339656,3+) index(10534)
Title: Elution from: 99.510 to 99.510 scan no 14845 cid35.00 polarity:+
Data file D12h-3_1.mgf

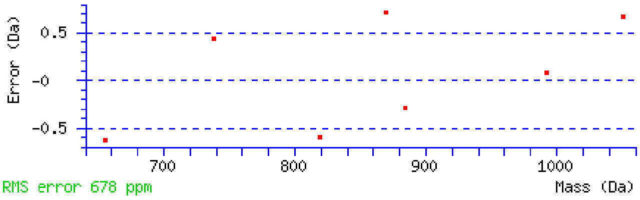
Click mouse within plot area to zoom in by factor of two about that point

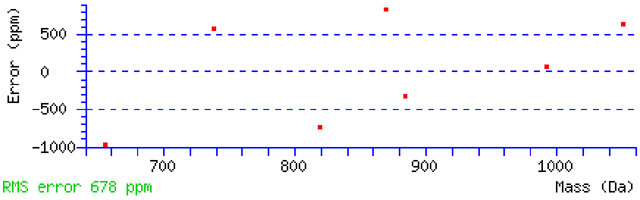
Or, Plot from 400 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



`Monoisotopic mass of neutral peptide Mr(calc): 2244.9910`
`Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)`
`Ions Score: 24  Expect: 0.031`
`Matches : 8/192 fragment ions using 17 most intense peaks   (help)`

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							18
2	203.1174	102.0624			185.1069	93.0571	V	2143.9536	1072.4804	2125.9300	1063.4686	2125.9430	1063.4751	17
3	333.1571	167.0822			315.1465	158.0769	E	2043.8881	1022.4477	2025.8645	1013.4359	2025.8776	1013.4424	16
4	435.2018	218.1045			417.1912	209.0992	T	1913.8485	957.4279	1895.8249	948.4161	1895.8379	948.4226	15
5	493.2203	247.1138			475.2097	238.1085	G	1811.8038	906.4055	1793.7802	897.3937	1793.7932	897.4002	14
6	653.3095	327.1584	635.2859	318.1466	635.2990	318.1531	R	1753.7853	877.3963	1735.7617	868.3845	1735.7747	868.3910	13
7	813.3988	407.2030	795.3752	398.1912	795.3882	398.1977	R	1593.6960	797.3517	1575.6725	788.3399	1575.6855	788.3464	12
8	977.4591	489.2332	959.4356	480.2214	959.4486	480.2279	Y	1433.6068	717.3070	1415.5832	708.2952	1415.5962	708.3017	11
9	1125.5246	563.2659	1107.5010	554.2541	1107.5140	554.2607	F	1269.5464	635.2768	1251.5228	626.2651	1251.5359	626.2716	10
10	1223.5744	612.2908	1205.5508	603.2790	1205.5638	603.2856	P	1121.4810	561.2441	1103.4574	552.2323	1103.4704	552.2388	9
11	1311.6035	***656.3054***	1293.5799	647.2936	1293.5929	647.3001	S	1023.4312	512.2192	1005.4076	503.2074	1005.4206	503.2139	8
12	1473.6282	***737.3177***	1455.6046	728.3059	1455.6176	728.3124	C	935.4021	468.2047	917.3785	459.1929	917.3915	459.1994	7
13	1637.6885	***819.3479***	1619.6650	810.3361	1619.6780	810.3426	Y	773.3774	387.1923	755.3538	378.1805	755.3668	378.1871	6
14	1767.7282	***884.3677***	1749.7046	875.3559	1749.7176	875.3624	E	609.3170	305.1622	591.2934	296.1504	591.3065	296.1569	5
15	1867.7936	934.4004	1849.7700	925.3887	1849.7830	925.3952	V	479.2774	240.1423	461.2538	231.1305	461.2668	231.1371	4
16	1981.8747	***991.4410***	1963.8511	982.4292	1963.8641	982.4357	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
17	2097.8987	***1049.4530***	2079.8751	1040.4412	2079.8881	1040.4477	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
18							K	149.1069	75.0571	131.0833	66.0453			1





AT4G19660.1

NCBI **BLAST** search of TVETGRRYFPSCYEVLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.7	2244.9910	0.0062	TVETGRRYFPSCYEVLDK
8.5	2244.9940	0.0032	NLASTSSSKLGNESSHGGQINK
7.9	2244.9971	0.0001	VEPDVSLYNAAIHGMCLRR
7.3	2245.0036	-0.0065	VFAPMENEINSPVSGFYPPK
7.2	2244.9906	0.0066	GMGEDNFPDLVPWLFETLK
6.3	2244.9944	0.0028	MAAGGFLTRAFDTMLKESGGK
4.9	2244.9971	0.0001	HMRANGVSKEVGCSWIELK
4.8	2244.9942	0.0029	MEILESKSDPSVDNLSSEVK
4.8	2245.0018	-0.0046	EARRVEDEVIVQMGSWADK
4.2	2244.9995	-0.0024	SSSTASSLTVRTVRYGECQK

AT4G19710.1

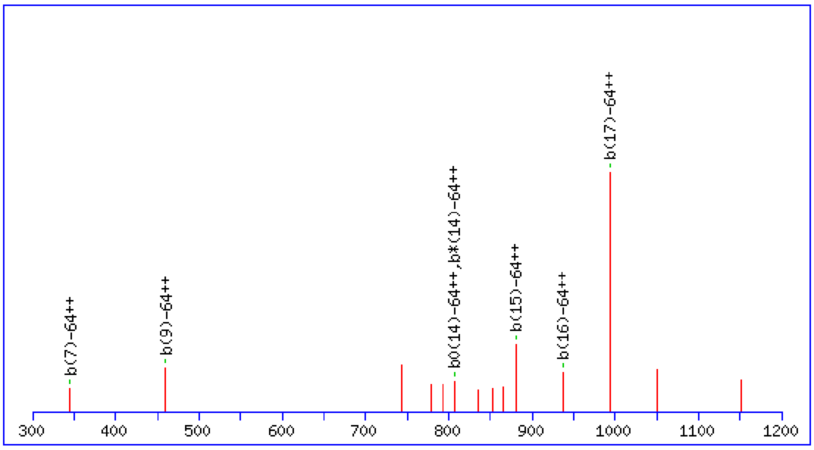
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLLSDIGIDLSRWRELLNEK**
Found in **AT4G19710.1** in **TAIR_Arabidopsis**, Symbols: AK-HSDH II, AK-HSDH | AK-HSDH/AK-HSDH II; aspartate kinase/ homoserine dehydrogenase | chr4:10725239-10729288 FORWARD

Match to Query 10508: 2445.198702 from(816.073510,3+) index(8784)
Title: Elution from: 77.846 to 77.846 scan no 11614 cid35.00 polarity:+
Data file C7-3_1.mgf

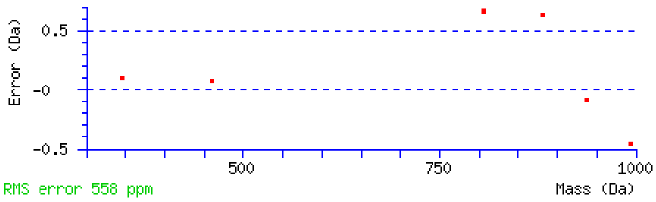
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

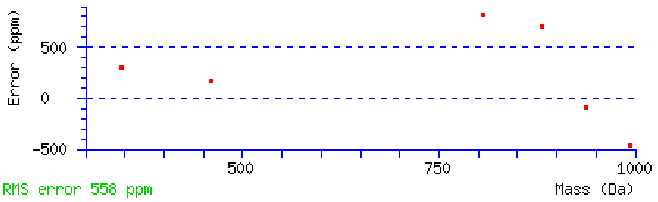


Monoisotopic mass of neutral peptide Mr(calc): 2445.1924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.014
Matches : 7/284 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	85.0414	43.0244					M							20
2	199.1225	100.0649					L	2298.1673	1149.5873	2280.1437	1140.5755	2280.1567	1140.5820	19
3	313.2036	157.1054					L	2184.0862	1092.5467	2166.0626	1083.5349	2166.0756	1083.5414	18
4	401.2327	201.1200			383.2221	192.1147	S	2070.0051	1035.5062	2051.9815	1026.4944	2051.9945	1026.5009	17
5	517.2567	259.1320			499.2461	250.1267	D	1981.9760	991.4917	1963.9524	982.4799	1963.9655	982.4864	16
6	631.3378	316.1725			613.3272	307.1672	I	1865.9520	933.4797	1847.9285	924.4679	1847.9415	924.4744	15
7	689.3563	***345.1818***			671.3457	336.1765	G	1751.8709	876.4391	1733.8474	867.4273	1733.8604	867.4338	14
8	803.4374	402.2223			785.4268	393.2170	I	1693.8524	847.4299	1675.8289	838.4181	1675.8419	838.4246	13
9	919.4613	***460.2343***			901.4508	451.2290	D	1579.7714	790.3893	1561.7478	781.3775	1561.7608	781.3840	12
10	1033.5424	517.2749			1015.5319	508.2696	L	1463.7474	732.3773	1445.7238	723.3655	1445.7368	723.3720	11
11	1121.5715	561.2894			1103.5609	552.2841	S	1349.6663	675.3368	1331.6427	666.3250	1331.6557	666.3315	10
12	1281.6608	641.3340	1263.6372	632.3222	1263.6502	632.3287	R	1261.6372	631.3222	1243.6136	622.3105	1243.6266	622.3170	9
13	1469.7341	735.3707	1451.7106	726.3589	1451.7236	726.3654	W	1101.5480	551.2776	1083.5244	542.2658	1083.5374	542.2723	8
14	1629.8234	815.4153	1611.7998	806.4035	1611.8128	806.4100	R	913.4746	457.2409	895.4510	448.2291	895.4640	448.2356	7
15	1759.8630	***880.4351***	1741.8394	871.4234	1741.8524	871.4299	E	753.3853	377.1963	735.3617	368.1845	735.3748	368.1910	6
16	1873.9441	***937.4757***	1855.9205	928.4639	1855.9335	928.4704	L	623.3457	312.1765	605.3221	303.1647	605.3351	303.1712	5
17	1988.0252	***994.5162***	1970.0016	985.5045	1970.0146	985.5110	L	509.2646	255.1359	491.2410	246.1241	491.2540	246.1307	4
18	2104.0622	1052.5347	2086.0386	1043.5230	2086.0516	1043.5295	N	395.1835	198.0954	377.1599	189.0836	377.1729	189.0901	3
19	2234.1018	1117.5546	2216.0783	1108.5428	2216.0913	1108.5493	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
20							K	149.1069	75.0571	131.0833	66.0453			1

AT4G19710.1





NCBI **BLAST** search of MLLSDIGIDLSRWRELLNEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.7	2445.1924	0.0063	MLLSDIGIDLSRWRELLNEK
4.3	2445.1938	0.0049	AVKSMPVAAACALAASKMQRPVR
2.8	2445.2033	-0.0046	ILNLSRNSMAGSIPEKISELSR
0.9	2445.1973	0.0014	RFTYSQVVIMTNNFQRILGK

Mascot: http://www.matrixscience.com/

AT4G19880.1

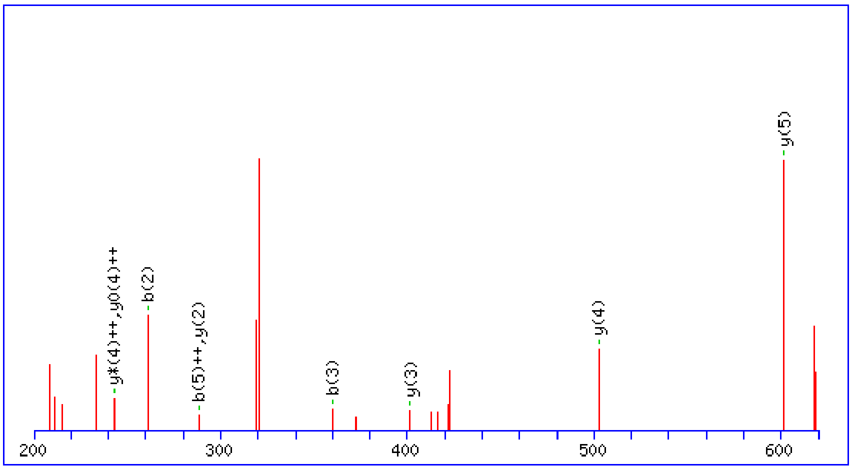
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFVTLIR**
Found in **AT4G19880.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45020.1); similar to Intracellular chloride channel [Medicago truncatula] (GB:ABC75353.2); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPr

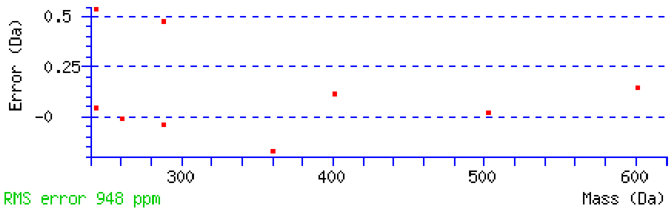
Match to Query 1474: 860.547960 from(431.281256,2+) index(6791)
Title: Elution from: 58.877 to 58.877 scan no 8724 cid35.00 polarity:+
Data file D1d-3_2.mgf

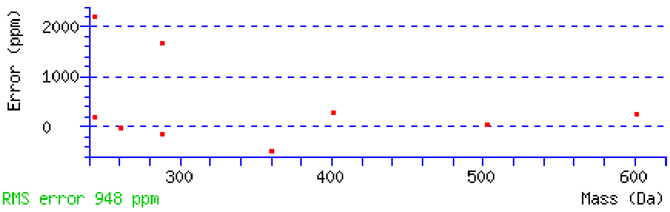
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 620 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 860.5484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.017
Matches : 9/48 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							7
2	**261.1598**	131.0835			F	748.4716	374.7394	731.4450	366.2262	730.4610	365.7341	6
3	**360.2282**	180.6177			V	***601.4032***	301.2052	584.3766	292.6920	583.3926	292.1999	5
4	461.2758	231.1416	443.2653	222.1363	T	***502.3348***	251.6710	485.3082	243.1577	484.3242	242.6657	4
5	574.3599	287.6836	556.3493	278.6783	L	***401.2871***	201.1472	384.2605	192.6339			3
6	687.4440	344.2256	669.4334	335.2203	I	***288.2030***	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LFVTLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.8	860.5484	-0.0004	LFVTLIR

AT4G19880.1

11.9	860.5484	-0.0004	LFVLTLR
6.2	860.5484	-0.0004	FVIKLNK
6.2	860.5484	-0.0004	LVFKLNK
0.6	860.5484	-0.0004	LFKNIVK

AT4G20050.1

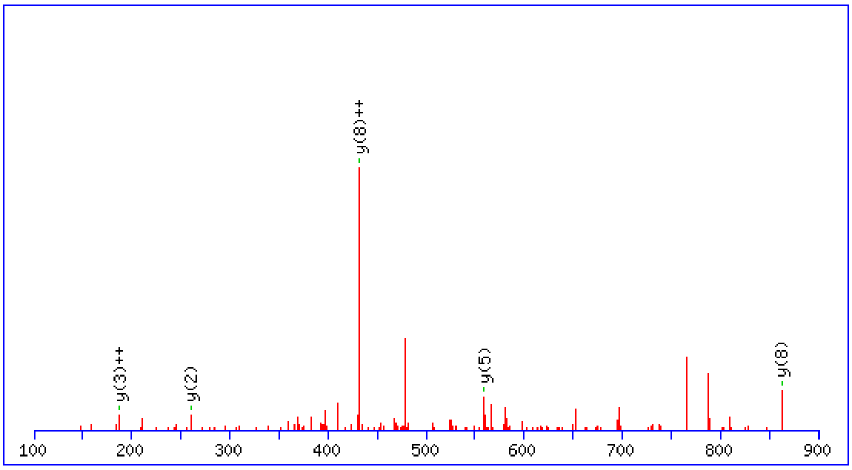
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDSTDAILK**
Found in **AT4G20050.1** in **TAIR_Arabidopsis**, Symbols: QRT3 | QRT3 (QUARTET 3) | chr4:10849921-10852100 REVERSE

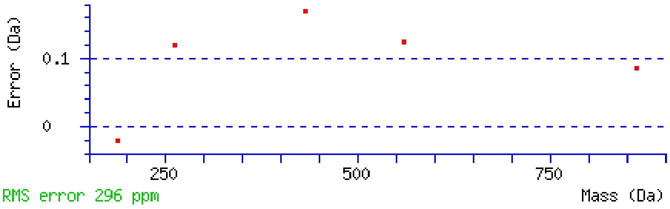
Match to Query 2451: 974.526000 from(488.270276,2+) index(4492)
Title: Elution from: 41.087 to 41.087 scan no 5541 cid35.00 polarity:+
Data file D12h-1_1.mgf

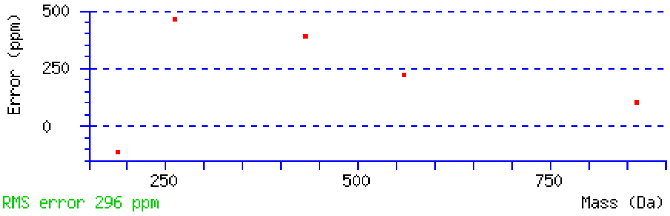
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 974.5284
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.037
Matches : 5/70 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							9
2	229.1183	115.0628	211.1077	106.0575	D	***862.4516***	431.7295	845.4251	423.2162	844.4411	422.7242	8
3	316.1503	158.5788	298.1397	149.5735	S	747.4247	374.2160	730.3981	365.7027	729.4141	365.2107	7
4	417.1980	209.1026	399.1874	200.0974	T	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
5	532.2249	266.6161	514.2144	257.6108	D	***559.3450***	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	603.2620	302.1347	585.2515	293.1294	A	444.3180	222.6627	427.2915	214.1494			4
7	716.3461	358.6767	698.3355	349.6714	I	373.2809	187.1441	356.2544	178.6308			3
8	829.4302	415.2187	811.4196	406.2134	L	***260.1969***	130.6021	243.1703	122.0888			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LDSTDAILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.6	974.5284	-0.0024	LDSTDAILK

AT4G20050.1

4.9	974.5284	-0.0024	IITIGGSVES
3.7	974.5257	0.0003	LSRSNRDK
2.1	974.5284	-0.0024	LSSLEADLK
2.0	974.5284	-0.0024	LSETLPSTK
1.7	974.5284	-0.0024	ELSDVTAIK
1.6	974.5284	-0.0024	LSKEEIEK
0.4	974.5284	-0.0024	ILSEVTADK

AT4G20260.1

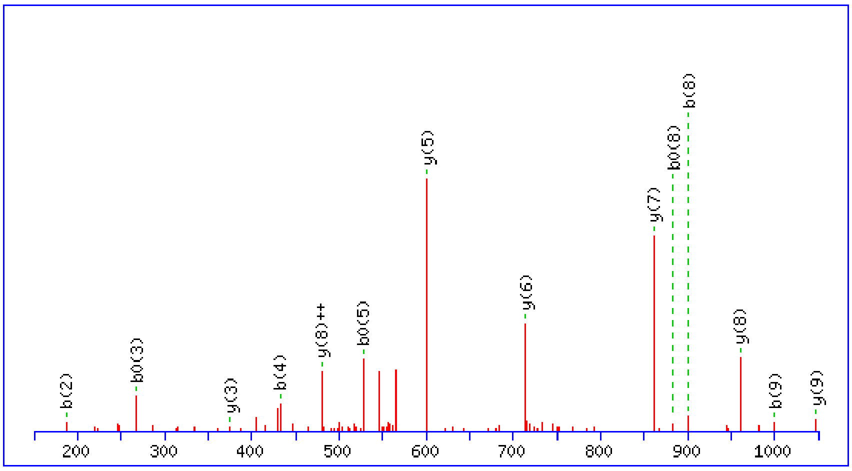
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVFLPEEVK**
Found in **AT4G20260.1** in **TAIR_Arabidopsis**, Symbols: | DREPP plasma membrane polypeptide family protein | chr4:10941603-10943237 FORWARD

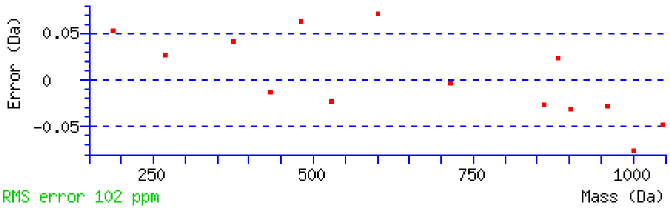
Match to Query 3273: 1145.633472 from(573.824012,2+) index(5671)
Title: Elution from: 51.846 to 51.846 scan no 7330 cid35.00 polarity:+
Data file D12h-2_3.mgf

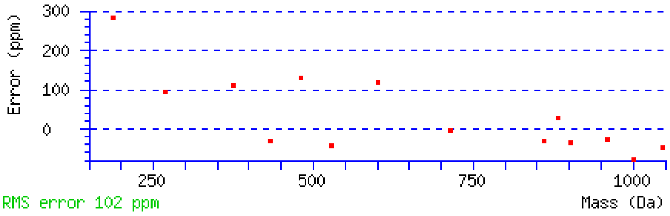
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1145.6332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.3e-005
Matches : 14/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			**V**							**10**
2	***187.1077***	94.0575	169.0972	85.0522	**S**	***1047.5721***	524.2897	1030.5455	515.7764	1029.5615	515.2844	**9**
3	286.1761	143.5917	268.1656	134.5864	**V**	***960.5401***	480.7737	943.5135	472.2604	942.5295	471.7684	**8**
4	***433.2445***	217.1259	415.2340	208.1206	**F**	***861.4716***	431.2395	844.4451	422.7262	843.4611	422.2342	**7**
5	546.3286	273.6679	528.3180	264.6627	**L**	***714.4032***	357.7053	697.3767	349.1920	696.3927	348.7000	**6**
6	643.3814	322.1943	625.3708	313.1890	**P**	***601.3192***	301.1632	584.2926	292.6499	583.3086	292.1579	**5**
7	772.4240	386.7156	754.4134	377.7103	**E**	504.2664	252.6368	487.2399	244.1236	486.2558	243.6316	**4**
8	***901.4666***	451.2369	883.4560	442.2316	**E**	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
9	***1000.5350***	500.7711	982.5244	491.7658	**V**	246.1812	123.5942	229.1547	115.0810			**2**
10					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VSVFLPEEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G20260.1

Score	Mr(calc)	Delta	Sequence
52.5	1145.6332	0.0002	VSVFLPEEVK
0.6	1145.6305	0.0029	DAQRFIQLR

AT4G20360.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GITINTATVEYETENR**
Found in **AT4G20360.1** in **TAIR_Arabidopsis**, Symbols: AtRab8D, AtRABE1b | AtRABE1b/AtRab8D (Arabidopsis Rab GTPase homolog E1b); translation elongation factor | chr4:10990047-10991477 FORWARD

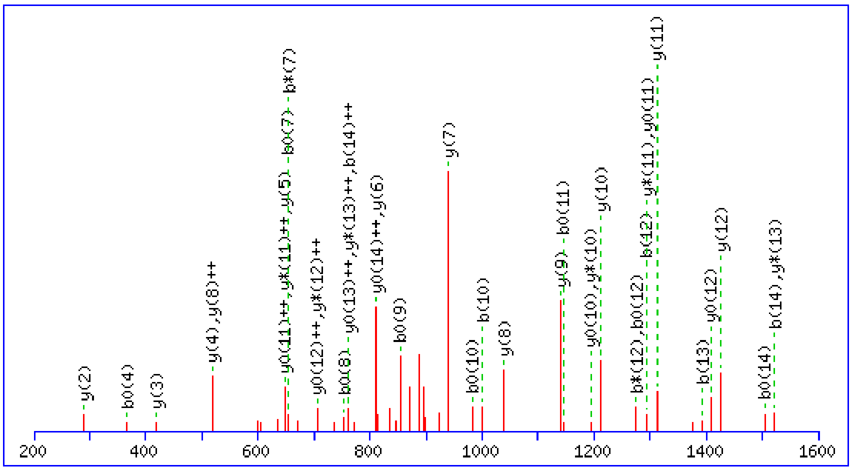
Match to Query 8701: 1809.872676 from(905.943614,2+) index(5655)
Title: Elution from: 53.360 to 53.360 scan no 7309 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

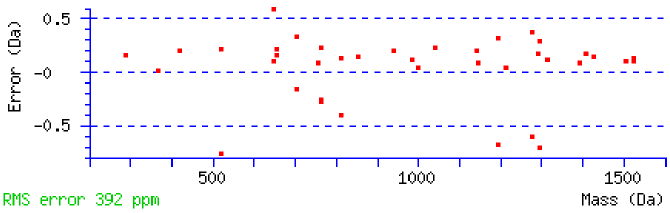
Show Y-axis ☐

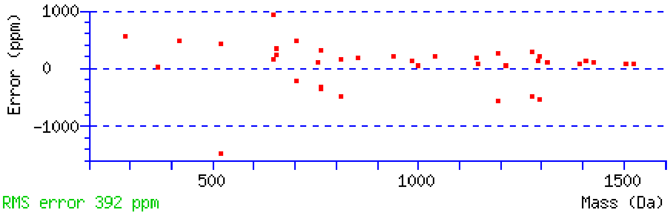


Monoisotopic mass of neutral peptide Mr(calc): 1809.8745
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 121 **Expect:** 2.6e-012
Matches : 40/164 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**16**
2	171.1128	86.0600					**I**	1753.8603	877.4338	1736.8337	868.9205	1735.8497	868.4285	**15**
3	272.1605	136.5839			254.1499	127.5786	**T**	1640.7762	820.8917	1623.7497	812.3785	1622.7657	811.8865	**14**
4	385.2445	193.1259			367.2340	184.1206	**I**	1539.7285	770.3679	1522.7020	761.8546	1521.7180	761.3626	**13**
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	**N**	***1426.6445***	713.8259	1409.6179	705.3126	1408.6339	704.8206	**12**
6	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	**T**	***1312.6016***	656.8044	1295.5750	648.2911	1294.5910	647.7991	**11**
7	671.3723	336.1898	654.3457	327.6765	653.3617	327.1845	**A**	***1211.5539***	606.2806	1194.5273	597.7673	1193.5433	597.2753	**10**
8	772.4199	386.7136	755.3934	378.2003	754.4094	377.7083	**T**	***1140.5168***	570.7620	1123.4902	562.2487	1122.5062	561.7567	**9**
9	871.4884	436.2478	854.4618	427.7345	853.4778	427.2425	**V**	***1039.4691***	520.2382	1022.4425	511.7249	1021.4585	511.2329	**8**
10	**1000.5310**	500.7691	983.5044	492.2558	982.5204	491.7638	**E**	***940.4007***	470.7040	923.3741	462.1907	922.3901	461.6987	**7**
11	1163.5943	582.3008	1146.5677	573.7875	1145.5837	573.2955	**Y**	***811.3581***	406.1827	794.3315	397.6694	793.3475	397.1774	**6**
12	**1292.6369**	646.8221	1275.6103	638.3088	1274.6263	637.8168	**E**	***648.2947***	324.6510	631.2682	316.1377	630.2842	315.6457	**5**
13	**1393.6846**	697.3459	1376.6580	688.8326	1375.6740	688.3406	**T**	***519.2522***	260.1297	502.2256	251.6164	501.2416	251.1244	**4**
14	**1522.7271**	761.8672	1505.7006	753.3539	1504.7166	752.8619	**E**	***418.2045***	209.6059	401.1779	201.0926	400.1939	200.6006	**3**
15	1636.7701	818.8887	1619.7435	810.3754	1618.7595	809.8834	**N**	***289.1619***	145.0846	272.1353	136.5713			**2**
16							**R**	175.1190	88.0631	158.0924	79.5498			**1**

AT4G20360.1





NCBI **BLAST** search of GITINTATVEYETENR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
120.7	1809.8745	-0.0018	GITINTATVEYETENR
5.0	1809.8753	-0.0026	CKIIFLETLCNDER

Mascot: http://www.matrixscience.com/

AT4G20890.1

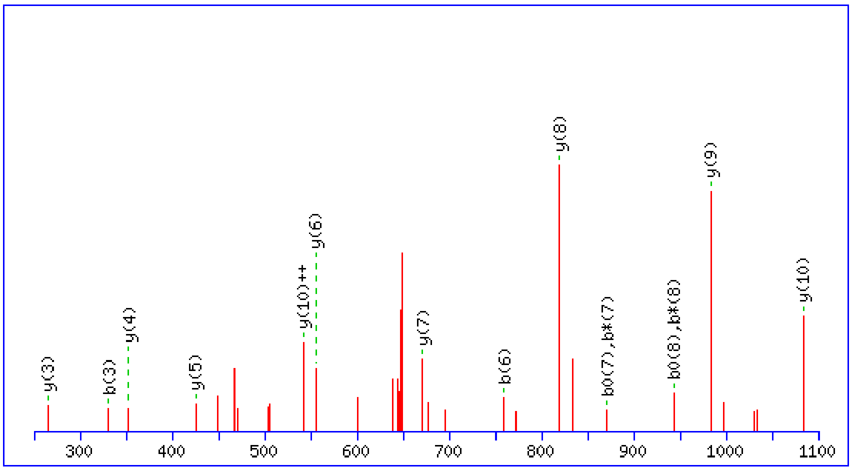
Mascot Search Results

Peptide View

MS/MS Fragmentation of **INVYFNEASGGK**
Found in **AT4G20890.1** in **TAIR_Arabidopsis**, Symbols: TUB9 | TUB9 (tubulin beta-9 chain); structural molecule | chr4:11182229-11183851 FORWARD

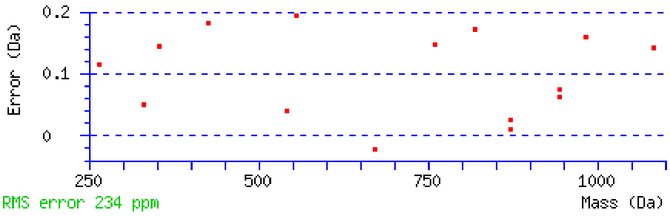
Match to Query 5005: 1312.583492 from(657.299022,2+) index(4587)
Title: Elution from: 42.023 to 42.023 scan no 5722 cid35.00 polarity:+
Data file C7-3_1.mgf

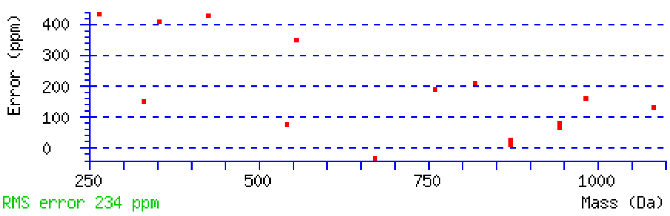
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1312.5858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 7.4e-006
Matches : 15/112 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							12
2	231.1254	116.0663	213.1018	107.0545			N	1199.5120	600.2596	1181.4884	591.2478	1181.5014	591.2543	11
3	**331.1908**	166.0990	313.1672	157.0873			V	***1083.4750***	542.2411	1065.4514	533.2293	1065.4644	533.2358	10
4	495.2512	248.1292	477.2276	239.1174			Y	***983.4095***	492.2084	965.3859	483.1966	965.3990	483.2031	9
5	643.3166	322.1620	625.2930	313.1502			F	***819.3492***	410.1782	801.3256	401.1664	801.3386	401.1729	8
6	**759.3536**	380.1805	741.3300	371.1687			N	***671.2837***	336.1455	653.2601	327.1337	653.2731	327.1402	7
7	889.3933	445.2003	871.3697	436.1885	871.3827	436.1950	E	***555.2467***	278.1270	537.2231	269.1152	537.2361	269.1217	6
8	961.4274	481.2173	943.4038	472.2056	943.4168	472.2121	A	***425.2071***	213.1072	407.1835	204.0954	407.1965	204.1019	5
9	1049.4565	525.2319	1031.4329	516.2201	1031.4459	516.2266	S	***353.1729***	177.0901	335.1494	168.0783	335.1624	168.0848	4
10	1107.4750	554.2411	1089.4514	545.2293	1089.4644	545.2358	G	***265.1439***	133.0756	247.1203	124.0638			3
11	1165.4935	583.2504	1147.4699	574.2386	1147.4829	574.2451	G	207.1254	104.0663	189.1018	95.0545			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of INVYFNEASGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G20890.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.5	1312.5858	-0.0023	INVYFNEASGGK
6.3	1312.5835	-0.0000	ADSVYTKDRDK

Mascot: http://www.matrixscience.com/

AT4G20980.1

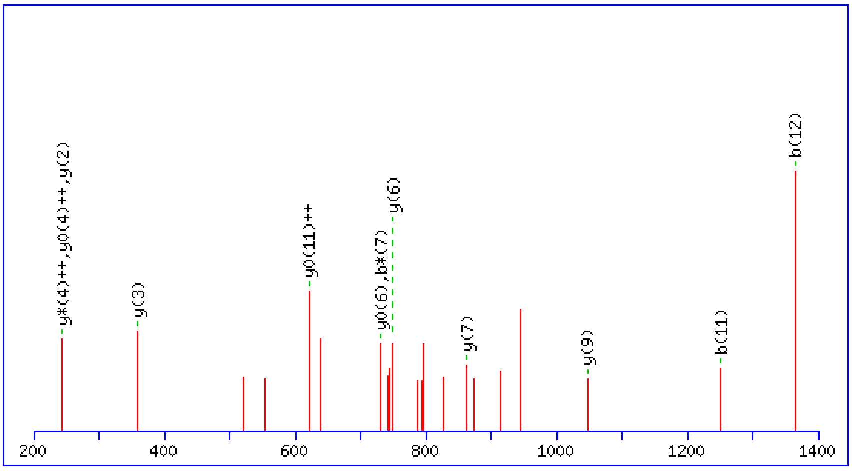
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFLTLNALNEFDPK**
Found in **AT4G20980.1** in **TAIR_Arabidopsis**, Symbols: | eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative | chr4:11217008-11218783 FORWARD

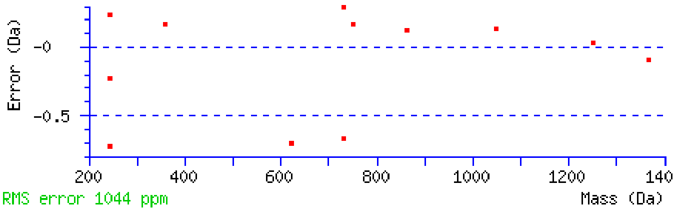
Match to Query 7126: 1607.818276 from(804.916414,2+) index(9610)
Title: Elution from: 88.615 to 88.615 scan no 13340 cid35.00 polarity:+
Data file D12h-3_2.mgf

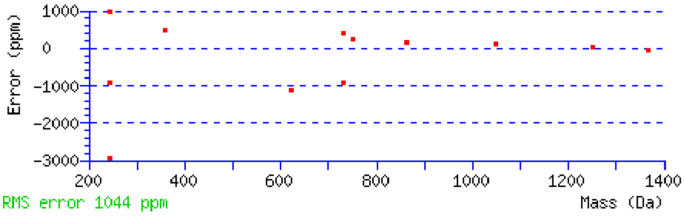
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1607.8195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00066
Matches : 12/142 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**14**
2	235.1077	118.0575			217.0972	109.0522	**F**	1521.7948	761.4010	1504.7682	752.8877	1503.7842	752.3957	**13**
3	348.1918	174.5995			330.1812	165.5942	**L**	1374.7264	687.8668	1357.6998	679.3535	1356.7158	678.8615	**12**
4	449.2395	225.1234			431.2289	216.1181	**T**	1261.6423	631.3248	1244.6157	622.8115	1243.6317	622.3195	**11**
5	562.3235	281.6654			544.3130	272.6601	**L**	1160.5946	580.8009	1143.5681	572.2877	1142.5840	571.7957	**10**
6	676.3665	338.6869	659.3399	330.1736	658.3559	329.6816	**N**	***1047.5106***	524.2589	1030.4840	515.7456	1029.5000	515.2536	**9**
7	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	**A**	933.4676	467.2374	916.4411	458.7242	915.4571	458.2322	**8**
8	860.4876	430.7475	843.4611	422.2342	842.4771	421.7422	**L**	***862.4305***	431.7189	845.4040	423.2056	844.4199	422.7136	**7**
9	974.5306	487.7689	957.5040	479.2556	956.5200	478.7636	**N**	***749.3464***	375.1769	732.3199	366.6636	731.3359	366.1716	**6**
10	1103.5731	552.2902	1086.5466	543.7769	1085.5626	543.2849	**E**	635.3035	318.1554	618.2770	309.6421	617.2930	309.1501	**5**
11	**1250.6416**	625.8244	1233.6150	617.3111	1232.6310	616.8191	**F**	506.2609	253.6341	489.2344	245.1208	488.2504	244.6288	**4**
12	**1365.6685**	683.3379	1348.6420	674.8246	1347.6579	674.3326	**D**	***359.1925***	180.0999	342.1660	171.5866	341.1819	171.0946	**3**
13	1462.7213	731.8643	1445.6947	723.3510	1444.7107	722.8590	**P**	***244.1656***	122.5864	227.1390	114.0731			**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SFLTLNALNEFDPK

AT4G20980.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.6	1607.8195	-0.0012	SFLTLNALNEFDPK

AT4G21150.1

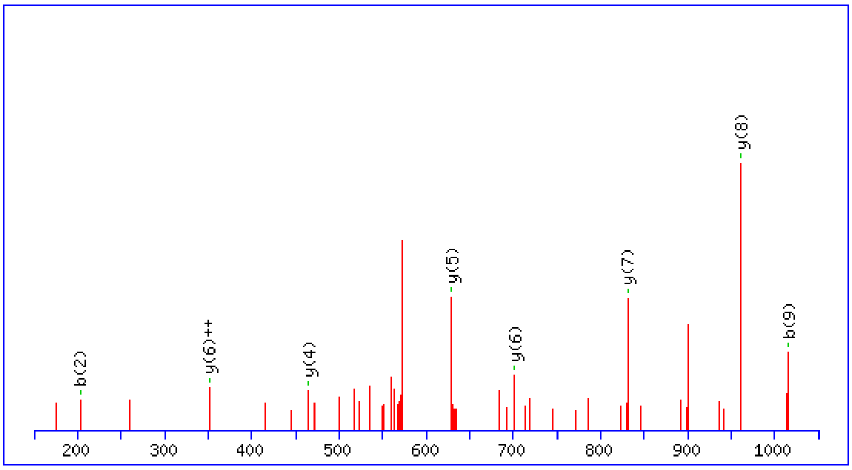
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLEEAYEALK**
Found in **AT4G21150.1** in **TAIR_Arabidopsis**, Symbols: | ribophorin II (RPN2) family protein | chr4:11278656-11283609 FORWARD

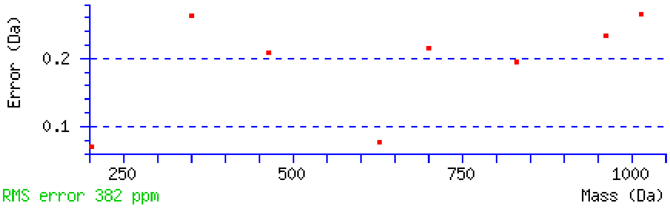
Match to Query 4054: 1162.539880 from(582.277216,2+) index(5841)
Title: Elution from: 51.011 to 51.011 scan no 7336 cid35.00 polarity:+
Data file C7-1_1.mgf

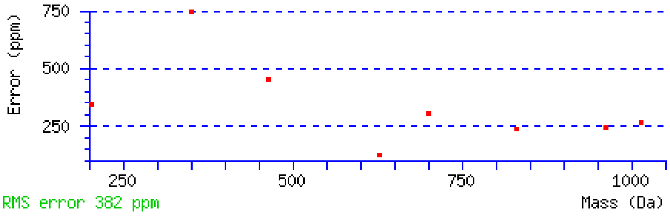
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1162.5384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00045
Matches : 8/84 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							10
2	**203.1174**	102.0624	185.1069	93.0571	L	1075.5166	538.2619	1057.4930	529.2502	1057.5061	529.2567	9
3	333.1571	167.0822	315.1465	158.0769	E	***961.4355***	481.2214	943.4119	472.2096	943.4250	472.2161	8
4	463.1967	232.1020	445.1861	223.0967	E	***831.3959***	416.2016	813.3723	407.1898	813.3853	407.1963	7
5	535.2308	268.1191	517.2203	259.1138	A	***701.3563***	351.1818	683.3327	342.1700	683.3457	342.1765	6
6	699.2912	350.1492	681.2806	341.1440	Y	***629.3221***	315.1647	611.2985	306.1529	611.3115	306.1594	5
7	829.3308	415.1691	811.3203	406.1638	E	***465.2618***	233.1345	447.2382	224.1227	447.2512	224.1292	4
8	901.3650	451.1861	883.3544	442.1808	A	335.2221	168.1147	317.1985	159.1029			3
9	**1015.4461**	508.2267	997.4355	499.2214	L	263.1880	132.0976	245.1644	123.0858			2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SLEEAYEALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G21150.1

43.1	1162.5384	0.0015	SLEEAYEALK
8.8	1162.5433	-0.0034	AEFDYLHKK
2.4	1162.5411	-0.0012	FIRQEAEEK
1.1	1162.5370	0.0028	SLGMLKDMEK
0.9	1162.5415	-0.0016	SLRIGQDNSR
0.5	1162.5419	-0.0021	GYICKHMIK
0.4	1162.5433	-0.0034	TLDVTPYWR
0.2	1162.5388	0.0010	DGKGSSTANALK
0.1	1162.5433	-0.0034	SLSFPQWASK
0.1	1162.5411	-0.0012	SLSSEWKNAK

AT4G21280.1

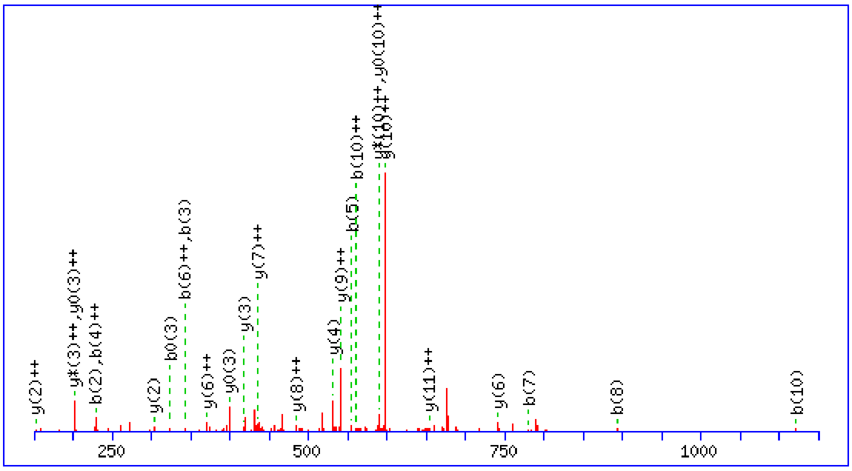
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIINVKPLIDRK**
Found in **AT4G21280.1** in **TAIR_Arabidopsis**, Symbols: PSBQ, PSBQA, PSBQ-1 | PSBQ/PSBQ-1/PSBQA; calcium ion binding | chr4:11334456-11335597 FORWARD

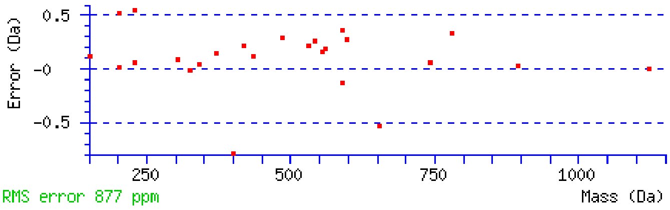
Match to Query 6004: 1422.853590 from(475.291806,3+) index(5702)
Title: Elution from: 50.205 to 50.205 scan no 7091 cid35.00 polarity:+
Data file D12h-1_1.mgf

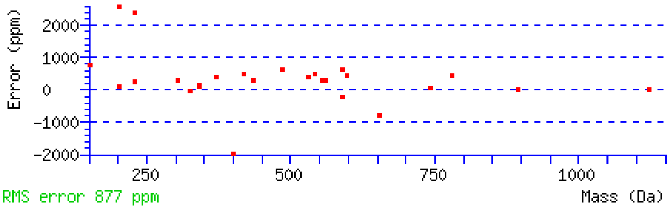
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1422.8558
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0014
Matches : 26/122 fragment ions using 62 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	***229.1183***	115.0628			211.1077	106.0575	I	1308.8362	654.9217	1291.8096	646.4085	1290.8256	645.9164	11
3	***342.2023***	171.6048			324.1918	162.5995	I	1195.7521	598.3797	1178.7256	589.8664	1177.7416	589.3744	10
4	456.2453	**228.6263**	439.2187	220.1130	438.2347	219.6210	N	1082.6681	541.8377	1065.6415	533.3244	1064.6575	532.8324	9
5	***555.3137***	278.1605	538.2871	269.6472	537.3031	269.1552	V	968.6251	484.8162	951.5986	476.3029	950.6146	475.8109	8
6	683.4087	**342.2080**	666.3821	333.6947	665.3981	333.2027	K	869.5567	435.2820	852.5302	426.7687	851.5461	426.2767	7
7	***780.4614***	390.7343	763.4349	382.2211	762.4509	381.7291	P	**741.4618**	371.2345	724.4352	362.7212	723.4512	362.2292	6
8	***893.5455***	447.2764	876.5189	438.7631	875.5349	438.2711	L	644.4090	322.7081	627.3824	314.1949	626.3984	313.7028	5
9	1006.6295	503.8184	989.6030	495.3051	988.6190	494.8131	I	**531.3249**	266.1661	514.2984	257.6528	513.3144	257.1608	4
10	***1121.6565***	**561.3319**	1104.6299	552.8186	1103.6459	552.3266	D	**418.2409**	209.6241	401.2143	201.1108	400.2303	200.6188	3
11	1277.7576	639.3824	1260.7310	630.8692	1259.7470	630.3772	R	**303.2139**	152.1106	286.1874	143.5973			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DIINVKPLIDRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G21280.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.6	1422.8558	-0.0022	DIINVKPLIDRK
12.2	1422.8558	-0.0023	QLASITVIGLVGPR
7.0	1422.8558	-0.0022	AGVLAVQISSLPLR

AT4G21430.1

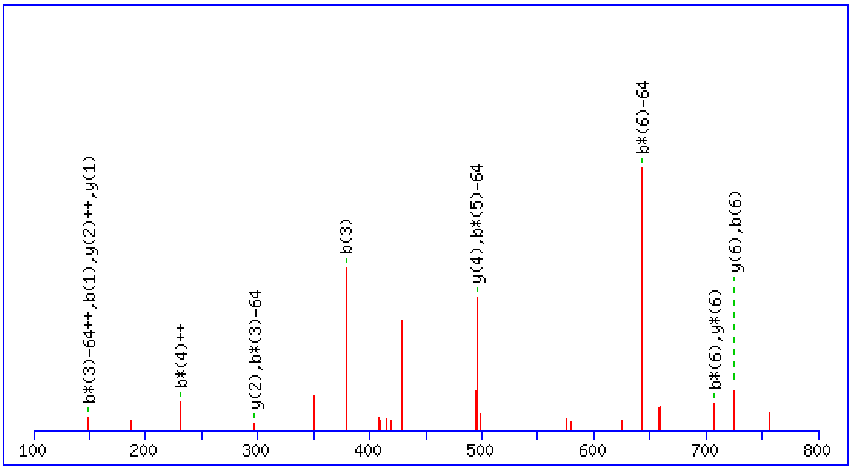
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQVVPFK**
Found in **AT4G21430.1** in **TAIR_Arabidopsis**, Symbols: B160 | B160; transcription factor | chr4:11407846-11412170 REVERSE

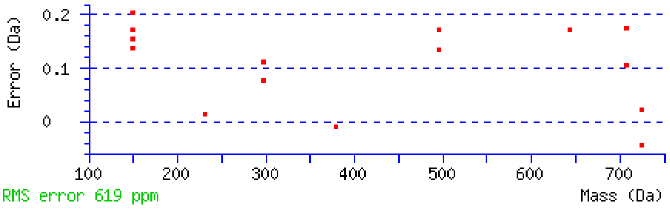
Match to Query 1421: 872.431396 from(437.222974,2+) index(4196)
Title: Elution from: 39.514 to 39.514 scan no 5326 cid35.00 polarity:+
Data file 0-2_2.mgf

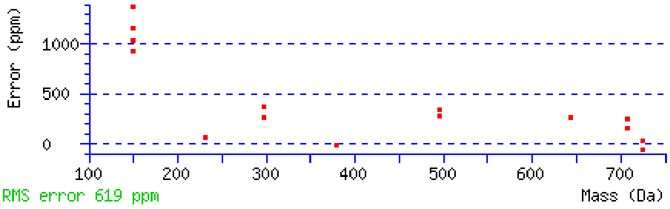
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 872.4308
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 **Expect:** 0.0039
Matches : 15/68 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**149.0397**	75.0235			M					7
2	279.0924	140.0498	261.0688	131.0380	Q	***725.4057***	363.2065	707.3821	354.1947	6
3	**379.1578**	190.0825	361.1342	181.0707	V	595.3530	298.1801	577.3294	289.1684	5
4	479.2233	240.1153	461.1997	231.1035	V	***495.2876***	248.1474	477.2640	239.1356	4
5	577.2731	289.1402	559.2495	280.1284	P	395.2221	198.1147	377.1985	189.1029	3
6	**725.3385**	363.1729	707.3149	354.1611	F	***297.1723***	149.0898	279.1487	140.0780	2
7					K	***149.1069***	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MQVVPFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.9	872.4308	0.0006	MQVVPFK
18.8	872.4313	0.0001	NLCLGRK

AT4G21430.1

10.0	872.4313	0.0001	AMGRAINK
7.8	872.4313	0.0001	NMKPKSR
5.1	872.4308	0.0006	MSIWLAK
3.1	872.4313	0.0001	NLGIKCR
2.7	872.4308	0.0006	MASLWLK
2.7	872.4308	0.0006	MSALWLK
2.2	872.4333	-0.0019	ETSSLSLK
1.0	872.4312	0.0002	DMIRAVR

AT4G21660.1

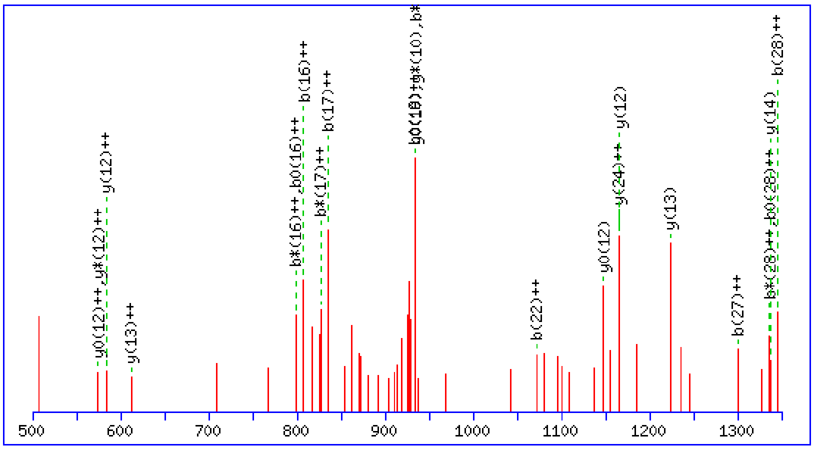
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MTADSTVALVHSVVSNGDVSNGNTSASSK**
Found in **AT4G21660.1** in **TAIR_Arabidopsis**, Symbols: | proline-rich spliceosome-associated (PSP) family protein | chr4:11506271-11509784 REVERSE

Match to Query 10699: 2834.338326 from(945.786718,3+) index(7303)
Title: Elution from: 63.856 to 63.856 scan no 9494 cid35.00 polarity:+
Data file C7-3_2.mgf

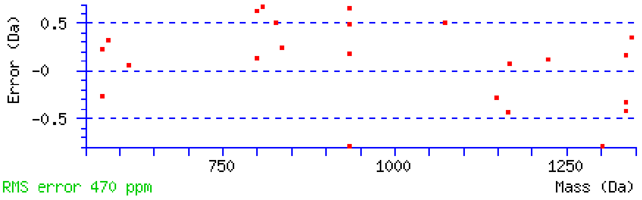
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

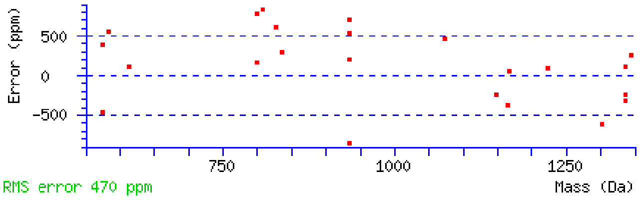


Monoisotopic mass of neutral peptide Mr(calc): 2834.3353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.039
Matches : 23/302 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							29
2	233.0954	117.0514			215.0849	108.0461	T	2704.3020	1352.6546	2687.2755	1344.1414	2686.2915	1343.6494	28
3	304.1326	152.5699			286.1220	143.5646	A	2603.2543	1302.1308	2586.2278	1293.6175	2585.2438	1293.1255	27
4	419.1595	210.0834			401.1489	201.0781	D	2532.2172	1266.6123	2515.1907	1258.0990	2514.2067	1257.6070	26
5	506.1915	253.5994			488.1810	244.5941	S	2417.1903	1209.0988	2400.1637	1200.5855	2399.1797	1200.0935	25
6	607.2392	304.1232			589.2286	295.1180	T	2330.1583	1165.5828	2313.1317	1157.0695	2312.1477	1156.5775	24
7	706.3076	353.6574			688.2971	344.6522	V	2229.1106	1115.0589	2212.0840	1106.5457	2211.1000	1106.0536	23
8	777.3447	389.1760			759.3342	380.1707	A	2130.0422	1065.5247	2113.0156	1057.0114	2112.0316	1056.5194	22
9	890.4288	445.7180			872.4182	436.7128	L	2059.0050	1030.0062	2041.9785	1021.4929	2040.9945	1021.0009	21
10	989.4972	495.2522			971.4866	486.2470	V	1945.9210	973.4641	1928.8944	964.9509	1927.9104	964.4588	20
11	1126.5561	563.7817			1108.5456	554.7764	H	1846.8526	923.9299	1829.8260	915.4166	1828.8420	914.9246	19
12	1213.5882	607.2977			1195.5776	598.2924	S	1709.7937	855.4005	1692.7671	846.8872	1691.7831	846.3952	18
13	1312.6566	656.8319			1294.6460	647.8266	V	1622.7616	811.8845	1605.7351	803.3712	1604.7511	802.8792	17
14	1411.7250	706.3661			1393.7144	697.3608	V	1523.6932	762.3502	1506.6667	753.8370	1505.6827	753.3450	16
15	1498.7570	749.8821			1480.7464	740.8769	S	1424.6248	712.8160	1407.5983	704.3028	1406.6142	703.8108	15
16	1612.7999	***806.9036***	1595.7734	798.3903	1594.7894	797.8983	N	**1337.5928**	669.3000	1320.5662	660.7868	1319.5822	660.2947	14
17	1669.8214	***835.4143***	1652.7948	826.9011	1651.8108	826.4091	G	**1223.5498**	612.2786	1206.5233	603.7653	1205.5393	603.2733	13
18	1784.8483	892.9278	1767.8218	884.4145	1766.8378	883.9225	D	**1166.5284**	583.7678	1149.5018	575.2546	1148.5178	574.7625	12
19	1883.9168	942.4620	1866.8902	933.9487	1865.9062	933.4567	V	1051.5014	526.2544	1034.4749	517.7411	1033.4909	517.2491	11
20	1970.9488	985.9780	1953.9222	977.4648	1952.9382	976.9727	S	952.4330	476.7202	935.4065	468.2069	934.4225	467.7149	10
21	2084.9917	1042.9995	2067.9652	1034.4862	2066.9811	1033.9942	N	865.4010	433.2041	848.3745	424.6909	847.3904	424.1989	9
22	2142.0132	***1071.5102***	2124.9866	1062.9970	2124.0026	1062.5049	G	751.3581	376.1827	734.3315	367.6694	733.3475	367.1774	8
23	2256.0561	1128.5317	2239.0296	1120.0184	2238.0455	1119.5264	N	694.3366	347.6719	677.3101	339.1587	676.3260	338.6667	7
24	2357.1038	1179.0555	2340.0772	1170.5423	2339.0932	1170.0502	T	580.2937	290.6505	563.2671	282.1372	562.2831	281.6452	6
25	2444.1358	1222.5715	2427.1093	1214.0583	2426.1252	1213.5663	S	479.2460	240.1266	462.2195	231.6134	461.2354	231.1214	5

26	2515.1729	1258.0901	2498.1464	1249.5768	2497.1624	1249.0848	**A**	392.2140	196.6106	375.1874	188.0974	374.2034	187.6053	**4**
27	2602.2049	***1301.6061***	2585.1784	1293.0928	2584.1944	1292.6008	**S**	321.1769	161.0921	304.1503	152.5788	303.1663	152.0868	**3**
28	2689.2370	***1345.1221***	2672.2104	1336.6089	2671.2264	1336.1168	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of MTADSTVALVHSVVSNGDVSNGNTSASSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.5	2834.3353	0.0031	MTADSTVALVHSVVSNGDVSNGNTSASSK
3.0	2834.3418	-0.0035	SYGTVSGSSSATEVGKTSAVSQIGSSGDTK
1.5	2834.3309	0.0074	STCKQWNFLFNDQIFTKMHFDK
1.4	2834.3439	-0.0056	RMSERDAAFGSNTSVGLGAYLGIMGSR
0.1	2834.3314	0.0070	MDMTELNTLTYDDLDSVSKLQKSR

Mascot: http://www.matrixscience.com/

AT4G21705.1

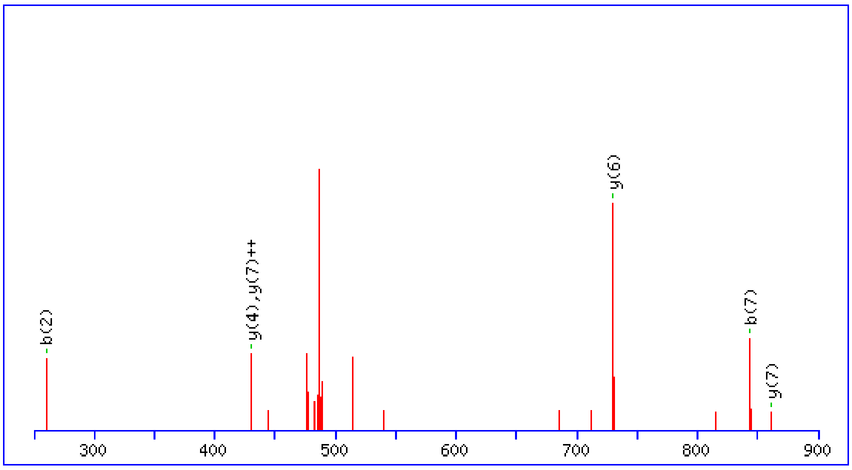
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QMYHALVK**
Found in **AT4G21705.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr4:11533269-11534829 REVERSE

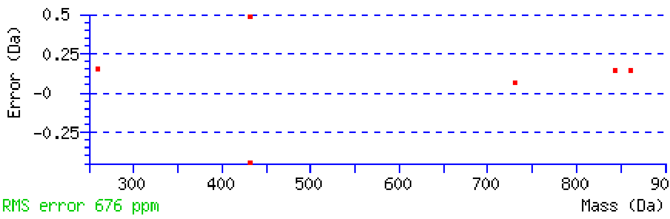
Match to Query 2268: 988.519276 from(495.266914,2+) index(784)
Title: Elution from: 13.108 to 13.108 scan no 1109 cid35.00 polarity:+
Data file D12h-1_3.mgf

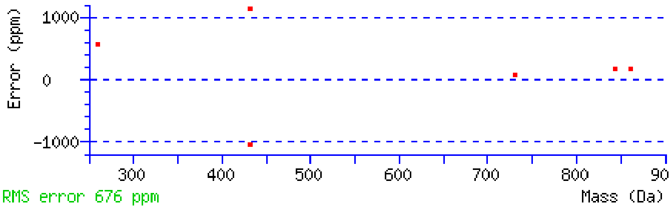
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 988.5164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0064
Matches : 6/56 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	129.0659	65.0366	112.0393	56.5233	Q					8
2	***260.1063***	130.5568	243.0798	122.0435	M	***861.4651***	431.2362	844.4386	422.7229	7
3	423.1697	212.0885	406.1431	203.5752	Y	***730.4246***	365.7160	713.3981	357.2027	6
4	560.2286	280.6179	543.2020	272.1047	H	567.3613	284.1843	550.3348	275.6710	5
5	631.2657	316.1365	614.2391	307.6232	A	***430.3024***	215.6548	413.2758	207.1416	4
6	744.3498	372.6785	727.3232	364.1652	L	359.2653	180.1363	342.2387	171.6230	3
7	***843.4182***	422.2127	826.3916	413.6994	V	246.1812	123.5942	229.1547	115.0810	2
8					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of QMYHALVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.6	988.5164	0.0029	QMYHALVK
25.2	988.5189	0.0004	KTEQENLK

AT4G21705.1

18.0	988.5189	0.0004	KEAADQSLK
15.8	988.5189	0.0004	ERLDSELK
10.7	988.5189	0.0004	NTSENIALK
10.3	988.5189	0.0004	DSRELEIK
9.5	988.5189	0.0004	SLAETNNLK
8.5	988.5189	0.0004	SDIDGKIGGK
6.0	988.5189	0.0004	NIEKEAGTK
5.1	988.5189	0.0004	ENGTKAELK

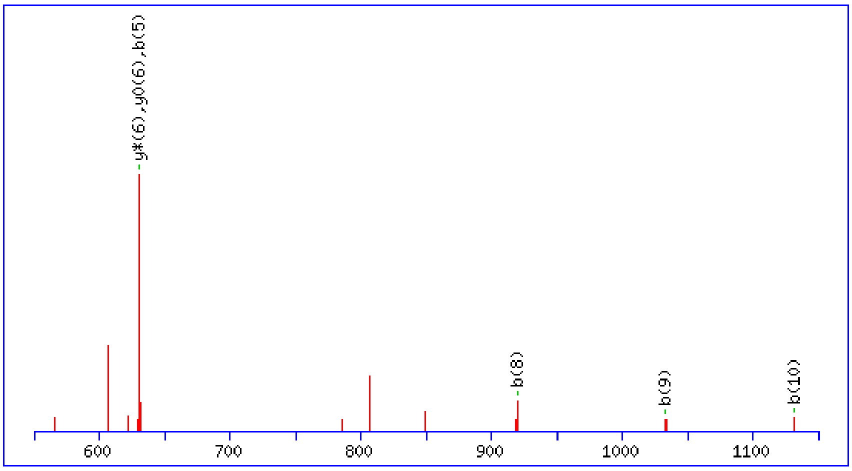
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEEKKMGTLVK**
Found in **AT4G21710.1** in **TAIR_Arabidopsis**, Symbols: EMB1989, RPB2, NRPB2 | NRPB2 (EMBRYO DEFECTIVE 1989); DNA binding | chr4:11535696-11542212 REVERSE

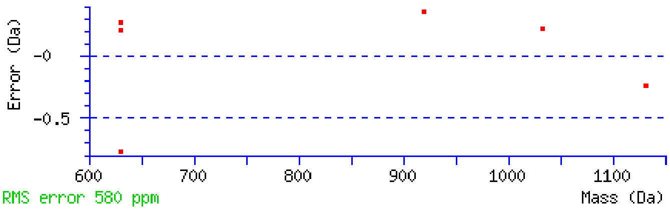
Match to Query 4391: 1276.673138 from(639.343845,2+) index(5734)
Title: Elution from: 51.081 to 51.081 scan no 7321 cid35.00 polarity:+
Data file C7-3_3.mgf

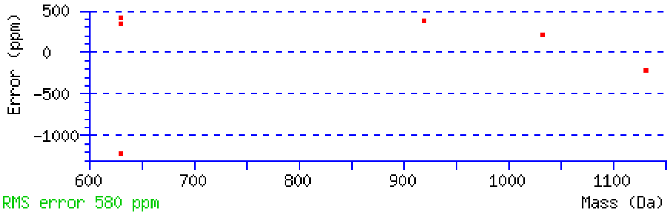
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1276.6697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0027
Matches : 6/108 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**11**
2	245.0768	123.0420			227.0662	114.0368	**E**	1162.6500	581.8286	1145.6235	573.3154	1144.6395	572.8234	**10**
3	374.1194	187.5633			356.1088	178.5581	**E**	1033.6074	517.3074	1016.5809	508.7941	1015.5969	508.3021	**9**
4	502.2144	251.6108	485.1878	243.0975	484.2038	242.6055	**K**	904.5648	452.7861	887.5383	444.2728	886.5543	443.7808	**8**
5	***630.3093***	315.6583	613.2828	307.1450	612.2988	306.6530	**K**	776.4699	388.7386	759.4433	380.2253	758.4593	379.7333	**7**
6	761.3498	381.1785	744.3233	372.6653	743.3393	372.1733	**M**	648.3749	324.6911	631.3484	316.1778	630.3643	315.6858	**6**
7	818.3713	409.6893	801.3447	401.1760	800.3607	400.6840	**G**	517.3344	259.1709	500.3079	250.6576	499.3239	250.1656	**5**
8	***919.4190***	460.2131	902.3924	451.6998	901.4084	451.2078	**T**	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	**4**
9	***1032.5030***	516.7551	1015.4765	508.2419	1014.4925	507.7499	**L**	359.2653	180.1363	342.2387	171.6230			**3**
10	***1131.5714***	566.2894	1114.5449	557.7761	1113.5609	557.2841	**V**	246.1812	123.5942	229.1547	115.0810			**2**
11							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of DEEKKMGTLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G21710.1

Score	Mr(calc)	Delta	Sequence
31.1	1276.6697	0.0035	DEEKKMGTLVK
5.3	1276.6703	0.0028	ELYLWDVVIQ
5.3	1276.6697	0.0035	MNSLTVEQVLK
5.1	1276.6697	0.0034	TTICQILSDVK
4.9	1276.6696	0.0035	EMLIKDQEKK
4.9	1276.6744	-0.0012	MVERVVNMRK
4.7	1276.6697	0.0035	MSGSLGLTPASLK
4.5	1276.6703	0.0028	LTYQTIFYTK
3.6	1276.6710	0.0021	MIISAHAVHGNK
2.8	1276.6744	-0.0012	RCVKQMVAAAK

Mascot: http://www.matrixscience.com/

AT4G22240.1

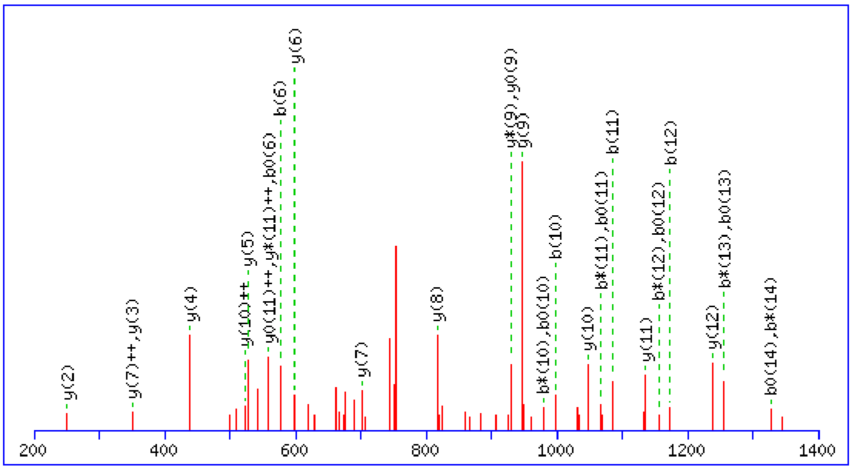
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLLTSVQDTASSVAR**
Found in **AT4G22240.1** in **TAIR_Arabidopsis**, Symbols: | plastid-lipid associated protein PAP, putative | chr4:11766102-11767239 REVERSE

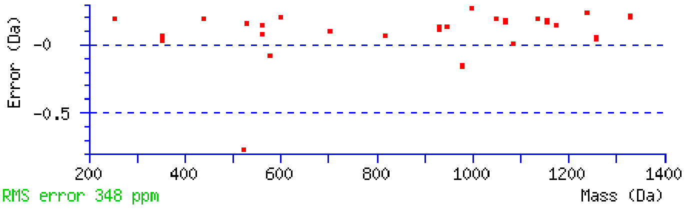
Match to Query 6829: 1522.732544 from(762.373548,2+) index(7098)
Title: Elution from: 62.415 to 62.415 scan no 9121 cid35.00 polarity:+
Data file 0-2_1.mgf

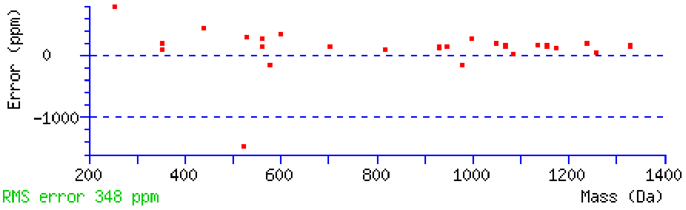
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1522.7329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 110 **Expect:** 9e-011
Matches : 32/144 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							15
2	173.1069	87.0571					L	1465.7217	733.3645	1447.6981	724.3527	1447.7112	724.3592	14
3	287.1880	144.0976					L	1351.6406	676.3240	1333.6170	667.3122	1333.6301	667.3187	13
4	389.2327	195.1200			371.2221	186.1147	T	***1237.5595***	619.2834	1219.5359	610.2716	1219.5490	610.2781	12
5	477.2617	239.1345			459.2512	230.1292	S	***1135.5148***	568.2610	1117.4912	559.2493	1117.5043	559.2558	11
6	**577.3272**	289.1672			559.3166	280.1620	V	***1047.4858***	524.2465	1029.4622	515.2347	1029.4752	515.2412	10
7	707.3798	354.1936	689.3563	345.1818	689.3693	345.1883	Q	***947.4203***	474.2138	929.3967	465.2020	929.4097	465.2085	9
8	823.4038	412.2055	805.3802	403.1938	805.3933	403.2003	D	***817.3677***	409.1875	799.3441	400.1757	799.3571	400.1822	8
9	925.4485	463.2279	907.4250	454.2161	907.4380	454.2226	T	***701.3437***	351.1755	683.3201	342.1637	683.3331	342.1702	7
10	**997.4827**	499.2450	979.4591	490.2332	979.4721	490.2397	A	***599.2990***	300.1531	581.2754	291.1413	581.2884	291.1478	6
11	**1085.5117**	543.2595	1067.4882	534.2477	1067.5012	534.2542	S	***527.2648***	264.1360	509.2412	255.1243	509.2543	255.1308	5
12	**1173.5408**	587.2740	1155.5172	578.2623	1155.5302	578.2688	S	***439.2358***	220.1215	421.2122	211.1097	421.2252	211.1162	4
13	1273.6063	637.3068	1255.5827	628.2950	1255.5957	628.3015	V	***351.2067***	176.1070	333.1831	167.0952			3
14	1345.6404	673.3238	1327.6168	664.3121	1327.6298	664.3186	A	***251.1412***	126.0743	233.1177	117.0625			2
15							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GLLTSVQDTASSVAR

AT4G22240.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
109.8	1522.7329	-0.0004	GLLTSVQDTASSVAR
0.8	1522.7282	0.0043	MAVTKLDPDSVRR

AT4G22300.1

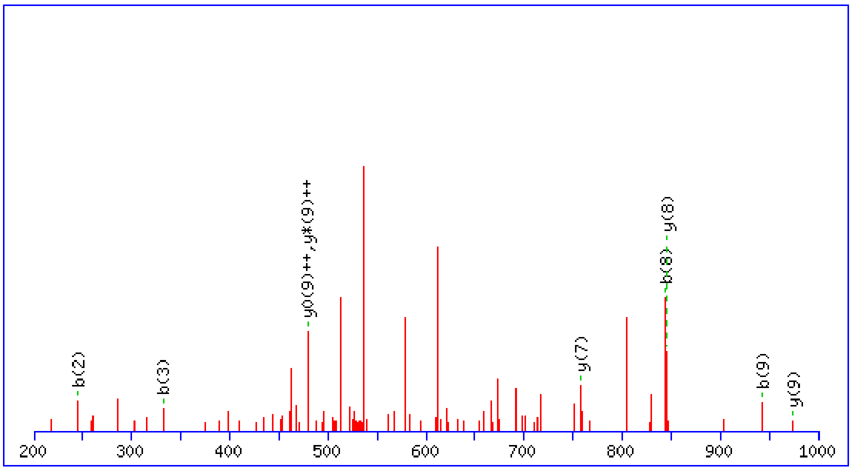
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DESSLLKAVK**
Found in **AT4G22300.1** in **TAIR_Arabidopsis**, Symbols: SOBER1 | SOBER1 (SUPPRESSOR OF AVRBST-ELICITED RESISTANCE 1); carboxylesterase | chr4:11787572-11791067 REVERSE

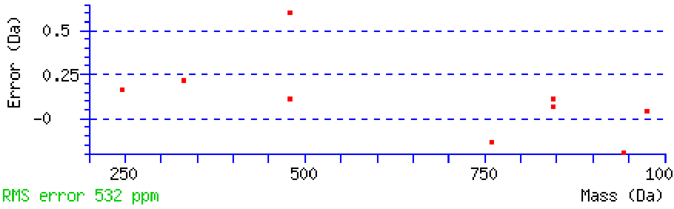
Match to Query 3328: 1088.610434 from(545.312493,2+) index(7921)
Title: Elution from: 69.611 to 69.611 scan no 10352 cid35.00 polarity:+
Data file D12h-1_2.mgf

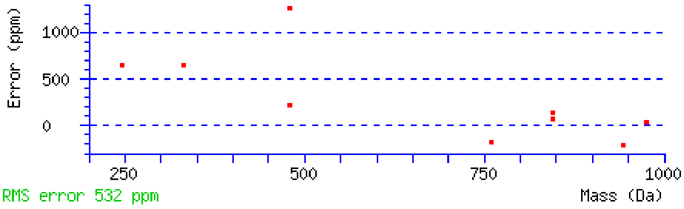
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1088.6077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.045
Matches : 9/84 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							10
2	***245.0768***	123.0420			227.0662	114.0368	E	***974.5881***	487.7977	957.5615	479.2844	956.5775	478.7924	9
3	***332.1088***	166.5581			314.0983	157.5528	S	***845.5455***	423.2764	828.5189	414.7631	827.5349	414.2711	8
4	419.1409	210.0741			401.1303	201.0688	S	***758.5135***	379.7604	741.4869	371.2471	740.5029	370.7551	7
5	532.2249	266.6161			514.2144	257.6108	L	671.4814	336.2443	654.4549	327.7311			6
6	645.3090	323.1581			627.2984	314.1529	L	558.3974	279.7023	541.3708	271.1890			5
7	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	K	445.3133	223.1603	428.2867	214.6470			4
8	***844.4411***	422.7242	827.4145	414.2109	826.4305	413.7189	A	317.2183	159.1128	300.1918	150.5995			3
9	***943.5095***	472.2584	926.4829	463.7451	925.4989	463.2531	V	246.1812	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DESSLLKAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G22300.1

Score	Mr(calc)	Delta	Sequence
20.9	1088.6077	0.0027	DESSLLKAVK
7.5	1088.6124	-0.0020	REIIKGSMR
5.1	1088.6077	0.0027	DEKSLKELK
4.2	1088.6124	-0.0020	MLAEKRIGR
1.2	1088.6124	-0.0020	LMLEQRRK
0.6	1088.6091	0.0014	FKRQTPQGK

AT4G22670.1

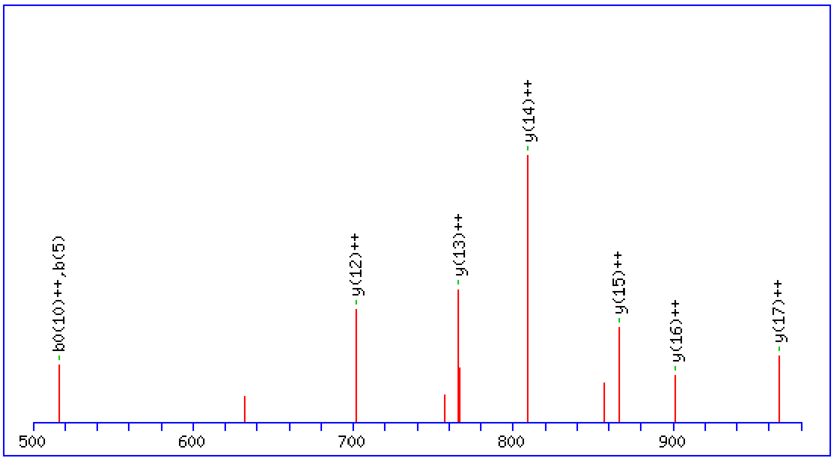
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMEALSEGNFDEAIEHLTR**
Found in **AT4G22670.1** in **TAIR_Arabidopsis**, Symbols: ATHIP1 | ATHIP1 (ARABIDOPSIS THALIANA HSP70-INTERACTING PROTEIN 1); binding | chr4:11918247-11920682 FORWARD

Match to Query 9643: 2131.986357 from(711.669395,3+) index(9181)
Title: Elution from: 81.145 to 81.145 scan no 12349 cid35.00 polarity:+
Data file D1d-3_2.mgf

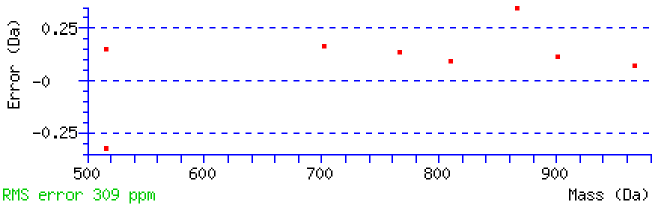
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 980 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

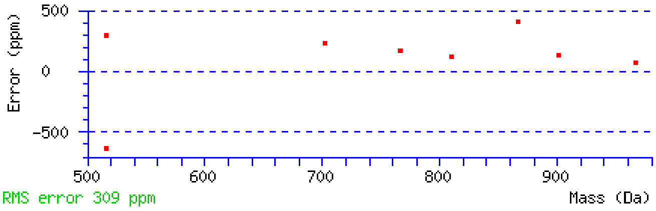


Monoisotopic mass of neutral peptide Mr(calc): 2131.9844
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 8.7e-005
Matches : 8/194 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							19
2	203.0849	102.0461					M	2061.9546	1031.4809	2044.9280	1022.9677	2043.9440	1022.4757	18
3	332.1275	166.5674			314.1169	157.5621	E	1930.9141	965.9607	1913.8876	957.4474	1912.9035	956.9554	17
4	403.1646	202.0859			385.1540	193.0806	A	1801.8715	901.4394	1784.8450	892.9261	1783.8610	892.4341	16
5	516.2486	258.6280			498.2381	249.6227	L	1730.8344	865.9208	1713.8079	857.4076	1712.8238	856.9156	15
6	603.2807	302.1440			585.2701	293.1387	S	1617.7503	809.3788	1600.7238	800.8655	1599.7398	800.3735	14
7	732.3233	366.6653			714.3127	357.6600	E	1530.7183	765.8628	1513.6918	757.3495	1512.7077	756.8575	13
8	789.3447	395.1760			771.3342	386.1707	G	1401.6757	701.3415	1384.6492	692.8282	1383.6652	692.3362	12
9	903.3877	452.1975	886.3611	443.6842	885.3771	443.1922	N	1344.6543	672.8308	1327.6277	664.3175	1326.6437	663.8255	11
10	1050.4561	525.7317	1033.4295	517.2184	1032.4455	516.7264	F	1230.6113	615.8093	1213.5848	607.2960	1212.6008	606.8040	10
11	1165.4830	583.2451	1148.4565	574.7319	1147.4725	574.2399	D	1083.5429	542.2751	1066.5164	533.7618	1065.5323	533.2698	9
12	1294.5256	647.7664	1277.4991	639.2532	1276.5150	638.7612	E	968.5160	484.7616	951.4894	476.2483	950.5054	475.7563	8
13	1365.5627	683.2850	1348.5362	674.7717	1347.5522	674.2797	A	839.4734	420.2403	822.4468	411.7271	821.4628	411.2350	7
14	1478.6468	739.8270	1461.6202	731.3138	1460.6362	730.8217	I	768.4363	384.7218	751.4097	376.2085	750.4257	375.7165	6
15	1607.6894	804.3483	1590.6628	795.8351	1589.6788	795.3430	E	655.3522	328.1797	638.3257	319.6665	637.3416	319.1745	5
16	1744.7483	872.8778	1727.7217	864.3645	1726.7377	863.8725	H	526.3096	263.6584	509.2831	255.1452	508.2990	254.6532	4
17	1857.8324	929.4198	1840.8058	920.9065	1839.8218	920.4145	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
18	1958.8800	979.9437	1941.8535	971.4304	1940.8695	970.9384	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT4G22670.1





NCBI **BLAST** search of AMEALSEGNFDEAIEHLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.2	2131.9844	0.0020	AMEALSEGNFDEAIEHLTR

Mascot: http://www.matrixscience.com/

AT4G23100.1

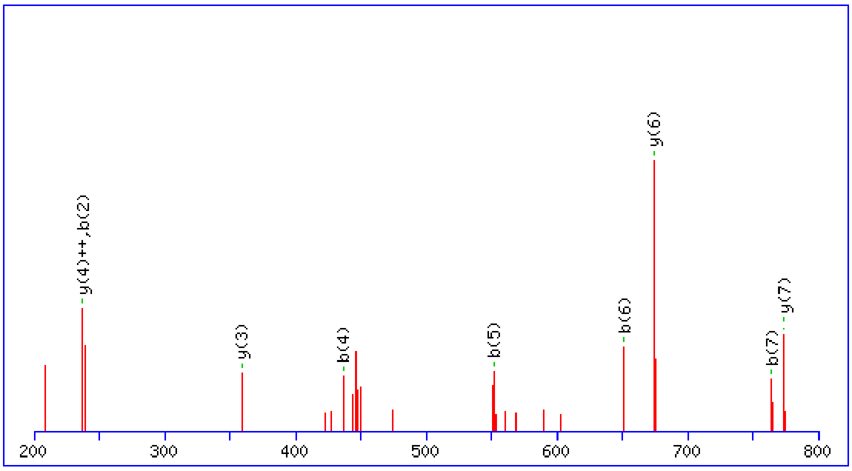
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVAEDVLK**
Found in **AT4G23100.1** in **TAIR_Arabidopsis**, Symbols: GSH1, CAD2, PAD2, RML1 | RML1 (ROOT MERISTEMLESS 1); glutamate-cysteine ligase | chr4:12103469-12106762 REVERSE

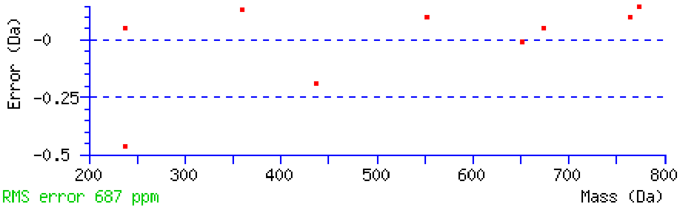
Match to Query 1640: 909.492628 from(455.753590,2+) index(684)
Title: Elution from: 11.615 to 11.615 scan no 973 cid35.00 polarity:+
Data file D12h-3_3.mgf

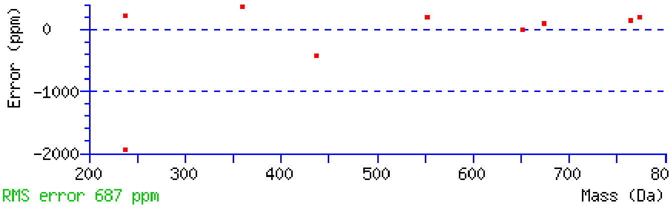
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 909.4920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0001
Matches : 9/58 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367			H							8
2	***237.1346***	119.0709			V	**773.4403**	387.2238	756.4138	378.7105	755.4298	378.2185	7
3	308.1717	154.5895			A	**674.3719**	337.6896	657.3454	329.1763	656.3614	328.6843	6
4	***437.2143***	219.1108	419.2037	210.1055	E	603.3348	302.1710	586.3083	293.6578	585.3243	293.1658	5
5	***552.2413***	276.6243	534.2307	267.6190	D	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
6	***651.3097***	326.1585	633.2991	317.1532	V	**359.2653**	180.1363	342.2387	171.6230			3
7	***764.3937***	382.7005	746.3832	373.6952	L	260.1969	130.6021	243.1703	122.0888			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HVAEDVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.5	909.4920	0.0007	HVAEDVLK

AT4G23100.1

4.3	909.4920	0.0007	YRETTIK
0.2	909.4933	-0.0007	HGRIYHK

Mascot: http://www.matrixscience.com/

AT4G23600.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGWLTLHDLDGVFR**
Found in **AT4G23600.1** in **TAIR_Arabidopsis**, Symbols: JR2, CORI3 | CORI3 (CORONATINE INDUCED 1, JASMONIC ACID RESPONSIVE 2); transaminase | chr4:12310667-12312895 FORWARD

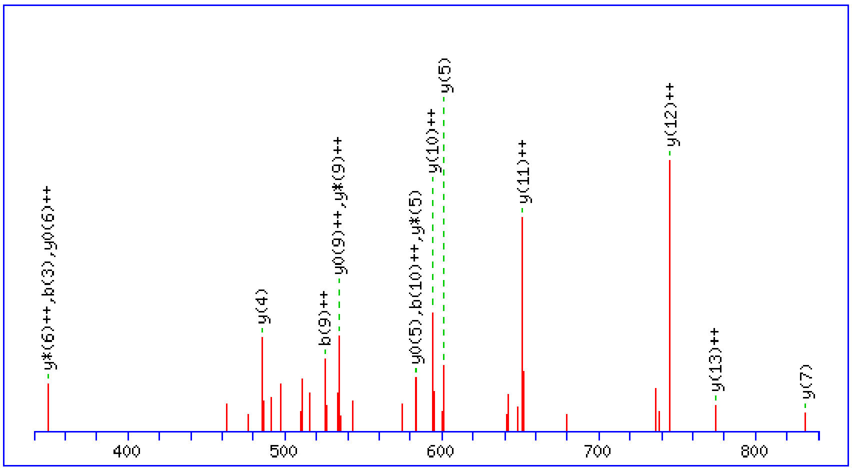
Match to Query 7738: 1648.770285 from(550.597371,3+) index(10029)
Title: Elution from: 92.097 to 92.097 scan no 13934 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 340 to 840 Da Full range

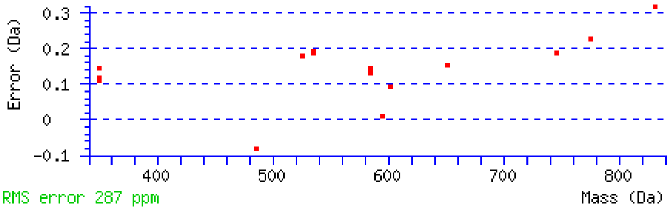
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

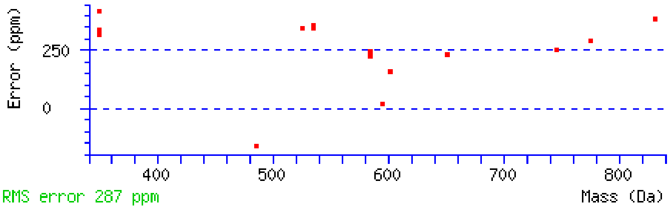


Monoisotopic mass of neutral peptide Mr(calc): 1648.7717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00021
Matches : 16/122 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							14
2	161.0705	81.0389	143.0599	72.0336	G	1547.7344	774.3708	1529.7108	765.3590	1529.7238	765.3655	13
3	349.1439	175.0756	331.1333	166.0703	W	1489.7159	745.3616	1471.6923	736.3498	1471.7053	736.3563	12
4	463.2250	232.1161	445.2144	223.1108	L	1301.6425	651.3249	1283.6189	642.3131	1283.6319	642.3196	11
5	565.2697	283.1385	547.2591	274.1332	T	1187.5614	594.2843	1169.5378	585.2725	1169.5508	585.2790	10
6	679.3508	340.1790	661.3402	331.1737	L	1085.5167	543.2620	1067.4931	534.2502	1067.5061	534.2567	9
7	819.4008	410.2040	801.3902	401.1988	H	971.4356	486.2214	953.4120	477.2096	953.4250	477.2161	8
8	935.4248	468.2160	917.4142	459.2107	D	***831.3855***	416.1964	813.3620	407.1846	813.3750	407.1911	7
9	1049.5059	**525.2566**	1031.4953	516.2513	L	715.3616	358.1844	697.3380	349.1726	697.3510	349.1791	6
10	1165.5299	**583.2686**	1147.5193	574.2633	D	***601.2805***	301.1439	583.2569	292.1321	583.2699	292.1386	5
11	1223.5484	612.2778	1205.5378	603.2725	G	***485.2565***	243.1319	467.2329	234.1201			4
12	1323.6138	662.3105	1305.6032	653.3053	V	427.2380	214.1226	409.2144	205.1108			3
13	1471.6793	736.3433	1453.6687	727.3380	F	327.1725	164.0899	309.1490	155.0781			2
14					R	179.1071	90.0572	161.0835	81.0454			1



RMS error 287 ppm



RMS error 287 ppm

NCBI **BLAST** search of TGWLTLHDLDGVFR

AT4G23600.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.2	1648.7717	-0.0015	TGWLTLHDLDGVFR
4.3	1648.7695	0.0007	WTGIPLSNLQQSER
2.7	1648.7722	-0.0019	RLNRWVEPESPSR
1.9	1648.7669	0.0034	ASAEVLGKGSYGTTYK
1.9	1648.7704	-0.0001	MVFISCHLSAHAKK
1.7	1648.7700	0.0003	RRLGSETNGIHQEK

AT4G23650.1

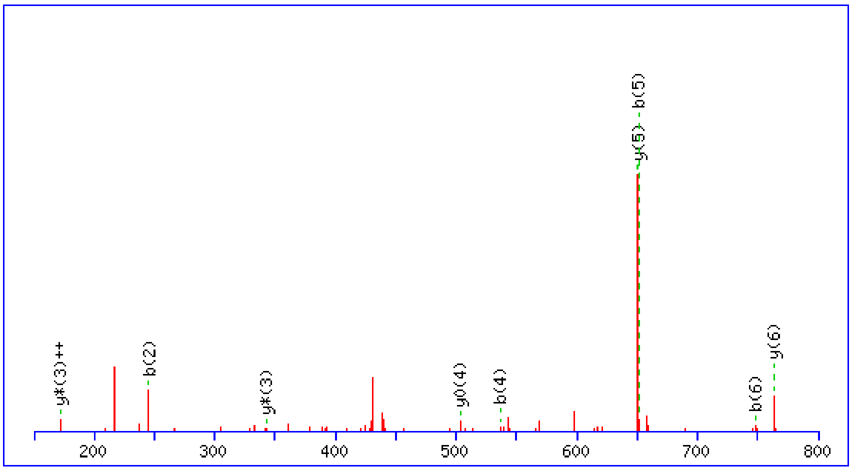
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLKYDPK**
Found in **AT4G23650.1** in **TAIR_Arabidopsis**, Symbols: CPK3, CDPK6 | CDPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); calmodulin-dependent protein kinase/ kinase | chr4:12324977-12327425 REVERSE

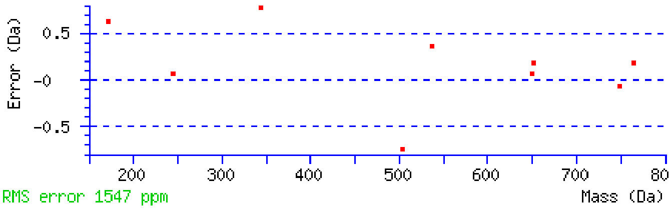
Match to Query 1619: 893.468248 from(447.741400,2+) index(5953)
Title: Elution from: 52.767 to 52.767 scan no 7517 cid35.00 polarity:+
Data file 0-2_1.mgf

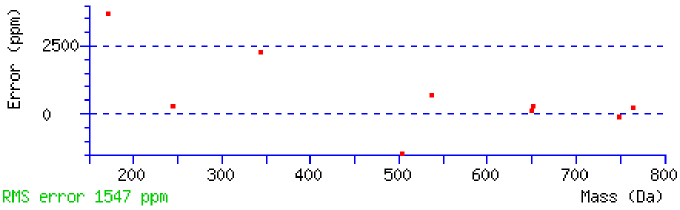
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 893.4680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.029
Matches : 9/56 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							7
2	***245.1318***	123.0696					L	**763.4349**	382.2211	746.4083	373.7078	745.4243	373.2158	6
3	373.2268	187.1170	356.2002	178.6038			K	**650.3508**	325.6790	633.3243	317.1658	632.3402	316.6738	5
4	***536.2901***	268.6487	519.2636	260.1354			Y	522.2558	261.6316	505.2293	253.1183	504.2453	252.6263	4
5	***651.3171***	326.1622	634.2905	317.6489	633.3065	317.1569	D	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
6	***748.3698***	374.6886	731.3433	366.1753	730.3593	365.6833	P	244.1656	122.5864	227.1390	114.0731			2
7							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of MLKYDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	893.4680	0.0002	MLKYDPK
17.4	893.4681	0.0002	MLFDIQK

AT4G23650.1

15.2	893.4681	0.0002	MLDQFLK
9.0	893.4681	0.0002	LMDQLFK

Mascot: http://www.matrixscience.com/

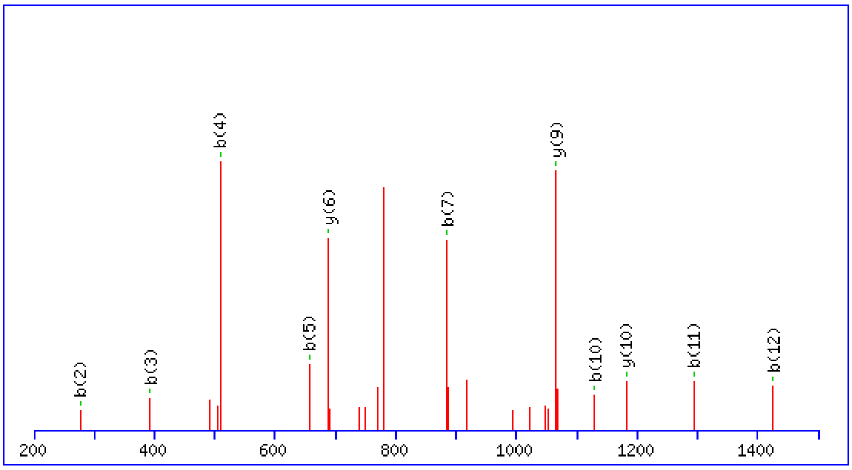
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNDDFPEPSGYMK**
Found in **AT4G23670.1** in **TAIR_Arabidopsis**, Symbols: | major latex protein-related / MLP-related | chr4:12332856-12333666 REVERSE

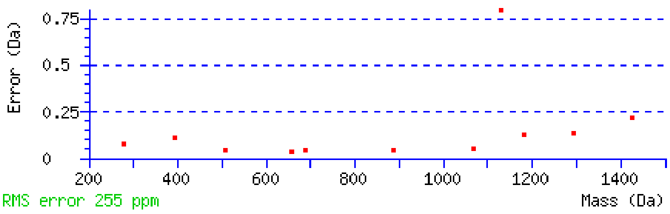
Match to Query 6814: 1572.625098 from(787.319825,2+) index(3543)
Title: Elution from: 34.390 to 34.390 scan no 4434 cid35.00 polarity:+
Data file D6h-1_3.mgf

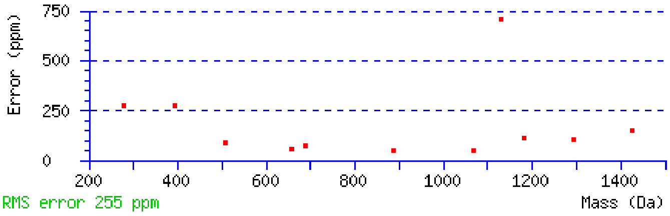
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1572.6239
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 1.2e-008
Matches : 11/132 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							13
2	*277.1335*	139.0704	259.1099	130.0586			N	1413.5419	707.2746	1395.5184	698.2628	1395.5314	698.2693	12
3	*393.1575*	197.0824	375.1339	188.0706	375.1469	188.0771	D	1297.5050	649.2561	1279.4814	640.2443	1279.4944	640.2508	11
4	*509.1815*	255.0944	491.1579	246.0826	491.1709	246.0891	D	**1181.4810**	591.2441	1163.4574	582.2323	1163.4704	582.2388	10
5	*657.2469*	329.1271	639.2233	320.1153	639.2364	320.1218	F	**1065.4570**	533.2321	1047.4334	524.2203	1047.4464	524.2269	9
6	755.2967	378.1520	737.2731	369.1402	737.2862	369.1467	P	917.3915	459.1994	899.3680	450.1876	899.3810	450.1941	8
7	*885.3364*	443.1718	867.3128	434.1600	867.3258	434.1665	E	819.3417	410.1745	801.3182	401.1627	801.3312	401.1692	7
8	983.3862	492.1967	965.3626	483.1849	965.3756	483.1914	P	**689.3021**	345.1547	671.2785	336.1429	671.2916	336.1494	6
9	1071.4152	536.2112	1053.3916	527.1995	1053.4047	527.2060	S	591.2523	296.1298	573.2287	287.1180	573.2418	287.1245	5
10	*1129.4337*	565.2205	1111.4101	556.2087	1111.4232	556.2152	G	503.2233	252.1153	485.1997	243.1035			4
11	*1293.4941*	647.2507	1275.4705	638.2389	1275.4835	638.2454	Y	445.2048	223.1060	427.1812	214.0942			3
12	*1425.5316*	713.2694	1407.5080	704.2576	1407.5210	704.2642	M	281.1444	141.0758	263.1208	132.0640			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RNDDFPEPSGYMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G23670.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.1	1572.6239	0.0012	RNDDFPEPSGYMK
7.0	1572.6221	0.0030	ARRDGEMGSSSPER
3.3	1572.6298	-0.0047	GQQSTVETESMQSK

Mascot: http://www.matrixscience.com/

AT4G23850.1

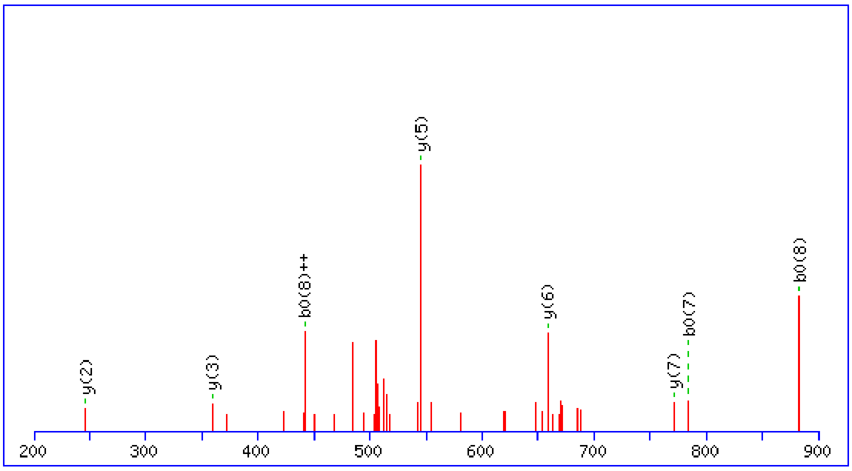
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFILGELVK**
Found in **AT4G23850.1** in **TAIR_Arabidopsis**, Symbols: | long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase | chr4:12403730-12408273 REVERSE

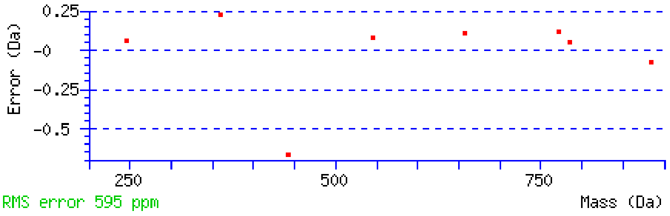
Match to Query 3132: 1046.600934 from(524.307743,2+) index(8936)
Title: Elution from: 78.569 to 78.569 scan no 11851 cid35.00 polarity:+
Data file D1d-3_1.mgf

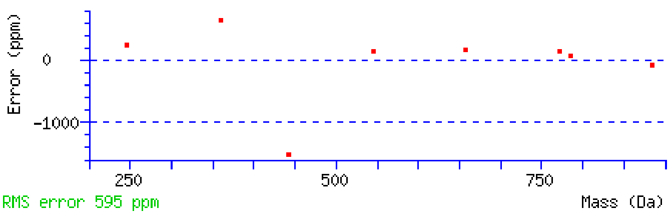
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1046.6012
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.01
Matches : 8/74 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							9
2	277.1183	139.0628	259.1077	130.0575	F	918.5659	459.7866	901.5393	451.2733	900.5553	450.7813	8
3	390.2023	195.6048	372.1918	186.5995	I	***771.4975***	386.2524	754.4709	377.7391	753.4869	377.2471	7
4	503.2864	252.1468	485.2758	243.1416	L	***658.4134***	329.7103	641.3869	321.1971	640.4028	320.7051	6
5	560.3079	280.6576	542.2973	271.6523	G	***545.3293***	273.1683	528.3028	264.6550	527.3188	264.1630	5
6	689.3505	345.1789	671.3399	336.1736	E	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
7	802.4345	401.7209	784.4240	392.7156	L	***359.2653***	180.1363	342.2387	171.6230			3
8	901.5029	451.2551	883.4924	442.2498	V	***246.1812***	123.5942	229.1547	115.0810			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EFILGELVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G23850.1

25.3	1046.6012	-0.0002	EFILGELVK

Mascot: http://www.matrixscience.com/

AT4G24190.1

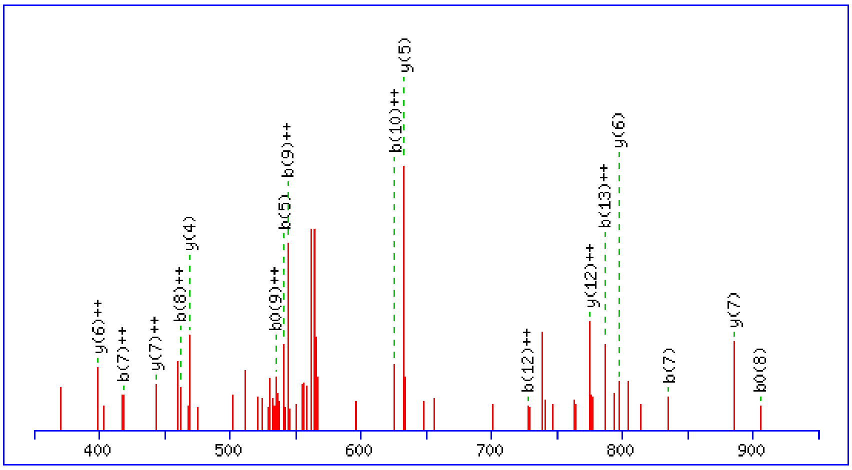
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APHDLYESYYNSNK**
Found in **AT4G24190.1** in **TAIR_Arabidopsis**, Symbols: SHD | SHD (SHEPHERD); ATP binding | chr4:12551912-12555861 REVERSE

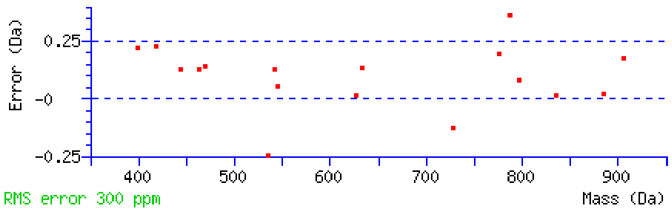
Match to Query 7952: 1718.692680 from(573.904836,3+) index(3309)
Title: Elution from: 30.694 to 30.694 scan no 4034 cid35.00 polarity:+
Data file D1d-3_3.mgf

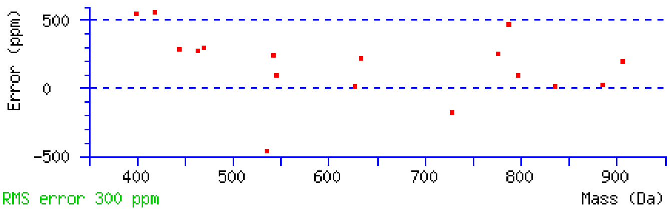
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1718.6915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.047
Matches : 17/126 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							14
2	171.0912	86.0492					P	1647.6646	824.3359	1629.6410	815.3241	1629.6540	815.3307	13
3	311.1412	156.0743					H	1549.6148	775.3110	1531.5912	766.2992	1531.6042	766.3058	12
4	427.1652	214.0862			409.1547	205.0810	D	1409.5648	705.2860	1391.5412	696.2742	1391.5542	696.2808	11
5	541.2463	271.1268			523.2358	262.1215	L	1293.5408	647.2740	1275.5172	638.2623	1275.5302	638.2688	10
6	705.3067	353.1570			687.2961	344.1517	Y	1179.4597	590.2335	1161.4361	581.2217	1161.4491	581.2282	9
7	835.3463	***418.1768***			817.3357	409.1715	E	1015.3993	508.2033	997.3758	499.1915	997.3888	499.1980	8
8	923.3754	***462.1913***			905.3648	453.1860	S	**885.3597**	443.1835	867.3361	434.1717	867.3492	434.1782	7
9	1087.4357	***544.2215***			1069.4252	535.2162	Y	**797.3307**	399.1690	779.3071	390.1572	779.3201	390.1637	6
10	1251.4961	***626.2517***			1233.4855	617.2464	Y	**633.2703**	317.1388	615.2467	308.1270	615.2597	308.1335	5
11	1367.5331	684.2702	1349.5095	675.2584	1349.5225	675.2649	N	**469.2099**	235.1086	451.1863	226.0968	451.1994	226.1033	4
12	1455.5622	***728.2847***	1437.5386	719.2729	1437.5516	719.2794	S	353.1729	177.0901	335.1493	168.0783	335.1624	168.0848	3
13	1571.5992	***786.3032***	1553.5756	777.2914	1553.5886	777.2979	N	265.1439	133.0756	247.1203	124.0638			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of APHDLYESYYNSNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G24190.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.7	1718.6915	0.0012	APHDLYESYYNSNK
0.1	1718.6948	-0.0022	GTHGYMDPTYISTNK

AT4G24280.1

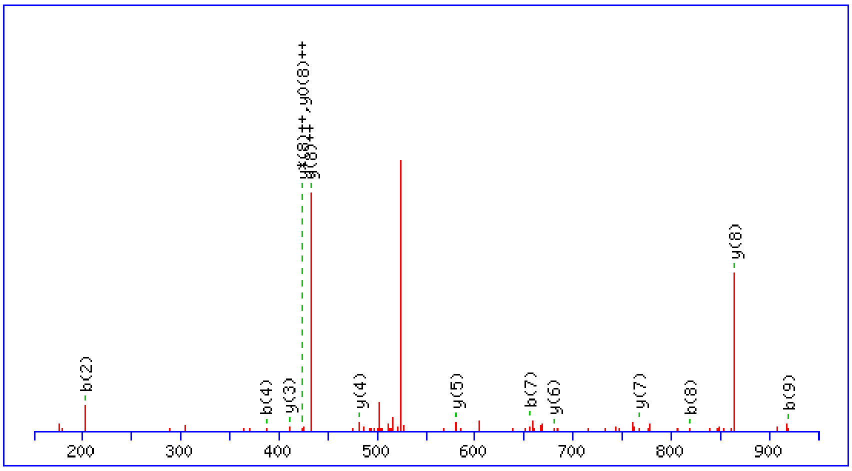
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTPSVVAYTK**
Found in **AT4G24280.1** in **TAIR_Arabidopsis**, Symbols: CPHSC70-1 | CPHSC70-1 (chloroplast heat shock protein 70-1); ATP binding / unfolded protein binding | chr4:12590104-12593447 FORWARD

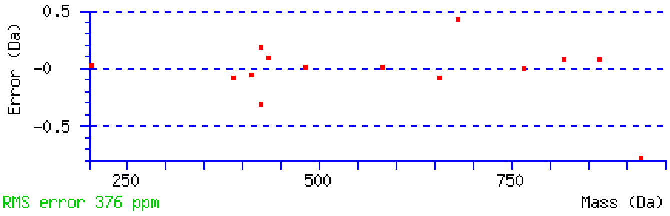
Match to Query 3266: 1065.570584 from(533.792568,2+) index(2195)
Title: Elution from: 25.463 to 25.463 scan no 2822 cid35.00 polarity:+
Data file 0-1_1.mgf

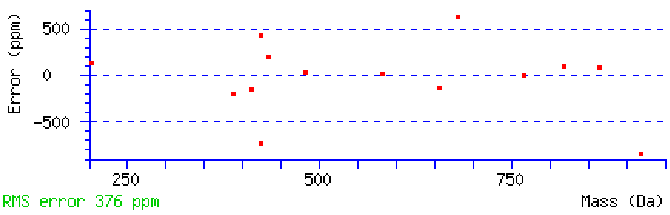
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1065.5706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0063
Matches : 14/88 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	***203.1026***	102.0550	185.0921	93.0497	T	965.5302	483.2688	948.5037	474.7555	947.5197	474.2635	9
3	300.1554	150.5813	282.1448	141.5761	P	***864.4825***	432.7449	847.4560	424.2316	846.4720	423.7396	8
4	***387.1874***	194.0974	369.1769	185.0921	S	***767.4298***	384.2185	750.4032	375.7053	749.4192	375.2132	7
5	486.2558	243.6316	468.2453	234.6263	V	***680.3978***	340.7025	663.3712	332.1892	662.3872	331.6972	6
6	585.3243	293.1658	567.3137	284.1605	V	***581.3293***	291.1683	564.3028	282.6550	563.3188	282.1630	5
7	***656.3614***	328.6843	638.3508	319.6790	A	***482.2609***	241.6341	465.2344	233.1208	464.2504	232.6288	4
8	***819.4247***	410.2160	801.4141	401.2107	Y	***411.2238***	206.1155	394.1973	197.6023	393.2132	197.1103	3
9	***920.4724***	460.7398	902.4618	451.7345	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TTPSVVAYTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G24280.1

Score	Mr(calc)	Delta	Sequence
28.5	1065.5706	-0.0000	TTPSVVAYTK
0.3	1065.5706	-0.0000	SSLLVDSFAK

AT4G24770.1

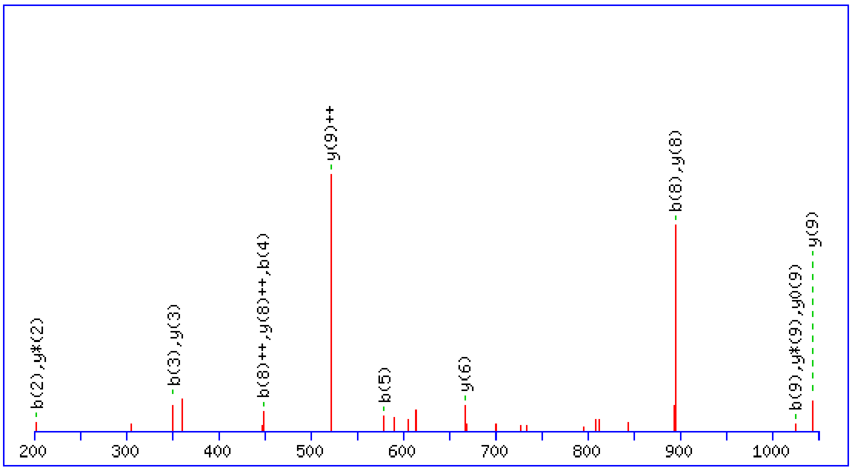
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEFPEPSEEAK**
Found in **AT4G24770.1** in **TAIR_Arabidopsis**, Symbols: ATRBP31, CP31, ATRBP33, RBP31 | RBP31 (31-KDA RNA BINDING PROTEIN); RNA binding / poly(U) binding | chr4:12766233-12767962 REVERSE

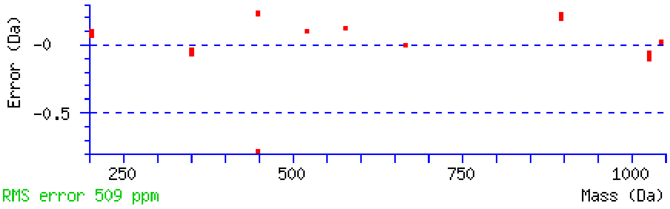
Match to Query 4661: 1244.519980 from(623.267266,2+) index(2432)
Title: Elution from: 27.003 to 27.003 scan no 3088 cid35.00 polarity:+
Data file 0-1_1.mgf

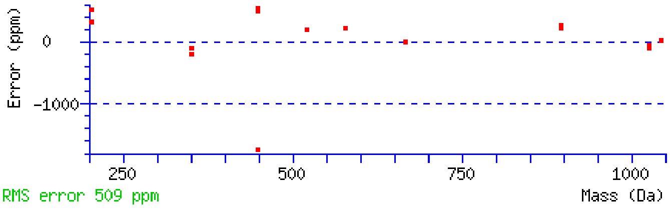
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1244.5205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 2.6e-005
Matches : 16/94 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							11
2	***203.0811***	102.0442	185.0705	93.0389	E	1173.4936	587.2505	1155.4701	578.2387	1155.4831	578.2452	10
3	***351.1465***	176.0769	333.1359	167.0716	F	**1043.4540**	522.2306	1025.4304	513.2189	1025.4435	513.2254	9
4	***449.1963***	225.1018	431.1857	216.0965	P	**895.3886**	448.1979	877.3650	439.1861	877.3780	439.1926	8
5	***579.2359***	290.1216	561.2254	281.1163	E	797.3388	399.1730	779.3152	390.1612	779.3282	390.1677	7
6	677.2857	339.1465	659.2752	330.1412	P	**667.2991**	334.1532	649.2756	325.1414	649.2886	325.1479	6
7	765.3148	383.1610	747.3042	374.1558	S	569.2493	285.1283	551.2258	276.1165	551.2388	276.1230	5
8	***895.3544***	448.1808	877.3439	439.1756	E	481.2203	241.1138	463.1967	232.1020	463.2097	232.1085	4
9	***1025.3940***	513.2007	1007.3835	504.1954	E	**351.1807**	176.0940	333.1571	167.0822	333.1701	167.0887	3
10	1097.4282	549.2177	1079.4176	540.2125	A	221.1410	111.0741	203.1174	102.0624			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AEFPEPSEEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G24770.1

Score	Mr(calc)	Delta	Sequence
50.1	1244.5205	-0.0005	AEFPEPSEEAK
0.6	1244.5218	-0.0018	MSKMKDFGGGR
0.4	1244.5232	-0.0032	YSRNFESEAK
0.3	1244.5184	0.0015	QASSAQGFFMR

AT4G24820.1

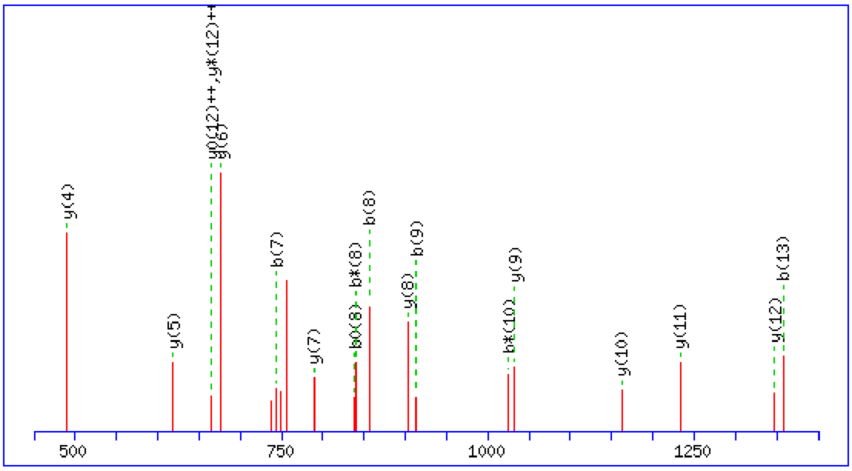
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IADAEENLGESEVR**
Found in **AT4G24820.1** in **TAIR_Arabidopsis**, Symbols: | 26S proteasome regulatory subunit, putative (RPN7) | chr4:12790481-12792609 REVERSE

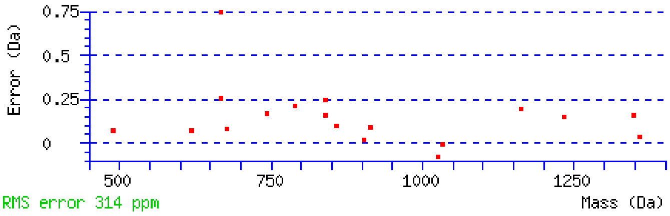
Match to Query 6678: 1530.716466 from(766.365509,2+) index(3009)
Title: Elution from: 29.154 to 29.154 scan no 3709 cid35.00 polarity:+
Data file D1d-3_2.mgf

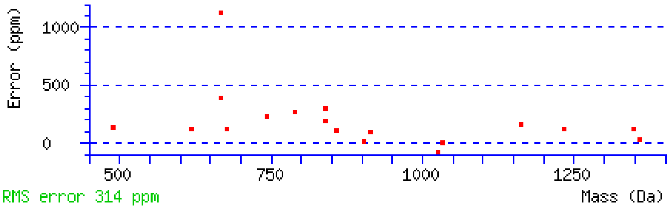
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1530.7161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 3.2e-010
Matches : 18/136 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							14
2	185.1285	93.0679					A	1418.6394	709.8233	1401.6128	701.3101	1400.6288	700.8181	13
3	300.1554	150.5813			282.1448	141.5761	D	***1347.6023***	674.3048	1330.5757	665.7915	1329.5917	665.2995	12
4	371.1925	186.0999			353.1819	177.0946	A	***1232.5753***	616.7913	1215.5488	608.2780	1214.5648	607.7860	11
5	500.2351	250.6212			482.2245	241.6159	E	***1161.5382***	581.2727	1144.5117	572.7595	1143.5277	572.2675	10
6	629.2777	315.1425			611.2671	306.1372	E	***1032.4956***	516.7515	1015.4691	508.2382	1014.4851	507.7462	9
7	**743.3206**	372.1640	726.2941	363.6507	725.3101	363.1587	N	***903.4530***	452.2302	886.4265	443.7169	885.4425	443.2249	8
8	**856.4047**	428.7060	839.3781	420.1927	838.3941	419.7007	L	***789.4101***	395.2087	772.3836	386.6954	771.3995	386.2034	7
9	**913.4262**	457.2167	896.3996	448.7034	895.4156	448.2114	G	***676.3260***	338.6667	659.2995	330.1534	658.3155	329.6614	6
10	1042.4687	521.7380	1025.4422	513.2247	1024.4582	512.7327	E	***619.3046***	310.1559	602.2780	301.6427	601.2940	301.1506	5
11	1129.5008	565.2540	1112.4742	556.7408	1111.4902	556.2487	S	***490.2620***	245.6346	473.2354	237.1214	472.2514	236.6293	4
12	1258.5434	629.7753	1241.5168	621.2620	1240.5328	620.7700	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
13	**1357.6118**	679.3095	1340.5852	670.7963	1339.6012	670.3042	V	274.1874	137.5973	257.1608	129.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IADAEENLGESEVR

AT4G24820.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
99.5	1530.7161	0.0003	IADAEENLGESEVR

Mascot: http://www.matrixscience.com/

AT4G24830.1

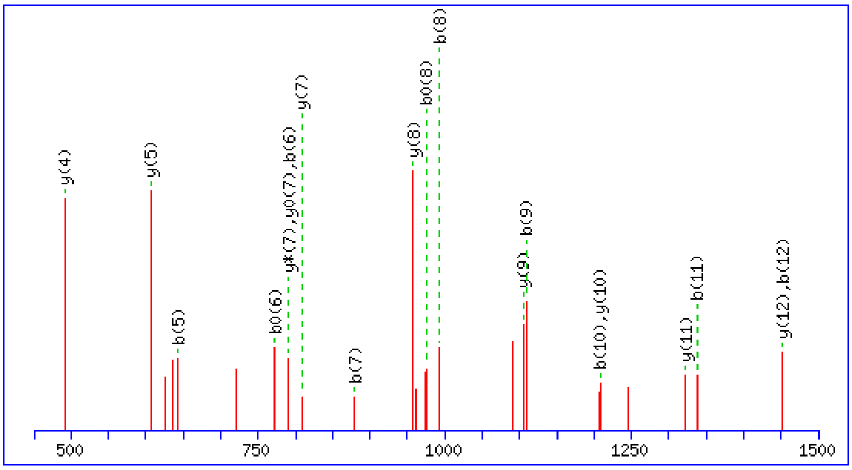
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FELTFFSLNPELK**
Found in **AT4G24830.1** in **TAIR_Arabidopsis**, Symbols: | arginosuccinate synthase family | chr4:12793095-12795867 REVERSE

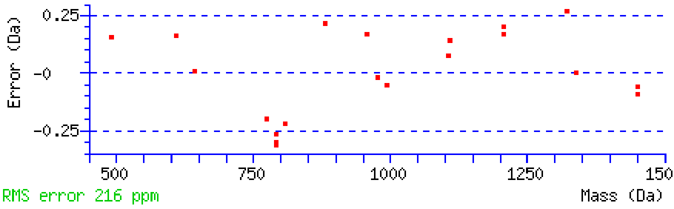
Match to Query 7200: 1598.781410 from(800.397981,2+) index(10604)
Title: Elution from: 103.574 to 103.574 scan no 15308 cid35.00 polarity:+
Data file D6h-1_2.mgf

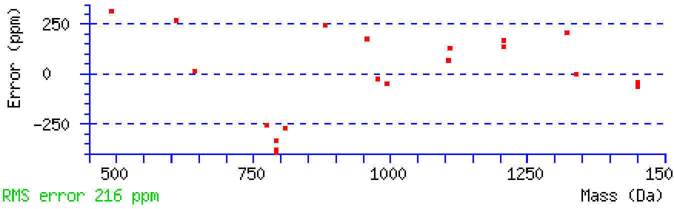
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1598.7791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 6.1e-009
Matches : 20/122 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							13
2	279.1124	140.0598			261.1018	131.0545	E	***1451.7209***	726.3641	1433.6973	717.3523	1433.7103	717.3588	12
3	393.1935	197.1004			375.1829	188.0951	L	***1321.6813***	661.3443	1303.6577	652.3325	1303.6707	652.3390	11
4	495.2382	248.1227			477.2276	239.1174	T	***1207.6002***	604.3037	1189.5766	595.2919	1189.5896	595.2984	10
5	***643.3036***	322.1554			625.2930	313.1502	F	***1105.5555***	553.2814	1087.5319	544.2696	1087.5449	544.2761	9
6	***791.3691***	396.1882			773.3585	387.1829	F	***957.4900***	479.2486	939.4664	470.2368	939.4794	470.2434	8
7	***879.3981***	440.2027			861.3876	431.1974	S	***809.4246***	405.2159	791.4010	396.2041	791.4140	396.2106	7
8	***993.4792***	497.2433			975.4687	488.2380	L	721.3955	361.2014	703.3719	352.1896	703.3849	352.1961	6
9	***1109.5162***	555.2617	1091.4926	546.2500	1091.5057	546.2565	N	***607.3144***	304.1608	589.2908	295.1490	589.3038	295.1556	5
10	***1207.5660***	604.2866	1189.5424	595.2749	1189.5555	595.2814	P	***491.2774***	246.1423	473.2538	237.1305	473.2668	237.1371	4
11	***1337.6056***	669.3065	1319.5821	660.2947	1319.5951	660.3012	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
12	***1451.6867***	726.3470	1433.6632	717.3352	1433.6762	717.3417	L	263.1880	132.0976	245.1644	123.0858			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FELTFFSLNPELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G24830.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.7	1598.7791	0.0023	FELTFFSLNPELK
9.1	1598.7815	-0.0001	MGNVIIGVMRKAMK
8.3	1598.7791	0.0024	LFKPFDELFVDSK
4.5	1598.7773	0.0041	RSYEVAAAESKQLK
2.4	1598.7829	-0.0015	FTLNQTMESIRLK
2.4	1598.7768	0.0046	FVYDKDVQVTELK
2.3	1598.7829	-0.0015	ISPLPKMVSPENPR
2.2	1598.7802	0.0012	SLLPVEPLVAECEK
1.5	1598.7795	0.0019	QQVQEDVKKFGFK
0.9	1598.7768	0.0046	EFALYVSAISNELK

AT4G24930.1

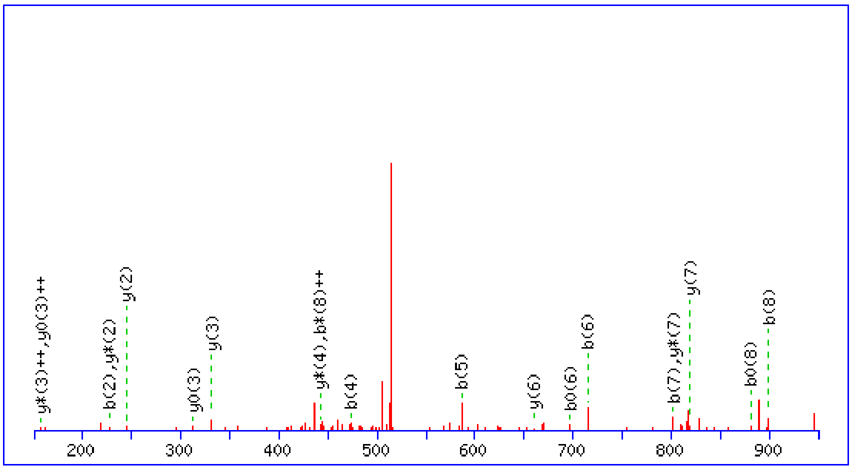
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLCSLQSPK**
Found in **AT4G24930.1** in **TAIR_Arabidopsis**, Symbols: | thylakoid lumenal 17.9 kDa protein, chloroplast | chr4:12821506-12822399 REVERSE

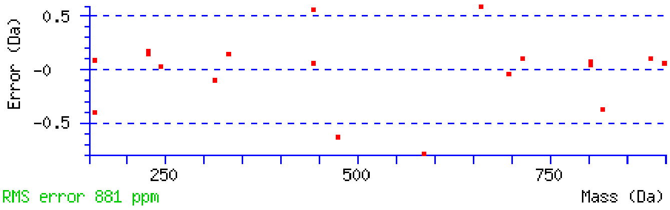
Match to Query 3037: 1044.565722 from(523.290137,2+) index(2408)
Title: Elution from: 26.541 to 26.541 scan no 3062 cid35.00 polarity:+
Data file C7-3_1.mgf

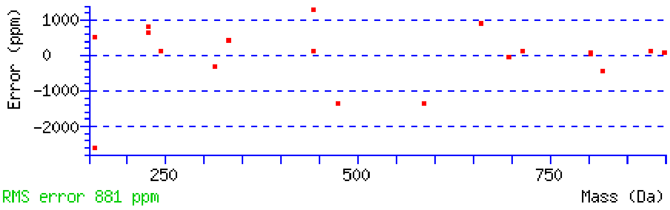
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1044.5638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.033
Matches : 19/76 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							9
2	***227.1754***	114.0913					L	932.4870	466.7471	915.4604	458.2339	914.4764	457.7418	8
3	387.2061	194.1067					C	**819.4029**	410.2051	802.3764	401.6918	801.3924	401.1998	7
4	***474.2381***	237.6227			456.2275	228.6174	S	**659.3723**	330.1898	642.3457	321.6765	641.3617	321.1845	6
5	***587.3221***	294.1647			569.3116	285.1594	L	572.3402	286.6738	555.3137	278.1605	554.3297	277.6685	5
6	***715.3807***	358.1940	698.3542	349.6807	697.3702	349.1887	Q	459.2562	230.1317	442.2296	221.6185	441.2456	221.1264	4
7	***802.4128***	401.7100	785.3862	393.1967	784.4022	392.7047	S	**331.1976**	166.1024	314.1710	157.5892	313.1870	157.0972	3
8	***899.4655***	450.2364	882.4390	441.7231	881.4550	441.2311	P	**244.1656**	122.5864	227.1390	114.0731			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LLCSLQSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.0	1044.5638	0.0020	LLCSLQSPK

AT4G24930.1

18.3	1044.5676	-0.0018	ENLTEKRR
14.8	1044.5676	-0.0019	SSVERRSPK
7.8	1044.5676	-0.0018	RLNEERTK
7.7	1044.5676	-0.0019	REVETQRK
5.5	1044.5676	-0.0019	RTQKEDIR
4.6	1044.5676	-0.0019	QALDSRISR
3.4	1044.5684	-0.0027	RNMMKLPR
3.2	1044.5651	0.0006	MPPKRNFR
3.0	1044.5638	0.0020	TIISDMLPR

AT4G25050.1

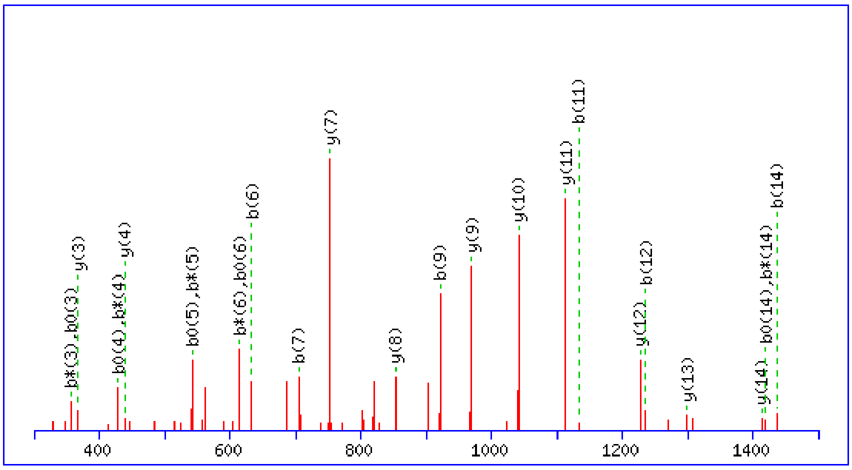
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQLALAADVPLTAESK**
Found in **AT4G25050.1** in **TAIR_Arabidopsis**, Symbols: ACP4 | ACP4 (ACYL CARRIER PROTEIN 4) | chr4:12870188-12871034 FORWARD

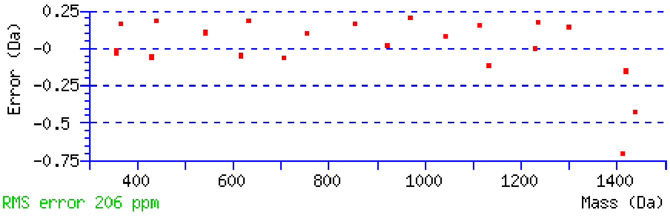
Match to Query 7704: 1672.824512 from(837.419532,2+) index(6832)
Title: Elution from: 59.459 to 59.459 scan no 8837 cid35.00 polarity:+
Data file C7-2_3.mgf

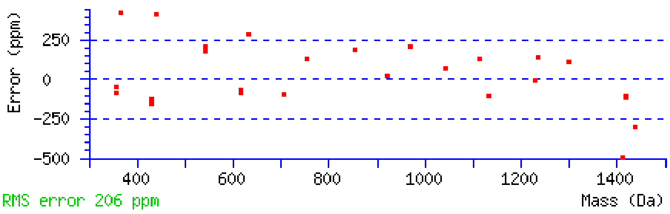
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1672.8244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 6.8e-011
Matches : 26/176 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							16
2	261.0996	131.0534	243.0760	122.0416	243.0890	122.0481	Q	1543.7920	772.3997	1525.7685	763.3879	1525.7815	763.3944	15
3	375.1806	188.0940	357.1571	179.0822	357.1701	179.0887	L	***1413.7394***	707.3733	1395.7158	698.3615	1395.7288	698.3681	14
4	447.2148	224.1110	429.1912	215.0992	429.2042	215.1058	A	***1299.6583***	650.3328	1281.6347	641.3210	1281.6477	641.3275	13
5	561.2959	281.1516	543.2723	272.1398	543.2853	272.1463	L	***1227.6241***	614.3157	1209.6006	605.3039	1209.6136	605.3104	12
6	**633.3300**	317.1687	615.3065	308.1569	615.3195	308.1634	A	***1113.5431***	557.2752	1095.5195	548.2634	1095.5325	548.2699	11
7	**705.3642**	353.1857	687.3406	344.1739	687.3536	344.1805	A	***1041.5089***	521.2581	1023.4853	512.2463	1023.4983	512.2528	10
8	821.3882	411.1977	803.3646	402.1859	803.3776	402.1924	D	***969.4748***	485.2410	951.4512	476.2292	951.4642	476.2357	9
9	**921.4536**	461.2304	903.4300	452.2187	903.4431	452.2252	V	***853.4508***	427.2290	835.4272	418.2172	835.4402	418.2237	8
10	1019.5034	510.2553	1001.4798	501.2436	1001.4929	501.2501	P	***753.3853***	377.1963	735.3617	368.1845	735.3748	368.1910	7
11	**1133.5845**	567.2959	1115.5609	558.2841	1115.5740	558.2906	L	655.3355	328.1714	637.3119	319.1596	637.3250	319.1661	6
12	**1235.6292**	618.3183	1217.6057	609.3065	1217.6187	609.3130	T	541.2544	271.1309	523.2308	262.1191	523.2439	262.1256	5
13	1307.6634	654.3353	1289.6398	645.3235	1289.6528	645.3300	A	***439.2097***	220.1085	421.1861	211.0967	421.1991	211.1032	4
14	**1437.7030**	719.3551	1419.6794	710.3434	1419.6924	710.3499	E	***367.1756***	184.0914	349.1520	175.0796	349.1650	175.0861	3
15	1525.7321	763.3697	1507.7085	754.3579	1507.7215	754.3644	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
16							K	149.1069	75.0571	131.0833	66.0453			1





AT4G25050.1

NCBI **BLAST** search of EQLALAADVPLTAESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.3	1672.8244	0.0001	EQLALAADVPLTAESK

Mascot: http://www.matrixscience.com/

AT4G25090.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLQAETK**
Found in **AT4G25090.1** in **TAIR_Arabidopsis**, Symbols: | respiratory burst oxidase, putative / NADPH oxidase, putative | chr4:12878940-12883609 REVERSE

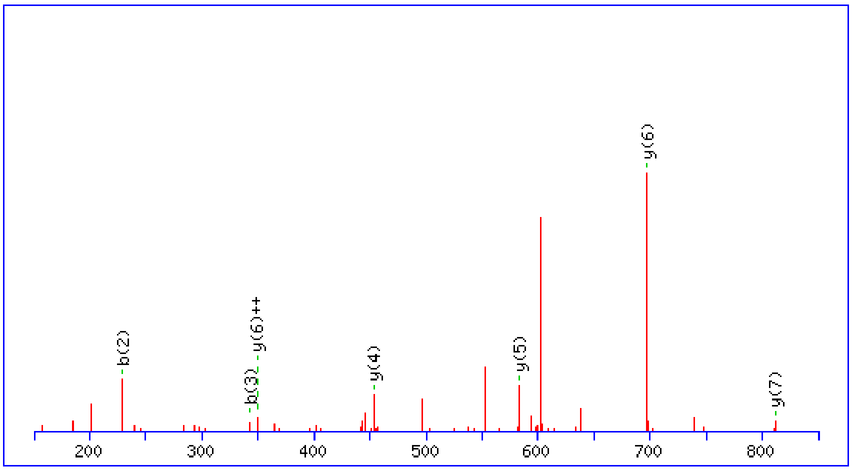
Match to Query 1459: 924.512140 from(463.263346,2+) index(4244)
Title: Elution from: 42.973 to 42.973 scan no 5476 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

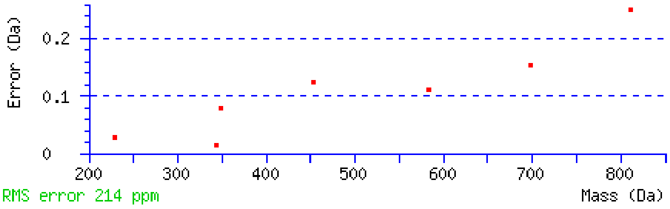
Label all possible matches ○ Label matches used for scoring ●

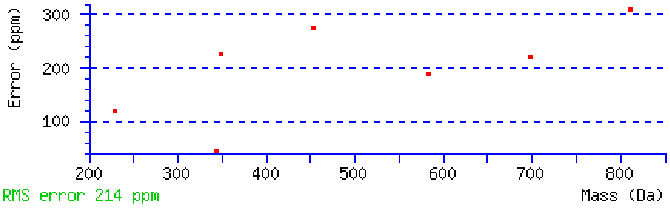
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 924.5140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.015
Matches : 7/66 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					**L**							**8**
2	**229.1695**	115.0884					**L**	***811.4402***	406.2237	793.4166	397.2120	793.4296	397.2185	**7**
3	**343.2506**	172.1289					**L**	***697.3591***	349.1832	679.3355	340.1714	679.3485	340.1779	**6**
4	473.3032	237.1552	455.2796	228.1435			**Q**	***583.2780***	292.1426	565.2544	283.1309	565.2674	283.1374	**5**
5	545.3374	273.1723	527.3138	264.1605			**A**	***453.2254***	227.1163	435.2018	218.1045	435.2148	218.1110	**4**
6	675.3770	338.1921	657.3534	329.1803	657.3664	329.1869	**E**	381.1912	191.0992	363.1676	182.0875	363.1806	182.0940	**3**
7	777.4217	389.2145	759.3981	380.2027	759.4111	380.2092	**T**	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	**2**
8							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of LLLQAETK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.8	924.5140	-0.0019	LLLQAETK

AT4G25090.1

4.7	924.5140	-0.0019	LPKSITEK
3.0	924.5140	-0.0019	IIVVTENK
3.0	924.5140	-0.0019	ILDGEKIK
3.0	924.5140	-0.0019	LIGEKVEK
3.0	924.5140	-0.0019	LLKEDVAK

AT4G25100.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYVDNLKK**
Found in **AT4G25100.1** in **TAIR_Arabidopsis**, Symbols: FSD1 | FSD1 (FE SUPEROXIDE DISMUTASE 1); iron superoxide dismutase | chr4:12884659-12886511 REVERSE

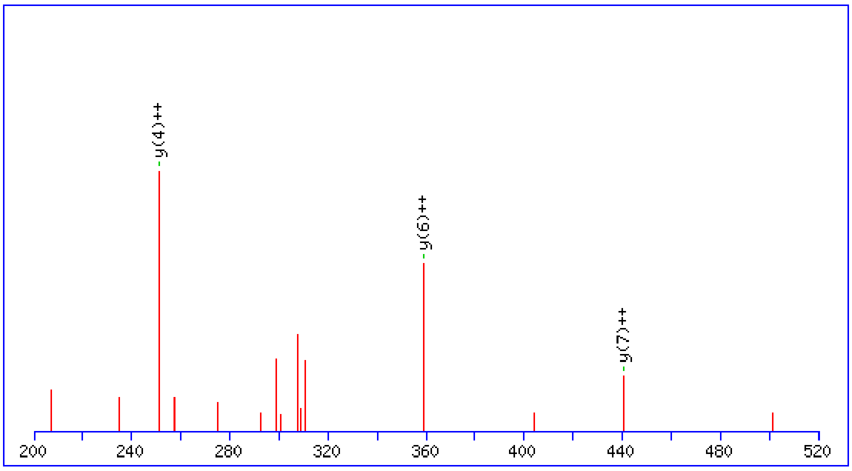
Match to Query 2163: 949.524534 from(317.515454,3+) index(635)
Title: Elution from: 12.001 to 12.001 scan no 957 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 520 Da Full range

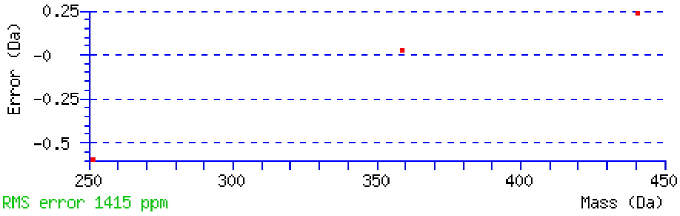
Label all possible matches ○ Label matches used for scoring ●

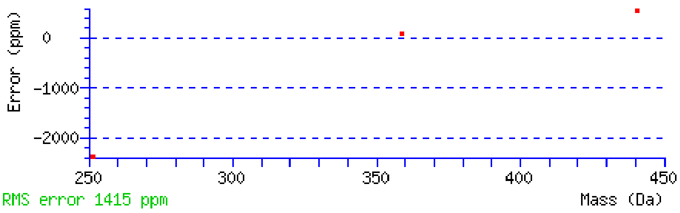
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 949.5233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.016
Matches : 3/62 fragment ions using 3 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							8
2	235.1077	118.0575					Y	879.4934	440.2504	862.4669	431.7371	861.4829	431.2451	7
3	334.1761	167.5917					V	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	6
4	449.2031	225.1052			431.1925	216.0999	D	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
5	563.2460	282.1266	546.2195	273.6134	545.2354	273.1214	N	502.3348	251.6710	485.3082	243.1577			4
6	676.3301	338.6687	659.3035	330.1554	658.3195	329.6634	L	388.2918	194.6496	371.2653	186.1363			3
7	804.4250	402.7162	787.3985	394.2029	786.4145	393.7109	K	275.2078	138.1075	258.1812	129.5942			2
8							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AYVDNLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.7	949.5233	0.0013	AYVDNLKK

AT4G25100.1

11.7	949.5266	-0.0021	MKEIKSSK
11.7	949.5266	-0.0021	SVAMLKSSK
3.2	949.5233	0.0013	IEVTGIYR
3.2	949.5233	0.0012	YSGQVVAVK
2.1	949.5246	-0.0001	HLLHFQR
1.6	949.5233	0.0013	KYASVPASK

AT4G25130.1

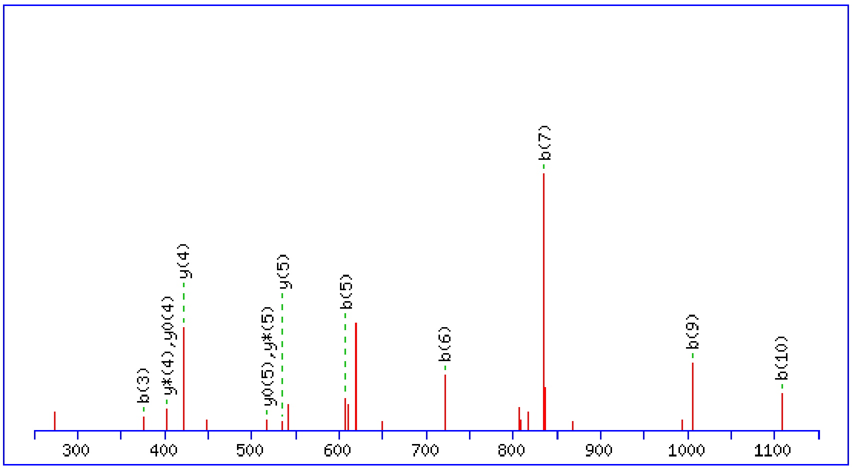
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RIVTEILPATK**
Found in **AT4G25130.1** in **TAIR_Arabidopsis**, Symbols: | peptide methionine sulfoxide reductase, putative | chr4:12898812-12900008 REVERSE

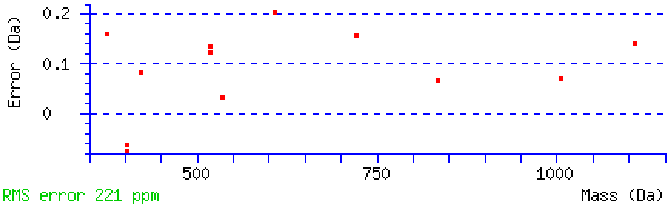
Match to Query 4717: 1254.710926 from(628.362739,2+) index(3557)
Title: Elution from: 33.591 to 33.591 scan no 4381 cid35.00 polarity:+
Data file D1d-3_1.mgf

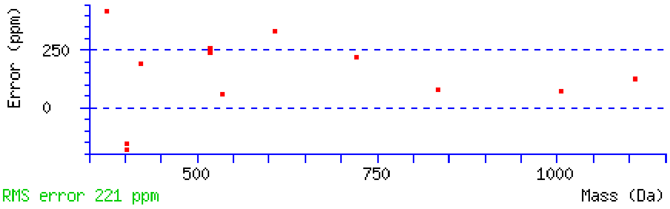
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1254.7106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 8.6e-005
Matches : 12/112 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							11
2	275.1776	138.0925	257.1540	129.0807			I	1095.6286	548.3179	1077.6050	539.3062	1077.6181	539.3127	10
3	***375.2431***	188.1252	357.2195	179.1134			V	981.5475	491.2774	963.5239	482.2656	963.5370	482.2721	9
4	477.2878	239.1475	459.2642	230.1357	459.2772	230.1422	T	881.4821	441.2447	863.4585	432.2329	863.4715	432.2394	8
5	***607.3274***	304.1673	589.3038	295.1556	589.3169	295.1621	E	779.4374	390.2223	761.4138	381.2105	761.4268	381.2170	7
6	***721.4085***	361.2079	703.3849	352.1961	703.3980	352.2026	I	649.3977	325.2025	631.3741	316.1907	631.3872	316.1972	6
7	***835.4896***	418.2484	817.4660	409.2367	817.4790	409.2432	L	**535.3166**	268.1620	517.2930	259.1502	517.3061	259.1567	5
8	933.5394	467.2733	915.5158	458.2616	915.5288	458.2681	P	**421.2355**	211.1214	403.2120	202.1096	403.2250	202.1161	4
9	***1005.5736***	503.2904	987.5500	494.2786	987.5630	494.2851	A	323.1857	162.0965	305.1622	153.0847	305.1752	153.0912	3
10	***1107.6183***	554.3128	1089.5947	545.3010	1089.6077	545.3075	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RIVTEILPATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G25130.1

Score	Mr(calc)	Delta	Sequence
40.6	1254.7106	0.0003	RIVTEILPATK
21.0	1254.7106	0.0003	TKSVLHITLTK
7.5	1254.7106	0.0003	ELQEIVRILK
3.3	1254.7106	0.0004	VEDILVRGLVK
0.9	1254.7106	0.0003	GILLNAVATQLK
0.5	1254.7133	-0.0023	TRPGTPVRIIK

AT4G25280.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MISSSSRSLK**
Found in **AT4G25280.1** in **TAIR_Arabidopsis**, Symbols: | adenylate kinase family protein | chr4:12939078-12940733 REVERSE

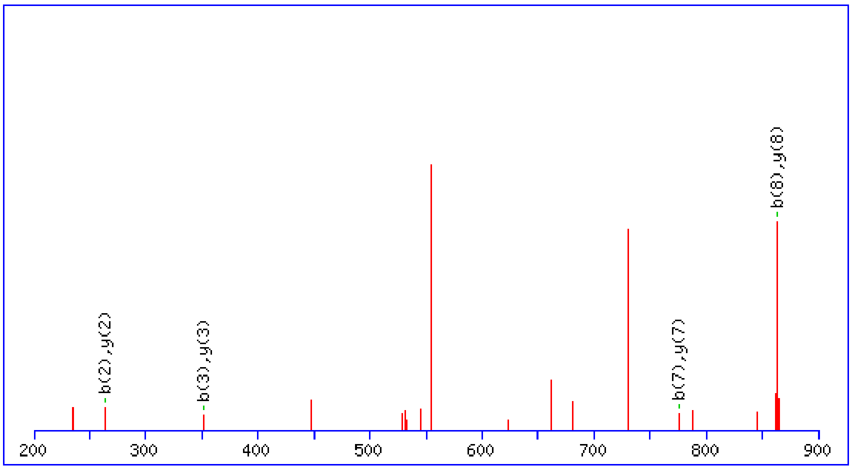
Match to Query 3030: 1124.528406 from(563.271479,2+) index(8105)
Title: Elution from: 76.068 to 76.068 scan no 10964 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

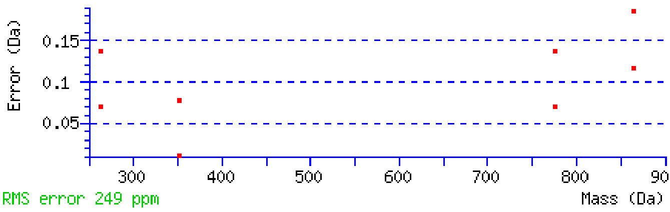
Label all possible matches ○ Label matches used for scoring ●

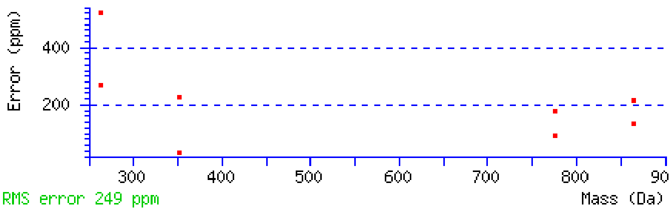
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1124.5288
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25  Expect: 0.025
Matches : 8/126 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							10
2	***263.1208***	132.0640					I	977.5036	489.2555	959.4801	480.2437	959.4931	480.2502	9
3	***351.1499***	176.0786			333.1393	167.0733	S	***863.4225***	432.2149	845.3990	423.2031	845.4120	423.2096	8
4	439.1789	220.0931			421.1684	211.0878	S	***775.3935***	388.2004	757.3699	379.1886	757.3829	379.1951	7
5	527.2080	264.1076			509.1974	255.1024	S	687.3644	344.1858	669.3408	335.1741	669.3538	335.1806	6
6	615.2371	308.1222			597.2265	299.1169	S	599.3354	300.1713	581.3118	291.1595	581.3248	291.1660	5
7	***775.3263***	388.1668	757.3027	379.1550	757.3157	379.1615	R	511.3063	256.1568	493.2827	247.1450	493.2957	247.1515	4
8	***863.3554***	432.1813	845.3318	423.1695	845.3448	423.1760	S	***351.2170***	176.1122	333.1935	167.1004	333.2065	167.1069	3
9	977.4365	489.2219	959.4129	480.2101	959.4259	480.2166	L	***263.1880***	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MISSSSRSLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G25280.1

Score	Mr(calc)	Delta	Sequence
25.1	1124.5288	-0.0004	MISSSSRSLK
23.3	1124.5299	-0.0015	LFSIEWYR
2.1	1124.5254	0.0030	RTFSADLSSK
2.0	1124.5254	0.0030	QEHEITNIK
1.2	1124.5281	0.0003	NNLLHQVDR

Mascot: http://www.matrixscience.com/

AT4G25370.1

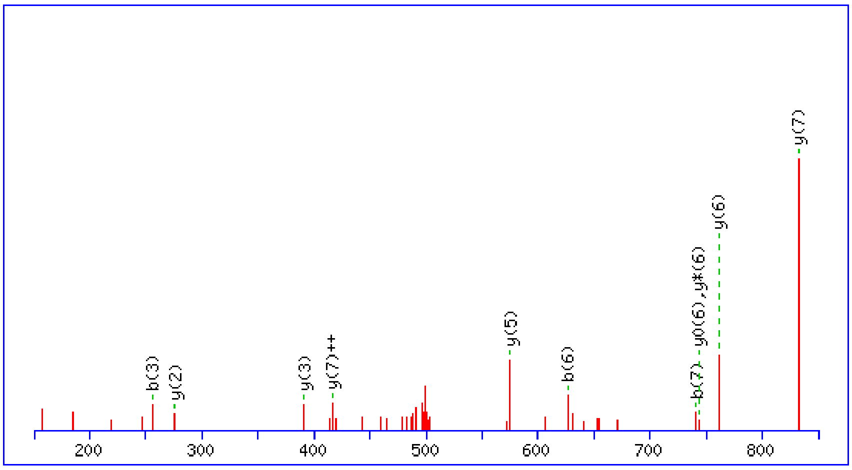
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIAWAIDEK**
Found in **AT4G25370.1** in **TAIR_Arabidopsis**, Symbols: | Clp amino terminal domain-containing protein | chr4:12972757-12974590 FORWARD

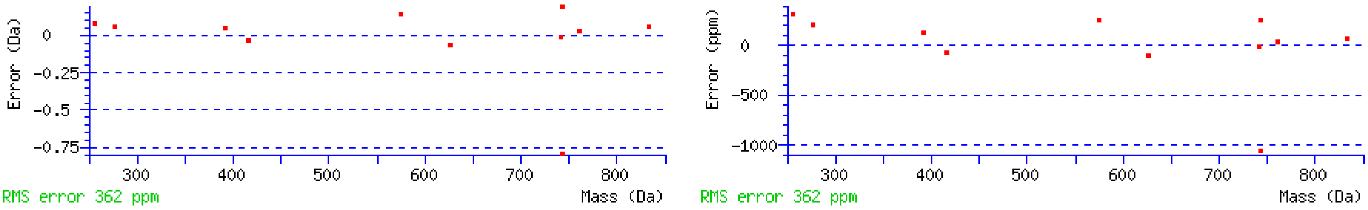
Match to Query 2707: 1015.533504 from(508.774028,2+) index(5084)
Title: Elution from: 45.243 to 45.243 scan no 6336 cid35.00 polarity:+
Data file C7-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1015.5338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00021
Matches : 11/66 fragment ions using 13 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258			A							9
2	185.1285	93.0679			I	945.5040	473.2556	928.4775	464.7424	927.4934	464.2504	8
3	**256.1656**	128.5864			A	***832.4199***	416.7136	815.3934	408.2003	814.4094	407.7083	7
4	442.2449	221.6261			W	***761.3828***	381.1951	744.3563	372.6818	743.3723	372.1898	6
5	513.2820	257.1446			A	***575.3035***	288.1554	558.2770	279.6421	557.2930	279.1501	5
6	**626.3661**	313.6867			I	504.2664	252.6368	487.2399	244.1236	486.2558	243.6316	4
7	**741.3930**	371.2001	723.3824	362.1949	D	***391.1823***	196.0948	374.1558	187.5815	373.1718	187.0895	3
8	870.4356	435.7214	852.4250	426.7162	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of AIAWAIDEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.7	1015.5338	-0.0003	AIAWAIDEK

AT4G25620.1

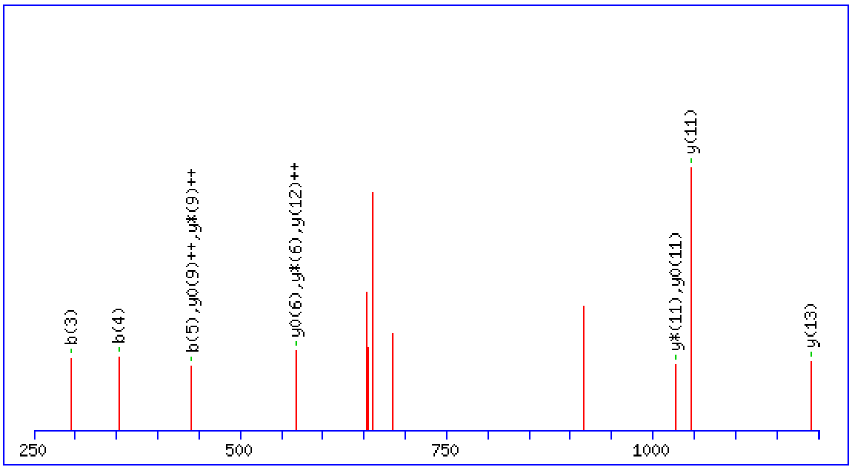
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGSGSITPAGQGSR**
Found in **AT4G25620.1** in **TAIR_Arabidopsis**, Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:13067456-13069305 REVERSE

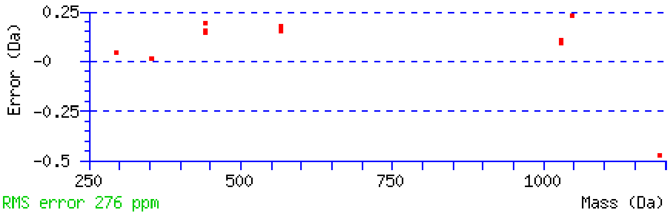
Match to Query 4929: 1338.592190 from(670.303371,2+) index(4520)
Title: Elution from: 41.860 to 41.860 scan no 5725 cid35.00 polarity:+
Data file 0-2_2.mgf

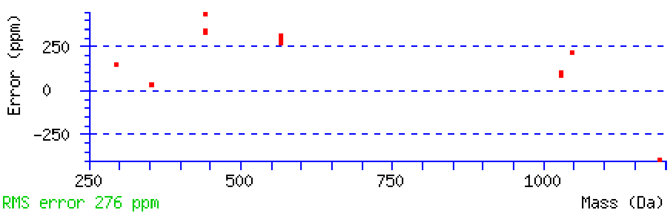
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1338.5888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.028
Matches : 12/130 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							14
2	207.0912	104.0492					G	***1191.5307***	596.2690	1173.5071	587.2572	1173.5201	587.2637	13
3	***295.1203***	148.0638			277.1097	139.0585	S	1133.5122	567.2597	1115.4886	558.2479	1115.5016	558.2544	12
4	***353.1388***	177.0730			335.1282	168.0677	G	***1045.4831***	523.2452	1027.4595	514.2334	1027.4726	514.2399	11
5	***441.1678***	221.0876			423.1573	212.0823	S	987.4646	494.2359	969.4410	485.2242	969.4541	485.2307	10
6	555.2489	278.1281			537.2384	269.1228	I	899.4356	450.2214	881.4120	441.2096	881.4250	441.2161	9
7	657.2937	329.1505			639.2831	320.1452	T	785.3545	393.1809	767.3309	384.1691	767.3439	384.1756	8
8	755.3435	378.1754			737.3329	369.1701	P	683.3097	342.1585	665.2862	333.1467	665.2992	333.1532	7
9	827.3776	414.1924			809.3670	405.1872	A	585.2599	293.1336	567.2364	284.1218	567.2494	284.1283	6
10	885.3961	443.2017			867.3855	434.1964	G	513.2258	257.1165	495.2022	248.1047	495.2152	248.1113	5
11	1015.4488	508.2280	997.4252	499.2162	997.4382	499.2227	Q	455.2073	228.1073	437.1837	219.0955	437.1967	219.1020	4
12	1073.4673	537.2373	1055.4437	528.2255	1055.4567	528.2320	G	325.1547	163.0810	307.1311	154.0692	307.1441	154.0757	3
13	1161.4963	581.2518	1143.4727	572.2400	1143.4858	572.2465	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FGSGSITPAGQGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G25620.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.2	1338.5888	0.0034	FGSGSITPAGQGSR
19.0	1338.5911	0.0011	QYSLWLDNQR
14.5	1338.5922	-0.0000	GMENKVSTGKDR
12.0	1338.5922	-0.0000	SKALCRADDASK
8.7	1338.5945	-0.0023	RSSCAIWLSDK
7.5	1338.5911	0.0011	YSPFGPDRLDR
6.2	1338.5911	0.0011	SDNPFSFPRQK
3.4	1338.5888	0.0034	VSFGLNAQASDGR
2.9	1338.5918	0.0004	EDKQFEMALAK
2.6	1338.5918	0.0004	FISMIDAELDR

AT4G25630.1

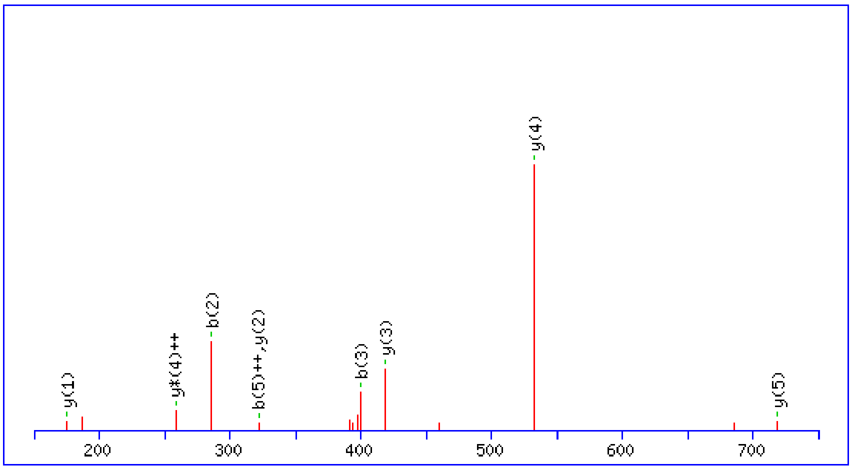
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VWNPFR**
Found in **AT4G25630.1** in **TAIR_Arabidopsis**, Symbols: ATFIB2, FIB2 | FIB2 (FIBRILLARIN 2) | chr4:13074248-13076214 FORWARD

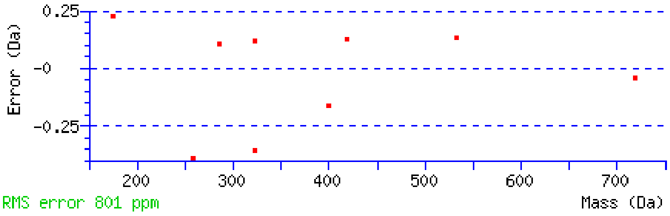
Match to Query 1094: 817.423646 from(409.719099,2+) index(5655)
Title: Elution from: 50.627 to 50.627 scan no 7207 cid35.00 polarity:+
Data file 0-2_2.mgf

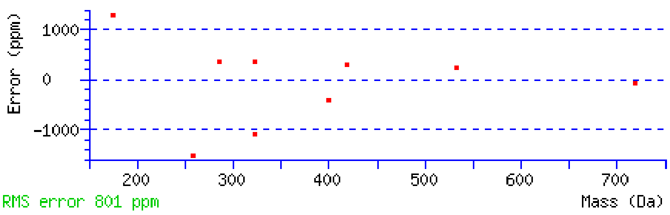
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 817.4235
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00014
Matches : 9/36 fragment ions using 11 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	100.0757	50.5415			V					6
2	**286.1550**	143.5811			W	*719.3624*	360.1848	702.3358	351.6715	5
3	**400.1979**	200.6026	383.1714	192.0893	N	*533.2831*	267.1452	516.2565	258.6319	4
4	497.2507	249.1290	480.2241	240.6157	P	*419.2401*	210.1237	402.2136	201.6104	3
5	644.3191	322.6632	627.2926	314.1499	F	*322.1874*	161.5973	305.1608	153.0840	2
6					R	*175.1190*	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of VWNPFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.6	817.4235	0.0001	VWNPFR
21.8	817.4229	0.0008	VGRSPMR
18.6	817.4228	0.0008	ERNLMR
4.9	817.4229	0.0008	ERCVVR

AT4G25740.1

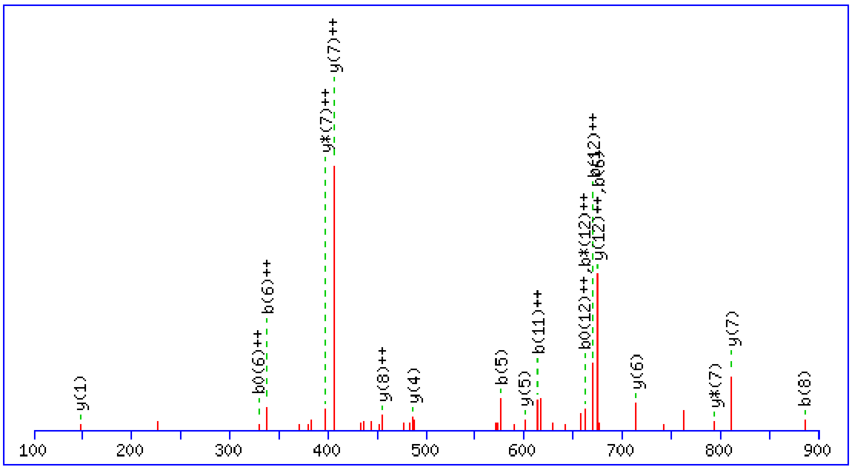
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HPLIDVPNLQVIK**
Found in **AT4G25740.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S10 (RPS10A) | chr4:13107497-13108760 REVERSE

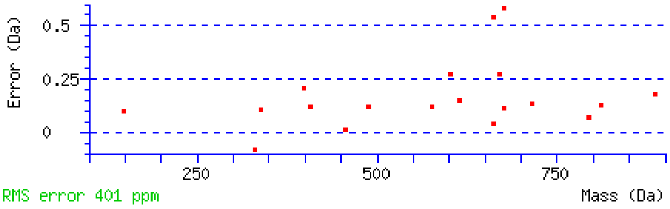
Match to Query 6301: 1484.872449 from(495.964759,3+) index(7441)
Title: Elution from: 64.587 to 64.587 scan no 9661 cid35.00 polarity:+
Data file D1d-3_2.mgf

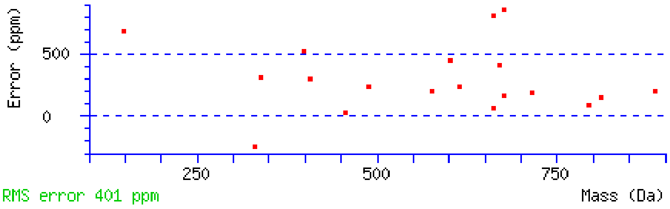
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1484.8715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.00058
Matches : 19/106 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.0662	69.5367					H							13
2	235.1190	118.0631					P	1348.8199	674.9136	1331.7933	666.4003	1330.8093	665.9083	12
3	348.2030	174.6051					L	1251.7671	626.3872	1234.7406	617.8739	1233.7565	617.3819	11
4	461.2871	231.1472					I	1138.6830	569.8452	1121.6565	561.3319	1120.6725	560.8399	10
5	**576.3140**	288.6606			558.3035	279.6554	D	1025.5990	513.3031	1008.5724	504.7898	1007.5884	504.2978	9
6	**675.3824**	**338.1949**			657.3719	329.1896	V	910.5720	455.7897	893.5455	447.2764			8
7	772.4352	386.7212			754.4246	377.7160	P	***811.5036***	406.2554	794.4771	397.7422			7
8	**886.4781**	443.7427	869.4516	435.2294	868.4676	434.7374	N	***714.4509***	357.7291	697.4243	349.2158			6
9	999.5622	500.2847	982.5356	491.7715	981.5516	491.2795	L	***600.4079***	300.7076	583.3814	292.1943			5
10	1127.6208	564.3140	1110.5942	555.8007	1109.6102	555.3087	Q	***487.3239***	244.1656	470.2973	235.6523			4
11	1226.6892	**613.8482**	1209.6626	605.3350	1208.6786	604.8429	V	359.2653	180.1363	342.2387	171.6230			3
12	1339.7732	**670.3903**	1322.7467	661.8770	1321.7627	661.3850	I	260.1969	130.6021	243.1703	122.0888			2
13							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HPLIDVPNLQVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G25740.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.8	1484.8715	0.0010	HPLIDVPNLQVIK
3.7	1484.8748	-0.0024	MLVLTKSSPKPLR
0.0	1484.8715	0.0010	ILGIYQVSSKHLK

AT4G26300.1

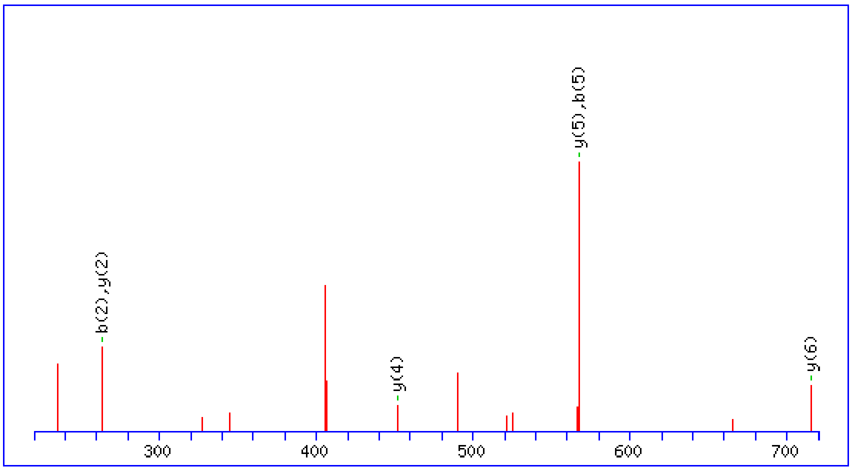
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFDVSLK**
Found in **AT4G26300.1** in **TAIR_Arabidopsis**, Symbols: EMB1027 | EMB1027 (EMBRYO DEFECTIVE 1027); ATP binding / arginine-tRNA ligase | chr4:13308409-13313118 REVERSE

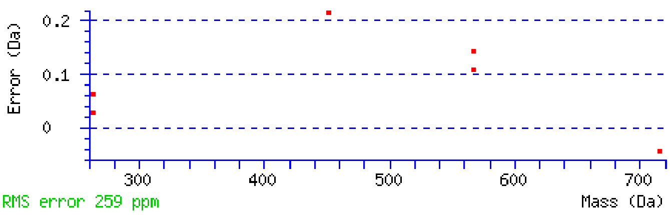
Match to Query 1258: 828.445560 from(415.230056,2+) index(5955)
Title: Elution from: 52.663 to 52.663 scan no 7494 cid35.00 polarity:+
Data file C7-2_1.mgf

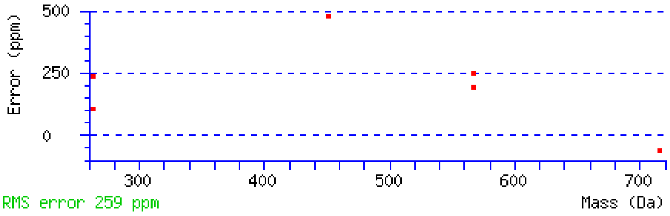
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 720 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 828.4457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.017
Matches : 6/52 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							7
2	**263.1538**	132.0805			F	***715.3719***	358.1896	697.3483	349.1778	697.3613	349.1843	6
3	379.1778	190.0925	361.1672	181.0873	D	***567.3065***	284.1569	549.2829	275.1451	549.2959	275.1516	5
4	479.2433	240.1253	461.2327	231.1200	V	***451.2825***	226.1449	433.2589	217.1331	433.2719	217.1396	4
5	**567.2723**	284.1398	549.2617	275.1345	S	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
6	681.3534	341.1803	663.3428	332.1751	L	***263.1880***	132.0976	245.1644	123.0858			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LFDVSLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.4	828.4457	-0.0002	LFDVSLK
13.0	828.4457	-0.0002	IYAVDLK

AT4G26300.1

13.0	828.4457	-0.0002	LFVSLDK
4.9	828.4457	-0.0002	IPYTSIK
4.9	828.4457	-0.0002	ISFDVIK
4.9	828.4457	-0.0002	LFELATK
4.9	828.4457	-0.0002	LYGVELK
3.1	828.4462	-0.0006	KTRGDIK
3.1	828.4444	0.0012	MIMGKLK
3.1	828.4462	-0.0006	RSVTGGLK

AT4G26530.1

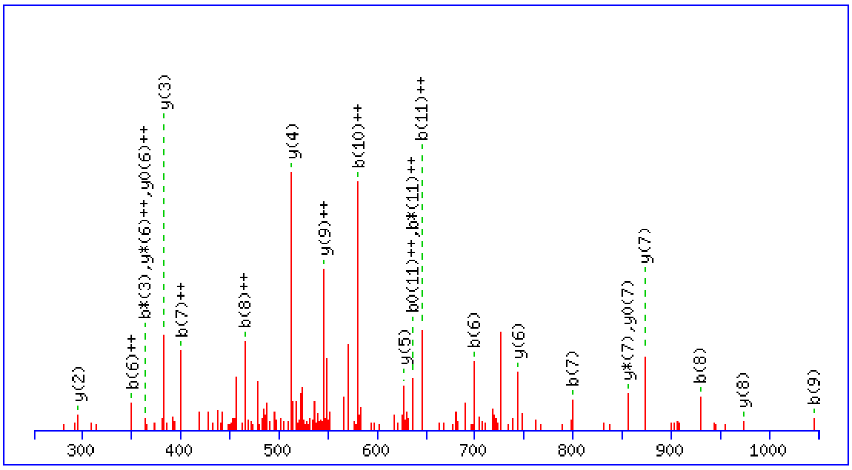
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RFASINVENIESNR**
Found in **AT4G26530.1** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr4:13391573-13392944 FORWARD

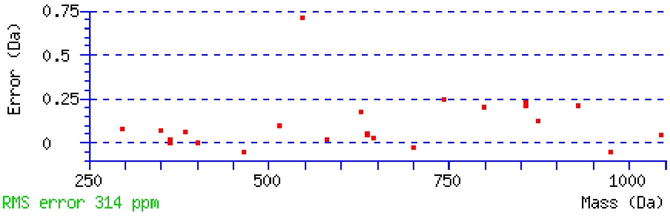
Match to Query 7841: 1670.765283 from(557.929037,3+) index(4501)
Title: Elution from: 43.579 to 43.579 scan no 5745 cid35.00 polarity:+
Data file D1d-2_1.mgf

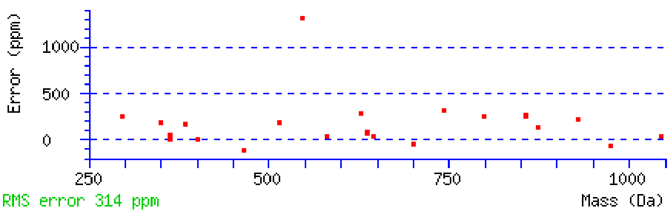
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1670.7647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 2.3e-005
Matches : 24/146 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							14
2	309.1620	155.0846	291.1384	146.0728			F	1511.6827	756.3450	1493.6591	747.3332	1493.6721	747.3397	13
3	381.1961	191.1017	363.1725	182.0899			A	1363.6173	682.3123	1345.5937	673.3005	1345.6067	673.3070	12
4	469.2252	235.1162	451.2016	226.1044	451.2146	226.1109	S	1291.5831	646.2952	1273.5595	637.2834	1273.5725	637.2899	11
5	583.3063	292.1568	565.2827	283.1450	565.2957	283.1515	I	1203.5540	602.2807	1185.5305	593.2689	1185.5435	593.2754	10
6	**699.3433**	**350.1753**	681.3197	341.1635	681.3327	341.1700	N	1089.4730	545.2401	1071.4494	536.2283	1071.4624	536.2348	9
7	**799.4087**	**400.2080**	781.3851	391.1962	781.3982	391.2027	V	***973.4360***	487.2216	955.4124	478.2098	955.4254	478.2163	8
8	**929.4484**	**465.2278**	911.4248	456.2160	911.4378	456.2225	E	***873.3705***	437.1889	855.3469	428.1771	855.3599	428.1836	7
9	**1045.4854**	523.2463	1027.4618	514.2345	1027.4748	514.2410	N	***743.3309***	372.1691	725.3073	363.1573	725.3203	363.1638	6
10	1159.5665	**580.2869**	1141.5429	571.2751	1141.5559	571.2816	I	***627.2939***	314.1506	609.2703	305.1388	609.2833	305.1453	5
11	1289.6061	**645.3067**	1271.5825	636.2949	1271.5955	636.3014	E	***513.2128***	257.1100	495.1892	248.0982	495.2022	248.1047	4
12	1377.6351	689.3212	1359.6116	680.3094	1359.6246	680.3159	S	***383.1732***	192.0902	365.1496	183.0784	365.1626	183.0849	3
13	1493.6721	747.3397	1475.6486	738.3279	1475.6616	738.3344	N	***295.1441***	148.0757	277.1205	139.0639			2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RFASINVENIESNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G26530.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.3	1670.7647	0.0006	RFASINVENIESNR
1.5	1670.7676	-0.0023	TYGGKVVPGAMDTAAAK
0.4	1670.7703	-0.0050	NGAAMISRPVFLSDR

AT4G26570.1

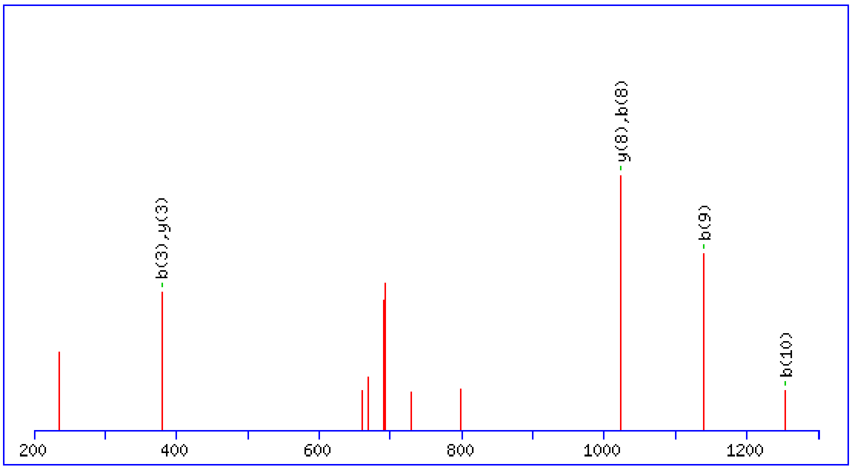
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDFSFQLYDLK**
Found in **AT4G26570.1** in **TAIR_Arabidopsis**, Symbols: CBL3 | ATCBL3 (CALCINEURIN B-LIKE 3) | chr4:13408614-13410004 REVERSE

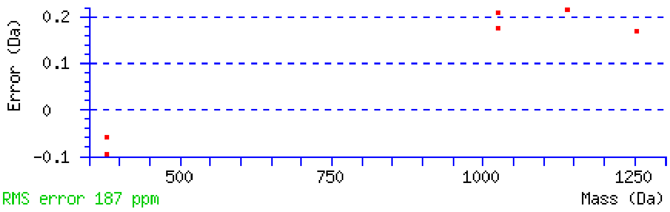
Match to Query 5191: 1400.663724 from(701.339138,2+) index(5595)
Title: Elution from: 49.848 to 49.848 scan no 7134 cid35.00 polarity:+
Data file D6h-2_3.mgf

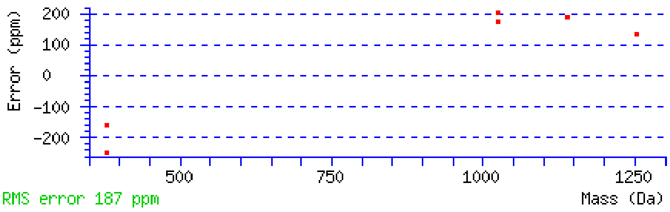
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1400.6638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.011
Matches : 6/104 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							11
2	231.1124	116.0598			213.1018	107.0545	D	1287.5900	644.2986	1269.5664	635.2868	1269.5794	635.2934	10
3	***379.1778***	190.0925			361.1672	181.0873	F	1171.5660	586.2866	1153.5424	577.2749	1153.5555	577.2814	9
4	467.2069	234.1071			449.1963	225.1018	S	**1023.5006**	512.2539	1005.4770	503.2421	1005.4900	503.2486	8
5	615.2723	308.1398			597.2617	299.1345	F	935.4715	468.2394	917.4479	459.2276	917.4609	459.2341	7
6	745.3250	373.1661	727.3014	364.1543	727.3144	364.1608	Q	787.4061	394.2067	769.3825	385.1949	769.3955	385.2014	6
7	859.4061	430.2067	841.3825	421.1949	841.3955	421.2014	L	657.3534	329.1803	639.3298	320.1686	639.3428	320.1751	5
8	***1023.4664***	512.2369	1005.4428	503.2251	1005.4559	503.2316	Y	543.2723	272.1398	525.2487	263.1280	525.2617	263.1345	4
9	***1139.4904***	570.2488	1121.4668	561.2370	1121.4798	561.2436	D	**379.2120**	190.1096	361.1884	181.0978	361.2014	181.1043	3
10	***1253.5715***	627.2894	1235.5479	618.2776	1235.5609	618.2841	L	263.1880	132.0976	245.1644	123.0858			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IDFSFQLYDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G26570.1

Score	Mr(calc)	Delta	Sequence
28.0	1400.6638	-0.0001	IDFSFQLYDLK
14.3	1400.6665	-0.0027	ALFNDRFFDLK
4.3	1400.6669	-0.0032	HFARHSSEAVLK
3.6	1400.6676	-0.0039	EKQMLHDEVKK
3.6	1400.6676	-0.0039	KSRYLEVMNTK
2.4	1400.6620	0.0017	EITSAQAAHNTLK
1.7	1400.6647	-0.0010	HLSQQQPATSRK
1.6	1400.6616	0.0021	DSSSYAFKLELK
1.6	1400.6665	-0.0028	FDAINWIHEIK
0.2	1400.6642	-0.0005	FYRELNSQTVK

AT4G26970.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVISEDFNSYGSR**
Found in **AT4G26970.1** in **TAIR_Arabidopsis**, Symbols: | aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr4:13543083-13548433 FORWARD

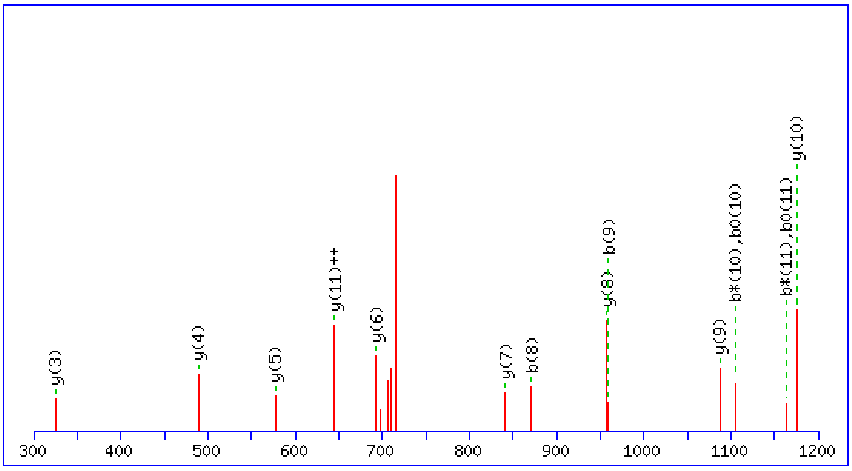
Match to Query 5596: 1446.598050 from(724.306301,2+) index(4568)
Title: Elution from: 41.427 to 41.427 scan no 5711 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1200 Da Full range

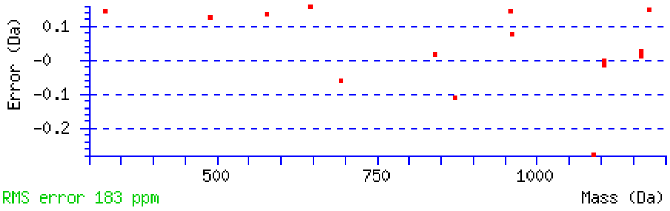
Label all possible matches ○ Label matches used for scoring ●

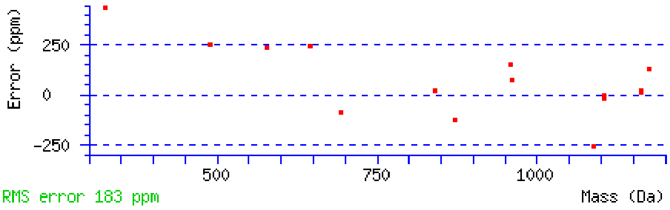
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1446.5970
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 3.5e-008
Matches : 15/122 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							13
2	159.0912	80.0492					V	1389.5857	695.2965	1371.5622	686.2847	1371.5752	686.2912	12
3	273.1723	137.0898					I	1289.5203	645.2638	1271.4967	636.2520	1271.5097	636.2585	11
4	361.2014	181.1043			343.1908	172.0990	S	***1175.4392***	588.2232	1157.4156	579.2114	1157.4286	579.2180	10
5	491.2410	246.1241			473.2304	237.1189	E	***1087.4101***	544.2087	1069.3865	535.1969	1069.3996	535.2034	9
6	607.2650	304.1361			589.2544	295.1309	D	***957.3705***	479.1889	939.3469	470.1771	939.3599	470.1836	8
7	755.3304	378.1689			737.3199	369.1636	F	***841.3465***	421.1769	823.3229	412.1651	823.3360	412.1716	7
8	**871.3674**	436.1874	853.3439	427.1756	853.3569	427.1821	N	***693.2811***	347.1442	675.2575	338.1324	675.2705	338.1389	6
9	**959.3965**	480.2019	941.3729	471.1901	941.3859	471.1966	S	***577.2441***	289.1257	559.2205	280.1139	559.2335	280.1204	5
10	1123.4569	562.2321	1105.4333	553.2203	1105.4463	553.2268	Y	***489.2150***	245.1111	471.1914	236.0994	471.2045	236.1059	4
11	1181.4754	591.2413	1163.4518	582.2295	1163.4648	582.2360	G	***325.1547***	163.0810	307.1311	154.0692	307.1441	154.0757	3
12	1269.5044	635.2559	1251.4808	626.2441	1251.4939	626.2506	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of GVISEDFNSYGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G26970.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.7	1446.5970	0.0011	GVISEDFNSYGSR
0.6	1446.5994	-0.0013	FFFFCDPHRR

AT4G27080.1

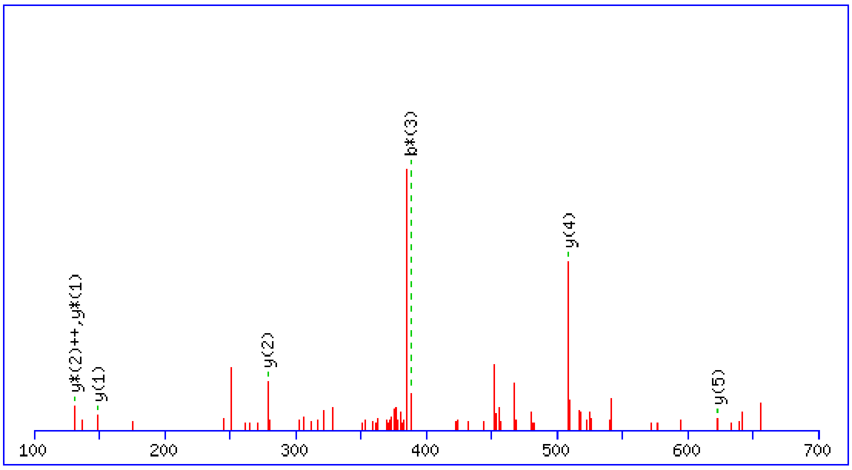
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RIMPQK**
Found in **AT4G27080.1** in **TAIR_Arabidopsis**, Symbols: ATPDIL5-4 | ATPDIL5-4 (PDI-LIKE 5-4) | chr4:13589162-13593341 FORWARD

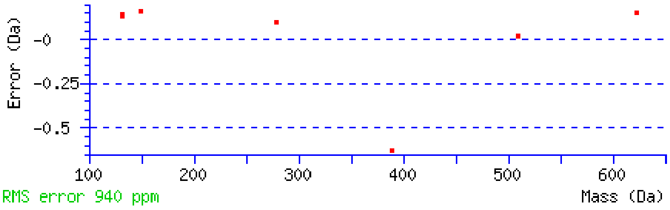
Match to Query 951: 782.410232 from(392.212392,2+) index(1284)
Title: Elution from: 19.067 to 19.067 scan no 1792 cid35.00 polarity:+
Data file 0-2_1.mgf

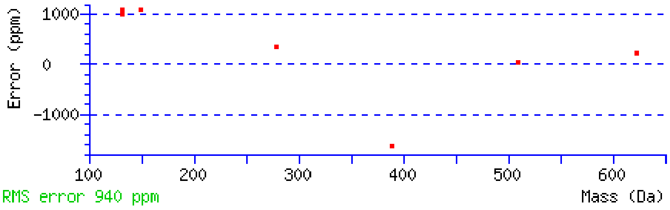
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 782.4099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.021
Matches : 7/40 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	161.0965	81.0519	143.0729	72.0401	R					6
2	275.1776	138.0925	257.1540	129.0807	I	***623.3279***	312.1676	605.3044	303.1558	5
3	407.2151	204.1112	389.1916	195.0994	M	***509.2468***	255.1271	491.2233	246.1153	4
4	505.2649	253.1361	487.2414	244.1243	P	377.2093	189.1083	359.1857	180.0965	3
5	635.3176	318.1624	617.2940	309.1506	Q	***279.1595***	140.0834	261.1359	131.0716	2
6					K	***149.1069***	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of RIMPQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.2	782.4099	0.0003	RIMPQK

Mascot: http://www.matrixscience.com/

AT4G27090.1

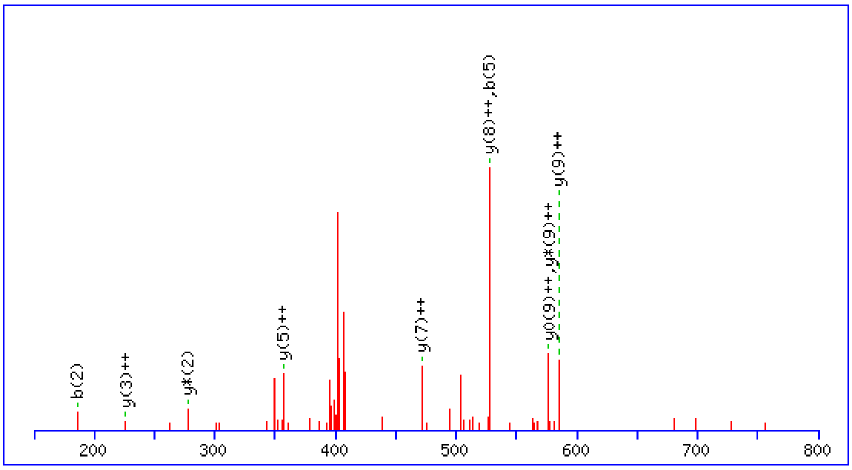
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLNDFDRFK**
Found in **AT4G27090.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L14 (RPL14B) | chr4:13594110-13595193 REVERSE

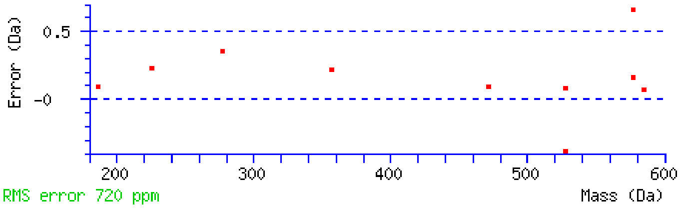
Match to Query 4489: 1238.603889 from(413.875239,3+) index(4394)
Title: Elution from: 39.533 to 39.533 scan no 5480 cid35.00 polarity:+
Data file D1d-3_2.mgf

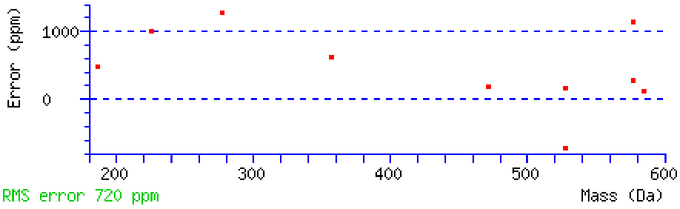
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1238.6044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.035
Matches : 10/92 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							10
2	**186.0873**	93.5473	169.0608	85.0340			N	1168.5745	584.7909	1151.5480	576.2776	1150.5640	575.7856	9
3	299.1714	150.0893	282.1448	141.5761			L	1054.5316	527.7694	1037.5051	519.2562	1036.5211	518.7642	8
4	413.2143	207.1108	396.1878	198.5975			N	941.4476	471.2274	924.4210	462.7141	923.4370	462.2221	7
5	**528.2413**	264.6243	511.2147	256.1110	510.2307	255.6190	D	827.4046	414.2060	810.3781	405.6927	809.3941	405.2007	6
6	675.3097	338.1585	658.2831	329.6452	657.2991	329.1532	F	712.3777	356.6925	695.3511	348.1792	694.3671	347.6872	5
7	790.3366	395.6719	773.3101	387.1587	772.3260	386.6667	D	565.3093	283.1583	548.2827	274.6450	547.2987	274.1530	4
8	946.4377	473.7225	929.4112	465.2092	928.4272	464.7172	R	450.2823	225.6448	433.2558	217.1315			3
9	1093.5061	547.2567	1076.4796	538.7434	1075.4956	538.2514	F	294.1812	147.5942	277.1547	139.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ANLNDFDRFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G27090.1

18.1	1238.6044	-0.0005	ANLNDFDRFK
0.3	1238.6044	-0.0005	KGSQWFETTR

AT4G27270.1

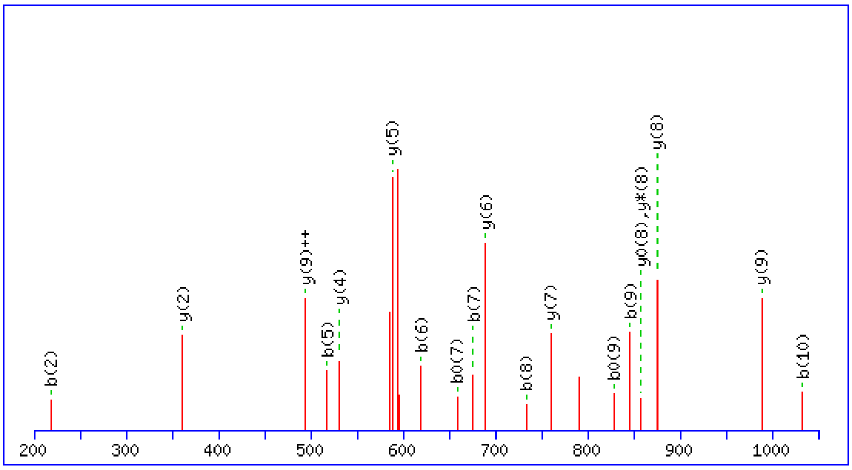
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFLDATGGLWR**
Found in **AT4G27270.1** in **TAIR_Arabidopsis**, Symbols: | quinone reductase family protein | chr4:13661464-13663249 REVERSE

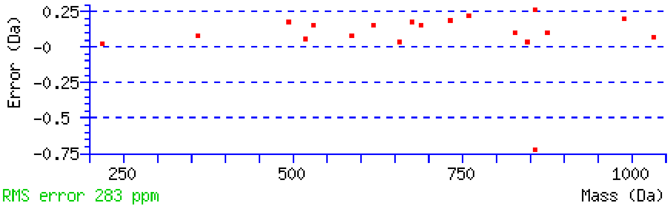
Match to Query 3621: 1205.621858 from(603.818205,2+) index(8025)
Title: Elution from: 75.357 to 75.357 scan no 10848 cid35.00 polarity:+
Data file D1d-1-2.mgf

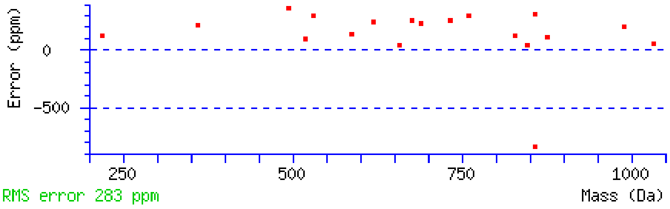
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1205.6193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 8.4e-008
Matches : 19/84 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			A							11
2	***219.1128***	110.0600			F	1135.5895	568.2984	1118.5629	559.7851	1117.5789	559.2931	10
3	332.1969	166.6021			L	***988.5211***	494.7642	971.4945	486.2509	970.5105	485.7589	9
4	447.2238	224.1155	429.2132	215.1103	D	***875.4370***	438.2221	858.4104	429.7089	857.4264	429.2169	8
5	***518.2609***	259.6341	500.2504	250.6288	A	***760.4101***	380.7087	743.3835	372.1954	742.3995	371.7034	7
6	***619.3086***	310.1579	601.2980	301.1527	T	***689.3729***	345.1901	672.3464	336.6768	671.3624	336.1848	6
7	***676.3301***	338.6687	658.3195	329.6634	G	***588.3253***	294.6663	571.2987	286.1530			5
8	***733.3515***	367.1794	715.3410	358.1741	G	***531.3038***	266.1555	514.2772	257.6423			4
9	***846.4356***	423.7214	828.4250	414.7162	L	474.2823	237.6448	457.2558	229.1315			3
10	***1032.5149***	516.7611	1014.5043	507.7558	W	***361.1983***	181.1028	344.1717	172.5895			2
11					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AFLDATGGLWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G27270.1

Score	Mr(calc)	Delta	Sequence
77.4	1205.6193	0.0026	AFLDATGGLWR
4.2	1205.6186	0.0032	MPSKESLSRR
0.9	1205.6252	-0.0033	TASIESSGVISR
0.7	1205.6186	0.0032	RLDGTMSLAAR
0.6	1205.6227	-0.0008	MLFSTVLSHR

Mascot: http://www.matrixscience.com/

AT4G27440.1

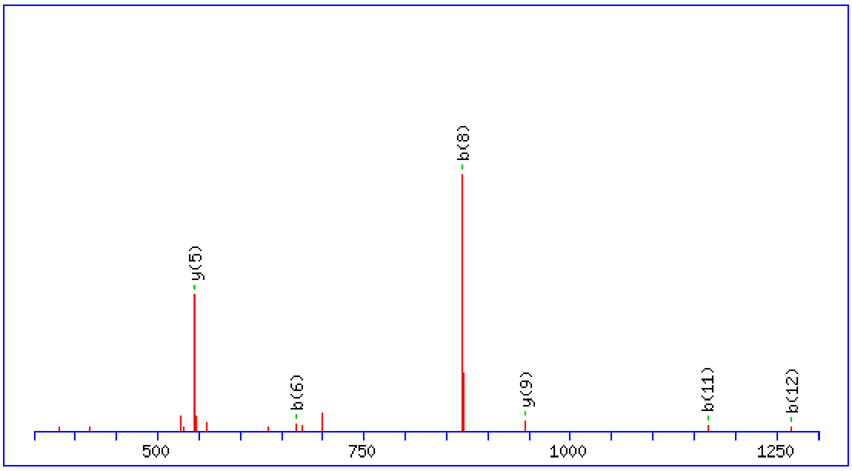
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RLAQVVSDPSLTK**
Found in **AT4G27440.1** in **TAIR_Arabidopsis**, Symbols: PORB | PORB (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B); oxidoreductase/ protochlorophyllide reductase | chr4:13725654-13727113 FORWARD

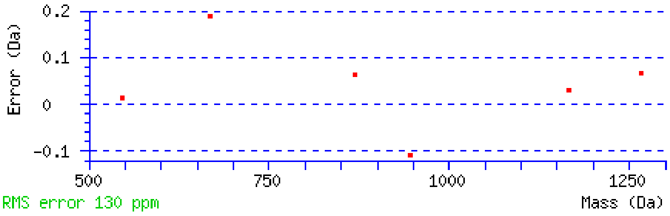
Match to Query 5647: 1412.795342 from(707.404947,2+) index(2680)
Title: Elution from: 26.814 to 26.814 scan no 3304 cid35.00 polarity:+
Data file D1d-3_2.mgf

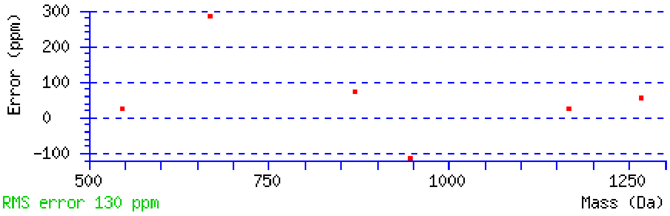
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1412.7987
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0015
Matches : 6/130 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							13
2	270.1925	135.5999	253.1659	127.0866			L	1257.7049	629.3561	1240.6783	620.8428	1239.6943	620.3508	12
3	341.2296	171.1184	324.2030	162.6051			A	1144.6208	572.8141	1127.5943	564.3008	1126.6103	563.8088	11
4	469.2881	235.1477	452.2616	226.6344			Q	1073.5837	537.2955	1056.5572	528.7822	1055.5732	528.2902	10
5	568.3566	284.6819	551.3300	276.1686			V	**945.5251**	473.2662	928.4986	464.7529	927.5146	464.2609	9
6	***667.4250***	334.2161	650.3984	325.7028			V	846.4567	423.7320	829.4302	415.2187	828.4462	414.7267	8
7	754.4570	377.7321	737.4304	369.2189	736.4464	368.7269	S	747.3883	374.1978	730.3618	365.6845	729.3777	365.1925	7
8	***869.4839***	435.2456	852.4574	426.7323	851.4734	426.2403	D	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
9	966.5367	483.7720	949.5102	475.2587	948.5261	474.7667	P	**545.3293**	273.1683	528.3028	264.6550	527.3188	264.1630	5
10	1053.5687	527.2880	1036.5422	518.7747	1035.5582	518.2827	S	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4
11	***1166.6528***	583.8300	1149.6262	575.3168	1148.6422	574.8248	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
12	***1267.7005***	634.3539	1250.6739	625.8406	1249.6899	625.3486	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RLAQVVSDPSLTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G27440.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1412.7987	-0.0034	RLAQVVSDPSLTK
9.7	1412.7915	0.0038	VIIEVLPEWSTK
3.7	1412.7922	0.0032	MREKASLLPNVR

AT4G27500.1

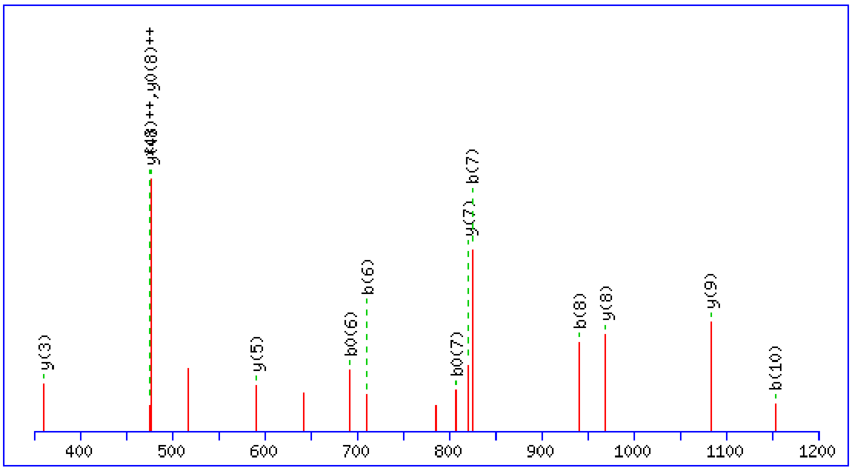
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SELFDLLDPLK**
Found in **AT4G27500.1** in **TAIR_Arabidopsis**, Symbols: PPI1 | PPI1 (PROTON PUMP INTERACTOR 1) | chr4:13743620-13745906 FORWARD

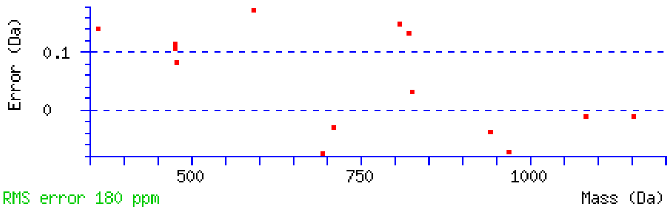
Match to Query 4719: 1300.652344 from(651.333448,2+) index(10515)
Title: Elution from: 103.782 to 103.782 scan no 15281 cid35.00 polarity:+
Data file 0-1_3.mgf

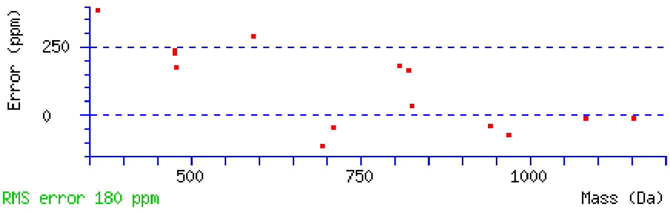
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1300.6559
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 7e-006
Matches : 14/94 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							11
2	219.0760	110.0416	201.0654	101.0363	E	1213.6341	607.3207	1195.6105	598.3089	1195.6235	598.3154	10
3	333.1571	167.0822	315.1465	158.0769	L	***1083.5945***	542.3009	1065.5709	533.2891	1065.5839	533.2956	9
4	481.2225	241.1149	463.2120	232.1096	F	***969.5134***	485.2603	951.4898	476.2485	951.5028	476.2550	8
5	597.2465	299.1269	579.2359	290.1216	D	***821.4479***	411.2276	803.4243	402.2158	803.4374	402.2223	7
6	**711.3276**	356.1674	693.3170	347.1622	L	705.4239	353.2156	687.4004	344.2038	687.4134	344.2103	6
7	**825.4087**	413.2080	807.3981	404.2027	L	***591.3428***	296.1751	573.3193	287.1633	573.3323	287.1698	5
8	**941.4327**	471.2200	923.4221	462.2147	D	***477.2617***	239.1345	459.2382	230.1227	459.2512	230.1292	4
9	1039.4825	520.2449	1021.4719	511.2396	P	***361.2378***	181.1225	343.2142	172.1107			3
10	**1153.5636**	577.2854	1135.5530	568.2801	L	263.1880	132.0976	245.1644	123.0858			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SELFDLLDPLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G27500.1

Score	Mr(calc)	Delta	Sequence
57.6	1300.6559	-0.0035	SELFDLLDPLK
10.5	1300.6538	-0.0015	FPIPGNMPRIK
5.1	1300.6516	0.0007	NKLPQANVCLK
3.9	1300.6504	0.0019	TPRSIFVYFR
0.4	1300.6516	0.0008	KLGGSLHCSVVK
0.0	1300.6489	0.0034	NTLPKLVEDMK

AT4G27520.1

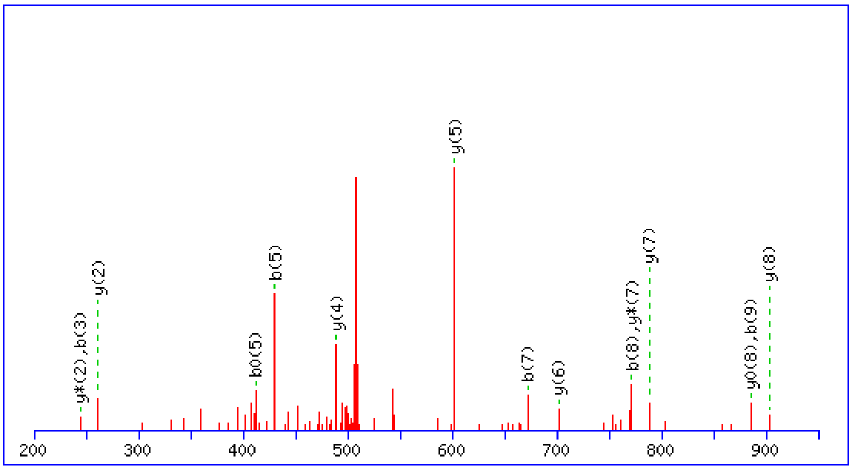
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GADSVLEVNK**
Found in **AT4G27520.1** in **TAIR_Arabidopsis**, Symbols: | plastocyanin-like domain-containing protein | chr4:13750674-13751825 REVERSE

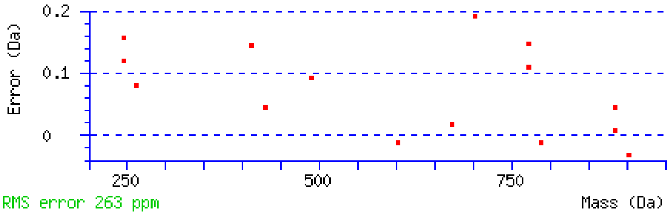
Match to Query 2860: 1030.526516 from(516.270534,2+) index(2231)
Title: Elution from: 24.721 to 24.721 scan no 2831 cid35.00 polarity:+
Data file C7-2_2.mgf

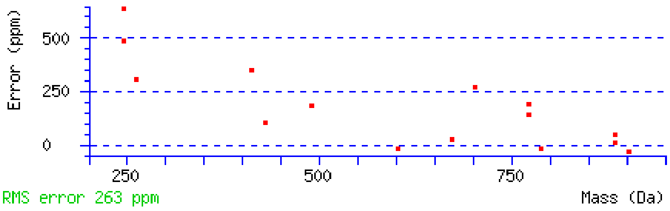
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1030.5295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 1.1e-006
Matches : 15/82 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	129.0659	65.0366					A	974.5153	487.7613	957.4888	479.2480	956.5047	478.7560	9
3	***244.0928***	122.5500			226.0822	113.5448	D	***903.4782***	452.2427	886.4516	443.7295	885.4676	443.2374	8
4	331.1248	166.0661			313.1143	157.0608	S	***788.4512***	394.7293	771.4247	386.2160	770.4407	385.7240	7
5	***430.1932***	215.6003			412.1827	206.5950	V	***701.4192***	351.2132	684.3927	342.7000	683.4087	342.2080	6
6	543.2773	272.1423			525.2667	263.1370	L	***602.3508***	301.6790	585.3243	293.1658	584.3402	292.6738	5
7	***672.3199***	336.6636			654.3093	327.6583	E	***489.2667***	245.1370	472.2402	236.6237	471.2562	236.1317	4
8	***771.3883***	386.1978			753.3777	377.1925	V	360.2241	180.6157	343.1976	172.1024			3
9	***885.4312***	443.2193	868.4047	434.7060	867.4207	434.2140	N	***261.1557***	131.0815	244.1292	122.5682			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GADSVLEVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G27520.1

67.8	1030.5295	-0.0030	GADSVLEVNK
14.0	1030.5295	-0.0030	AVDSGKTEPK
13.9	1030.5270	-0.0005	MVLQNPWK
5.9	1030.5295	-0.0029	DLKEGENVK
4.4	1030.5236	0.0029	WVHAYIDK
3.9	1030.5295	-0.0029	SRLEPTSEL
1.2	1030.5295	-0.0029	NVSENIDKI

Mascot: http://www.matrixscience.com/

AT4G27595.1

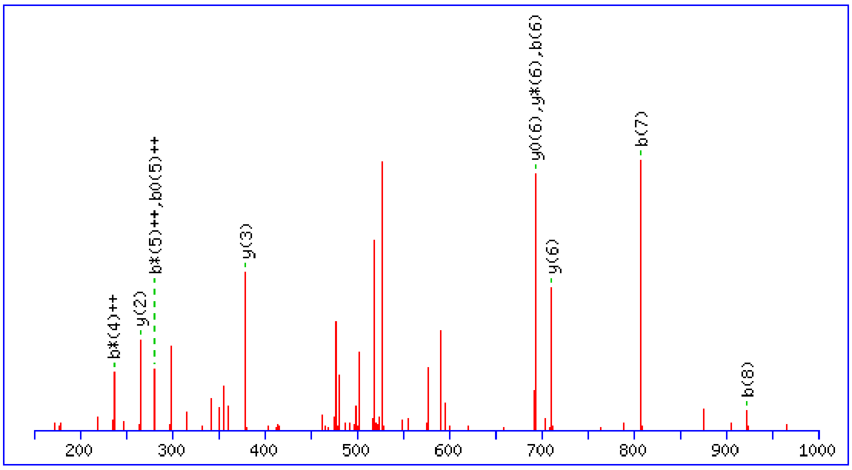
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLKQSLLDK**
Found in **AT4G27595.1** in **TAIR_Arabidopsis**, Symbols: | protein transport protein-related | chr4:13772825-13776524 REVERSE

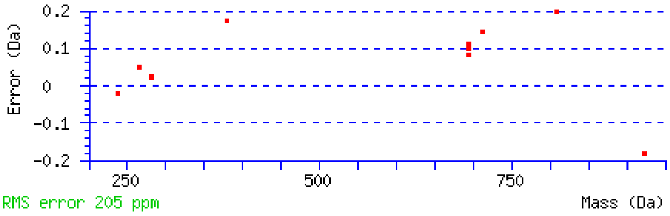
Match to Query 3040: 1070.571562 from(536.293057,2+) index(7578)
Title: Elution from: 67.617 to 67.617 scan no 9966 cid35.00 polarity:+
Data file D6h-1_2.mgf

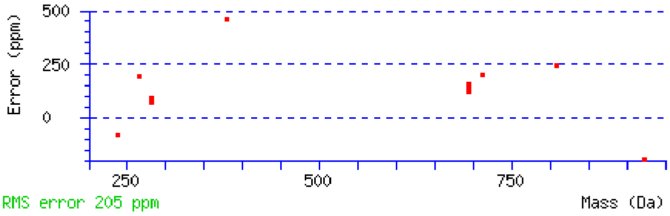
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1070.5746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.031
Matches : 11/86 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	231.1254	116.0663	213.1018	107.0545			L	955.5449	478.2761	937.5213	469.2643	937.5343	469.2708	8
3	361.2144	181.1108	343.1908	172.0990			K	841.4638	421.2355	823.4402	412.2237	823.4532	412.2303	7
4	491.2671	246.1372	473.2435	237.1254			Q	***711.3748***	356.1910	693.3512	347.1792	693.3642	347.1857	6
5	579.2961	290.1517	561.2725	281.1399	561.2855	281.1464	S	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	5
6	***693.3772***	347.1922	675.3536	338.1805	675.3666	338.1870	L	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
7	***807.4583***	404.2328	789.4347	395.2210	789.4477	395.2275	L	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	3
8	***923.4823***	462.2448	905.4587	453.2330	905.4717	453.2395	D	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NLKQSLLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.2	1070.5746	-0.0031	NLKQSLLDK

17.4	1070.5746	-0.0031	INENKLLSK
17.3	1070.5746	-0.0030	KITELTPTR
13.7	1070.5746	-0.0031	LLENSKLNK
12.6	1070.5699	0.0017	IMGRDKPIK
10.9	1070.5746	-0.0030	TLGLGAATVAGK
4.6	1070.5746	-0.0030	EVTELRALK
3.7	1070.5746	-0.0031	DSKGSLVPKK
3.3	1070.5746	-0.0030	GDILQGTVKK
3.3	1070.5746	-0.0030	NLVEKTVQK

Mascot: http://www.matrixscience.com/

AT4G27700.1

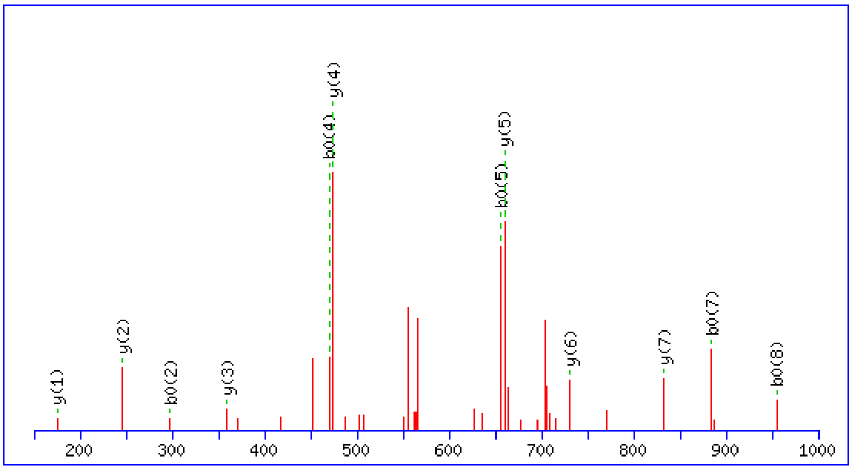
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EWTAWDIAR**
Found in **AT4G27700.1** in **TAIR_Arabidopsis**, Symbols: | rhodanese-like domain-containing protein | chr4:13826547-13827679 REVERSE

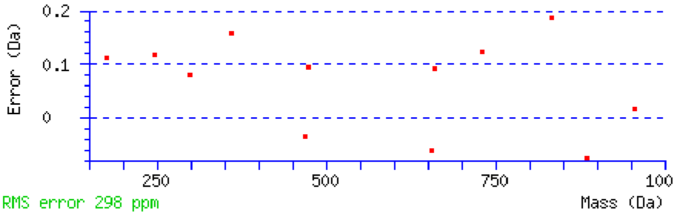
Match to Query 3656: 1146.546704 from(574.280628,2+) index(7231)
Title: Elution from: 63.852 to 63.852 scan no 9459 cid35.00 polarity:+
Data file D12h-1_3.mgf

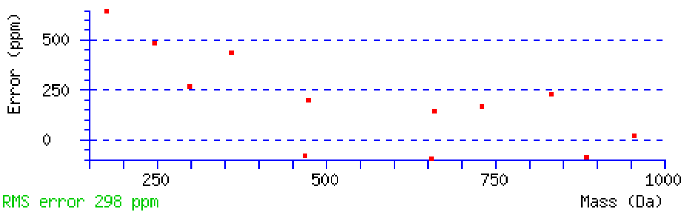
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1146.5458
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 5.5e-005
Matches : 12/74 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							9
2	316.1292	158.5682	298.1186	149.5629	W	1018.5105	509.7589	1001.4839	501.2456	1000.4999	500.7536	8
3	417.1769	209.0921	399.1663	200.0868	T	**832.4312**	416.7192	815.4046	408.2060	814.4206	407.7139	7
4	488.2140	244.6106	470.2034	235.6053	A	**731.3835**	366.1954	714.3570	357.6821	713.3729	357.1901	6
5	674.2933	337.6503	656.2827	328.6450	W	**660.3464**	330.6768	643.3198	322.1636	642.3358	321.6715	5
6	789.3202	395.1638	771.3097	386.1585	D	**474.2671**	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	902.4043	451.7058	884.3937	442.7005	I	**359.2401**	180.1237	342.2136	171.6104			3
8	973.4414	487.2243	955.4308	478.2191	A	**246.1561**	123.5817	229.1295	115.0684			2
9					R	**175.1190**	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EWTAWDIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.1	1146.5458	0.0009	EWTAWDIAR

AT4G27700.1

2.6	1146.5451	0.0016	MDDSLSPRAR

Mascot: http://www.matrixscience.com/

AT4G27860.1

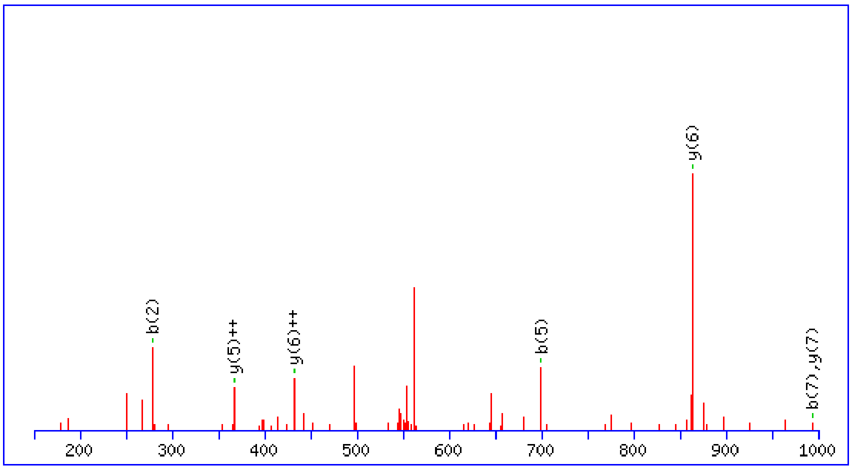
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEKRQEYK**
Found in **AT4G27860.1** in **TAIR_Arabidopsis**, Symbols: | integral membrane family protein | chr4:13873814-13876246 FORWARD

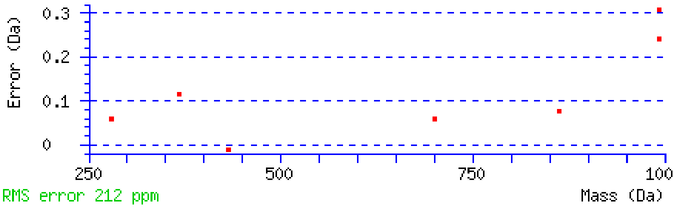
Match to Query 3643: 1140.503230 from(571.258891,2+) index(2383)
Title: Elution from: 27.252 to 27.252 scan no 3047 cid35.00 polarity:+
Data file D6h-2_2.mgf

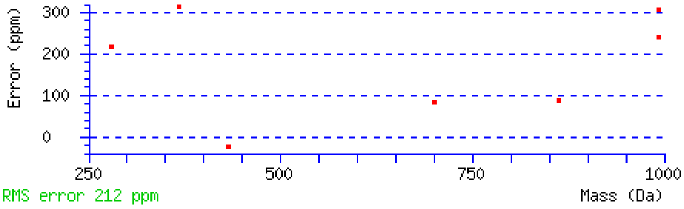
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1140.5026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.035
Matches : 7/110 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235					M							8
2	***279.0793***	140.0433			261.0688	131.0380	E	**993.4774**	497.2424	975.4538	488.2306	975.4669	488.2371	7
3	409.1684	205.0878	391.1448	196.0760	391.1578	196.0825	K	**863.4378**	432.2225	845.4142	423.2107	845.4272	423.2173	6
4	569.2576	285.1324	551.2340	276.1207	551.2471	276.1272	R	733.3488	367.1780	715.3252	358.1662	715.3382	358.1727	5
5	***699.3103***	350.1588	681.2867	341.1470	681.2997	341.1535	Q	573.2595	287.1334	555.2359	278.1216	555.2489	278.1281	4
6	829.3499	415.1786	811.3263	406.1668	811.3393	406.1733	E	443.2069	222.1071	425.1833	213.0953	425.1963	213.1018	3
7	***993.4103***	497.2088	975.3867	488.1970	975.3997	488.2035	Y	313.1672	157.0873	295.1437	148.0755			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MEKRQEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.5	1140.5026	0.0007	MEKRQEYK

AT4G27860.1

15.7	1140.5026	0.0007	LYSAAMTGSAR
14.3	1140.5053	-0.0020	MHVHNTNKK
10.5	1140.4999	0.0033	EIYSEMKSK
9.8	1140.5052	-0.0020	MRNQSFSVR
8.4	1140.5026	0.0007	CSNGTKFSVK
8.0	1140.5012	0.0020	MEMMLRKR
7.1	1140.5030	0.0002	MASRQGSKSR
6.4	1140.5045	-0.0013	WRGHHSVSR
6.3	1140.5012	0.0020	MEMMLRKR

AT4G28750.1

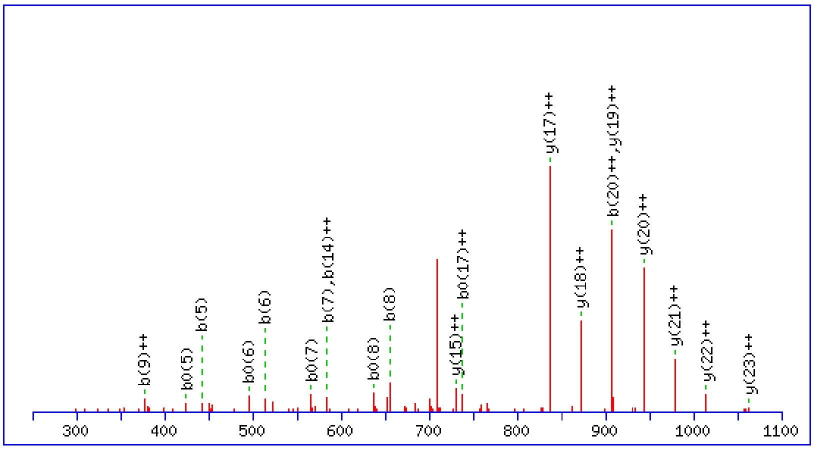
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSPAAAAAPDGATATKPKPPPIGPK**
Found in **AT4G28750.1** in **TAIR_Arabidopsis**, Symbols: PSAE-1 | PSAE-1 (PSA E1 KNOCKOUT); catalytic | chr4:14202957-14203894 REVERSE

Match to Query 10332: 2325.231066 from(776.084298,3+) index(2501)
Title: Elution from: 27.377 to 27.377 scan no 3159 cid35.00 polarity:+
Data file D12h-3_1.mgf

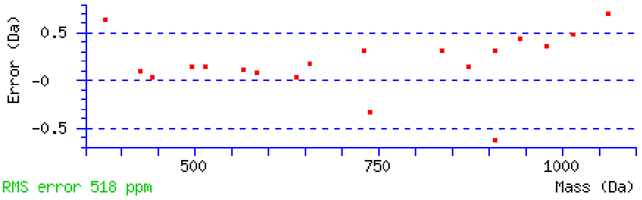
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

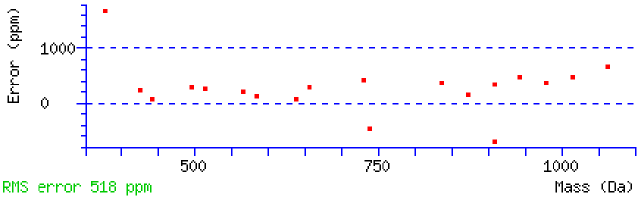


Monoisotopic mass of neutral peptide Mr(calc): 2325.2328
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1e-005
Matches : 20/238 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							25
2	203.0662	102.0368			185.0557	93.0315	S	2211.2132	1106.1102	2194.1866	1097.5970	2193.2026	1097.1050	24
3	300.1190	150.5631			282.1084	141.5579	P	2124.1812	1062.5942	2107.1546	1054.0809	2106.1706	1053.5889	23
4	371.1561	186.0817			353.1456	177.0764	A	2027.1284	1014.0678	2010.1019	1005.5546	2009.1178	1005.0626	22
5	**442.1932**	221.6003			424.1827	212.5950	A	1956.0913	978.5493	1939.0647	970.0360	1938.0807	969.5440	21
6	**513.2304**	257.1188			495.2198	248.1135	A	1885.0542	943.0307	1868.0276	934.5175	1867.0436	934.0254	20
7	**584.2675**	292.6374			566.2569	283.6321	A	1814.0171	907.5122	1796.9905	898.9989	1796.0065	898.5069	19
8	**655.3046**	328.1559			637.2940	319.1506	A	1742.9799	871.9936	1725.9534	863.4803	1724.9694	862.9883	18
9	752.3573	**376.6823**			734.3468	367.6770	P	1671.9428	836.4751	1654.9163	827.9618	1653.9323	827.4698	17
10	867.3843	434.1958			849.3737	425.1905	D	1574.8901	787.9487	1557.8635	779.4354	1556.8795	778.9434	16
11	924.4058	462.7065			906.3952	453.7012	G	1459.8631	730.4352	1442.8366	721.9219	1441.8526	721.4299	15
12	995.4429	498.2251			977.4323	489.2198	A	1402.8417	701.9245	1385.8151	693.4112	1384.8311	692.9192	14
13	1096.4905	548.7489			1078.4800	539.7436	T	1331.8046	666.4059	1314.7780	657.8926	1313.7940	657.4006	13
14	1167.5277	**584.2675**			1149.5171	575.2622	A	1230.7569	615.8821	1213.7303	607.3688	1212.7463	606.8768	12
15	1268.5753	634.7913			1250.5648	625.7860	T	1159.7198	580.3635	1142.6932	571.8502	1141.7092	571.3582	11
16	1396.6703	698.8388	1379.6438	690.3255	1378.6597	689.8335	K	1058.6721	529.8397	1041.6455	521.3264			10
17	1493.7231	747.3652	1476.6965	738.8519	1475.7125	738.3599	P	930.5771	465.7922	913.5506	457.2789			9
18	1621.8180	811.4127	1604.7915	802.8994	1603.8075	802.4074	K	833.5244	417.2658	816.4978	408.7525			8
19	1718.8708	859.9390	1701.8442	851.4258	1700.8602	850.9338	P	705.4294	353.2183	688.4028	344.7051			7
20	1815.9236	**908.4654**	1798.8970	899.9521	1797.9130	899.4601	P	608.3766	304.6920	591.3501	296.1787			6
21	1912.9763	956.9918	1895.9498	948.4785	1894.9658	947.9865	P	511.3239	256.1656	494.2973	247.6523			5
22	2026.0604	1013.5338	2009.0338	1005.0206	2008.0498	1004.5285	I	414.2711	207.6392	397.2445	199.1259			4
23	2083.0818	1042.0446	2066.0553	1033.5313	2065.0713	1033.0393	G	301.1870	151.0972	284.1605	142.5839			3
24	2180.1346	1090.5709	2163.1081	1082.0577	2162.1240	1081.5657	P	244.1656	122.5864	227.1390	114.0731			2
25							K	147.1128	74.0600	130.0863	65.5468			1

AT4G28750.1





NCBI **BLAST** search of DSPAAAAAPDGATATKPKPPPIGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.6	2325.2328	-0.0018	DSPAAAAAPDGATATKPKPPPIGPK
1.4	2325.2250	0.0061	LKIVEAVIETKDDMLPPNER

Mascot: http://www.matrixscience.com/

AT4G29060.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPAPVVTEASSEESGNTATAESIK**
Found in **AT4G29060.1** in **TAIR_Arabidopsis**, Symbols: EMB2726 | EMB2726 (EMBRYO DEFECTIVE 2726); translation elongation factor | chr4:14317750-14321321 FORWARD

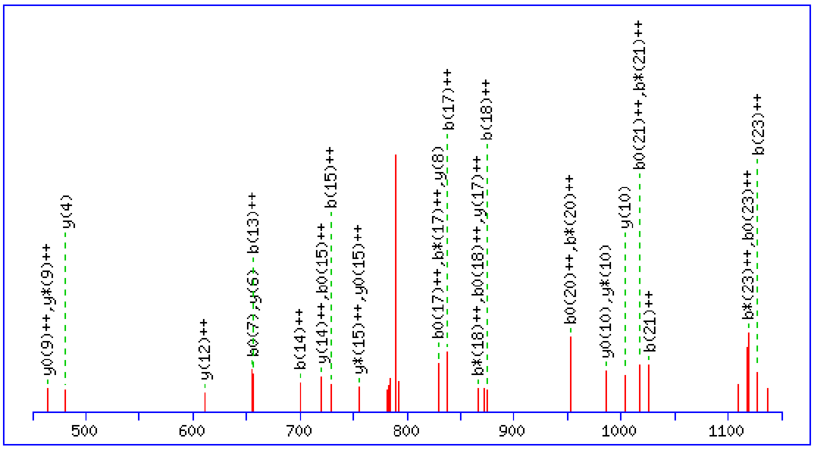
Match to Query 10147: 2401.059081 from(801.360303,3+) index(3789)
Title: Elution from: 35.752 to 35.752 scan no 4721 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1150 Da Full range

Label all possible matches ○ Label matches used for scoring ●

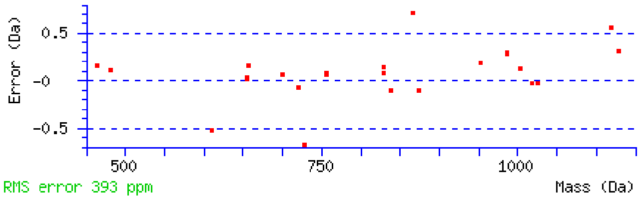
Show Y-axis ☐

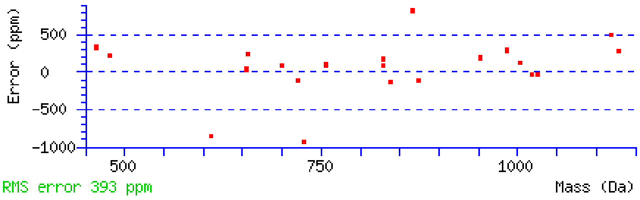


Monoisotopic mass of neutral peptide Mr(calc): 2401.0569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00073
Matches : 32/242 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							24
2	201.1018	101.0545			183.0912	92.0492	P	2300.0195	1150.5134	2281.9959	1141.5016	2282.0089	1141.5081	23
3	273.1359	137.0716			255.1254	128.0663	A	2201.9697	1101.4885	2183.9461	1092.4767	2183.9591	1092.4832	22
4	371.1857	186.0965			353.1752	177.0912	P	2129.9355	1065.4714	2111.9119	1056.4596	2111.9250	1056.4661	21
5	471.2512	236.1292			453.2406	227.1239	V	2031.8857	1016.4465	2013.8621	1007.4347	2013.8752	1007.4412	20
6	571.3166	286.1620			553.3061	277.1567	V	1931.8203	966.4138	1913.7967	957.4020	1913.8097	957.4085	19
7	673.3613	337.1843			655.3508	328.1790	T	1831.7548	916.3810	1813.7312	907.3693	1813.7443	907.3758	18
8	803.4010	402.2041			785.3904	393.1988	E	1729.7101	865.3587	1711.6865	856.3469	1711.6995	856.3534	17
9	875.4351	438.2212			857.4246	429.2159	A	1599.6705	800.3389	1581.6469	791.3271	1581.6599	791.3336	16
10	963.4642	482.2357			945.4536	473.2304	S	1527.6363	764.3218	1509.6127	755.3100	1509.6258	755.3165	15
11	1051.4933	526.2503			1033.4827	517.2450	S	1439.6073	720.3073	1421.5837	711.2955	1421.5967	711.3020	14
12	1181.5329	591.2701			1163.5223	582.2648	E	1351.5782	676.2927	1333.5546	667.2809	1333.5676	667.2875	13
13	1311.5725	***656.2899***			1293.5619	647.2846	E	1221.5386	611.2729	1203.5150	602.2611	1203.5280	602.2676	12
14	1399.6016	***700.3044***			1381.5910	691.2991	S	1091.4989	546.2531	1073.4754	537.2413	1073.4884	537.2478	11
15	1457.6201	***729.3137***			1439.6095	720.3084	G	***1003.4699***	502.2386	985.4463	493.2268	985.4593	493.2333	10
16	1573.6571	787.3322	1555.6335	778.3204	1555.6465	778.3269	N	945.4514	473.2293	927.4278	464.2175	927.4408	464.2240	9
17	1675.7018	***838.3545***	1657.6782	829.3427	1657.6912	829.3492	T	***829.4144***	415.2108	811.3908	406.1990	811.4038	406.2055	8
18	1747.7359	***874.3716***	1729.7123	865.3598	1729.7254	865.3663	A	727.3697	364.1885	709.3461	355.1767	709.3591	355.1832	7
19	1849.7806	925.3940	1831.7571	916.3822	1831.7701	916.3887	T	***655.3355***	328.1714	637.3119	319.1596	637.3250	319.1661	6
20	1921.8148	961.4110	1903.7912	952.3992	1903.8042	952.4058	A	553.2908	277.1490	535.2672	268.1373	535.2802	268.1438	5
21	2051.8544	***1026.4308***	2033.8308	1017.4191	2033.8439	1017.4256	E	***481.2567***	241.1320	463.2331	232.1202	463.2461	232.1267	4
22	2139.8835	1070.4454	2121.8599	1061.4336	2121.8729	1061.4401	S	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
23	2253.9646	***1127.4859***	2235.9410	1118.4741	2235.9540	1118.4806	I	263.1880	132.0976	245.1644	123.0858			2
24							K	149.1069	75.0571	131.0833	66.0453			1

AT4G29060.1





NCBI **BLAST** search of TPAPVVTEASSEESGNTATAESIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.4	2401.0569	0.0022	TPAPVVTEASSEESGNTATAESIK
8.9	2401.0636	-0.0045	MAQMVAMPVAHSLSLICNWAK
4.3	2401.0636	-0.0045	MAQMVAMPVAHSLSLICNWAK
3.7	2401.0626	-0.0036	GCDQRTVRELFYEMTIVEK
2.6	2401.0663	-0.0072	GYSSVYALLEAEGHDKFAYQK
0.4	2401.0519	0.0072	QGLVEAFYELFNVMEKNGCK
0.1	2401.0660	-0.0069	GETTSTIMFGQRAMKVENMVK

Mascot: http://www.matrixscience.com/

AT4G29840.1

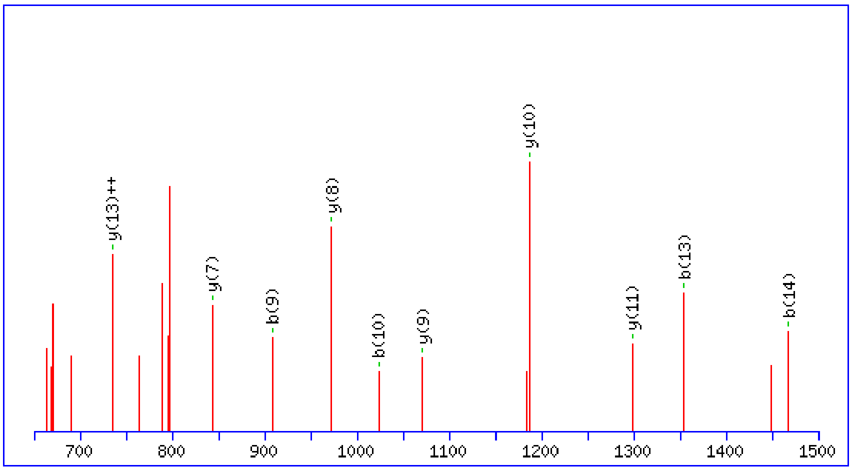
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGGLLDVEHDMEALK**
Found in **AT4G29840.1** in **TAIR_Arabidopsis**, Symbols: TS, MTO2 | MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase | chr4:14599440-14601020 REVERSE

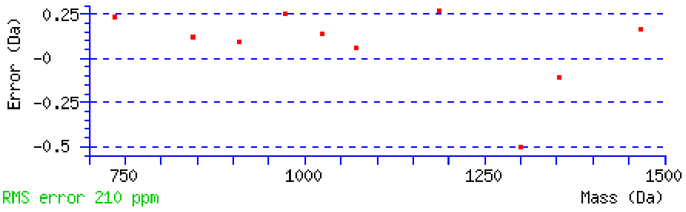
Match to Query 7109: 1612.777580 from(807.396066,2+) index(8507)
Title: Elution from: 78.384 to 78.384 scan no 11407 cid35.00 polarity:+
Data file D1d-1_1.mgf

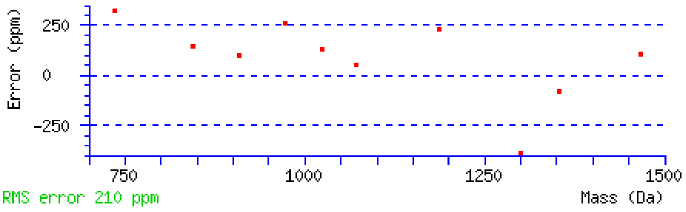
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1612.7767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 9e-005
Matches : 10/134 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							15
2	145.0608	73.0340	127.0502	64.0287	G	1526.7519	763.8796	1509.7254	755.3663	1508.7414	754.8743	14
3	202.0822	101.5448	184.0717	92.5395	G	1469.7305	735.3689	1452.7039	726.8556	1451.7199	726.3636	13
4	315.1663	158.0868	297.1557	149.0815	L	1412.7090	706.8581	1395.6824	698.3449	1394.6984	697.8529	12
5	428.2504	214.6288	410.2398	205.6235	L	***1299.6249***	650.3161	1282.5984	641.8028	1281.6144	641.3108	11
6	543.2773	272.1423	525.2667	263.1370	D	***1186.5409***	593.7741	1169.5143	585.2608	1168.5303	584.7688	10
7	642.3457	321.6765	624.3352	312.6712	V	***1071.5139***	536.2606	1054.4874	527.7473	1053.5034	527.2553	9
8	771.3883	386.1978	753.3777	377.1925	E	***972.4455***	486.7264	955.4190	478.2131	954.4349	477.7211	8
9	***908.4472***	454.7272	890.4367	445.7220	H	***843.4029***	422.2051	826.3764	413.6918	825.3923	413.1998	7
10	***1023.4742***	512.2407	1005.4636	503.2354	D	706.3440	353.6756	689.3175	345.1624	688.3334	344.6704	6
11	1154.5146	577.7610	1136.5041	568.7557	M	591.3171	296.1622	574.2905	287.6489	573.3065	287.1569	5
12	1283.5572	642.2823	1265.5467	633.2770	E	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
13	***1354.5944***	677.8008	1336.5838	668.7955	A	331.2340	166.1206	314.2074	157.6074			3
14	***1467.6784***	734.3428	1449.6679	725.3376	L	260.1969	130.6021	243.1703	122.0888			2
15					K	147.1128	74.0600	130.0863	65.5468			1





AT4G29840.1

NCBI **BLAST** search of SGGLLDVEHDMEALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.3	1612.7767	0.0009	SGGLLDVEHDMEALK
0.5	1612.7807	-0.0031	SGMIDDVFIGDFLGK

AT4G29900.1

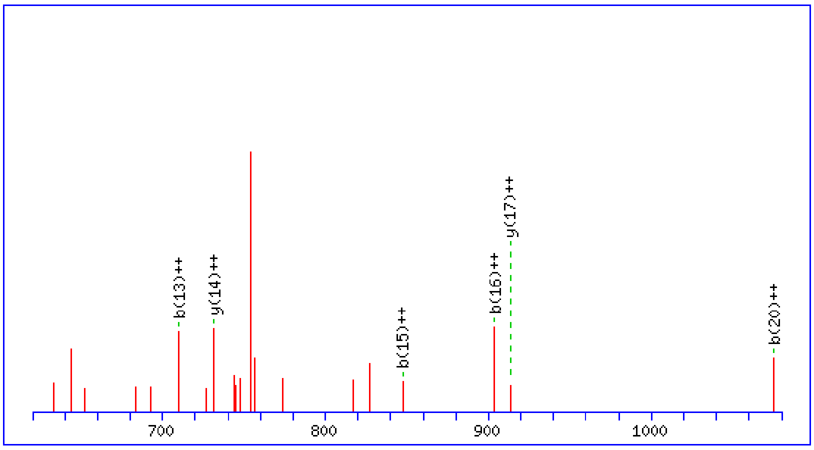
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFTGHTKNEQGGPQFIGGKTK**
Found in **AT4G29900.1** in **TAIR_Arabidopsis**, Symbols: ATACA10, ACA10 | ACA10 (autoinhibited Ca2+ -ATPase 10); calcium-transporting ATPase/ calmodulin binding | chr4:14611231-14618781 REVERSE

Match to Query 10186: 2294.143854 from(765.721894,3+) index(6124)
Title: Elution from: 53.661 to 53.661 scan no 7746 cid35.00 polarity:+
Data file C7-2_2.mgf

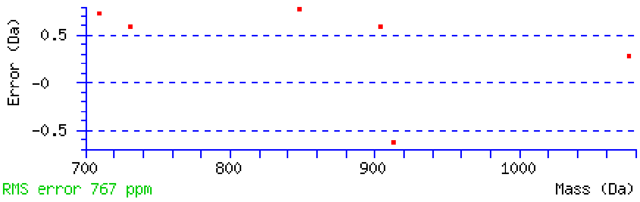
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 620 to 1080 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

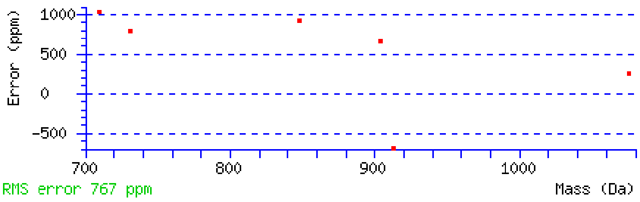


Monoisotopic mass of neutral peptide Mr(calc): 2294.1444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.047
Matches : 6/222 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							21
2	311.1390	156.0731					F	2132.0883	1066.5478	2115.0618	1058.0345	2114.0778	1057.5425	20
3	412.1867	206.5970			394.1761	197.5917	T	1985.0199	993.0136	1967.9934	984.5003	1967.0094	984.0083	19
4	469.2082	235.1077			451.1976	226.1024	G	1883.9722	942.4898	1866.9457	933.9765	1865.9617	933.4845	18
5	606.2671	303.6372			588.2565	294.6319	H	1826.9508	913.9790	1809.9242	905.4658	1808.9402	904.9737	17
6	707.3148	354.1610			689.3042	345.1557	T	1689.8919	845.4496	1672.8653	836.9363	1671.8813	836.4443	16
7	835.4097	418.2085	818.3832	409.6952	817.3992	409.2032	K	1588.8442	794.9257	1571.8176	786.4125	1570.8336	785.9204	15
8	949.4526	475.2300	932.4261	466.7167	931.4421	466.2247	N	1460.7492	730.8782	1443.7227	722.3650	1442.7387	721.8730	14
9	1078.4952	539.7513	1061.4687	531.2380	1060.4847	530.7460	E	1346.7063	673.8568	1329.6797	665.3435	1328.6957	664.8515	13
10	1206.5538	603.7805	1189.5273	595.2673	1188.5432	594.7753	Q	1217.6637	609.3355	1200.6372	600.8222	1199.6531	600.3302	12
11	1263.5753	632.2913	1246.5487	623.7780	1245.5647	623.2860	G	1089.6051	545.3062	1072.5786	536.7929	1071.5946	536.3009	11
12	1320.5967	660.8020	1303.5702	652.2887	1302.5862	651.7967	G	1032.5837	516.7955	1015.5571	508.2822	1014.5731	507.7902	10
13	1417.6495	***709.3284***	1400.6230	700.8151	1399.6389	700.3231	P	975.5622	488.2847	958.5356	479.7715	957.5516	479.2795	9
14	1545.7081	773.3577	1528.6815	764.8444	1527.6975	764.3524	Q	878.5094	439.7584	861.4829	431.2451	860.4989	430.7531	8
15	1692.7765	***846.8919***	1675.7499	838.3786	1674.7659	837.8866	F	750.4509	375.7291	733.4243	367.2158	732.4403	366.7238	7
16	1805.8606	***903.4339***	1788.8340	894.9206	1787.8500	894.4286	I	603.3824	302.1949	586.3559	293.6816	585.3719	293.1896	6
17	1862.8820	931.9447	1845.8555	923.4314	1844.8715	922.9394	G	490.2984	245.6528	473.2718	237.1396	472.2878	236.6475	5
18	1919.9035	960.4554	1902.8769	951.9421	1901.8929	951.4501	G	433.2769	217.1421	416.2504	208.6288	415.2663	208.1368	4
19	2047.9985	1024.5029	2030.9719	1015.9896	2029.9879	1015.4976	K	376.2554	188.6314	359.2289	180.1181	358.2449	179.6261	3
20	2149.0461	***1075.0267***	2132.0196	1066.5134	2131.0356	1066.0214	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT4G29900.1





NCBI **BLAST** search of YFTGHTKNEQGGPQFIGGKTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	2294.1444	-0.0005	YFTGHTKNEQGGPQFIGGKTK
15.0	2294.1503	-0.0064	GNADIIQISGHDGGTGASPISSIK
6.2	2294.1385	0.0053	LNMVEDSATMLKEALILEDK
4.3	2294.1399	0.0040	SDDTASIVTKAWLEVKGMGMR
2.4	2294.1424	0.0015	TGSMVVGVTADEISTKERETGK
1.0	2294.1444	-0.0005	ILQALGGHENVVGFHNAFEDK
0.3	2294.1498	-0.0059	NLLTEMETVTNIMREVELK

Mascot: http://www.matrixscience.com/

AT4G30100.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FRAGTSFNLEEAR**
Found in **AT4G30100.1** in **TAIR_Arabidopsis**, Symbols: | tRNA-splicing endonuclease positive effector-related | chr4:14714197-14719341 FORWARD

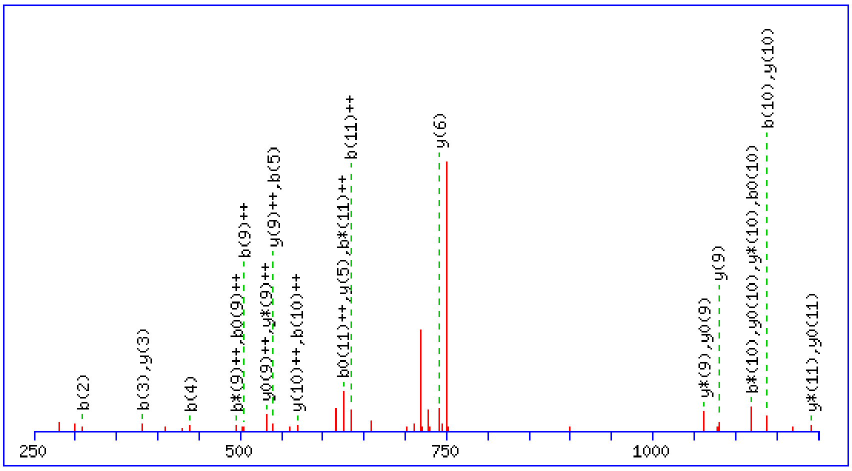
Match to Query 6207: 1516.679428 from(759.346990,2+) index(3266)
Title: Elution from: 35.207 to 35.207 scan no 4195 cid35.00 polarity:+
Data file D1d-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1200 Da Full range

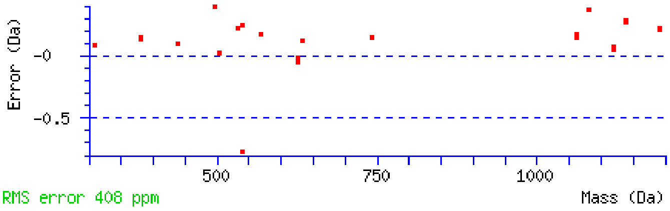
Label all possible matches ○ Label matches used for scoring ●

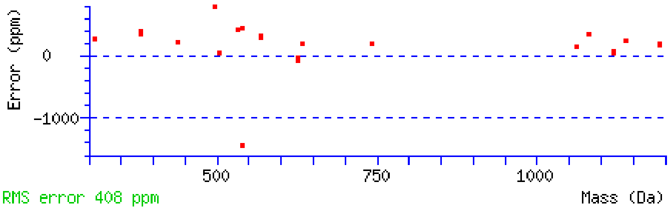
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1516.6779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0033
Matches : 29/130 fragment ions using 31 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	149.0727	75.0400					F							13
2	***309.1620***	155.0846	291.1384	146.0728			R	1369.6197	685.3135	1351.5961	676.3017	1351.6092	676.3082	12
3	***381.1961***	191.1017	363.1725	182.0899			A	1209.5305	605.2689	1191.5069	596.2571	1191.5199	596.2636	11
4	***439.2146***	220.1110	421.1910	211.0992			G	***1137.4963***	569.2518	1119.4727	560.2400	1119.4858	560.2465	10
5	***541.2593***	271.1333	523.2358	262.1215	523.2488	262.1280	T	***1079.4778***	540.2425	1061.4542	531.2308	1061.4673	531.2373	9
6	629.2884	315.1478	611.2648	306.1360	611.2778	306.1426	S	977.4331	489.2202	959.4095	480.2084	959.4225	480.2149	8
7	777.3538	389.1806	759.3303	380.1688	759.3433	380.1753	F	889.4040	445.2057	871.3805	436.1939	871.3935	436.2004	7
8	893.3908	447.1991	875.3673	438.1873	875.3803	438.1938	N	***741.3386***	371.1729	723.3150	362.1611	723.3280	362.1677	6
9	1007.4719	***504.2396***	989.4484	495.2278	989.4614	495.2343	L	***625.3016***	313.1544	607.2780	304.1426	607.2910	304.1492	5
10	***1137.5116***	***569.2594***	1119.4880	560.2476	1119.5010	560.2541	E	511.2205	256.1139	493.1969	247.1021	493.2099	247.1086	4
11	1267.5512	***634.2792***	1249.5276	625.2674	1249.5406	625.2740	E	***381.1809***	191.0941	363.1573	182.0823	363.1703	182.0888	3
12	1339.5854	670.2963	1321.5618	661.2845	1321.5748	661.2910	A	251.1412	126.0743	233.1177	117.0625			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FRAGTSFNLEEAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G30100.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.8	1516.6779	0.0016	FRAGTSFNLEEAR
6.8	1516.6761	0.0034	FRAEAICVEFMK
2.7	1516.6812	-0.0018	QSSDFMVKQQRK
2.6	1516.6812	-0.0018	MGFTVVSRSGSPTR
2.5	1516.6774	0.0020	SDTTESLFWIFR
2.2	1516.6786	0.0009	DGMSIKYVTDVTR
2.1	1516.6758	0.0036	QWQARAMRAGFR
2.1	1516.6761	0.0034	AIVEVFACCYLR
2.0	1516.6835	-0.0041	SSLAFNCKTPAFR
1.8	1516.6832	-0.0038	NGLIHDHHHRQK

AT4G30160.1

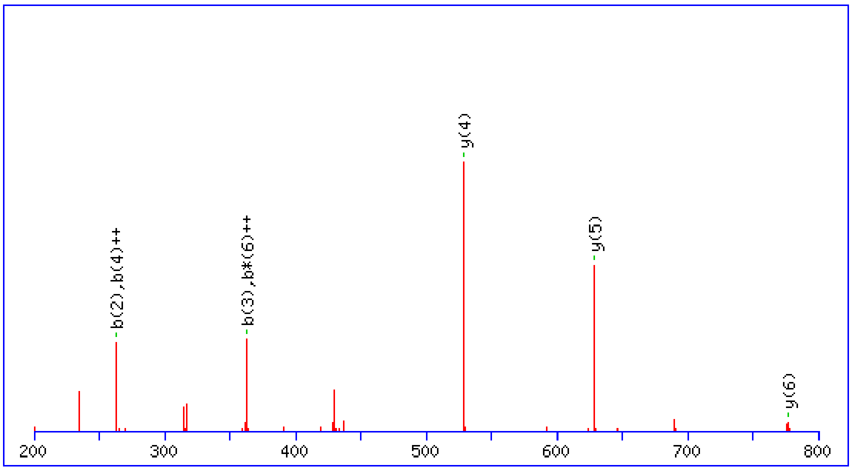
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFVCRGK**
Found in **AT4G30160.1** in **TAIR_Arabidopsis**, Symbols: ATVLN4, VLN4 | VLN4 (ARABIDOPSIS THALIANA VILLIN 4); actin binding | chr4:14754534-14759517 FORWARD

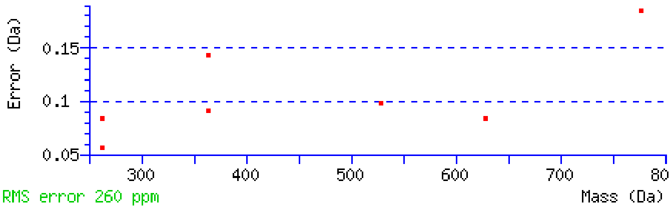
Match to Query 1573: 890.442104 from(446.228328,2+) index(4643)
Title: Elution from: 42.921 to 42.921 scan no 5816 cid35.00 polarity:+
Data file D12h-3_1.mgf

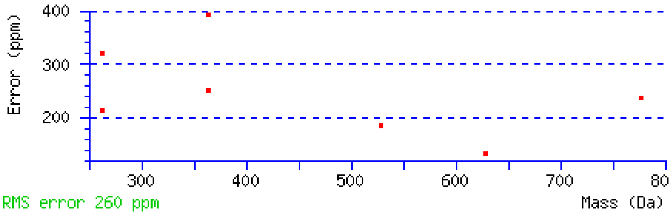
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 890.4440
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.03
Matches : 7/40 fragment ions using 6 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	115.0884	58.0478			**L**					**7**
2	**263.1538**	132.0805			**F**	***777.3702***	389.1888	759.3467	380.1770	**6**
3	**363.2193**	182.1133			**V**	***629.3048***	315.1560	611.2812	306.1442	**5**
4	525.2440	263.1256			**C**	***529.2393***	265.1233	511.2158	256.1115	**4**
5	685.3332	343.1703	667.3097	334.1585	**R**	367.2146	184.1109	349.1910	175.0992	**3**
6	743.3517	372.1795	725.3282	363.1677	**G**	207.1254	104.0663	189.1018	95.0545	**2**
7					**K**	149.1069	75.0571	131.0833	66.0453	**1**





NCBI **BLAST** search of LFVCRGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.1	890.4440	-0.0019	LFVCRGK
18.5	890.4414	0.0007	IFQSMLK

AT4G30160.1

13.6	890.4414	0.0007	MVNYVLK
13.6	890.4414	0.0007	YCSLVLK
9.3	890.4414	0.0007	EMSKFLK
7.9	890.4448	-0.0027	IMSLKMK
7.9	890.4414	0.0007	LFSLMQK
4.0	890.4445	-0.0024	IMRQRR
2.1	890.4418	0.0003	IMTVRSR
0.1	890.4448	-0.0027	SLKMMLK

AT4G30190.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDQSALTGESLPVTK**
Found in **AT4G30190.1** in **TAIR_Arabidopsis**, Symbols: PMA2, AHA2 | AHA2 (Arabidopsis H(+)-ATPase 2); ATPase | chr4:14770826-14775926 REVERSE

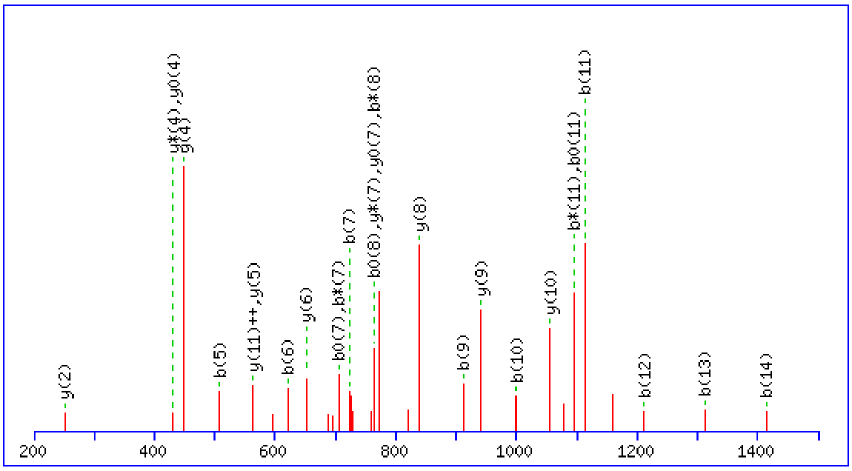
Match to Query 6632: 1560.755992 from(781.385272,2+) index(4471)
Title: Elution from: 40.715 to 40.715 scan no 5592 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

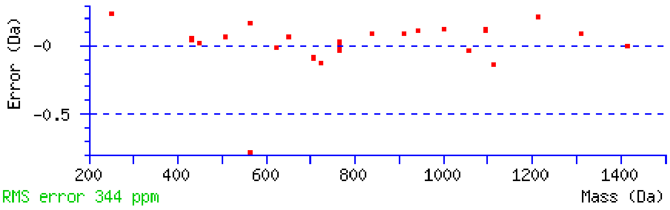
Label all possible matches ○ Label matches used for scoring ●

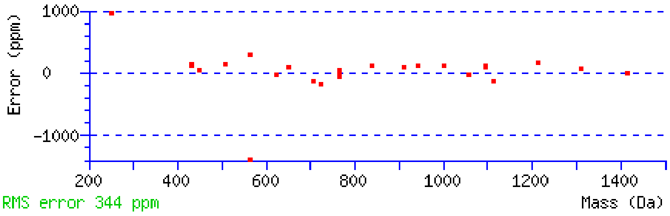
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1560.7589
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 5.2e-008
Matches : 27/160 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							15
2	217.0967	109.0520			199.0861	100.0467	D	1461.7008	731.3540	1443.6772	722.3422	1443.6902	722.3487	14
3	347.1493	174.0783	329.1258	165.0665	329.1388	165.0730	Q	1345.6768	673.3420	1327.6532	664.3302	1327.6662	664.3368	13
4	435.1784	218.0928	417.1548	209.0811	417.1678	209.0876	S	1215.6241	608.3157	1197.6006	599.3039	1197.6136	599.3104	12
5	***507.2126***	254.1099	489.1890	245.0981	489.2020	245.1046	A	1127.5951	564.3012	1109.5715	555.2894	1109.5845	555.2959	11
6	***621.2937***	311.1505	603.2701	302.1387	603.2831	302.1452	L	**1055.5609**	528.2841	1037.5374	519.2723	1037.5504	519.2788	10
7	***723.3384***	362.1728	705.3148	353.1610	705.3278	353.1675	T	**941.4798**	471.2436	923.4563	462.2318	923.4693	462.2383	9
8	781.3569	391.1821	763.3333	382.1703	763.3463	382.1768	G	**839.4351**	420.2212	821.4115	411.2094	821.4246	411.2159	8
9	***911.3965***	456.2019	893.3729	447.1901	893.3859	447.1966	E	781.4166	391.2120	763.3930	382.2002	763.4061	382.2067	7
10	***999.4256***	500.2164	981.4020	491.2046	981.4150	491.2111	S	**651.3770**	326.1921	633.3534	317.1803	633.3664	317.1869	6
11	***1113.5067***	557.2570	1095.4831	548.2452	1095.4961	548.2517	L	**563.3479**	282.1776	545.3243	273.1658	545.3374	273.1723	5
12	***1211.5565***	606.2819	1193.5329	597.2701	1193.5459	597.2766	P	**449.2668**	225.1371	431.2433	216.1253	431.2563	216.1318	4
13	***1311.6219***	656.3146	1293.5983	647.3028	1293.6113	647.3093	V	351.2170	176.1122	333.1935	167.1004	333.2065	167.1069	3
14	***1413.6666***	707.3369	1395.6430	698.3252	1395.6561	698.3317	T	**251.1516**	126.0794	233.1280	117.0676	233.1410	117.0741	2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT4G30190.1

NCBI **BLAST** search of VDQSALTGESLPVTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.9	1560.7589	-0.0029	VDQSALTGESLPVTK
14.4	1560.7569	-0.0009	LTRAIMEEHTLAR
7.3	1560.7540	0.0020	NSEIGNLVRRNHK
0.3	1560.7535	0.0025	ENYLGHSIKAPVGR

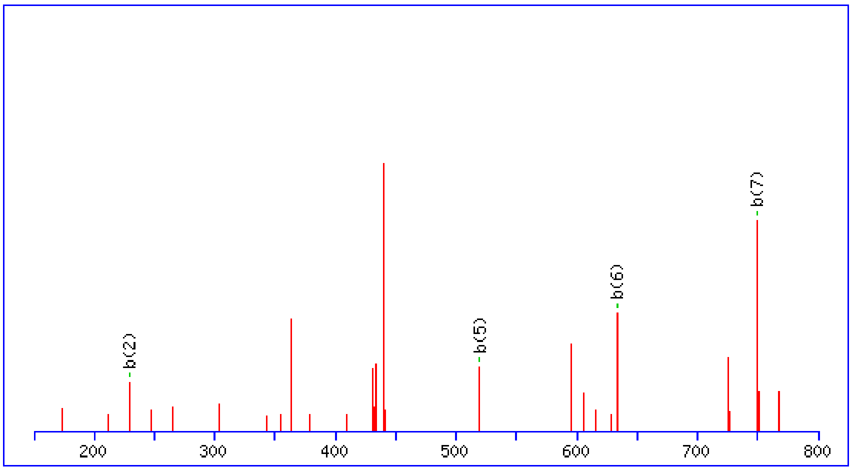
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLSLSLDK**
Found in **AT4G30290.1** in **TAIR_Arabidopsis**, Symbols: ATXTH19 | ATXTH19 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 19); hydrolase, acting on glycosyl bonds | chr4:14828960-14829971 REVERSE

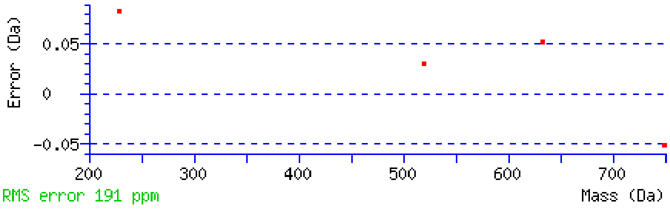
Match to Query 1617: 896.503764 from(449.259158,2+) index(1357)
Title: Elution from: 17.217 to 17.217 scan no 1764 cid35.00 polarity:+
Data file D1d-3_3.mgf

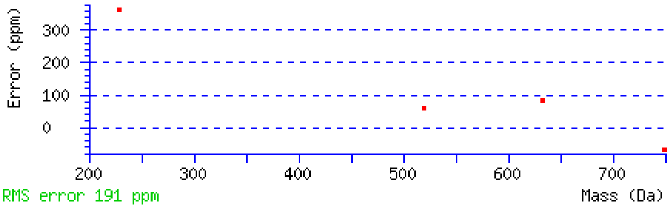
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 896.5061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0016
Matches : 4/64 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							8
2	*229.1695*	115.0884			L	783.4323	392.2198	765.4087	383.2080	765.4217	383.2145	7
3	317.1985	159.1029	299.1880	150.0976	S	669.3512	335.1792	651.3276	326.1674	651.3406	326.1739	6
4	431.2796	216.1435	413.2691	207.1382	L	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	5
5	*519.3087*	260.1580	501.2981	251.1527	S	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
6	*633.3898*	317.1985	615.3792	308.1933	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
7	*749.4138*	375.2105	731.4032	366.2052	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LLSLSLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.3	896.5061	-0.0023	LLSLSLDK

AT4G30290.1

29.3	896.5061	-0.0023	LLSTVLDK
16.1	896.5061	-0.0023	VTLLSIDK
5.9	896.5014	0.0024	ILIGCLAK
3.0	896.5061	-0.0023	SSIIIEVK
3.0	896.5061	-0.0023	TISLVDLK
3.0	896.5061	-0.0023	LLSLVDTK
1.6	896.5061	-0.0023	SVLIEISK
1.3	896.5061	-0.0023	LTITIEAK
1.1	896.5061	-0.0023	VSISLLEK

AT4G30530.1

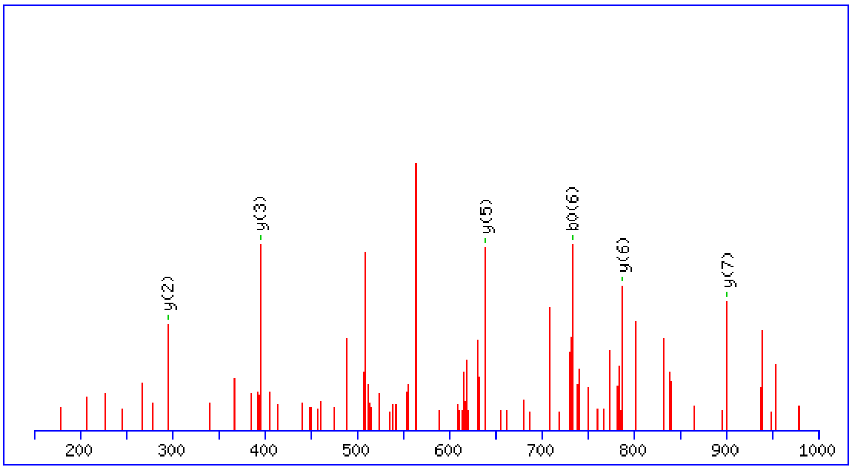
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EILFEIVDR**
Found in **AT4G30530.1** in **TAIR_Arabidopsis**, Symbols: | defense-related protein, putative | chr4:14920611-14922292 FORWARD

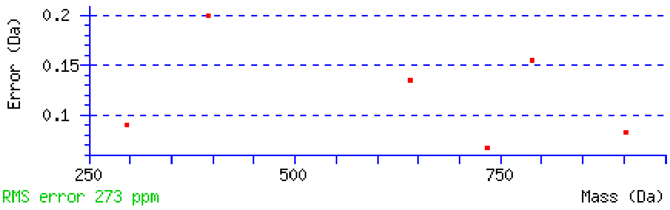
Match to Query 3813: 1144.579680 from(573.297116,2+) index(8476)
Title: Elution from: 75.900 to 75.900 scan no 11224 cid35.00 polarity:+
Data file 0-3_1.mgf

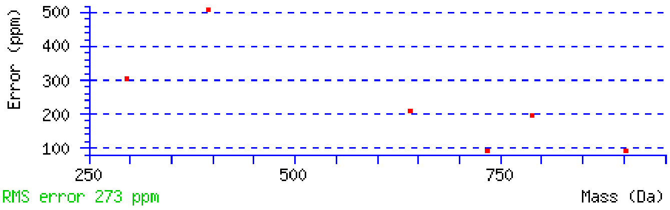
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1144.5772
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.005
Matches : 6/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							9
2	245.1280	123.0676	227.1174	114.0624	I	1015.5449	508.2761	997.5213	499.2643	997.5343	499.2708	8
3	359.2091	180.1082	341.1985	171.1029	L	***901.4638***	451.2355	883.4402	442.2237	883.4532	442.2303	7
4	507.2746	254.1409	489.2640	245.1356	F	***787.3827***	394.1950	769.3591	385.1832	769.3721	385.1897	6
5	637.3142	319.1607	619.3036	310.1554	E	***639.3172***	320.1623	621.2937	311.1505	621.3067	311.1570	5
6	751.3953	376.2013	733.3847	367.1960	I	509.2776	255.1424	491.2540	246.1307	491.2671	246.1372	4
7	851.4607	426.2340	833.4502	417.2287	V	***395.1965***	198.1019	377.1729	189.0901	377.1860	189.0966	3
8	967.4847	484.2460	949.4741	475.2407	D	***295.1311***	148.0692	277.1075	139.0574	277.1205	139.0639	2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EILFEIVDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.6	1144.5772	0.0025	EILFEIVDR

AT4G30530.1

7.9	1144.5777	0.0020	EIIIRDTNR
4.2	1144.5777	0.0020	RDDIIGATLR
3.6	1144.5799	-0.0002	DNWSKLLVR

Mascot: http://www.matrixscience.com/

AT4G30600.1

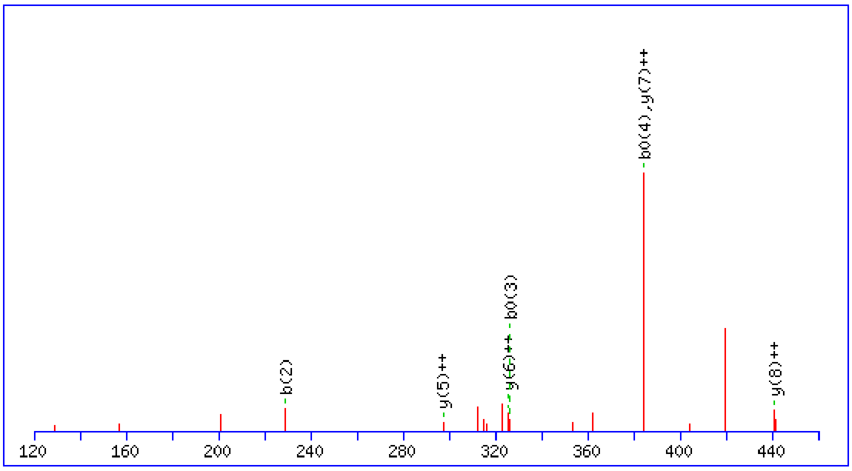
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIDGILLTK**
Found in **AT4G30600.1** in **TAIR_Arabidopsis**, Symbols: | signal recognition particle receptor alpha subunit family protein | chr4:14938148-14940606 REVERSE

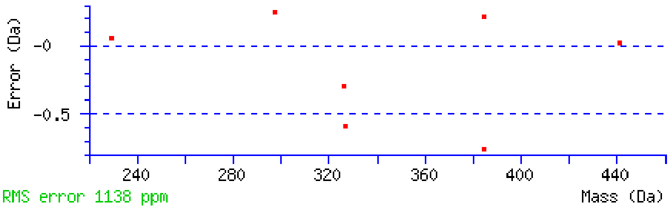
Match to Query 2038: 994.589595 from(332.537141,3+) index(2448)
Title: Elution from: 27.176 to 27.176 scan no 3126 cid35.00 polarity:+
Data file D12h-2_3.mgf

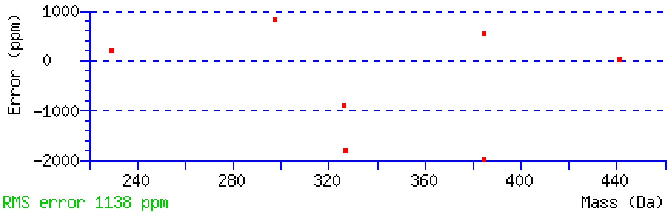
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 460 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.5923
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.02
Matches : 7/74 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							9
2	229.1695	115.0884			I	881.5185	441.2629	863.4949	432.2511	863.5079	432.2576	8
3	345.1935	173.1004	327.1829	164.0951	D	767.4374	384.2223	749.4138	375.2105	749.4268	375.2170	7
4	403.2120	202.1096	385.2014	193.1043	G	651.4134	326.2103	633.3898	317.1985	633.4028	317.2050	6
5	517.2930	259.1502	499.2825	250.1449	I	593.3949	297.2011	575.3713	288.1893	575.3843	288.1958	5
6	631.3741	316.1907	613.3636	307.1854	L	479.3138	240.1605	461.2902	231.1487	461.3032	231.1552	4
7	745.4552	373.2313	727.4447	364.2260	L	365.2327	183.1200	347.2091	174.1082	347.2221	174.1147	3
8	847.5000	424.2536	829.4894	415.2483	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LIDGILLTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G30600.1

16.9	994.5923	-0.0027	LIDGILLTK
14.5	994.5876	0.0020	IILPCLKK
10.0	994.5923	-0.0027	LLLVTLGEK

AT4G30720.1

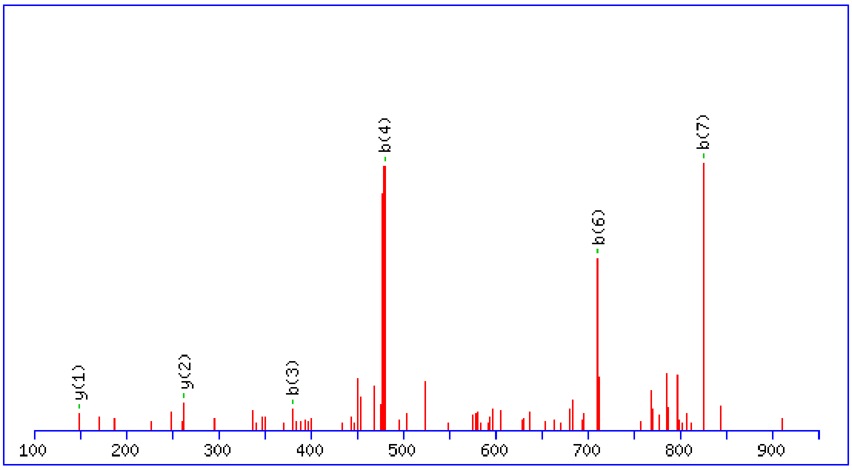
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFDVLNLK**
Found in **AT4G30720.1** in **TAIR_Arabidopsis**, Symbols: | oxidoreductase | chr4:14972218-14975467 REVERSE

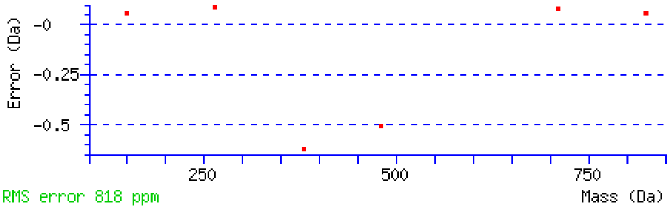
Match to Query 2384: 972.477470 from(487.246011,2+) index(1307)
Title: Elution from: 19.338 to 19.338 scan no 1828 cid35.00 polarity:+
Data file C7-2_1.mgf

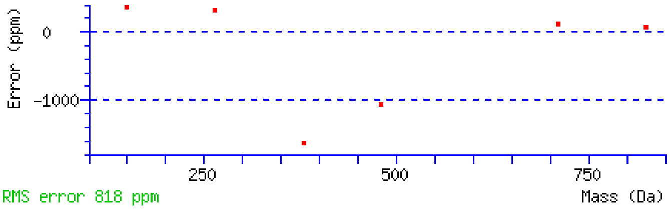
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.022
Matches : 6/64 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							8
2	265.0967	133.0520			247.0861	124.0467	F	857.4609	429.2341	839.4374	420.2223	839.4504	420.2288	7
3	***381.1207***	191.0640			363.1101	182.0587	D	709.3955	355.2014	691.3719	346.1896	691.3849	346.1961	6
4	***481.1861***	241.0967			463.1756	232.0914	V	593.3715	297.1894	575.3479	288.1776			5
5	595.2672	298.1373			577.2567	289.1320	L	493.3061	247.1567	475.2825	238.1449			4
6	***711.3042***	356.1558	693.2806	347.1440	693.2937	347.1505	N	379.2250	190.1161	361.2014	181.1043			3
7	***825.3853***	413.1963	807.3617	404.1845	807.3748	404.1910	L	**263.1880**	132.0976	245.1644	123.0858			2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DFDVLNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.5	972.4776	-0.0002	DFDVLNLK
25.1	972.4754	0.0021	GSTSQEILK

AT4G30720.1

20.9	972.4776	-0.0002	FVSVPATDK
19.3	972.4776	-0.0002	VPYEQSLK
18.0	972.4803	-0.0029	RSSPSWLK
17.8	972.4799	-0.0024	LFEEWLK
16.2	972.4776	-0.0002	IFTKPDDK
15.7	972.4803	-0.0028	DTARAWLK
14.0	972.4803	-0.0028	FIDNPKAR
13.4	972.4776	-0.0001	FLGLDVGDK

AT4G30800.1

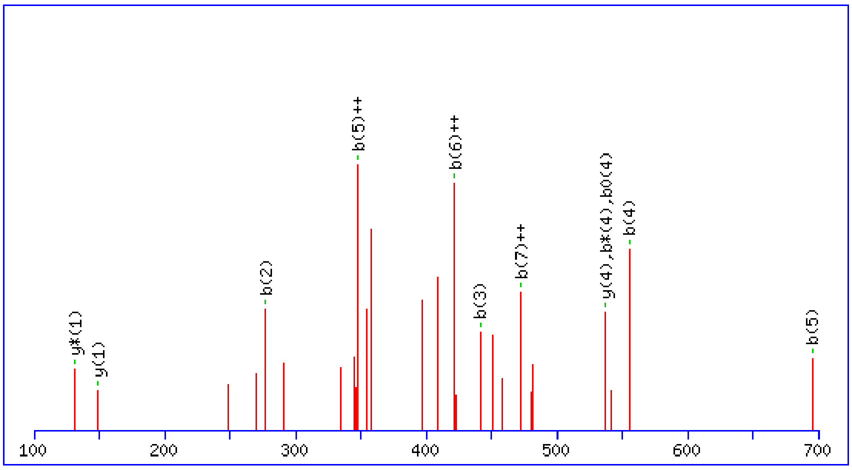
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RDYLHFVK**
Found in **AT4G30800.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S11 (RPS11B) | chr4:15001222-15002398 FORWARD

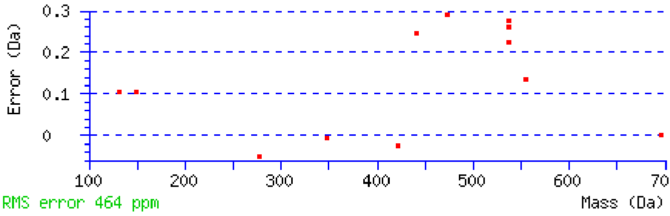
Match to Query 3344: 1090.534266 from(364.518698,3+) index(3183)
Title: Elution from: 31.149 to 31.149 scan no 3947 cid35.00 polarity:+
Data file C7-1_1.mgf

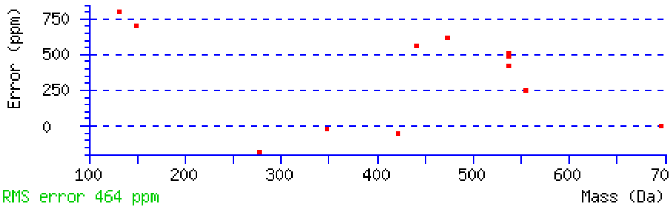
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1090.5352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0011
Matches : 12/70 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							8
2	***277.1205***	139.0639	259.0969	130.0521	259.1099	130.0586	D	931.4532	466.2303	913.4296	457.2185	913.4427	457.2250	7
3	***441.1809***	221.0941	423.1573	212.0823	423.1703	212.0888	Y	815.4293	408.2183	797.4057	399.2065			6
4	***555.2620***	278.1346	537.2384	269.1228	537.2514	269.1293	L	651.3689	326.1881	633.3453	317.1763			5
5	***695.3120***	***348.1596***	677.2884	339.1478	677.3014	339.1543	H	**537.2878**	269.1475	519.2642	260.1357			4
6	843.3774	***422.1924***	825.3538	413.1806	825.3669	413.1871	F	397.2378	199.1225	379.2142	190.1107			3
7	943.4429	***472.2251***	925.4193	463.2133	925.4323	463.2198	V	249.1723	125.0898	231.1487	116.0780			2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RDYLHFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.2	1090.5352	-0.0009	RDYLHFVK
12.6	1090.5359	-0.0016	YICIGDLVK

9.8	1090.5359	-0.0016	LYEAACLLK
9.7	1090.5329	0.0013	FVVQGNREK
8.8	1090.5330	0.0013	RSFSQNPIK
8.5	1090.5363	-0.0021	VRSGIQMSAK
5.0	1090.5337	0.0006	EKLQSIMSK
4.8	1090.5337	0.0006	MATKVSLEGK
3.8	1090.5363	-0.0021	MTTSPIRVR
3.6	1090.5329	0.0013	FRQLQQEK

AT4G30920.1

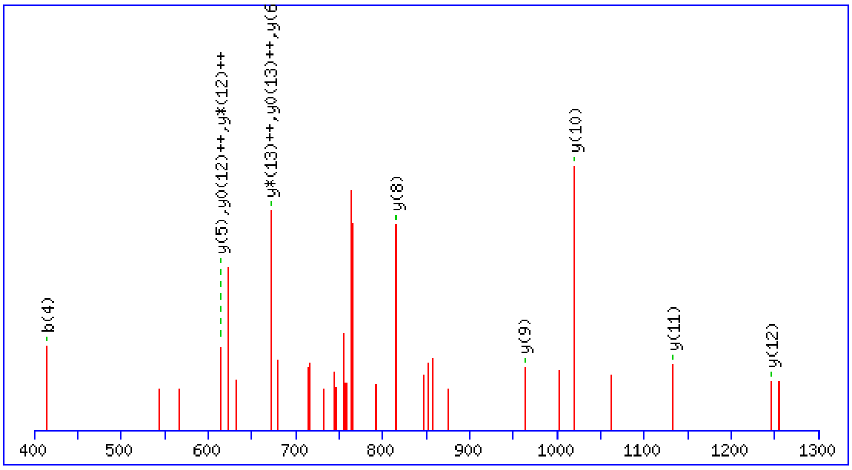
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVDIIGFGSGPELEK**
Found in **AT4G30920.1** in **TAIR_Arabidopsis**, Symbols: | cytosol aminopeptidase family protein | chr4:15046595-15049310 REVERSE

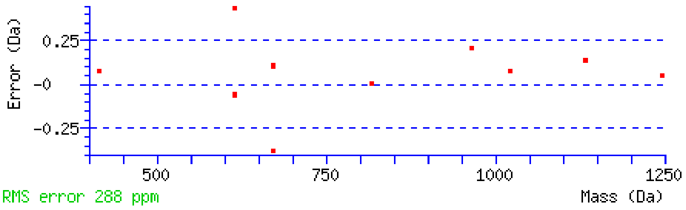
Match to Query 6598: 1546.787212 from(774.400882,2+) index(7583)
Title: Elution from: 67.249 to 67.249 scan no 9966 cid35.00 polarity:+
Data file D12h-3_2.mgf

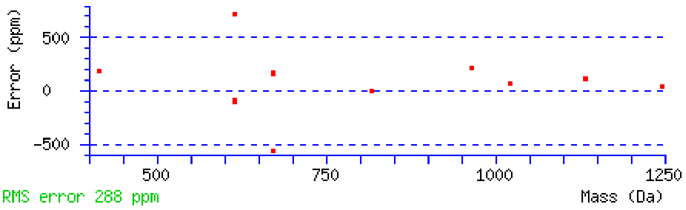
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1546.7879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 2.2e-006
Matches : 12/138 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	**S**							**15**
2	187.1077	94.0575	169.0972	85.0522	**V**	1460.7631	730.8852	1443.7366	722.3719	1442.7526	721.8799	**14**
3	302.1347	151.5710	284.1241	142.5657	**D**	1361.6947	681.3510	1344.6682	672.8377	1343.6842	672.3457	**13**
4	415.2187	208.1130	397.2082	199.1077	**I**	***1246.6678***	623.8375	1229.6412	615.3243	1228.6572	614.8322	**12**
5	528.3028	264.6550	510.2922	255.6498	**I**	***1133.5837***	567.2955	1116.5572	558.7822	1115.5732	558.2902	**11**
6	585.3243	293.1658	567.3137	284.1605	**G**	***1020.4997***	510.7535	1003.4731	502.2402	1002.4891	501.7482	**10**
7	732.3927	366.7000	714.3821	357.6947	**F**	***963.4782***	482.2427	946.4516	473.7295	945.4676	473.2374	**9**
8	789.4141	395.2107	771.4036	386.2054	**G**	***816.4098***	408.7085	799.3832	400.1953	798.3992	399.7032	**8**
9	876.4462	438.7267	858.4356	429.7214	**S**	759.3883	380.1978	742.3618	371.6845	741.3777	371.1925	**7**
10	933.4676	467.2374	915.4571	458.2322	**G**	***672.3563***	336.6818	655.3297	328.1685	654.3457	327.6765	**6**
11	1030.5204	515.7638	1012.5098	506.7585	**P**	***615.3348***	308.1710	598.3083	299.6578	597.3243	299.1658	**5**
12	1159.5630	580.2851	1141.5524	571.2798	**E**	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	**4**
13	1272.6470	636.8272	1254.6365	627.8219	**L**	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	**3**
14	1401.6896	701.3485	1383.6791	692.3432	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
15					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SVDIIGFGSGPELEK

AT4G30920.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.2	1546.7879	-0.0007	SVDIIGFGSGPELEK
0.7	1546.7912	-0.0040	IAELTGLSVEEAMGK

Mascot: http://www.matrixscience.com/

AT4G31300.1

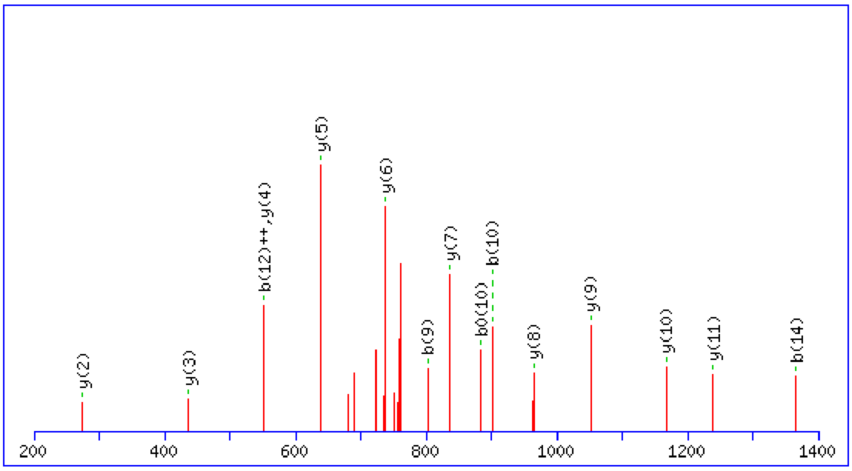
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSAADSQVVSDYVR**
Found in **AT4G31300.1** in **TAIR_Arabidopsis**, Symbols: PBA1 | PBA1 (20S proteasome beta subunit A 1); peptidase | chr4:15188933-15190941 FORWARD

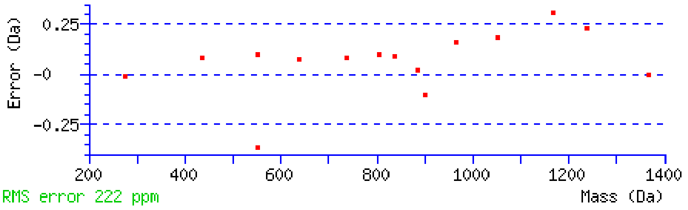
Match to Query 6284: 1539.716606 from(770.865579,2+) index(3546)
Title: Elution from: 35.193 to 35.193 scan no 4504 cid35.00 polarity:+
Data file D12h-2_3.mgf

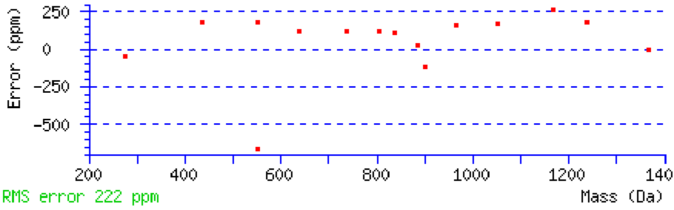
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1539.7165
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 104 **Expect:** 1.1e-010
Matches : 15/148 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	145.0608	73.0340			127.0502	64.0287	G	1453.6918	727.3495	1436.6652	718.8362	1435.6812	718.3442	14
3	232.0928	116.5500			214.0822	107.5448	S	1396.6703	698.8388	1379.6438	690.3255	1378.6597	689.8335	13
4	303.1299	152.0686			285.1193	143.0633	A	1309.6383	655.3228	1292.6117	646.8095	1291.6277	646.3175	12
5	374.1670	187.5872			356.1565	178.5819	A	***1238.6012***	619.8042	1221.5746	611.2909	1220.5906	610.7989	11
6	489.1940	245.1006			471.1834	236.0953	D	***1167.5640***	584.2857	1150.5375	575.7724	1149.5535	575.2804	10
7	576.2260	288.6166			558.2154	279.6114	S	***1052.5371***	526.7722	1035.5106	518.2589	1034.5265	517.7669	9
8	704.2846	352.6459	687.2580	344.1327	686.2740	343.6406	Q	***965.5051***	483.2562	948.4785	474.7429	947.4945	474.2509	8
9	**803.3530**	402.1801	786.3264	393.6669	785.3424	393.1748	V	***837.4465***	419.2269	820.4199	410.7136	819.4359	410.2216	7
10	**902.4214**	451.7143	885.3949	443.2011	884.4108	442.7091	V	***738.3781***	369.6927	721.3515	361.1794	720.3675	360.6874	6
11	989.4534	495.2304	972.4269	486.7171	971.4429	486.2251	S	***639.3097***	320.1585	622.2831	311.6452	621.2991	311.1532	5
12	1104.4804	552.7438	1087.4538	544.2305	1086.4698	543.7385	D	***552.2776***	276.6425	535.2511	268.1292	534.2671	267.6372	4
13	1267.5437	634.2755	1250.5172	625.7622	1249.5331	625.2702	Y	***437.2507***	219.1290	420.2241	210.6157			3
14	**1366.6121**	683.8097	1349.5856	675.2964	1348.6016	674.8044	V	***274.1874***	137.5973	257.1608	129.0840			2
15							R	175.1190	88.0631	158.0924	79.5498			1





AT4G31300.1

NCBI **BLAST** search of SGSAADSQVVSDYVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
104.2	1539.7165	0.0001	SGSAADSQVVSDYVR
1.7	1539.7140	0.0026	CTTFEALAANTWR

AT4G31300.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEAEQLVVK**
Found in **AT4G31300.2** in **TAIR_Arabidopsis**, Symbols: PBA1 | PBA1 (20S proteasome beta subunit A 1); peptidase | chr4:15188933-15190941 FORWARD

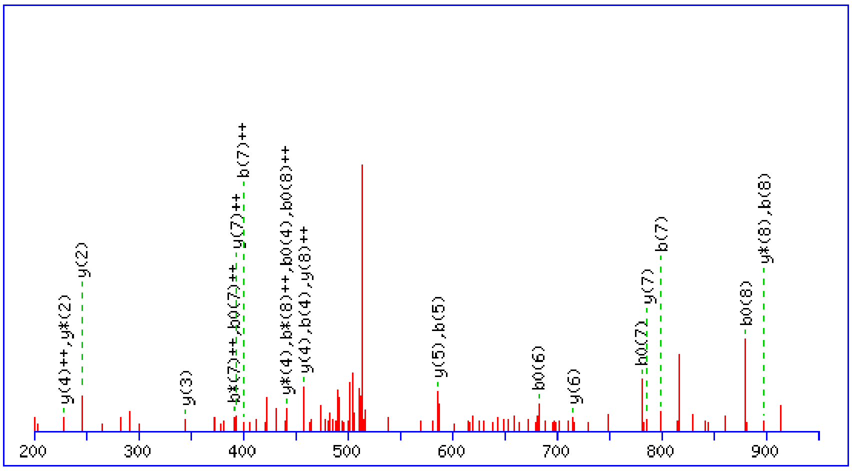
Match to Query 2810: 1043.551226 from(522.782889,2+) index(1983)
Title: Elution from: 23.434 to 23.434 scan no 2554 cid35.00 polarity:+
Data file D6h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

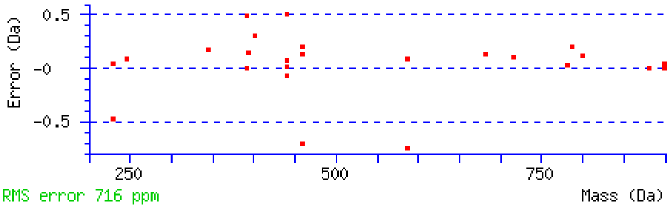
Label all possible matches ○ Label matches used for scoring ●

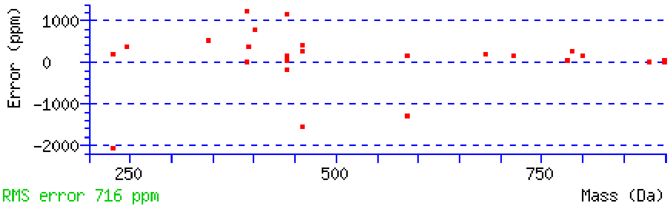
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1043.5499
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27  Expect: 0.0069
Matches : 25/78 fragment ions using 43 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	259.0925	130.0499			241.0819	121.0446	E	915.5146	458.2609	898.4880	449.7477	897.5040	449.2556	8
3	330.1296	165.5684			312.1190	156.5631	A	***786.4720***	393.7396	769.4454	385.2264	768.4614	384.7343	7
4	**459.1722**	230.0897			441.1616	221.0844	E	***715.4349***	358.2211	698.4083	349.7078	697.4243	349.2158	6
5	**587.2307**	294.1190	570.2042	285.6057	569.2202	285.1137	Q	***586.3923***	293.6998	569.3657	285.1865			5
6	700.3148	350.6610	683.2883	342.1478	682.3042	341.6558	L	***458.3337***	229.6705	441.3071	221.1572			4
7	**799.3832**	400.1953	782.3567	391.6820	781.3727	391.1900	V	***345.2496***	173.1285	328.2231	164.6152			3
8	**898.4516**	449.7295	881.4251	441.2162	880.4411	440.7242	V	***246.1812***	123.5942	229.1547	115.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EEAEQLVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G31300.2

26.8	1043.5499	0.0014	EEAEQLVVK
14.9	1043.5499	0.0014	SKEIPDEVK
12.3	1043.5499	0.0013	EVDENVIVK
6.4	1043.5499	0.0013	DVEENVLVK
1.1	1043.5499	0.0014	EEENLALVK

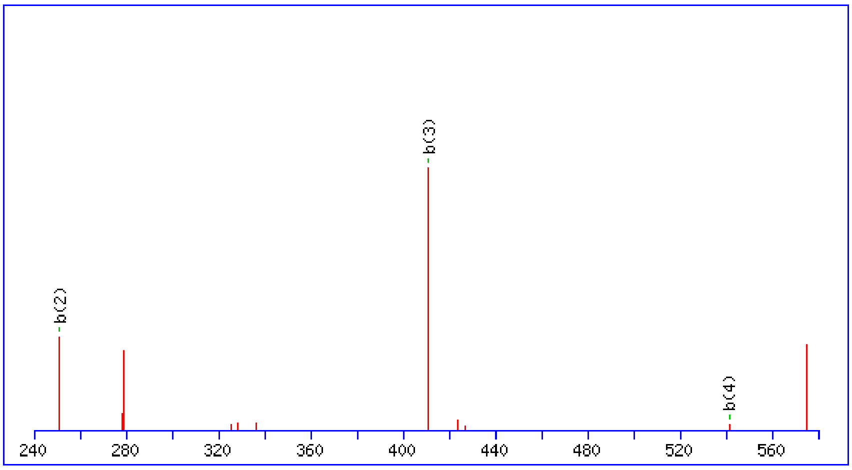
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFRKK**
Found in **AT4G31460.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L28 family protein | chr4:15259779-15260853 REVERSE

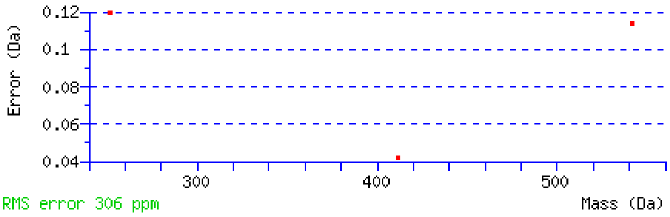
Match to Query 601: 688.386914 from(345.200733,2+) index(3869)
Title: Elution from: 35.578 to 35.578 scan no 4811 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 240 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

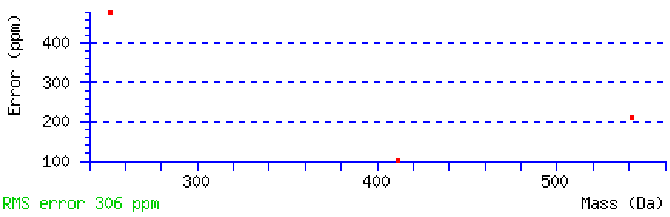


Monoisotopic mass of neutral peptide Mr(calc): 688.3880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.012
Matches : 3/36 fragment ions using 4 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	103.0520	52.0296			85.0414	43.0244	**T**					**5**
2	***251.1174***	126.0624			233.1069	117.0571	**F**	587.3506	294.1789	569.3270	285.1671	**4**
3	***411.2067***	206.1070	393.1831	197.0952	393.1961	197.1017	**R**	439.2852	220.1462	421.2616	211.1344	**3**
4	***541.2957***	271.1515	523.2721	262.1397	523.2852	262.1462	**K**	279.1959	140.1016	261.1723	131.0898	**2**
5							**K**	149.1069	75.0571	131.0833	66.0453	**1**



RMS error 306 ppm



RMS error 306 ppm

NCBI **BLAST** search of TFRKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.6	688.3880	-0.0011	TFRKK
18.1	688.3876	-0.0007	YLFLK
17.4	688.3876	-0.0007	IYIFK
17.4	688.3876	-0.0007	IYLFK
15.2	688.3880	-0.0011	RTFKK

10.3	688.3880	-0.0011	FKKTR
10.3	688.3880	-0.0011	FKTKR
10.3	688.3880	-0.0011	VPAHKK
8.4	688.3880	-0.0011	KFTRK
8.4	688.3876	-0.0007	YLLFK

Mascot: http://www.matrixscience.com/

AT4G31700.1

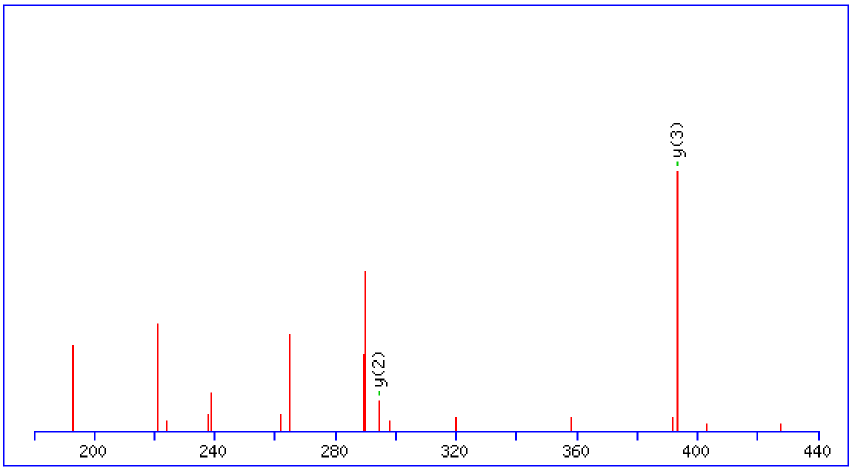
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYVFK**
Found in **AT4G31700.1** in **TAIR_Arabidopsis**, Symbols: RPS6 | RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome | chr4:15346312-15347720 REVERSE

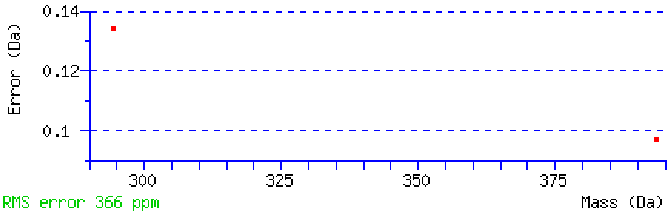
Match to Query 480: 612.326904 from(307.170728,2+) index(1384)
Title: Elution from: 20.762 to 20.762 scan no 1933 cid35.00 polarity:+
Data file D6h-2_2.mgf

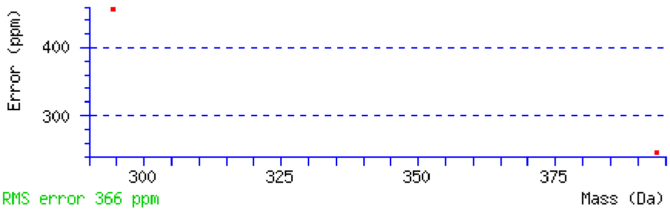
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 180 to 440 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 612.3271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 13 **Expect:** 0.048
Matches : 2/24 fragment ions using 3 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.5180	G					5
2	221.0921	111.0497	Y	556.3130	278.6601	539.2864	270.1468	4
3	320.1605	160.5839	V	*393.2496*	197.1285	376.2231	188.6152	3
4	467.2289	234.1181	F	*294.1812*	147.5942	277.1547	139.0810	2
5			K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of GYVFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.2	612.3271	-0.0002	GYVFK

Mascot: http://www.matrixscience.com/

AT4G31780.1

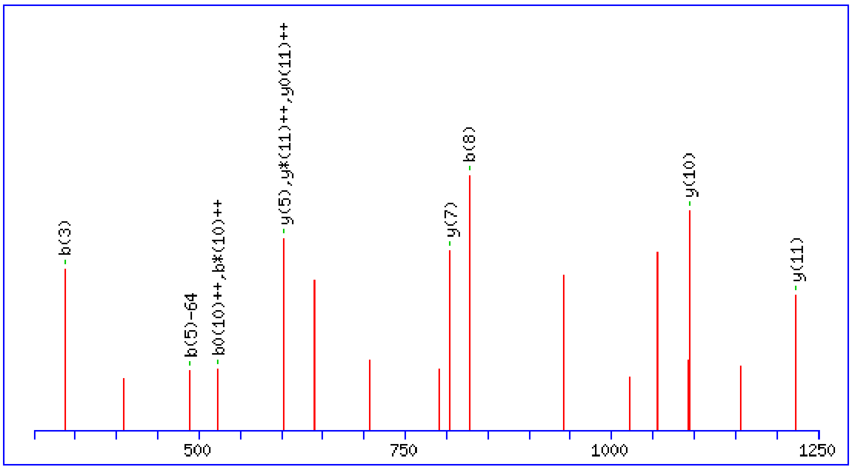
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGKTLASLSFNTK**
Found in **AT4G31780.1** in **TAIR_Arabidopsis**, Symbols: MGDA, MGD1 | MGD1 (MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE A); 1,2-diacylglycerol 3-beta-galactosyltransferase/ transferase, transferring glycosyl groups | chr4:15374228-15376879 FORWARD

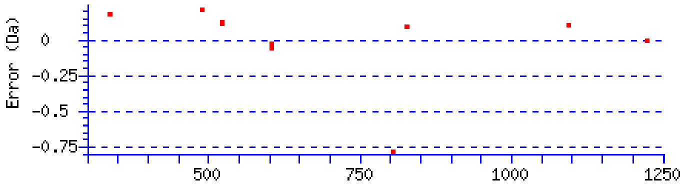
Match to Query 5443: 1428.688060 from(715.351306,2+) index(10473)
Title: Elution from: 103.134 to 103.134 scan no 15242 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

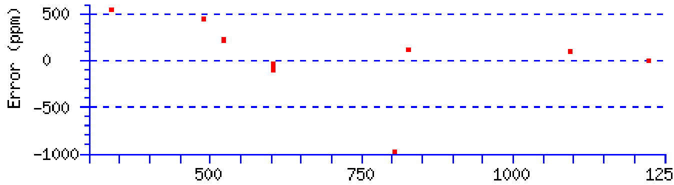


```
Monoisotopic mass of neutral peptide Mr(calc): 1428.6859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21  Expect: 0.035
Matches : 11/194 fragment ions using 15 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	149.0397	75.0235					M							13
2	207.0582	104.0327					G	1281.6608	641.3340	1263.6372	632.3222	1263.6502	632.3287	12
3	**337.1472**	169.0773	319.1237	160.0655			K	***1223.6423***	612.3248	1205.6187	603.3130	1205.6317	603.3195	11
4	439.1920	220.0996	421.1684	211.0878	421.1814	211.0943	T	***1093.5532***	547.2802	1075.5296	538.2685	1075.5427	538.2750	10
5	553.2731	277.1402	535.2495	268.1284	535.2625	268.1349	L	991.5085	496.2579	973.4849	487.2461	973.4979	487.2526	9
6	625.3072	313.1572	607.2836	304.1454	607.2966	304.1520	A	877.4274	439.2173	859.4038	430.2055	859.4168	430.2121	8
7	713.3363	357.1718	695.3127	348.1600	695.3257	348.1665	S	***805.3933***	403.2003	787.3697	394.1885	787.3827	394.1950	7
8	**827.4174**	414.2123	809.3938	405.2005	809.4068	405.2070	L	717.3642	359.1857	699.3406	350.1739	699.3536	350.1805	6
9	915.4464	458.2269	897.4228	449.2151	897.4359	449.2216	S	***603.2831***	302.1452	585.2595	293.1334	585.2725	293.1399	5
10	1063.5119	532.2596	1045.4883	523.2478	1045.5013	523.2543	F	515.2540	258.1307	497.2304	249.1189	497.2435	249.1254	4
11	1179.5489	590.2781	1161.5253	581.2663	1161.5383	581.2728	N	367.1886	184.0979	349.1650	175.0861	349.1780	175.0926	3
12	1281.5936	641.3004	1263.5700	632.2886	1263.5830	632.2951	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
13							K	149.1069	75.0571	131.0833	66.0453			1



RMS error 377 ppm



RMS error 377 ppm

AT4G31780.1

NCBI **BLAST** search of MGKTLASLSFNTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.5	1428.6859	0.0021	MGKTLASLSFNTK

AT4G31840.1

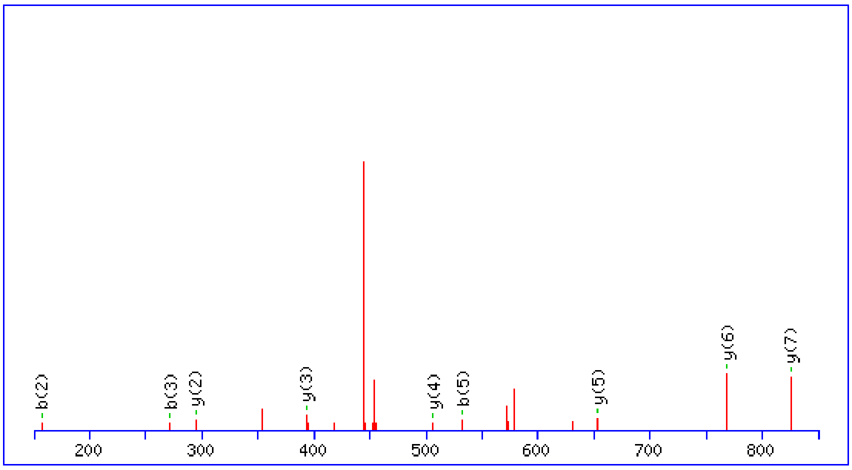
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGDFIVFK**
Found in **AT4G31840.1** in **TAIR_Arabidopsis**, Symbols: | plastocyanin-like domain-containing protein | chr4:15401804-15402432 FORWARD

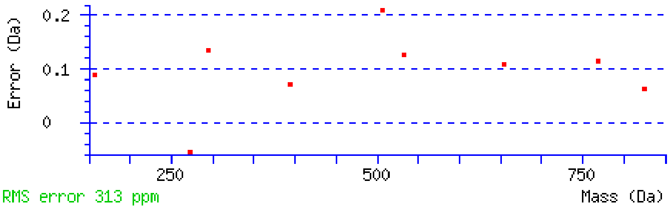
Match to Query 1730: 923.511252 from(462.762902,2+) index(6499)
Title: Elution from: 57.606 to 57.606 scan no 8419 cid35.00 polarity:+
Data file D6h-2_3.mgf

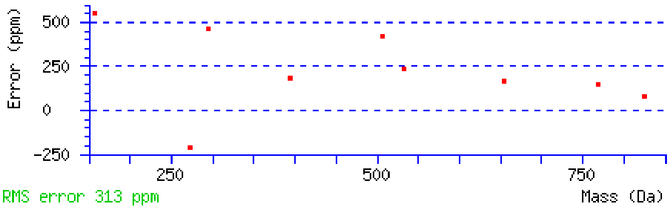
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 923.5117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 1.4e-005
Matches : 9/56 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							8
2	**157.0972**	79.0522			G	***825.4505***	413.2289	808.4240	404.7156	807.4400	404.2236	7
3	**272.1241**	136.5657	254.1135	127.5604	D	***768.4291***	384.7182	751.4025	376.2049	750.4185	375.7129	6
4	419.1925	210.0999	401.1819	201.0946	F	***653.4021***	327.2047	636.3756	318.6914			5
5	**532.2766**	266.6419	514.2660	257.6366	I	***506.3337***	253.6705	489.3071	245.1572			4
6	631.3450	316.1761	613.3344	307.1709	V	***393.2496***	197.1285	376.2231	188.6152			3
7	778.4134	389.7103	760.4028	380.7051	F	***294.1812***	147.5942	277.1547	139.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VGDFIVFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.4	923.5117	-0.0004	VGDFIVFK
3.4	923.5117	-0.0004	EVVGFVFK

Mascot: http://www.matrixscience.com/

AT4G31990.1

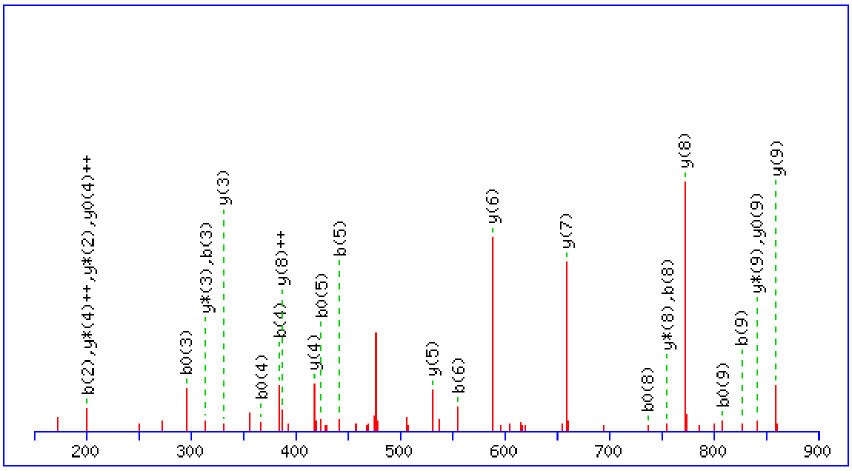
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISLAGLSLAK**
Found in **AT4G31990.1** in **TAIR_Arabidopsis**, Symbols: AAT3, ATAAT1 | ASP5 (ASPARTATE AMINOTRANSFERASE 5) | chr4:15471080-15473527 REVERSE

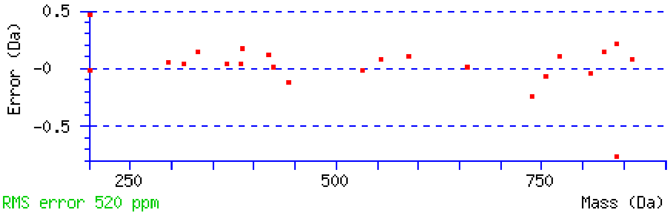
Match to Query 1796: 971.601974 from(486.808263,2+) index(6231)
Title: Elution from: 57.559 to 57.559 scan no 8150 cid35.00 polarity:+
Data file D1d-1_3.mgf

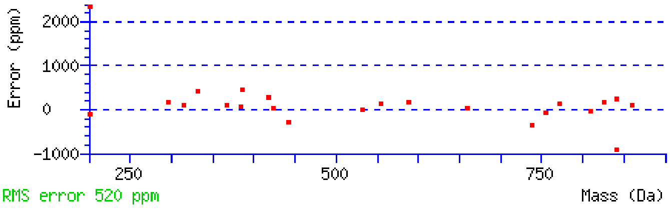
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 971.6015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 3.4e-006
Matches : 27/82 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			**I**							**10**
2	***201.1234***	101.0653	183.1128	92.0600	**S**	***859.5247***	430.2660	842.4982	421.7527	841.5142	421.2607	**9**
3	***314.2074***	157.6074	296.1969	148.6021	**L**	***772.4927***	386.7500	755.4662	378.2367	754.4822	377.7447	**8**
4	***385.2445***	193.1259	367.2340	184.1206	**A**	***659.4087***	330.2080	642.3821	321.6947	641.3981	321.2027	**7**
5	***442.2660***	221.6366	424.2554	212.6314	**G**	***588.3715***	294.6894	571.3450	286.1761	570.3610	285.6841	**6**
6	***555.3501***	278.1787	537.3395	269.1734	**L**	***531.3501***	266.1787	514.3235	257.6654	513.3395	257.1734	**5**
7	642.3821	321.6947	624.3715	312.6894	**S**	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	**4**
8	***755.4662***	378.2367	737.4556	369.2314	**L**	***331.2340***	166.1206	314.2074	157.6074			**3**
9	***826.5033***	413.7553	808.4927	404.7500	**A**	218.1499	109.5786	201.1234	101.0653			**2**
10					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ISLAGLSLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G31990.1

Score	Mr(calc)	Delta	Sequence
59.0	971.6015	0.0005	ISLAGLSLAK
7.3	971.6015	0.0005	ELAIKASLK

Mascot: http://www.matrixscience.com/

AT4G32260.1

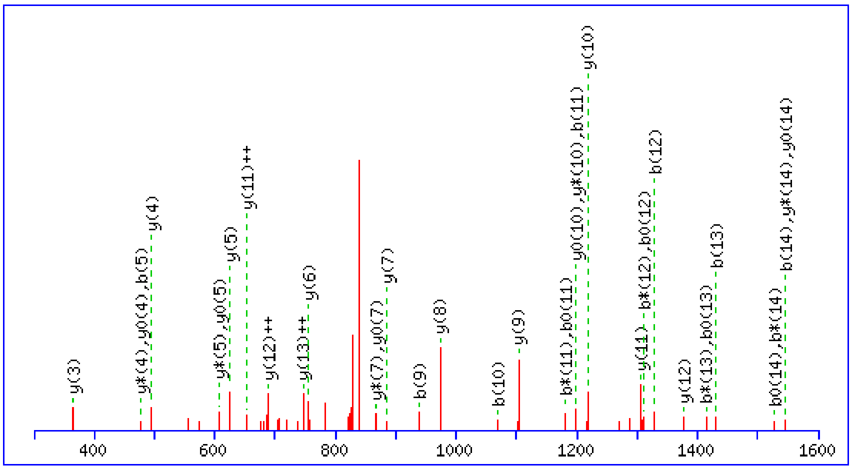
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALASLESQKEETIK**
Found in **AT4G32260.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase family | chr4:15573865-15574592 REVERSE

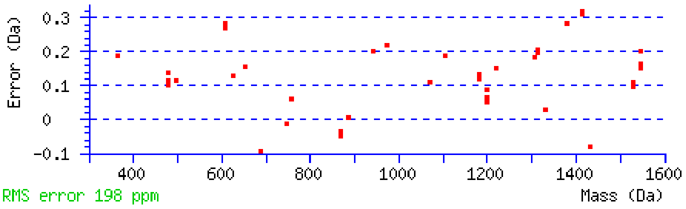
Match to Query 8341: 1692.812170 from(847.413361,2+) index(3533)
Title: Elution from: 33.504 to 33.504 scan no 4347 cid35.00 polarity:+
Data file C7-1_1.mgf

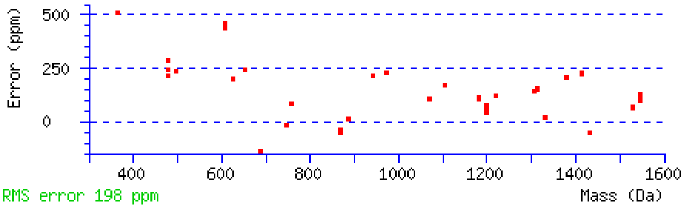
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1692.8142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 7.2e-010
Matches : 38/148 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							15
2	203.0811	102.0442			185.0705	93.0389	A	1563.7819	782.3946	1545.7583	773.3828	1545.7713	773.3893	14
3	317.1622	159.0847			299.1516	150.0794	L	1491.7477	746.3775	1473.7241	737.3657	1473.7372	737.3722	13
4	389.1963	195.1018			371.1857	186.0965	A	***1377.6666***	689.3370	1359.6430	680.3252	1359.6561	680.3317	12
5	***477.2254***	239.1163			459.2148	230.1110	S	***1305.6325***	653.3199	1287.6089	644.3081	1287.6219	644.3146	11
6	591.3065	296.1569			573.2959	287.1516	L	***1217.6034***	609.3053	1199.5798	600.2936	1199.5928	600.3001	10
7	721.3461	361.1767			703.3355	352.1714	E	***1103.5223***	552.2648	1085.4987	543.2530	1085.5117	543.2595	9
8	809.3752	405.1912			791.3646	396.1859	S	***973.4827***	487.2450	955.4591	478.2332	955.4721	478.2397	8
9	***939.4278***	470.2175	921.4042	461.2057	921.4172	461.2123	Q	***885.4536***	443.2304	867.4300	434.2187	867.4431	434.2252	7
10	***1069.5168***	535.2621	1051.4933	526.2503	1051.5063	526.2568	K	***755.4010***	378.2041	737.3774	369.1923	737.3904	369.1988	6
11	***1199.5565***	600.2819	1181.5329	591.2701	1181.5459	591.2766	E	***625.3119***	313.1596	607.2884	304.1478	607.3014	304.1543	5
12	***1329.5961***	665.3017	1311.5725	656.2899	1311.5855	656.2964	E	***495.2723***	248.1398	477.2487	239.1280	477.2617	239.1345	4
13	***1431.6408***	716.3240	1413.6172	707.3122	1413.6302	707.3188	T	***365.2327***	183.1200	347.2091	174.1082	347.2221	174.1147	3
14	***1545.7219***	773.3646	1527.6983	764.3528	1527.7113	764.3593	I	263.1880	132.0976	245.1644	123.0858			2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EALASLESQKEETIK

AT4G32260.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.5	1692.8142	-0.0021	EALASLESQKEETIK
21.9	1692.8142	-0.0020	EKTIQEEAEISATVK
13.9	1692.8117	0.0004	QVFPEIGEINISAMK
11.1	1692.8144	-0.0022	MQVISPSSPAPRFAGK
6.6	1692.8088	0.0034	ILDRYGKQHADDLK
6.6	1692.8095	0.0027	IEAKVEQMKAEAEAK
2.7	1692.8110	0.0012	NVKKEAGISWFEHK
2.2	1692.8165	-0.0043	GSESEDLVVPLFSLGK
1.3	1692.8110	0.0012	GSITLKVHYHEFNK
0.9	1692.8119	0.0003	IFVMSFMRNPRFK

Mascot: http://www.matrixscience.com/

AT4G32410.1

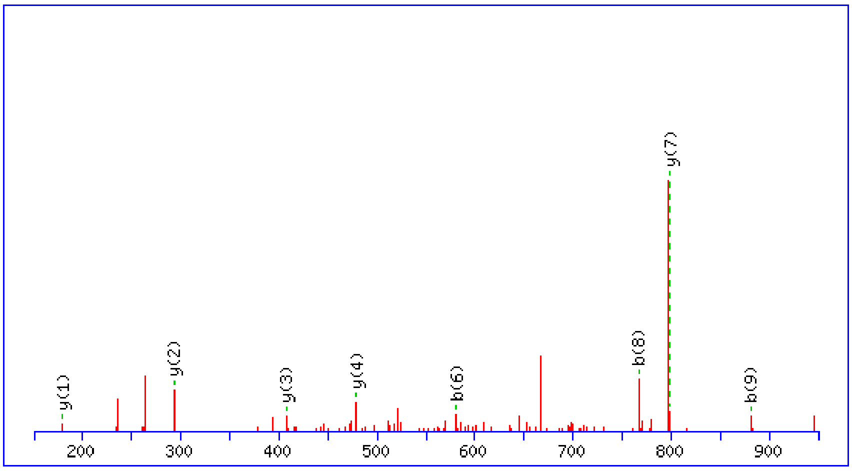
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAGAMNALIR**
Found in **AT4G32410.1** in **TAIR_Arabidopsis**, Symbols: CESA1, RSW1 | CESA1 (CELLULOSE SYNTHASE 1); transferase, transferring glycosyl groups | chr4:15641015-15646394 REVERSE

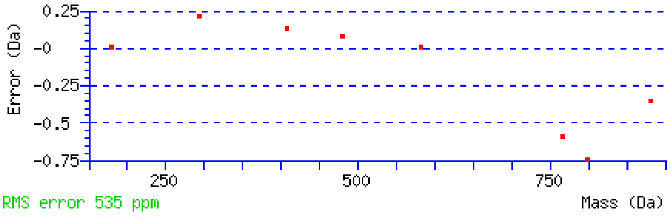
Match to Query 2949: 1058.545654 from(530.280103,2+) index(5733)
Title: Elution from: 50.886 to 50.886 scan no 7403 cid35.00 polarity:+
Data file D12h-3_3.mgf

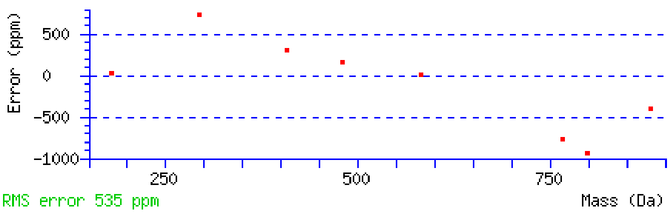
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1058.5465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.038
Matches : 8/72 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	131.0963	66.0518	113.0727	57.0400	K					10
2	203.1305	102.0689	185.1069	93.0571	A	929.4648	465.2360	911.4412	456.2242	9
3	261.1490	131.0781	243.1254	122.0663	G	857.4306	429.2189	839.4070	420.2071	8
4	333.1831	167.0952	315.1595	158.0834	A	***799.4121***	400.2097	781.3885	391.1979	7
5	465.2206	233.1140	447.1970	224.1022	M	727.3780	364.1926	709.3544	355.1808	6
6	**581.2576**	291.1324	563.2340	282.1207	N	595.3404	298.1739	577.3169	289.1621	5
7	653.2918	327.1495	635.2682	318.1377	A	***479.3034***	240.1554	461.2799	231.1436	4
8	**767.3729**	384.1901	749.3493	375.1783	L	***407.2693***	204.1383	389.2457	195.1265	3
9	**881.4540**	441.2306	863.4304	432.2188	I	***293.1882***	147.0977	275.1646	138.0859	2
10					R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of KAGAMNALIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G32410.1

Score	Mr(calc)	Delta	Sequence
23.6	1058.5465	-0.0009	KAGAMNALIR
17.2	1058.5438	0.0018	LGTVMELLR
16.5	1058.5465	-0.0008	EMRLVGALR
16.5	1058.5438	0.0018	KCLGLESIK
16.3	1058.5438	0.0018	MEQGTIKIK
15.3	1058.5465	-0.0008	LRMALDVAR
13.9	1058.5431	0.0025	WASKGINIR
13.8	1058.5465	-0.0008	MQKPKVGTR
12.0	1058.5438	0.0018	KEMEAAKIK
10.7	1058.5438	0.0018	LMAQNLLTK

AT4G32470.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYLQDMLALVER**
Found in **AT4G32470.1** in **TAIR_Arabidopsis**, Symbols: | ubiquinol-cytochrome C reductase complex 14 kDa protein, putative | chr4:15669647-15671101 REVERSE

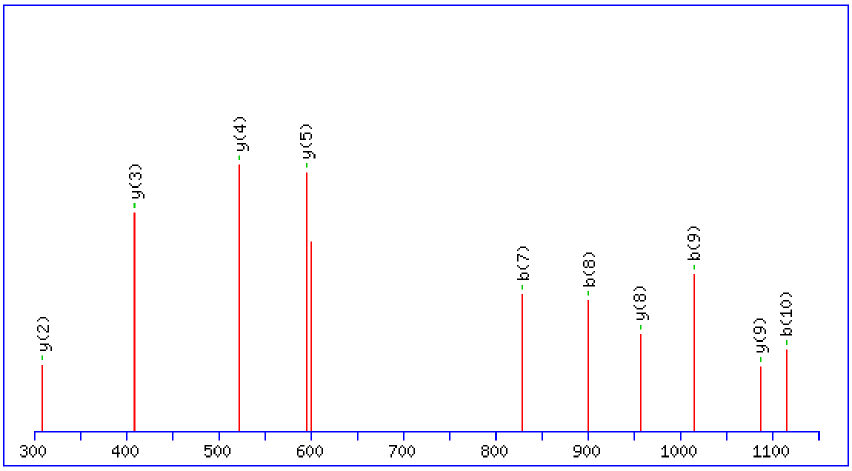
Match to Query 5466: 1422.676402 from(712.345477,2+) index(10686)
Title: Elution from: 108.159 to 108.159 scan no 15568 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1150 Da Full range

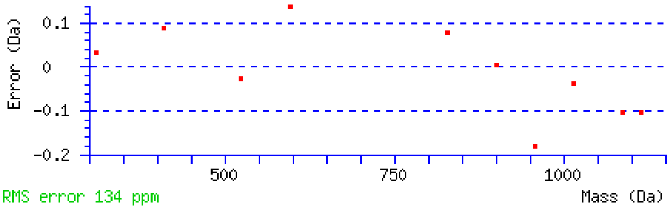
Label all possible matches ○ Label matches used for scoring ●

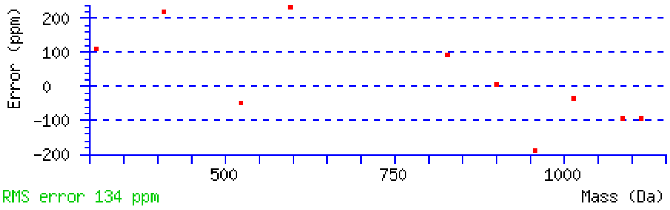
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1422.6753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 8.7e-006
Matches : 10/116 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					**G**							**12**
2	223.0861	112.0467					**Y**	1365.6641	683.3357	1347.6405	674.3239	1347.6536	674.3304	**11**
3	337.1672	169.0873					**L**	1201.6038	601.3055	1183.5802	592.2937	1183.5932	592.3002	**10**
4	467.2199	234.1136	449.1963	225.1018			**Q**	***1087.5227***	544.2650	1069.4991	535.2532	1069.5121	535.2597	**9**
5	583.2439	292.1256	565.2203	283.1138	565.2333	283.1203	**D**	***957.4700***	479.2386	939.4464	470.2269	939.4594	470.2334	**8**
6	715.2814	358.1443	697.2578	349.1325	697.2708	349.1390	**M**	841.4460	421.2267	823.4225	412.2149	823.4355	412.2214	**7**
7	**829.3625**	415.1849	811.3389	406.1731	811.3519	406.1796	**L**	709.4085	355.2079	691.3849	346.1961	691.3980	346.2026	**6**
8	**901.3966**	451.2020	883.3730	442.1902	883.3861	442.1967	**A**	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	**5**
9	**1015.4777**	508.2425	997.4541	499.2307	997.4672	499.2372	**L**	***523.2933***	262.1503	505.2697	253.1385	505.2827	253.1450	**4**
10	**1115.5432**	558.2752	1097.5196	549.2634	1097.5326	549.2699	**V**	***409.2122***	205.1097	391.1886	196.0979	391.2016	196.1044	**3**
11	1245.5828	623.2950	1227.5592	614.2832	1227.5722	614.2898	**E**	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	**2**
12							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of GYLQDMLALVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G32470.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.1	1422.6753	0.0011	GYLQDMLALVER
17.7	1422.6724	0.0040	NFEQQNQIVKR
11.5	1422.6753	0.0011	KPGSDYILMVER
5.9	1422.6747	0.0018	SYDKLHFNPRK
5.9	1422.6805	-0.0041	DSDELSLSRVKR
5.9	1422.6758	0.0007	ECREKVTVVAGR
5.9	1422.6758	0.0007	TAICDRVADVKR
5.2	1422.6787	-0.0023	MATAVVMNGELKK
5.0	1422.6758	0.0006	AGEMRDAAIVRAK
5.0	1422.6758	0.0006	MQELSREKINR

AT4G32560.1

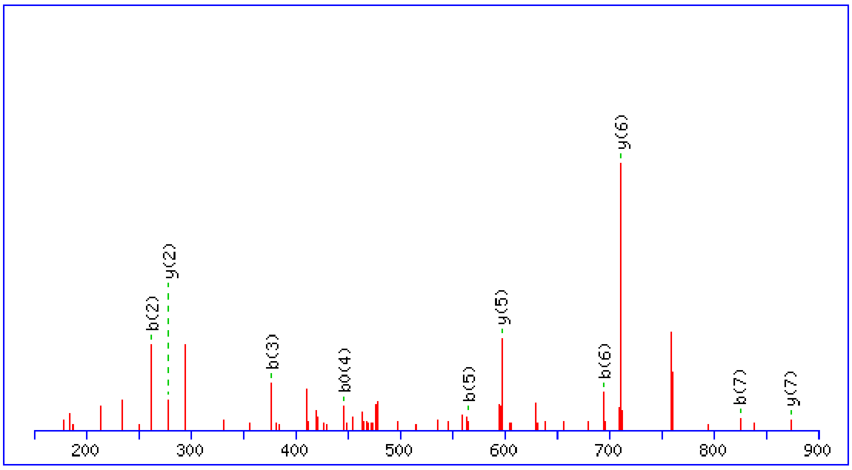
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCLSVKEK**
Found in **AT4G32560.1** in **TAIR_Arabidopsis**, Symbols: | paramyosin-related | chr4:15713872-15716041 FORWARD

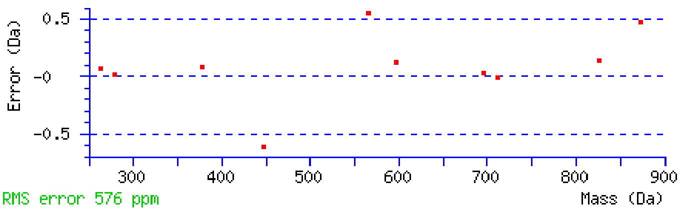
Match to Query 2150: 972.494058 from(487.254305,2+) index(5657)
Title: Elution from: 50.174 to 50.174 scan no 7189 cid35.00 polarity:+
Data file D12h-1_3.mgf

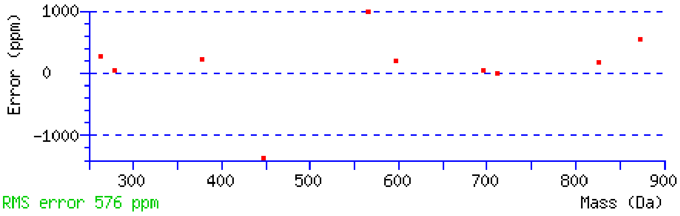
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [150] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.027
Matches : 10/66 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							8
2	***263.0974***	132.0524					C	***873.4359***	437.2216	855.4123	428.2098	855.4253	428.2163	7
3	***377.1785***	189.0929					L	***711.4111***	356.2092	693.3876	347.1974	693.4006	347.2039	6
4	465.2076	233.1074			447.1970	224.1022	S	***597.3300***	299.1687	579.3065	290.1569	579.3195	290.1634	5
5	***565.2731***	283.1402			547.2625	274.1349	V	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	4
6	***695.3621***	348.1847	677.3385	339.1729	677.3515	339.1794	K	409.2355	205.1214	391.2120	196.1096	391.2250	196.1161	3
7	***825.4017***	413.2045	807.3781	404.1927	807.3911	404.1992	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VCLSVKEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	972.4940	0.0000	VCLSVKEK
20.2	972.4940	0.0000	MKLNESIK

AT4G32560.1

14.9	972.4940	0.0000	MGSGEKILK
14.9	972.4940	0.0000	QMAKDLIK
13.8	972.4940	0.0000	VLQTMVQK
12.0	972.4940	0.0000	KMTVQDLK
10.4	972.4963	-0.0022	NMTIPFLK
10.3	972.4940	0.0000	MKVDTKPK
9.6	972.4940	0.0000	MTVLVEVR
7.6	972.4940	0.0000	QSASVVMIK

AT4G33010.1

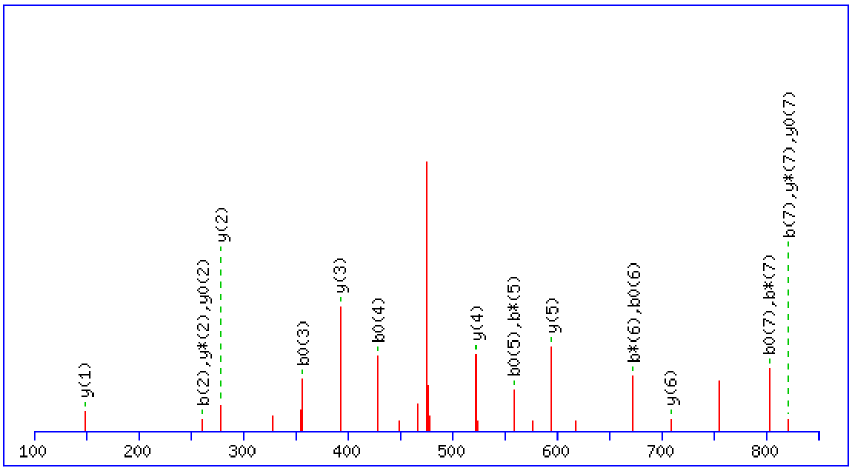
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEIAQIEK**
Found in **AT4G33010.1** in **TAIR_Arabidopsis**, Symbols: ATGLDP1 | ATGLDP1 (ARABIDOPSIS THALIANA GLYCINE DECARBOXYLASE P-PROTEIN 1); glycine dehydrogenase (decarboxylating) | chr4:15926855-15931153 REVERSE

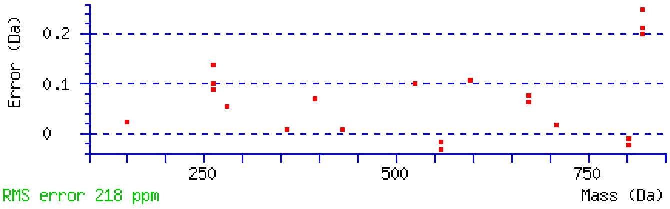
Match to Query 2132: 968.467472 from(485.241012,2+) index(1478)
Title: Elution from: 19.862 to 19.862 scan no 1977 cid35.00 polarity:+
Data file 0-3_2.mgf

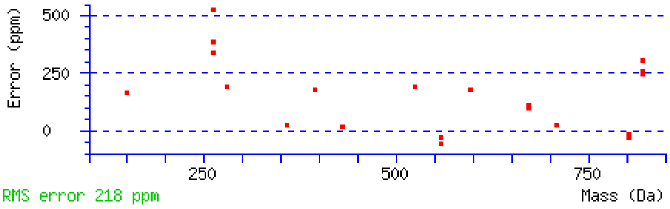
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.4675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 2e-005
Matches : 20/74 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							8
2	**261.0865**	131.0469			243.0760	122.0416	E	839.4351	420.2212	821.4115	411.2094	821.4246	411.2159	7
3	375.1676	188.0875			357.1571	179.0822	I	***709.3955***	355.2014	691.3719	346.1896	691.3849	346.1961	6
4	447.2018	224.1045			429.1912	215.0992	A	***595.3144***	298.1608	577.2908	289.1490	577.3038	289.1556	5
5	577.2544	289.1309	559.2308	280.1191	559.2439	280.1256	Q	***523.2802***	262.1438	505.2567	253.1320	505.2697	253.1385	4
6	691.3355	346.1714	673.3119	337.1596	673.3250	337.1661	I	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	**821.3752**	411.1912	803.3516	402.1794	803.3646	402.1859	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EEIAQIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.4	968.4675	0.0000	EEIAQIEK

AT4G33010.1

34.7	968.4675	0.0000	DLAAAEIEK
33.9	968.4672	0.0003	FMFQLFK
23.3	968.4675	0.0000	DIDVQIEK
17.2	968.4675	-0.0000	APSDSLELK
17.2	968.4650	0.0025	FKKMDYK
17.2	968.4675	0.0000	EAQELLEK
17.2	968.4701	-0.0027	SQQQPLQK
17.2	968.4675	0.0000	VEVQDLEK
17.1	968.4650	0.0025	MYIYNKK

Mascot: http://www.matrixscience.com/

AT4G33070.1

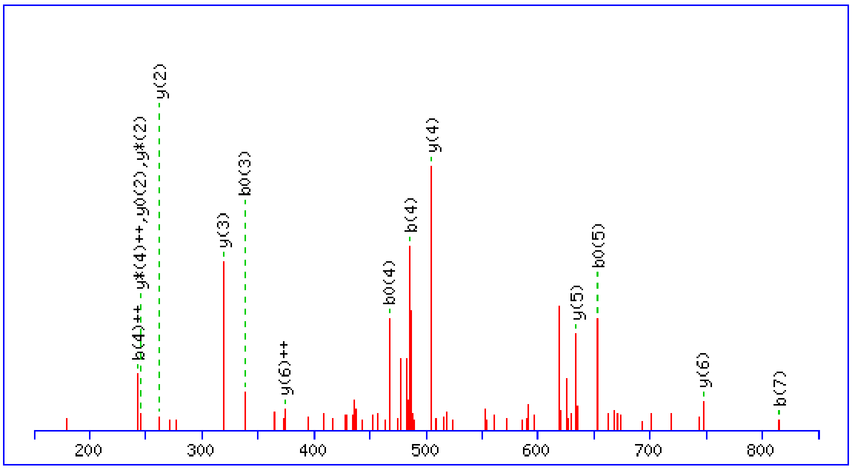
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLEWGSR**
Found in **AT4G33070.1** in **TAIR_Arabidopsis**, Symbols: | pyruvate decarboxylase, putative | chr4:15952522-15954679 REVERSE

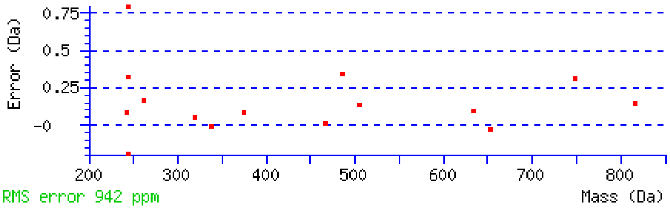
Match to Query 2318: 988.496314 from(495.255433,2+) index(5365)
Title: Elution from: 48.504 to 48.504 scan no 6798 cid35.00 polarity:+
Data file D6h-1_2.mgf

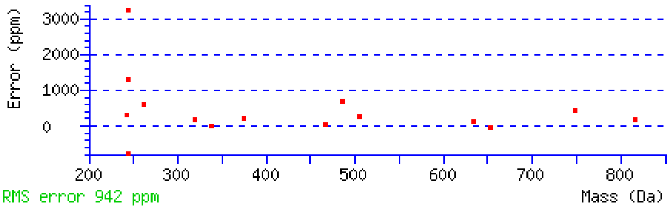
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 988.4978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.001
Matches : 16/68 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							8
2	**243.1339**	122.0706	225.1234	113.0653	L	860.4625	430.7349	843.4359	422.2216	842.4519	421.7296	7
3	356.2180	178.6126	338.2074	169.6074	L	***747.3784***	374.1928	730.3519	365.6796	729.3678	365.1876	6
4	**485.2606**	243.1339	467.2500	234.1287	E	***634.2944***	317.6508	617.2678	309.1375	616.2838	308.6455	5
5	671.3399	336.1736	653.3293	327.1683	W	***505.2518***	253.1295	488.2252	244.6162	487.2412	244.1242	4
6	728.3614	364.6843	710.3508	355.6790	G	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	3
7	**815.3934**	408.2003	797.3828	399.1951	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
8					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ELLEWGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.6	988.4978	-0.0015	ELLEWGSR
6.2	988.4978	-0.0015	EIGVPGFDR

AT4G33070.1

3.9	988.4978	-0.0015	AWEVDTLR
0.3	988.4938	0.0025	GKGNGSGVDAK

AT4G33090.1

{MATRIX SCIENCE} Mascot Search Results

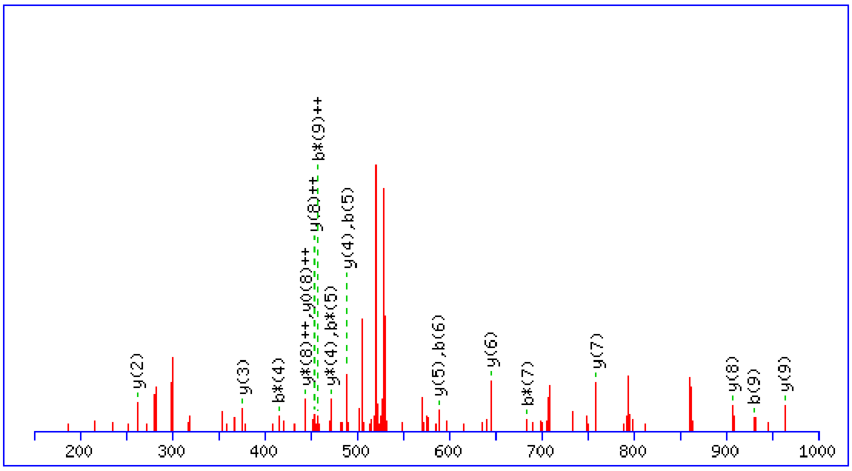
Peptide View

MS/MS Fragmentation of **LGFNGVLNDK**
Found in **AT4G33090.1** in **TAIR_Arabidopsis**, Symbols: APM1, ATAPM1 | APM1 (AMINOPEPTIDASE M1) | chr4:15965918-15970421 REVERSE

Match to Query 3334: 1075.565450 from(538.790001,2+) index(5560)
Title: Elution from: 49.240 to 49.240 scan no 6884 cid35.00 polarity:+
Data file 0-1_1.mgf

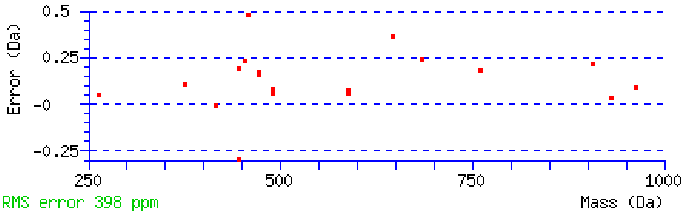
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

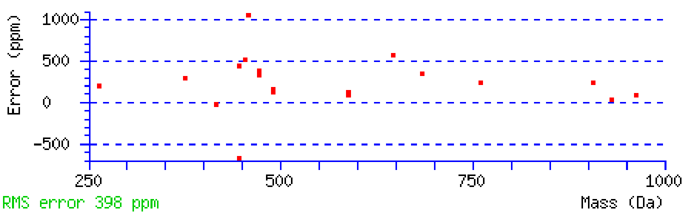


Monoisotopic mass of neutral peptide Mr(calc): 1075.5662
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 8.7e-005
Matches : 19/84 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							10
2	171.1128	86.0600					G	***963.4894***	482.2483	946.4629	473.7351	945.4789	473.2431	9
3	318.1812	159.5942					F	***906.4680***	453.7376	889.4414	445.2243	888.4574	444.7323	8
4	432.2241	216.6157	415.1976	208.1024			N	***759.3995***	380.2034	742.3730	371.6901	741.3890	371.1981	7
5	**489.2456**	245.1264	472.2191	236.6132			G	***645.3566***	323.1819	628.3301	314.6687	627.3461	314.1767	6
6	**588.3140**	294.6606	571.2875	286.1474			V	***588.3352***	294.6712	571.3086	286.1579	570.3246	285.6659	5
7	701.3981	351.2027	684.3715	342.6894			L	***489.2667***	245.1370	472.2402	236.6237	471.2562	236.1317	4
8	815.4410	408.2241	798.4145	399.7109			N	***376.1827***	188.5950	359.1561	180.0817	358.1721	179.5897	3
9	**930.4680**	465.7376	913.4414	457.2243	912.4574	456.7323	D	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 398 ppm



RMS error 398 ppm

NCBI **BLAST** search of LGFNGVLNDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G33090.1

Score	Mr(calc)	Delta	Sequence
45.1	1075.5662	-0.0008	LGFNGVLNDK
5.4	1075.5662	-0.0007	LANAANFIDK
3.6	1075.5662	-0.0007	LESKFNGGPK
3.1	1075.5669	-0.0014	QRRMISNR
3.1	1075.5669	-0.0014	QRRMLSNR

AT4G33130.1

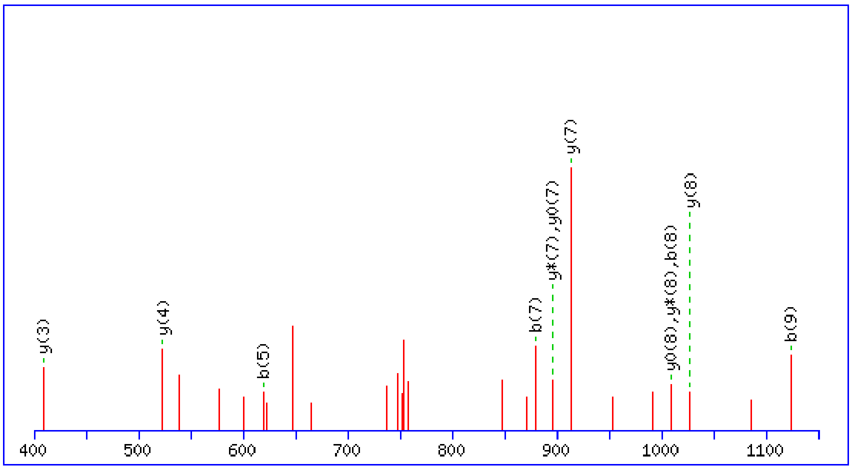
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQQQLQEEINLR**
Found in **AT4G33130.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13000.2); similar to transcription factor [Arabidopsis thaliana] (TAIR:AT3G13000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65161.1) | chr4:15979440-1598065

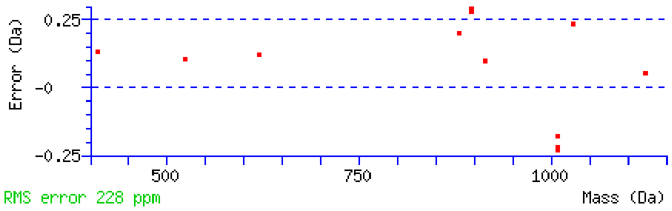
Match to Query 6775: 1530.747114 from(766.380833,2+) index(7385)
Title: Elution from: 65.649 to 65.649 scan no 9605 cid35.00 polarity:+
Data file D12h-3_1.mgf

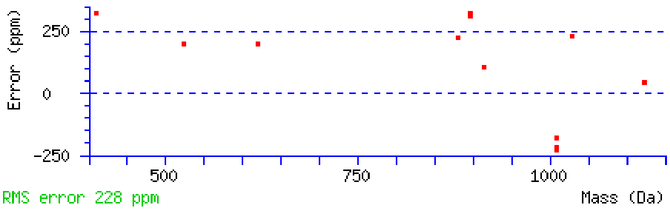
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1530.7510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0085
Matches : 12/110 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**12**
2	245.1410	123.0741	227.1174	114.0624			**Q**	1417.6772	709.3423	1399.6536	700.3305	1399.6667	700.3370	**11**
3	375.1937	188.1005	357.1701	179.0887			**Q**	1287.6246	644.3159	1269.6010	635.3041	1269.6140	635.3106	**10**
4	505.2463	253.1268	487.2227	244.1150			**Q**	1157.5719	579.2896	1139.5484	570.2778	1139.5614	570.2843	**9**
5	***619.3274***	310.1673	601.3038	301.1556			**L**	***1027.5193***	514.2633	1009.4957	505.2515	1009.5087	505.2580	**8**
6	749.3801	375.1937	731.3565	366.1819			**Q**	***913.4382***	457.2227	895.4146	448.2109	895.4276	448.2175	**7**
7	***879.4197***	440.2135	861.3961	431.2017	861.4091	431.2082	**E**	783.3855	392.1964	765.3620	383.1846	765.3750	383.1911	**6**
8	***1009.4593***	505.2333	991.4357	496.2215	991.4488	496.2280	**E**	653.3459	327.1766	635.3223	318.1648	635.3353	318.1713	**5**
9	***1123.5404***	562.2738	1105.5168	553.2621	1105.5299	553.2686	**I**	***523.3063***	262.1568	505.2827	253.1450			**4**
10	1239.5774	620.2923	1221.5538	611.2806	1221.5668	611.2871	**N**	***409.2252***	205.1162	391.2016	196.1044			**3**
11	1353.6585	677.3329	1335.6349	668.3211	1335.6479	668.3276	**L**	293.1882	147.0977	275.1646	138.0859			**2**
12							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of LQQQLQEEINLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G33130.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	1530.7510	-0.0039	LQQQLQEEINLR
7.2	1530.7459	0.0012	AYSKYLCPVSKAK
5.6	1530.7436	0.0035	GDILEIMDPNLRK
1.1	1530.7463	0.0008	DGKTPLHVATMRGK
0.2	1530.7510	-0.0039	VDTTTEHRLLQAK

AT4G33250.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVLAEAVNMDGASLDK**
Found in **AT4G33250.1** in **TAIR_Arabidopsis**, Symbols: TIF3K1, ATTIF3K1, EIF3K | EIF3K (eukaryotic translation initiation factor 3K) | chr4:16039070-16040621 REVERSE

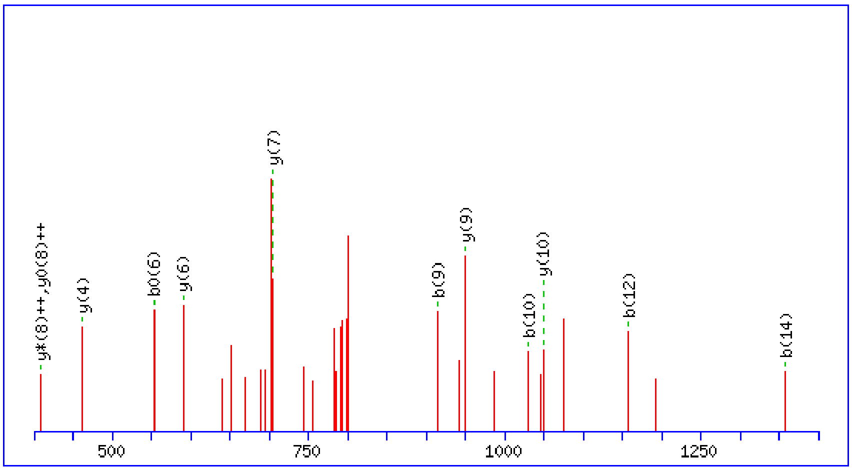
Match to Query 7342: 1618.785434 from(810.399993,2+) index(6709)
Title: Elution from: 59.841 to 59.841 scan no 8693 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1400 Da Full range

Label all possible matches ○ Label matches used for scoring ●

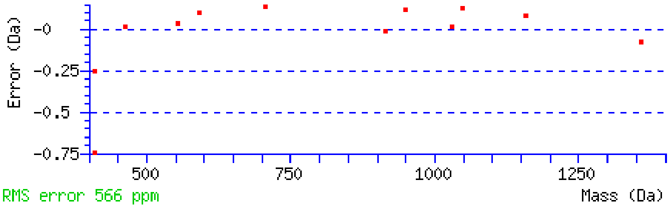
Show Y-axis ☐

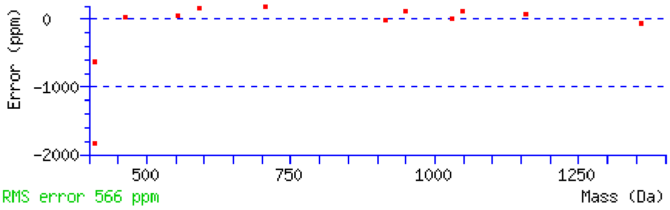


Monoisotopic mass of neutral peptide Mr(calc): 1618.7872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0038
Matches : 12/164 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	187.1077	94.0575			169.0972	85.0522	V	1532.7625	766.8849	1515.7359	758.3716	1514.7519	757.8796	15
3	300.1918	150.5995			282.1812	141.5942	L	1433.6941	717.3507	1416.6675	708.8374	1415.6835	708.3454	14
4	371.2289	186.1181			353.2183	177.1128	A	1320.6100	660.8086	1303.5835	652.2954	1302.5994	651.8034	13
5	500.2715	250.6394			482.2609	241.6341	E	1249.5729	625.2901	1232.5463	616.7768	1231.5623	616.2848	12
6	571.3086	286.1579			553.2980	277.1527	A	1120.5303	560.7688	1103.5038	552.2555	1102.5197	551.7635	11
7	670.3770	335.6921			652.3665	326.6869	V	***1049.4932***	525.2502	1032.4666	516.7370	1031.4826	516.2449	10
8	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	N	***950.4248***	475.7160	933.3982	467.2027	932.4142	466.7107	9
9	***915.4604***	458.2339	898.4339	449.7206	897.4499	449.2286	M	836.3818	418.6946	819.3553	410.1813	818.3713	409.6893	8
10	***1030.4874***	515.7473	1013.4608	507.2340	1012.4768	506.7420	D	***705.3414***	353.1743	688.3148	344.6610	687.3308	344.1690	7
11	1087.5088	544.2581	1070.4823	535.7448	1069.4983	535.2528	G	***590.3144***	295.6608	573.2879	287.1476	572.3039	286.6556	6
12	***1158.5459***	579.7766	1141.5194	571.2633	1140.5354	570.7713	A	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
13	1245.5780	623.2926	1228.5514	614.7794	1227.5674	614.2873	S	***462.2558***	231.6316	445.2293	223.1183	444.2453	222.6263	4
14	***1358.6620***	679.8347	1341.6355	671.3214	1340.6515	670.8294	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
15	1473.6890	737.3481	1456.6624	728.8349	1455.6784	728.3428	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT4G33250.1





NCBI **BLAST** search of SVLAEAVNMDGASLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.0	1618.7872	-0.0018	SVLAEAVNMDGASLDK

Mascot: http://www.matrixscience.com/

AT4G33390.1

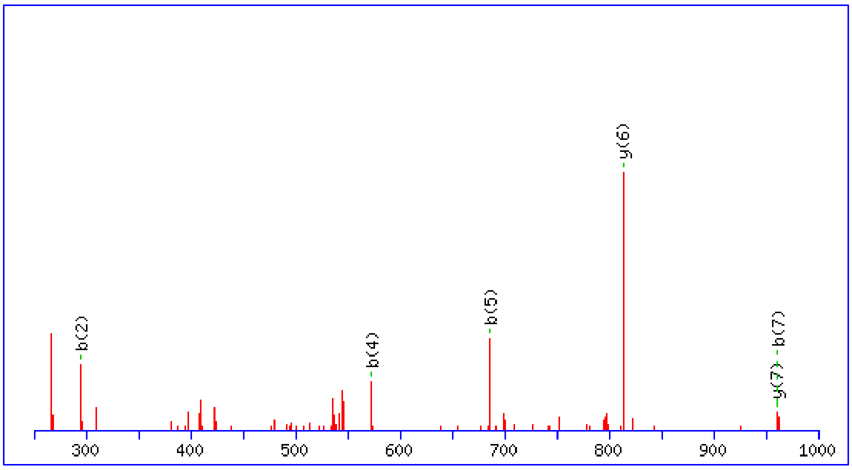
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFMFLMKK**
Found in **AT4G33390.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26570.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61337.1); contains InterPro domain Protein of unknown function DUF827, plant (InterPro:IPR008545) | chr4:16

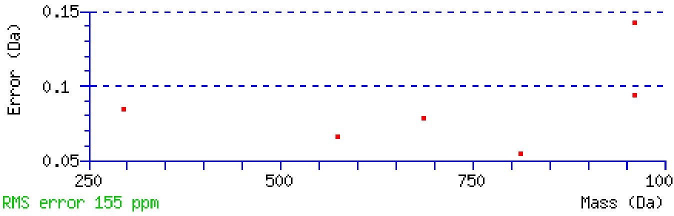
Match to Query 3095: 1106.566624 from(554.290588,2+) index(7504)
Title: Elution from: 68.522 to 68.522 scan no 9903 cid35.00 polarity:+
Data file D1d-2_1.mgf

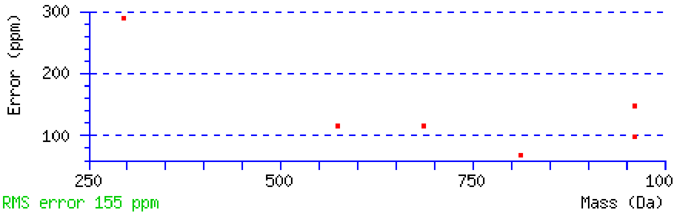
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1106.5657
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.037
Matches : 6/70 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	148.0757	74.5415			F					8
2	*295.1441*	148.0757			F	**960.5045**	480.7559	943.4780	472.2426	7
3	426.1846	213.5959			M	**813.4361**	407.2217	796.4096	398.7084	6
4	*573.2530*	287.1301			F	682.3956	341.7015	665.3691	333.1882	5
5	*686.3371*	343.6722			L	535.3272	268.1673	518.3007	259.6540	4
6	833.3725	417.1899			M	422.2432	211.6252	405.2166	203.1119	3
7	*961.4674*	481.2374	944.4409	472.7241	K	275.2078	138.1075	258.1812	129.5942	2
8					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of FFMFLMKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G33390.1

Score	Mr(calc)	Delta	Sequence	Site Analysis
21.0	1106.5657	0.0010	FFMFLMKK	Oxidation M6 96.77%
6.3	1106.5657	0.0010	FFMFLMKK	Oxidation M3 3.23%
4.6	1106.5641	0.0025	VSQIEEKMK	
4.3	1106.5641	0.0025	SNLEEKLMK	
1.3	1106.5641	0.0025	ETKSLMPSAK	

AT4G33510.1

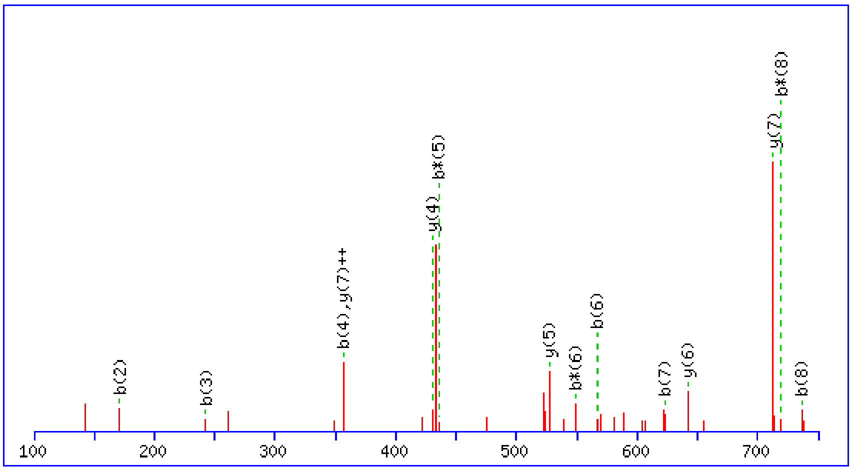
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GIANPLGIK**
Found in **AT4G33510.1** in **TAIR_Arabidopsis**, Symbols: DHS2 | DHS2 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE); 3-deoxy-7-phosphoheptulonate synthase | chr4:16116499-16118552 FORWARD

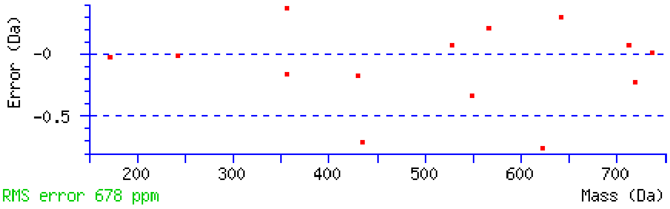
Match to Query 1436: 881.534634 from(441.774593,2+) index(4529)
Title: Elution from: 40.640 to 40.640 scan no 5694 cid35.00 polarity:+
Data file 0-2_3.mgf

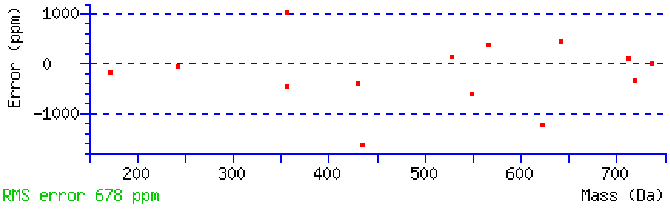
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 881.5334
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.00039
Matches : 14/58 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	58.0287	29.5180			G					9
2	***171.1128***	86.0600			I	825.5193	413.2633	808.4927	404.7500	8
3	***242.1499***	121.5786			A	**712.4352**	356.7212	695.4087	348.2080	7
4	***356.1928***	178.6001	339.1663	170.0868	N	**641.3981**	321.2027	624.3715	312.6894	6
5	453.2456	227.1264	436.2191	218.6132	P	**527.3552**	264.1812	510.3286	255.6679	5
6	***566.3297***	283.6685	549.3031	275.1552	L	**430.3024**	215.6548	413.2758	207.1416	4
7	***623.3511***	312.1792	606.3246	303.6659	G	317.2183	159.1128	300.1918	150.5995	3
8	***736.4352***	368.7212	719.4087	360.2080	I	260.1969	130.6021	243.1703	122.0888	2
9					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of GIANPLGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G33510.1

35.9	881.5334	0.0012	GIANPLGIK
9.0	881.5334	0.0012	AGNLPLGLK

AT4G33680.1

MATRIX SCIENCE

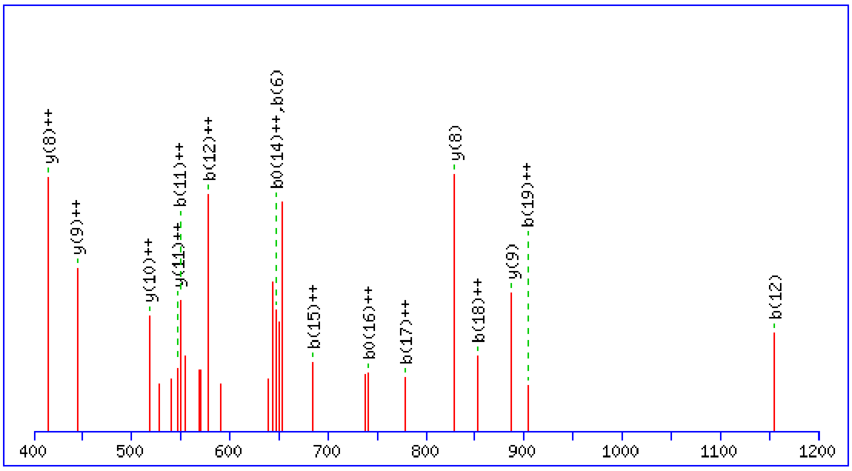
Mascot Search Results

Peptide View

MS/MS Fragmentation of **THVVTTPGSGFGPGGEGFVR**
Found in **AT4G33680.1** in **TAIR_Arabidopsis**, Symbols: AGD2 | AGD2 (ABERRANT GROWTH AND DEATH 2); transaminase | chr4:16171850-16174633 REVERSE

Match to Query 8650: 1982.890611 from(661.970813,3+) index(4478)
Title: Elution from: 41.029 to 41.029 scan no 5633 cid35.00 polarity:+
Data file C7-3_3.mgf

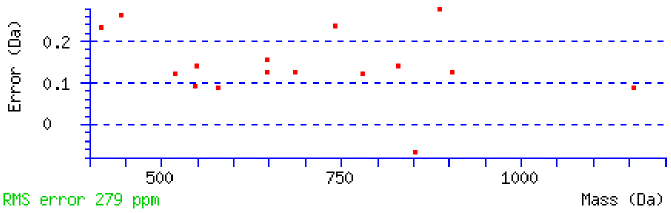
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

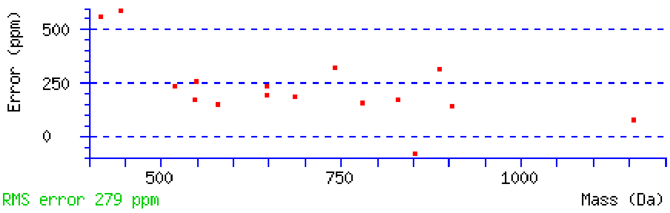


Monoisotopic mass of neutral peptide Mr(calc): 1982.8904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00067
Matches : 16/182 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							20
2	243.1020	122.0546	225.0914	113.0494	H	1881.8531	941.4302	1863.8295	932.4184	1863.8425	932.4249	19
3	343.1675	172.0874	325.1569	163.0821	V	1741.8030	871.4052	1723.7795	862.3934	1723.7925	862.3999	18
4	443.2329	222.1201	425.2223	213.1148	V	1641.7376	821.3724	1623.7140	812.3606	1623.7270	812.3672	17
5	545.2776	273.1424	527.2671	264.1372	T	1541.6721	771.3397	1523.6486	762.3279	1523.6616	762.3344	16
6	**647.3223**	324.1648	629.3118	315.1595	T	1439.6274	720.3174	1421.6039	711.3056	1421.6169	711.3121	15
7	745.3721	373.1897	727.3616	364.1844	P	1337.5827	669.2950	1319.5591	660.2832	1319.5722	660.2897	14
8	803.3906	402.1990	785.3801	393.1937	G	1239.5329	620.2701	1221.5093	611.2583	1221.5224	611.2648	13
9	891.4197	446.2135	873.4091	437.2082	S	1181.5144	591.2609	1163.4908	582.2491	1163.5039	582.2556	12
10	949.4382	475.2227	931.4276	466.2175	G	1093.4854	547.2463	1075.4618	538.2345	1075.4748	538.2410	11
11	1097.5036	***549.2555***	1079.4931	540.2502	F	1035.4669	518.2371	1017.4433	509.2253	1017.4563	509.2318	10
12	**1155.5221**	***578.2647***	1137.5116	569.2594	G	**887.4014**	444.2043	869.3778	435.1926	869.3908	435.1991	9
13	1253.5719	627.2896	1235.5614	618.2843	P	**829.3829**	415.1951	811.3593	406.1833	811.3723	406.1898	8
14	1311.5904	656.2989	1293.5799	647.2936	G	731.3331	366.1702	713.3095	357.1584	713.3226	357.1649	7
15	1369.6089	***685.3081***	1351.5984	676.3028	G	673.3146	337.1609	655.2910	328.1492	655.3041	328.1557	6
16	1499.6486	750.3279	1481.6380	741.3226	E	615.2961	308.1517	597.2725	299.1399	597.2856	299.1464	5
17	1557.6671	***779.3372***	1539.6565	770.3319	G	485.2565	243.1319	467.2329	234.1201			4
18	1705.7325	***853.3699***	1687.7219	844.3646	F	427.2380	214.1226	409.2144	205.1108			3
19	1805.7980	***903.4026***	1787.7874	894.3973	V	279.1725	140.0899	261.1490	131.0781			2
20					R	179.1071	90.0572	161.0835	81.0454			1

AT4G33680.1





NCBI **BLAST** search of THVVTTPGSGFGPGGEGFVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	1982.8904	0.0002	THVVTTPGSGFGPGGEGFVR
13.1	1982.8905	0.0002	TEEHQVFTLGAKQEWR
8.0	1982.8950	-0.0044	MKMLDEVFVYMGVMLK
7.9	1982.8904	0.0002	FSDGFRFGLGAEVGVSTGR
3.9	1982.8959	-0.0053	EEVEGKASSEPIGDQIFK
3.0	1982.8863	0.0043	GLDELSEDGINMIVSEVK
3.0	1982.8889	0.0017	LCSQLAELEVESLDQAR
2.4	1982.8912	-0.0006	AKLGYDPLEVNPEDMVR
1.5	1982.8961	-0.0054	LYCIERGGTFTTWTVR
0.7	1982.8909	-0.0003	KMDLDFLFHMFFLAR

Mascot: http://www.matrixscience.com/

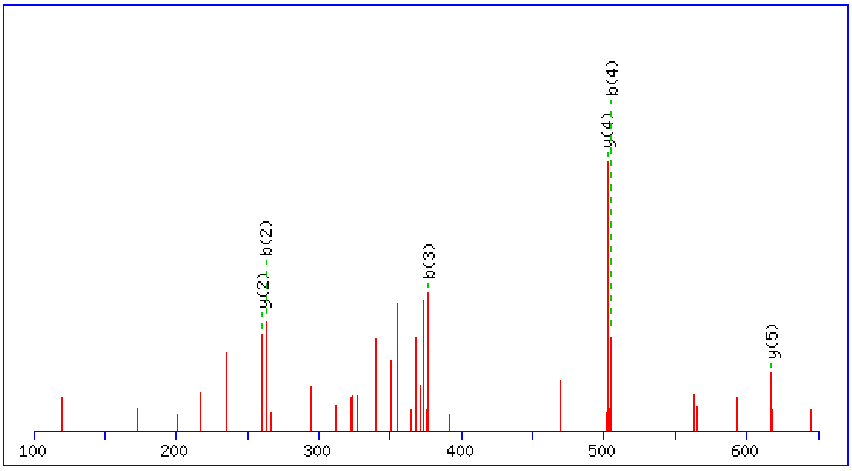
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDLELK**
Found in **AT4G33760.1** in **TAIR_Arabidopsis**, Symbols: | tRNA synthetase class II (D, K and N) family protein | chr4:16189287-16193262 REVERSE

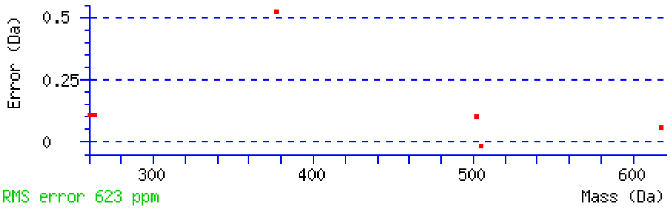
Match to Query 813: 763.412130 from(382.713341,2+) index(4904)
Title: Elution from: 44.720 to 44.720 scan no 6209 cid35.00 polarity:+
Data file 0-2_2.mgf

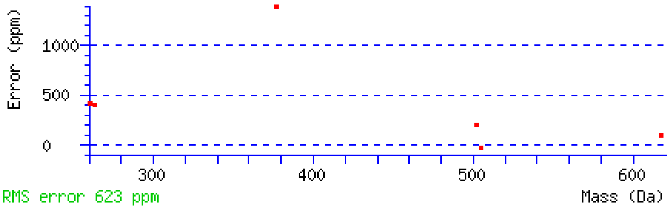
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 763.4116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.021
Matches : 6/44 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							6
2	***263.1026***	132.0550	245.0921	123.0497	D	***617.3505***	309.1789	600.3239	300.6656	599.3399	300.1736	5
3	***376.1867***	188.5970	358.1761	179.5917	L	***502.3235***	251.6654	485.2970	243.1521	484.3130	242.6601	4
4	***505.2293***	253.1183	487.2187	244.1130	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
5	618.3134	309.6603	600.3028	300.6550	L	***260.1969***	130.6021	243.1703	122.0888			2
6					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FDLELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.4	763.4116	0.0005	FDIELK
22.4	763.4116	0.0005	FDLELK
7.7	763.4116	0.0005	FVEELK

AT4G33760.1

6.9	763.4116	0.0005	FEDILK
1.5	763.4123	-0.0001	RMKSAR

AT4G34050.1

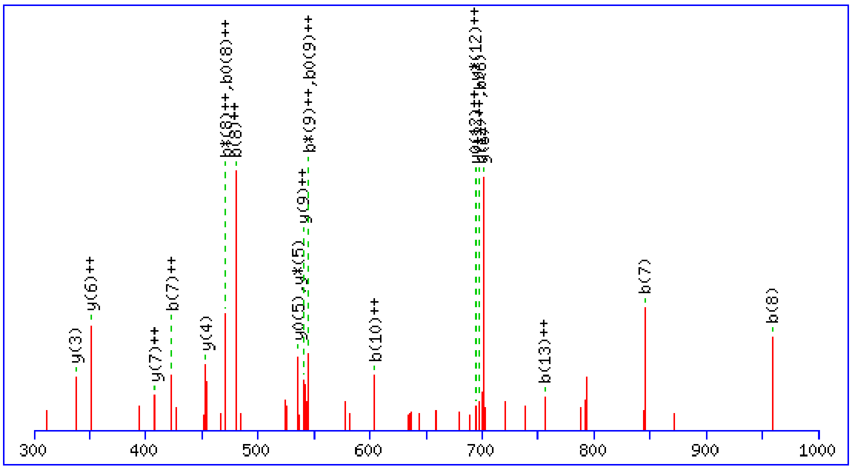
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHGTYDFIFVDADK**
Found in **AT4G34050.1** in **TAIR_Arabidopsis**, Symbols: | caffeoyl-CoA 3-O-methyltransferase, putative | chr4:16310849-16311978 FORWARD

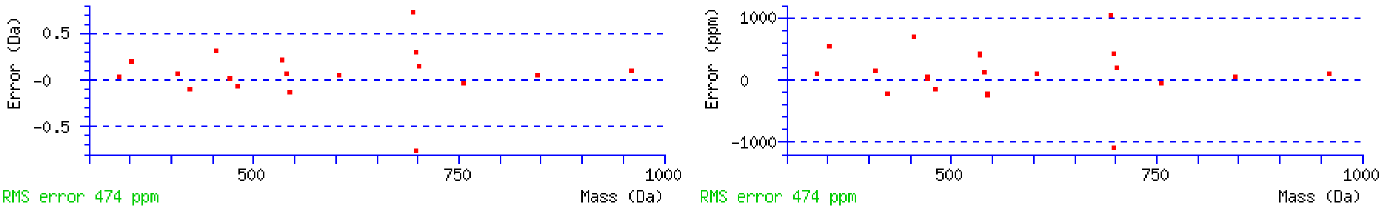
Match to Query 7632: 1658.693259 from(553.905029,3+) index(7001)
Title: Elution from: 61.901 to 61.901 scan no 9096 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1658.6937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0058
Matches : 22/148 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							14
2	257.0943	129.0508	239.0707	120.0390			H	1543.6640	772.3356	1525.6404	763.3238	1525.6534	763.3304	13
3	315.1128	158.0600	297.0892	149.0482			G	1403.6140	702.3106	1385.5904	693.2988	1385.6034	693.3053	12
4	417.1575	209.0824	399.1339	200.0706	399.1469	200.0771	T	1345.5955	673.3014	1327.5719	664.2896	1327.5849	664.2961	11
5	581.2179	291.1126	563.1943	282.1008	563.2073	282.1073	Y	1243.5508	622.2790	1225.5272	613.2672	1225.5402	613.2737	10
6	**697.2418**	349.1246	679.2183	340.1128	679.2313	340.1193	D	1079.4904	540.2488	1061.4668	531.2370	1061.4798	531.2436	9
7	**845.3073**	***423.1573***	827.2837	414.1455	827.2967	414.1520	F	963.4664	482.2369	945.4428	473.2251	945.4559	473.2316	8
8	**959.3884**	***480.1978***	941.3648	471.1860	941.3778	471.1926	I	815.4010	408.2041	797.3774	399.1923	797.3904	399.1988	7
9	1107.4538	554.2306	1089.4303	545.2188	1089.4433	545.2253	F	**701.3199**	351.1636	683.2963	342.1518	683.3093	342.1583	6
10	1207.5193	***604.2633***	1189.4957	595.2515	1189.5087	595.2580	V	553.2544	277.1309	535.2308	268.1191	535.2439	268.1256	5
11	1323.5433	662.2753	1305.5197	653.2635	1305.5327	653.2700	D	**453.1890**	227.0981	435.1654	218.0863	435.1784	218.0928	4
12	1395.5774	***698.2923***	1377.5538	689.2806	1377.5669	689.2871	A	**337.1650**	169.0861	319.1414	160.0743	319.1544	160.0809	3
13	1511.6014	***756.3043***	1493.5778	747.2925	1493.5908	747.2991	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
14							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of NHGTYDFIFVDADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G34050.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.3	1658.6937	-0.0004	NHGTYDFIFVDADK
10.8	1658.6915	0.0018	GDSKTDDSAAFAAAWK
4.8	1658.6948	-0.0016	MRGTTENTDLFDPK
4.3	1658.6971	-0.0038	GFDMKVKWEDDAGK
3.0	1658.6894	0.0039	SHTWHEAPSMQVAR
2.3	1658.6948	-0.0016	EIELYSTNQECVR

AT4G34100.1

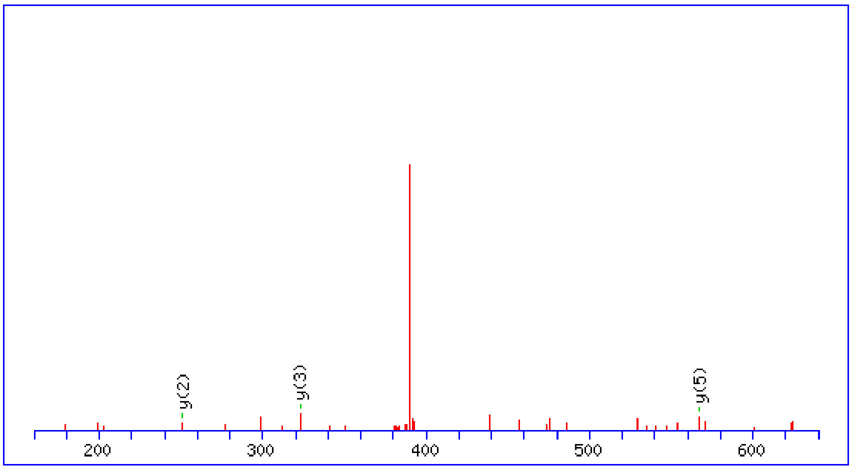
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDIQAAR**
Found in **AT4G34100.1** in **TAIR_Arabidopsis**, Symbols: | protein binding / zinc ion binding | chr4:16330595-16334869 FORWARD

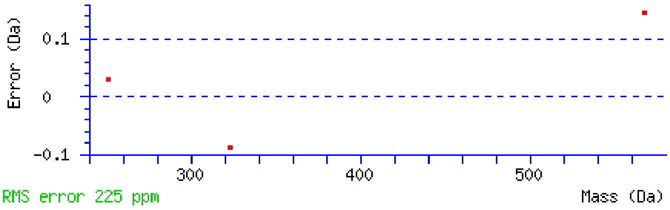
Match to Query 978: 796.404998 from(399.209775,2+) index(1222)
Title: Elution from: 17.948 to 17.948 scan no 1683 cid35.00 polarity:+
Data file 0-3_2.mgf

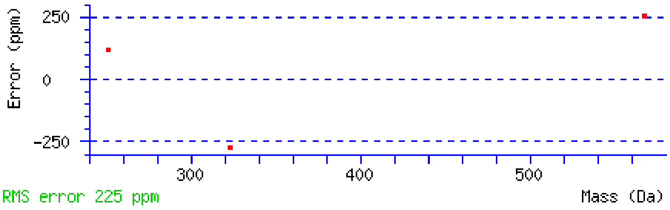
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 160 to 640 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 796.4069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.038
Matches : 3/54 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							7
2	231.1124	116.0598			213.1018	107.0545	D	683.3331	342.1702	665.3095	333.1584	665.3225	333.1649	6
3	345.1935	173.1004			327.1829	164.0951	I	***567.3091***	284.1582	549.2856	275.1464			5
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	Q	453.2280	227.1177	435.2045	218.1059			4
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	A	***323.1754***	162.0913	305.1518	153.0795			3
6	619.3144	310.1608	601.2908	301.1490	601.3038	301.1556	A	***251.1412***	126.0743	233.1177	117.0625			2
7							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LDIQAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.1	796.4043	0.0007	DILEATK
24.1	796.4069	-0.0019	LDIQAAR
24.1	796.4069	-0.0019	NLIEAAR

AT4G34100.1

20.5	796.4069	-0.0019	QILDAAR
14.8	796.4069	-0.0019	ALVADAAR
11.5	796.4043	0.0007	ILDEATK
8.6	796.4069	-0.0019	DGVLGIGR
7.6	796.4069	-0.0019	SKLADPR
7.6	796.4070	-0.0020	SLLSNPR
7.6	796.4070	-0.0020	SLSLNPR

AT4G34110.1

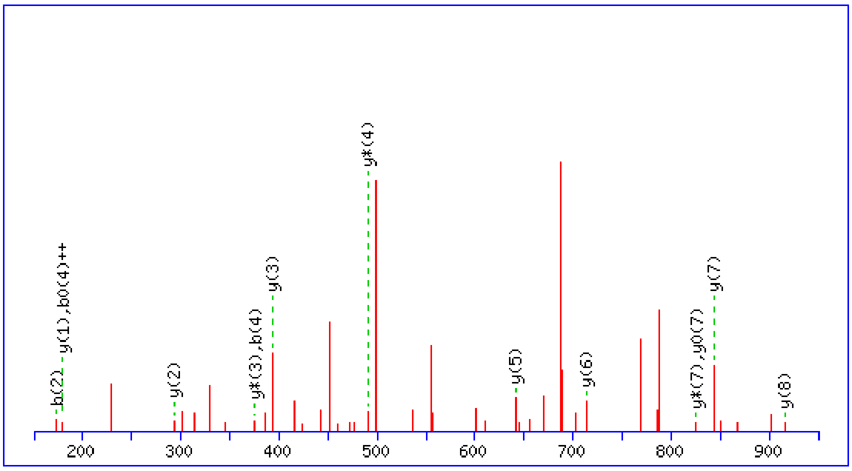
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAEAMDVLR**
Found in **AT4G34110.1** in **TAIR_Arabidopsis**, Symbols: PABP2, PAB2 | PAB2 (POLY(A) BINDING PROTEIN 2); RNA binding | chr4:16337714-16339896 FORWARD

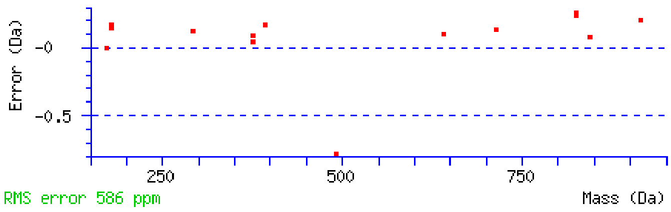
Match to Query 2493: 1014.483196 from(508.248874,2+) index(3711)
Title: Elution from: 35.190 to 35.190 scan no 4638 cid35.00 polarity:+
Data file C7-3_3.mgf

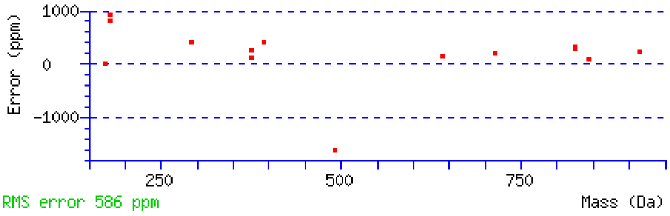
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1014.4812
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.038
Matches : 14/70 fragment ions using 44 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	101.0727	51.0400			V							9
2	173.1069	87.0571			A	***915.4231***	458.2152	897.3995	449.2034	897.4125	449.2099	8
3	303.1465	152.0769	285.1359	143.0716	E	***843.3889***	422.1981	825.3653	413.1863	825.3784	413.1928	7
4	375.1807	188.0940	357.1701	179.0887	A	***713.3493***	357.1783	695.3257	348.1665	695.3387	348.1730	6
5	507.2182	254.1127	489.2076	245.1074	M	***641.3151***	321.1612	623.2916	312.1494	623.3046	312.1559	5
6	623.2421	312.1247	605.2316	303.1194	D	509.2776	255.1424	491.2540	246.1307	491.2671	246.1372	4
7	723.3076	362.1574	705.2970	353.1522	V	***393.2536***	197.1305	375.2301	188.1187			3
8	837.3887	419.1980	819.3781	410.1927	L	***293.1882***	147.0977	275.1646	138.0859			2
9					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VAEAMDVLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G34110.1

23.5	1014.4812	0.0020	VAEAMDVLR
9.6	1014.4813	0.0019	MPISPSSLR
9.4	1014.4812	0.0020	LNDILEMR
6.1	1014.4805	0.0027	IGKDGAFHR
4.1	1014.4835	-0.0003	EMLGWKPK
3.5	1014.4839	-0.0007	HSKVCTLR
2.9	1014.4812	0.0020	ENLMELVR
1.4	1014.4812	0.0020	IACLEEIR
0.5	1014.4812	0.0020	IMEIVDQR
0.5	1014.4839	-0.0007	LMGRSPSPR

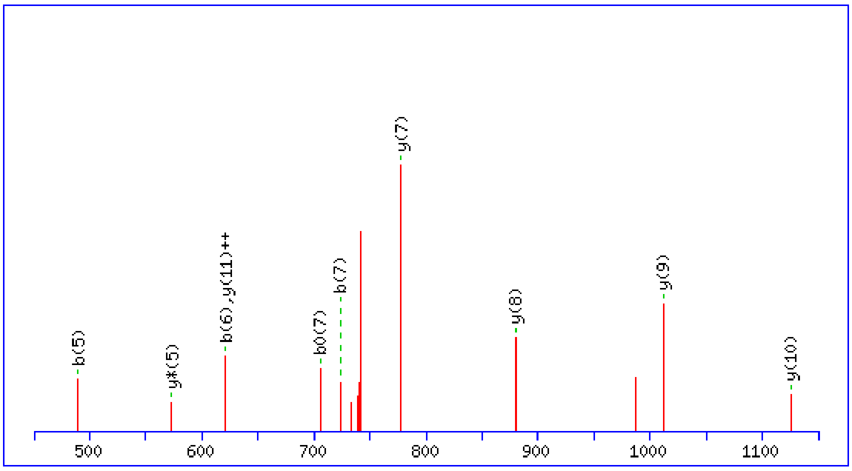
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGDLMTPSPLVVR**
Found in **AT4G34120.1** in **TAIR_Arabidopsis**, Symbols: LEJ1 | LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1) | chr4:16341198-16342897 FORWARD

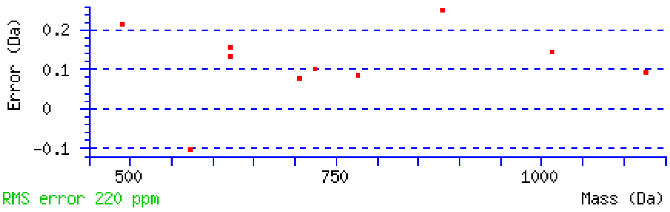
Match to Query 6532: 1498.777570 from(750.396061,2+) index(7545)
Title: Elution from: 66.231 to 66.231 scan no 9737 cid35.00 polarity:+
Data file C7-3_1.mgf

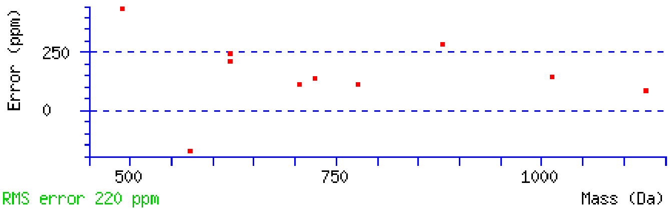
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1498.7772
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0022
Matches : 10/114 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400			V							14
2	201.1382	101.0727			V	1399.7190	700.3631	1381.6954	691.3514	1381.7084	691.3579	13
3	259.1567	130.0820			G	1299.6536	650.3304	1281.6300	641.3186	1281.6430	641.3251	12
4	375.1807	188.0940	357.1701	179.0887	D	1241.6351	621.3212	1223.6115	612.3094	1223.6245	612.3159	11
5	**489.2618**	245.1345	471.2512	236.1292	L	***1125.6111***	563.3092	1107.5875	554.2974	1107.6005	554.3039	10
6	**621.2993**	311.1533	603.2887	302.1480	M	***1011.5300***	506.2686	993.5064	497.2568	993.5194	497.2633	9
7	**723.3440**	362.1756	705.3334	353.1703	T	***879.4925***	440.2499	861.4689	431.2381	861.4819	431.2446	8
8	821.3938	411.2005	803.3832	402.1952	P	***777.4477***	389.2275	759.4242	380.2157	759.4372	380.2222	7
9	909.4228	455.2151	891.4123	446.2098	S	679.3980	340.2026	661.3744	331.1908	661.3874	331.1973	6
10	1007.4726	504.2400	989.4621	495.2347	P	591.3689	296.1881	573.3453	287.1763			5
11	1121.5537	561.2805	1103.5432	552.2752	L	493.3191	247.1632	475.2955	238.1514			4
12	1221.6192	611.3132	1203.6086	602.3080	V	379.2380	190.1226	361.2144	181.1108			3
13	1321.6846	661.3460	1303.6741	652.3407	V	279.1725	140.0899	261.1490	131.0781			2
14					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VVGDLMTPSPLVVR

AT4G34120.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.0	1498.7772	0.0004	VVGDLMTPSPLVVR
6.7	1498.7769	0.0007	RVPKLNRPPDQR
1.9	1498.7769	0.0007	GNTPLHIAVRKNR
1.9	1498.7738	0.0038	KLKIGEGGFGSVYK

AT4G34200.1

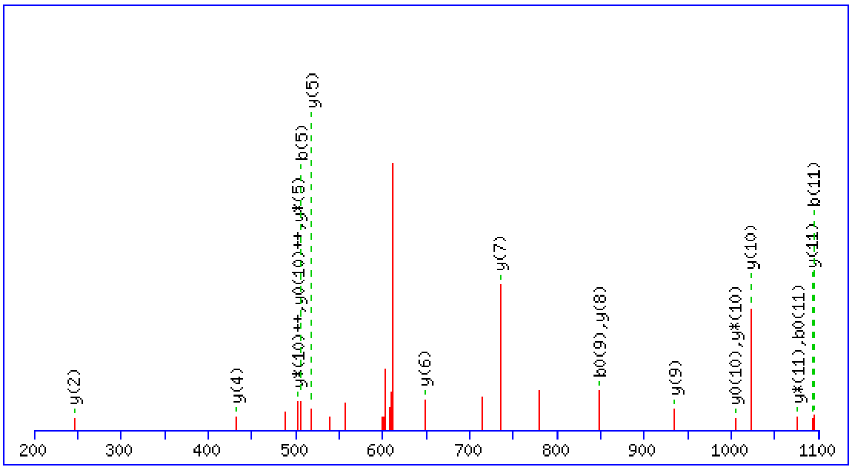
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FASSLSESGEVK**
Found in **AT4G34200.1** in **TAIR_Arabidopsis**, Symbols: EDA9 | EDA9 (embryo sac development arrest 9); NAD binding / amino acid binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor / phosphoglycerate dehydrogenase | chr4:

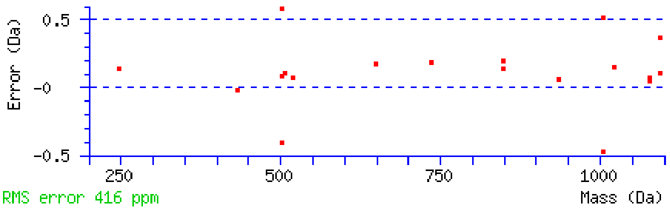
Match to Query 3960: 1239.598300 from(620.806426,2+) index(1952)
Title: Elution from: 25.974 to 25.974 scan no 2621 cid35.00 polarity:+
Data file D1d-1_1.mgf

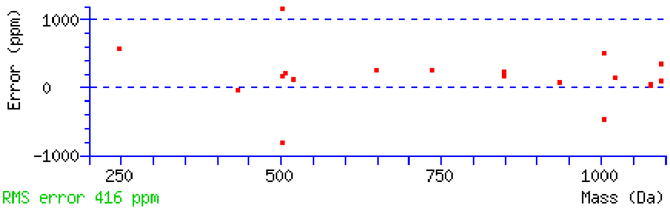
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1239.5983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 89 **Expect:** 3.6e-009
Matches : 19/102 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			**F**							**12**
2	219.1128	110.0600			**A**	***1093.5372***	547.2722	1076.5106	538.7589	1075.5266	538.2669	**11**
3	306.1448	153.5761	288.1343	144.5708	**S**	***1022.5000***	511.7537	1005.4735	503.2404	1004.4895	502.7484	**10**
4	393.1769	197.0921	375.1663	188.0868	**S**	***935.4680***	468.2376	918.4415	459.7244	917.4575	459.2324	**9**
5	**506.2609**	253.6341	488.2504	244.6288	**L**	***848.4360***	424.7216	831.4094	416.2084	830.4254	415.7163	**8**
6	593.2930	297.1501	575.2824	288.1448	**S**	***735.3519***	368.1796	718.3254	359.6663	717.3414	359.1743	**7**
7	722.3355	361.6714	704.3250	352.6661	**E**	***648.3199***	324.6636	631.2933	316.1503	630.3093	315.6583	**6**
8	809.3676	405.1874	791.3570	396.1821	**S**	***519.2773***	260.1423	502.2508	251.6290	501.2667	251.1370	**5**
9	866.3890	433.6982	848.3785	424.6929	**G**	***432.2453***	216.6263	415.2187	208.1130	414.2347	207.6210	**4**
10	995.4316	498.2195	977.4211	489.2142	**E**	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
11	**1094.5000**	547.7537	1076.4895	538.7484	**V**	***246.1812***	123.5942	229.1547	115.0810			**2**
12					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of FASSLSESGEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G34200.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.7	1239.5983	0.0000	FASSLSESGEVK
5.6	1239.5956	0.0027	KHDGNNNKEGK
1.7	1239.5983	0.0000	VYNDSISSEVK
1.3	1239.5996	-0.0013	VYAATHGQEHK
0.6	1239.5983	0.0000	TKEDSSIFDAK
0.5	1239.6005	-0.0022	KWFCGVCRK

AT4G34220.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIDGAIR**
Found in **AT4G34220.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr4:16381657-16384058 REVERSE

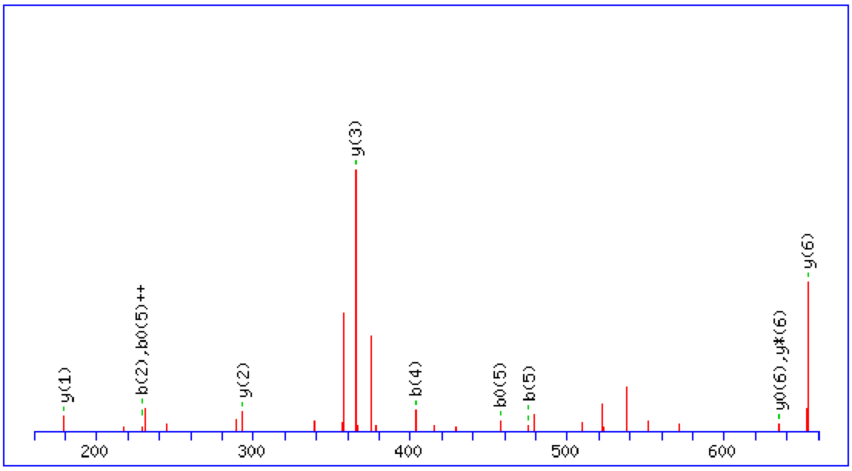
Match to Query 838: 766.420590 from(384.217571,2+) index(2750)
Title: Elution from: 28.284 to 28.284 scan no 3458 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 160 to 660 Da Full range

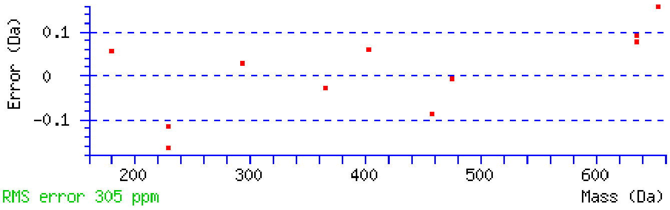
Label all possible matches ○ Label matches used for scoring ●

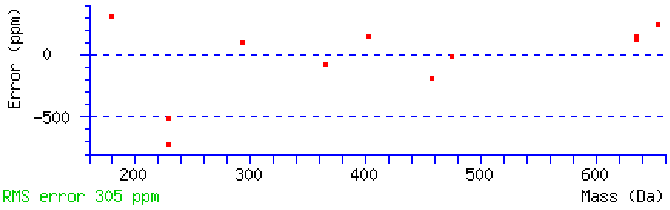
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 766.4197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.022
Matches : 11/48 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			L							7
2	***229.1695***	115.0884			I	***653.3459***	327.1766	635.3223	318.1648	635.3354	318.1713	6
3	345.1935	173.1004	327.1829	164.0951	D	539.2648	270.1360	521.2412	261.1243	521.2543	261.1308	5
4	***403.2120***	202.1096	385.2014	193.1043	G	423.2408	212.1241	405.2173	203.1123			4
5	***475.2461***	238.1267	457.2355	229.1214	A	***365.2223***	183.1148	347.1988	174.1030			3
6	589.3272	295.1672	571.3166	286.1620	I	***293.1882***	147.0977	275.1646	138.0859			2
7					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LIDGAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.3	766.4197	0.0009	LIDGAIR
25.1	766.4197	0.0009	LGVEALR

AT4G34220.1

23.2	766.4197	0.0009	INELLR
23.2	766.4197	0.0009	LNLEIR
22.5	766.4197	0.0009	TPSIALR
14.1	766.4197	0.0009	IAVDIAR
14.1	766.4197	0.0009	IGEVLAR
13.4	766.4197	0.0009	LEVQIR
12.3	766.4197	0.0009	LINEIR
12.3	766.4197	0.0009	LINELR

Mascot: http://www.matrixscience.com/

AT4G34290.1

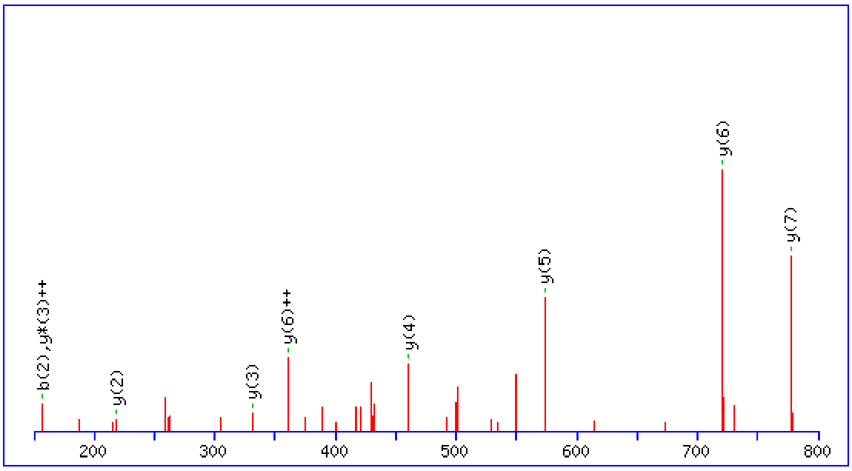
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGFLEIAK**
Found in **AT4G34290.1** in **TAIR_Arabidopsis**, Symbols: | SWIB complex BAF60b domain-containing protein | chr4:16410887-16412126 FORWARD

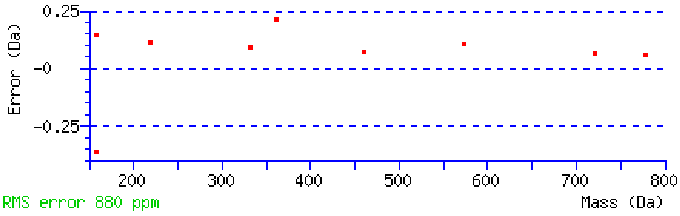
Match to Query 1217: 875.511782 from(438.763167,2+) index(5589)
Title: Elution from: 53.065 to 53.065 scan no 7233 cid35.00 polarity:+
Data file D1d-1_1.mgf

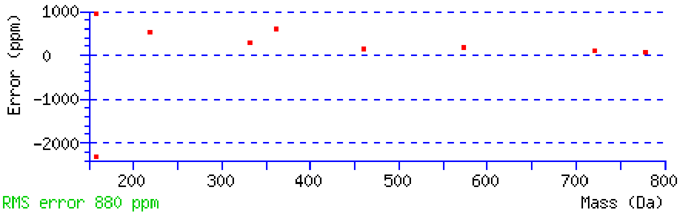
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 875.5116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 4.3e-005
Matches : 9/56 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415			V							8
2	157.0972	79.0522			G	*777.4505*	389.2289	760.4240	380.7156	759.4400	380.2236	7
3	304.1656	152.5864			F	*720.4291*	360.7182	703.4025	352.2049	702.4185	351.7129	6
4	417.2496	209.1285			L	*573.3606*	287.1840	556.3341	278.6707	555.3501	278.1787	5
5	546.2922	273.6498	528.2817	264.6445	E	*460.2766*	230.6419	443.2500	222.1287	442.2660	221.6366	4
6	659.3763	330.1918	641.3657	321.1865	I	*331.2340*	166.1206	314.2074	157.6074			3
7	730.4134	365.7103	712.4028	356.7051	A	*218.1499*	109.5786	201.1234	101.0653			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VGFLEIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.6	875.5116	0.0001	VGFLEIAK

AT4G34290.1

Mascot: http://www.matrixscience.com/

AT4G34620.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **STSQHVSPITGEILN**
Found in **AT4G34620.1** in **TAIR_Arabidopsis**, Symbols: SSR16 | SSR16 (ribosomal protein S16); structural constituent of ribosome | chr4:16535089-16536097 REVERSE

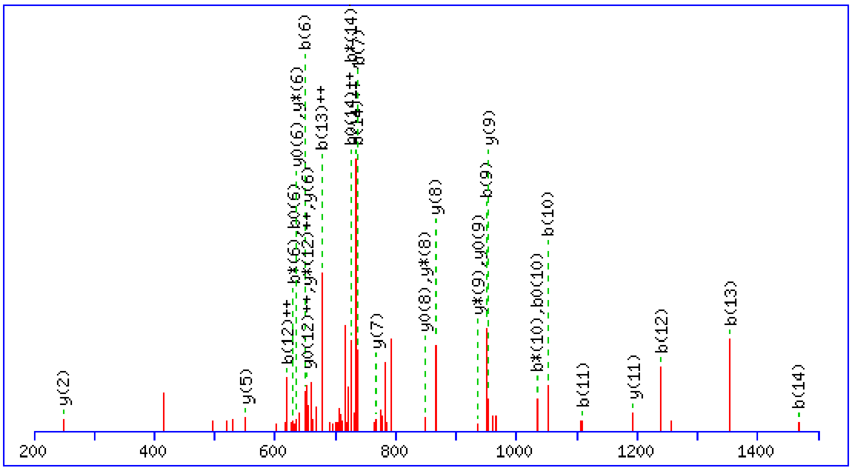
Match to Query 7158: 1600.742300 from(801.378426,2+) index(4591)
Title: Elution from: 44.214 to 44.214 scan no 5851 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

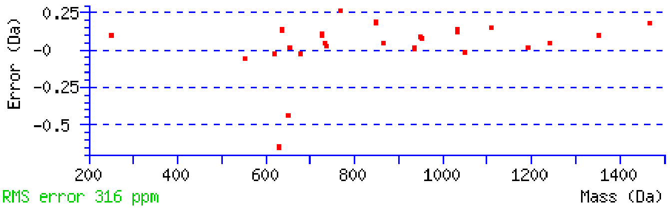
Label all possible matches ○ Label matches used for scoring ●

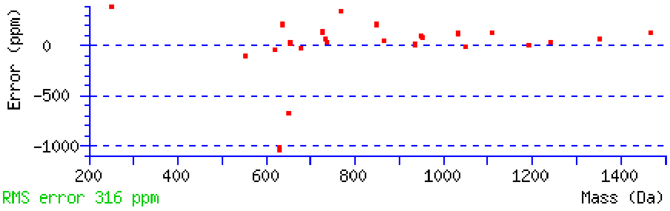
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1600.7435
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 2.2e-005
Matches : 32/156 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							15
2	191.0811	96.0442			173.0705	87.0389	T	1513.7217	757.3645	1495.6981	748.3527	1495.7112	748.3592	14
3	279.1101	140.0587			261.0996	131.0534	S	1411.6770	706.3421	1393.6534	697.3304	1393.6664	697.3369	13
4	409.1628	205.0850	391.1392	196.0732	391.1522	196.0797	Q	1323.6479	662.3276	1305.6244	653.3158	1305.6374	653.3223	12
5	549.2128	275.1100	531.1892	266.0982	531.2022	266.1047	H	***1193.5953***	597.3013	1175.5717	588.2895	1175.5847	588.2960	11
6	***649.2782***	325.1428	631.2546	316.1310	631.2677	316.1375	V	1053.5453	527.2763	1035.5217	518.2645	1035.5347	518.2710	10
7	***737.3073***	369.1573	719.2837	360.1455	719.2967	360.1520	S	***953.4798***	477.2436	935.4563	468.2318	935.4693	468.2383	9
8	835.3571	418.1822	817.3335	409.1704	817.3465	409.1769	P	***865.4508***	433.2290	847.4272	424.2172	847.4402	424.2237	8
9	***949.4382***	475.2227	931.4146	466.2109	931.4276	466.2175	I	***767.4010***	384.2041	749.3774	375.1923	749.3904	375.1988	7
10	***1051.4829***	526.2451	1033.4593	517.2333	1033.4723	517.2398	T	***653.3199***	327.1636	635.2963	318.1518	635.3093	318.1583	6
11	***1109.5014***	555.2543	1091.4778	546.2425	1091.4908	546.2491	G	***551.2752***	276.1412	533.2516	267.1294	533.2646	267.1359	5
12	***1239.5410***	**620.2742**	1221.5174	611.2624	1221.5305	611.2689	E	493.2567	247.1320	475.2331	238.1202	475.2461	238.1267	4
13	***1353.6221***	**677.3147**	1335.5985	668.3029	1335.6116	668.3094	I	363.2170	182.1122	345.1935	173.1004			3
14	***1467.7032***	**734.3553**	1449.6796	725.3435	1449.6927	725.3500	L	***249.1359***	125.0716	231.1124	116.0598			2
15							N	135.0548	68.0311	117.0313	59.0193			1





AT4G34620.1

NCBI **BLAST** search of STSQHVSPITGEILN
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.8	1600.7435	-0.0012	STSQHVSPITGEILN
0.0	1600.7457	-0.0034	NNDGEIKFGYSLVK

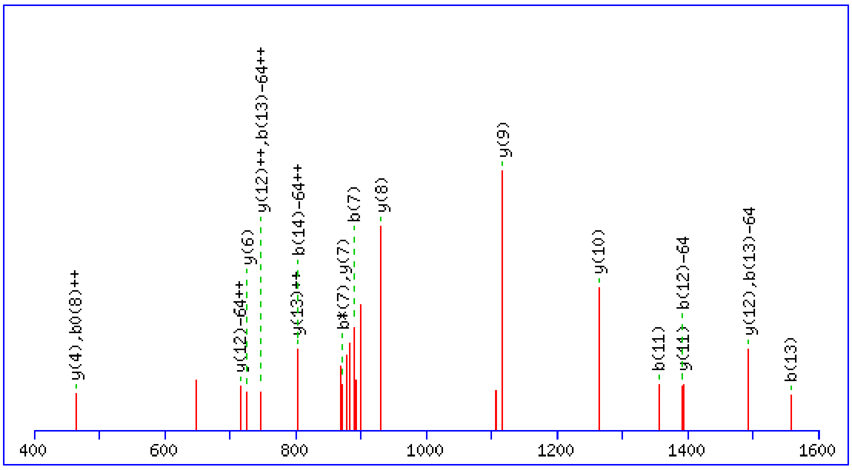
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVLTQFWGMDFTTDK**
Found in **AT4G34670.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S3A (RPS3aB) | chr4:16548729-16550227 FORWARD

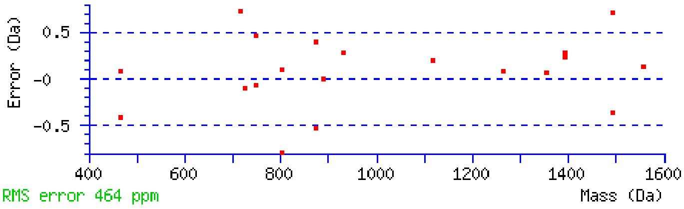
Match to Query 8601: 1817.829928 from(909.922240,2+) index(9886)
Title: Elution from: 92.605 to 92.605 scan no 13922 cid35.00 polarity:+
Data file 0-2_2.mgf

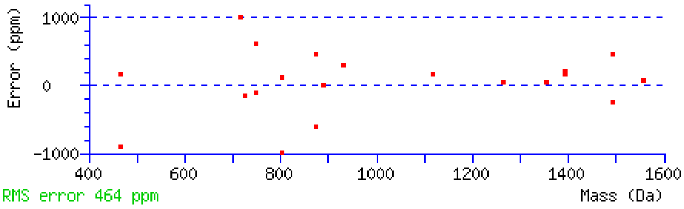
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1817.8295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 63 **Expect:** 9e-007
Matches : 20/244 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	214.1186	107.5629	197.0921	99.0497			V	1704.7938	852.9005	1687.7672	844.3873	1686.7832	843.8952	14
3	327.2027	164.1050	310.1761	155.5917			L	1605.7254	803.3663	1588.6988	794.8531	1587.7148	794.3610	13
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	T	***1492.6413***	746.8243	1475.6148	738.3110	1474.6307	737.8190	12
5	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	Q	***1391.5936***	696.3005	1374.5671	687.7872	1373.5831	687.2952	11
6	703.3774	352.1923	686.3508	343.6790	685.3668	343.1870	F	***1263.5351***	632.2712	1246.5085	623.7579	1245.5245	623.2659	10
7	**889.4567**	445.2320	872.4301	436.7187	871.4461	436.2267	W	***1116.4666***	558.7370	1099.4401	550.2237	1098.4561	549.7317	9
8	946.4781	473.7427	929.4516	465.2294	928.4676	464.7374	G	***930.3873***	465.6973	913.3608	457.1840	912.3768	456.6920	8
9	1093.5135	547.2604	1076.4870	538.7471	1075.5030	538.2551	M	***873.3659***	437.1866	856.3393	428.6733	855.3553	428.1813	7
10	1208.5405	604.7739	1191.5139	596.2606	1190.5299	595.7686	D	***726.3305***	363.6689	709.3039	355.1556	708.3199	354.6636	6
11	**1355.6089**	678.3081	1338.5823	669.7948	1337.5983	669.3028	F	611.3035	306.1554	594.2770	297.6421	593.2930	297.1501	5
12	1456.6566	728.8319	1439.6300	720.3186	1438.6460	719.8266	T	***464.2351***	232.6212	447.2086	224.1079	446.2245	223.6159	4
13	**1557.7042**	779.3558	1540.6777	770.8425	1539.6937	770.3505	T	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
14	1672.7312	836.8692	1655.7046	828.3560	1654.7206	827.8639	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1





AT4G34670.1

NCBI **BLAST** search of NVLTQFWGMDFTTDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.6	1817.8295	0.0005	NVLTQFWGMDFTTDK

AT4G34860.1

{MATRIX SCIENCE} Mascot Search Results

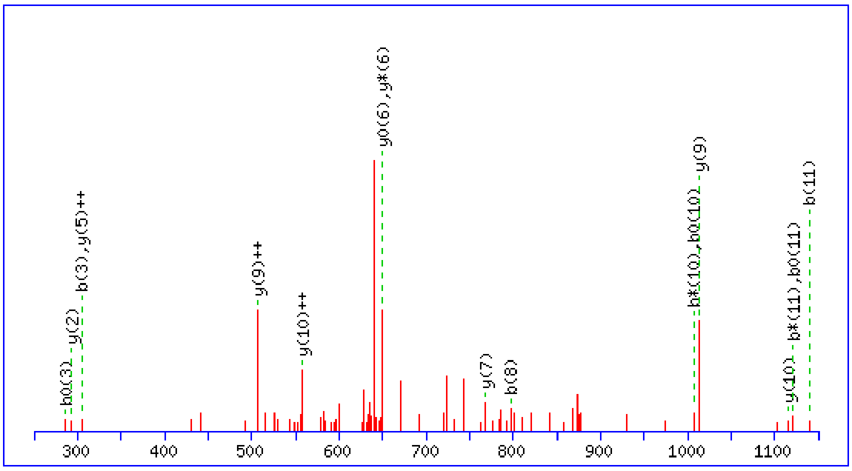
Peptide View

MS/MS Fragmentation of **SLTELTGSPQLR**
Found in **AT4G34860.1** in **TAIR_Arabidopsis**, Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr4:16609960-16612024 REVERSE

Match to Query 5105: 1316.651452 from(659.333002,2+) index(9969)
Title: Elution from: 88.335 to 88.335 scan no 13443 cid35.00 polarity:+
Data file C7-1_1.mgf

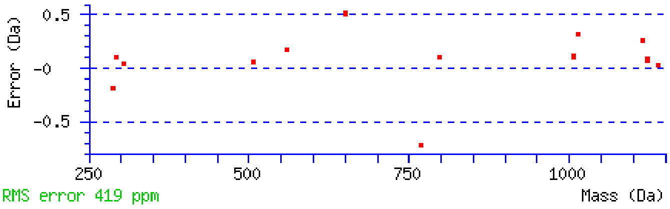
Click mouse within plot area to zoom in by factor of two about that point

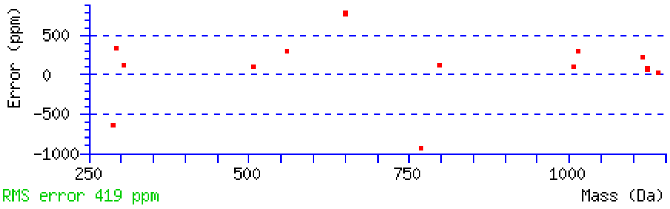
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1316.6512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.038
Matches : 17/106 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	203.1174	102.0624			185.1069	93.0571	L	1229.6295	615.3184	1211.6059	606.3066	1211.6189	606.3131	11
3	***305.1622***	153.0847			287.1516	144.0794	T	***1115.5484***	558.2778	1097.5248	549.2660	1097.5378	549.2725	10
4	435.2018	218.1045			417.1912	209.0992	E	***1013.5036***	507.2555	995.4801	498.2437	995.4931	498.2502	9
5	549.2829	275.1451			531.2723	266.1398	L	883.4640	442.2356	865.4404	433.2239	865.4534	433.2304	8
6	651.3276	326.1674			633.3170	317.1622	T	***769.3829***	385.1951	751.3593	376.1833	751.3723	376.1898	7
7	709.3461	355.1767			691.3355	346.1714	G	667.3382	334.1727	649.3146	325.1609	649.3276	325.1675	6
8	***797.3752***	399.1912			779.3646	390.1859	S	609.3197	305.1635	591.2961	296.1517	591.3091	296.1582	5
9	895.4250	448.2161			877.4144	439.2108	P	521.2906	261.1490	503.2671	252.1372			4
10	1025.4776	513.2424	1007.4540	504.2306	1007.4670	504.2372	Q	423.2408	212.1241	405.2173	203.1123			3
11	***1139.5587***	570.2830	1121.5351	561.2712	1121.5481	561.2777	L	***293.1882***	147.0977	275.1646	138.0859			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SLTELTGSPQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G34860.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.6	1316.6512	0.0002	SLTELTGSPQLR
10.1	1316.6512	0.0002	SDVITAAQEIVR
7.2	1316.6512	0.0002	DSVIESSLPAKR
6.0	1316.6535	-0.0020	NDPVESLLLFR
3.4	1316.6514	0.0001	GHPRVMAYVLR
1.0	1316.6512	0.0002	KTAGDLAGPSASVK

AT4G34870.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEMELFADTTPNTAENFR**
Found in **AT4G34870.1** in **TAIR_Arabidopsis**, Symbols: ATCYP1, ROC5 | ROC5 (ROTAMASE CYP 5); peptidyl-prolyl cis-trans isomerase | chr4:16614456-16614974 FORWARD

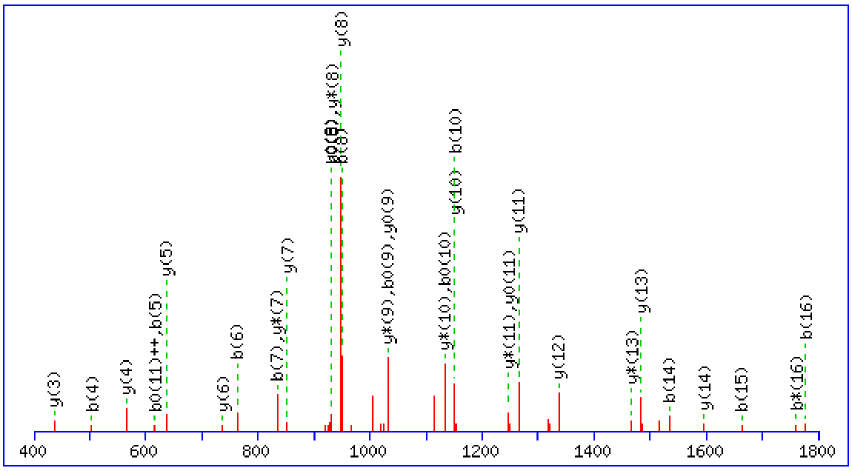
Match to Query 9546: 2097.966694 from(1049.990623,2+) index(8655)
Title: Elution from: 75.965 to 75.965 scan no 11510 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

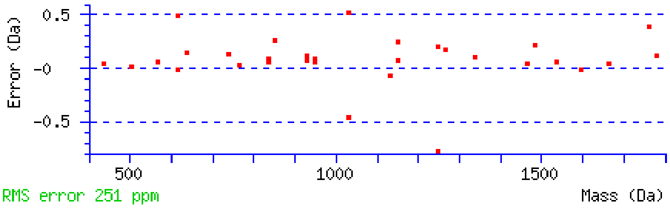
Show Y-axis ☐

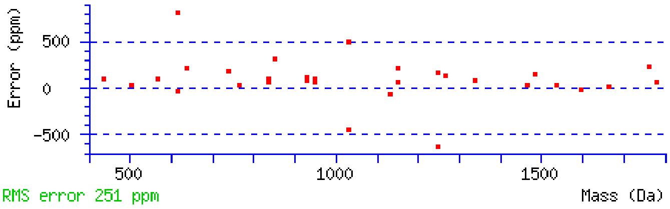


Monoisotopic mass of neutral peptide Mr(calc): 2097.9677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 95 **Expect:** 7.9e-010
Matches : 34/174 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							18
2	243.1339	122.0706			225.1234	113.0653	E	1985.8909	993.4491	1968.8644	984.9358	1967.8804	984.4438	17
3	374.1744	187.5908			356.1639	178.5856	M	1856.8483	928.9278	1839.8218	920.4145	1838.8378	919.9225	16
4	***503.2170***	252.1121			485.2064	243.1069	E	1725.8079	863.4076	1708.7813	854.8943	1707.7973	854.4023	15
5	***616.3011***	308.6542			598.2905	299.6489	L	***1596.7653***	798.8863	1579.7387	790.3730	1578.7547	789.8810	14
6	***763.3695***	382.1884			745.3589	373.1831	F	***1483.6812***	742.3442	1466.6547	733.8310	1465.6706	733.3390	13
7	***834.4066***	417.7069			816.3960	408.7017	A	***1336.6128***	668.8100	1319.5862	660.2968	1318.6022	659.8047	12
8	***949.4335***	475.2204			931.4230	466.2151	D	***1265.5757***	633.2915	1248.5491	624.7782	1247.5651	624.2862	11
9	1050.4812	525.7443			1032.4707	516.7390	T	***1150.5487***	575.7780	1133.5222	567.2647	1132.5382	566.7727	10
10	***1151.5289***	576.2681			1133.5183	567.2628	T	1049.5010	525.2542	1032.4745	516.7409	1031.4905	516.2489	9
11	1248.5817	624.7945			1230.5711	615.7892	P	***948.4534***	474.7303	931.4268	466.2170	930.4428	465.7250	8
12	1362.6246	681.8159	1345.5980	673.3027	1344.6140	672.8107	N	***851.4006***	426.2039	834.3741	417.6907	833.3900	417.1987	7
13	1463.6723	732.3398	1446.6457	723.8265	1445.6617	723.3345	T	***737.3577***	369.1825	720.3311	360.6692	719.3471	360.1772	6
14	***1534.7094***	767.8583	1517.6828	759.3451	1516.6988	758.8530	A	***636.3100***	318.6586	619.2835	310.1454	618.2994	309.6534	5
15	***1663.7520***	832.3796	1646.7254	823.8664	1645.7414	823.3743	E	***565.2729***	283.1401	548.2463	274.6268	547.2623	274.1348	4
16	***1777.7949***	889.4011	1760.7684	880.8878	1759.7843	880.3958	N	***436.2303***	218.6188	419.2037	210.1055			3
17	1924.8633	962.9353	1907.8368	954.4220	1906.8528	953.9300	F	322.1874	161.5973	305.1608	153.0840			2
18							R	175.1190	88.0631	158.0924	79.5498			1

AT4G34870.1





NCBI **BLAST** search of IEMELFADTTPNTAENFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.4	2097.9677	-0.0010	IEMELFADTTPNTAENFR
4.6	2097.9711	-0.0044	SALSMLKHDSEGKEFMEK
1.5	2097.9679	-0.0012	KNEMMMIPAAAASSSKEMR
1.5	2097.9679	-0.0012	KNEMMMIPAAAASSSKEMR

Mascot: http://www.matrixscience.com/

AT4G35000.1

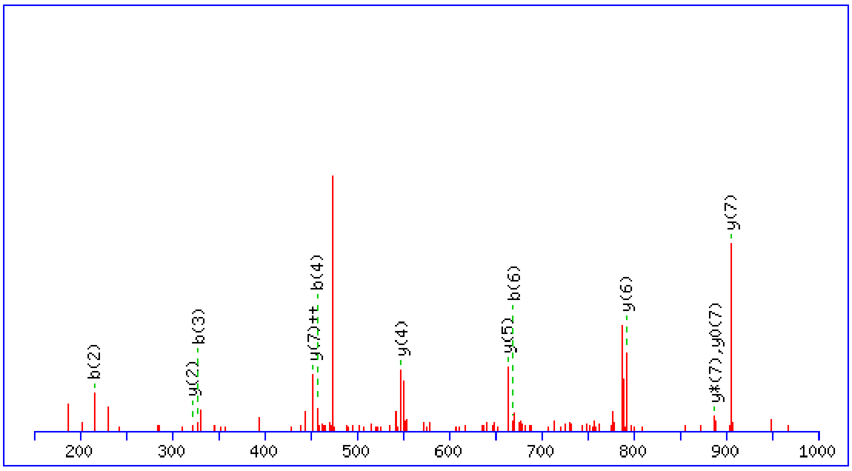
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLLEDPEFR**
Found in **AT4G35000.1** in **TAIR_Arabidopsis**, Symbols: APX3 | APX3 (ASCORBATE PEROXIDASE 3); L-ascorbate peroxidase | chr4:16665012-16667546 REVERSE

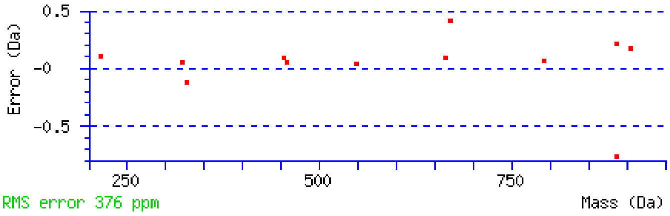
Match to Query 3024: 1118.563790 from(560.289171,2+) index(5073)
Title: Elution from: 46.919 to 46.919 scan no 6497 cid35.00 polarity:+
Data file D12h-2_3.mgf

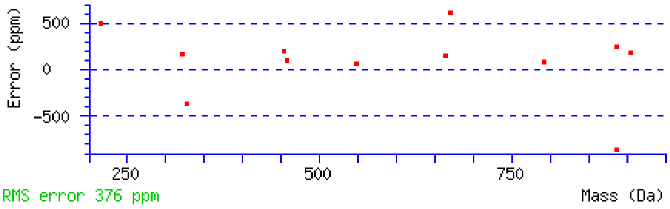
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1118.5608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.018
Matches : 12/76 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							9
2	***215.1390***	108.0731	197.1285	99.0679	L	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	8
3	***328.2231***	164.6152	310.2125	155.6099	L	***905.4363***	453.2218	888.4098	444.7085	887.4258	444.2165	7
4	***457.2657***	229.1365	439.2551	220.1312	E	***792.3523***	396.6798	775.3257	388.1665	774.3417	387.6745	6
5	572.2926	286.6499	554.2821	277.6447	D	***663.3097***	332.1585	646.2831	323.6452	645.2991	323.1532	5
6	***669.3454***	335.1763	651.3348	326.1710	P	***548.2827***	274.6450	531.2562	266.1317	530.2722	265.6397	4
7	798.3880	399.6976	780.3774	390.6923	E	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
8	945.4564	473.2318	927.4458	464.2266	F	***322.1874***	161.5973	305.1608	153.0840			2
9					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TLLEDPEFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT4G35000.1

24.6	1118.5608	0.0030	TLLEDPEFR
1.2	1118.5641	-0.0003	TLMQEQLEK

Mascot: http://www.matrixscience.com/

AT4G35090.1

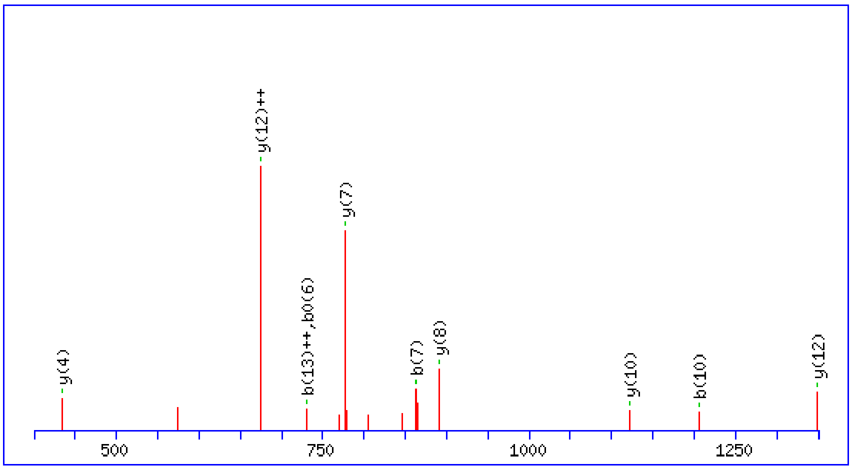
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWPEDILPLQPVGR**
Found in **AT4G35090.1** in **TAIR_Arabidopsis**, Symbols: CAT2 | CAT2 (CATALASE 2); catalase | chr4:16700942-16703220 REVERSE

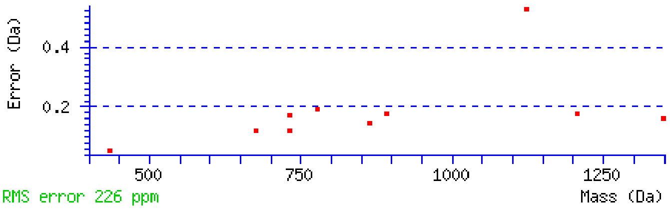
Match to Query 7712: 1638.812260 from(820.413406,2+) index(10040)
Title: Elution from: 91.726 to 91.726 scan no 13776 cid35.00 polarity:+
Data file C7-3_1.mgf

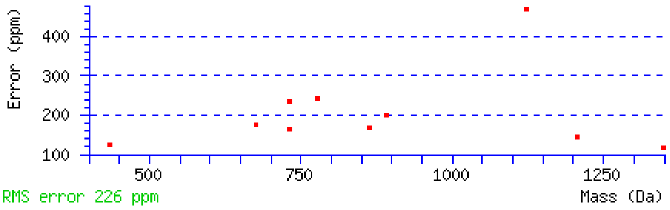
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1638.8108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0012
Matches : 10/120 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							14
2	291.1254	146.0663			273.1148	137.0610	W	1537.7734	769.3903	1519.7498	760.3785	1519.7628	760.3850	13
3	389.1752	195.0912			371.1646	186.0859	P	***1349.7000***	675.3536	1331.6764	666.3418	1331.6894	666.3483	12
4	519.2148	260.1110			501.2042	251.1058	E	1251.6502	626.3287	1233.6266	617.3169	1233.6396	617.3234	11
5	635.2388	318.1230			617.2282	309.1177	D	***1121.6106***	561.3089	1103.5870	552.2971	1103.6000	552.3036	10
6	749.3199	375.1636			731.3093	366.1583	I	1005.5866	503.2969	987.5630	494.2851			9
7	**863.4010**	432.2041			845.3904	423.1988	L	***891.5055***	446.2564	873.4819	437.2446			8
8	961.4508	481.2290			943.4402	472.2237	P	***777.4244***	389.2158	759.4008	380.2040			7
9	1075.5319	538.2696			1057.5213	529.2643	L	679.3746	340.1909	661.3510	331.1791			6
10	**1205.5845**	603.2959	1187.5609	594.2841	1187.5740	594.2906	Q	565.2935	283.1504	547.2699	274.1386			5
11	1303.6343	652.3208	1285.6107	643.3090	1285.6238	643.3155	P	***435.2408***	218.1241	417.2173	209.1123			4
12	1403.6998	702.3535	1385.6762	693.3417	1385.6892	693.3482	V	337.1910	169.0992	319.1675	160.0874			3
13	1461.7183	731.3628	1443.6947	722.3510	1443.7077	722.3575	G	237.1256	119.0664	219.1020	110.0546			2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TWPEDILPLQPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G35090.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.0	1638.8108	0.0015	TWPEDILPLQPVGR
2.2	1638.8085	0.0037	KRDSGLNVFEEVVK
1.0	1638.8168	-0.0046	ERPIIACGKTFGIR
0.7	1638.8086	0.0037	ILSPTASVSSAFIGNR
0.7	1638.8120	0.0003	LKSMNEISSLVNLR

AT4G35100.1

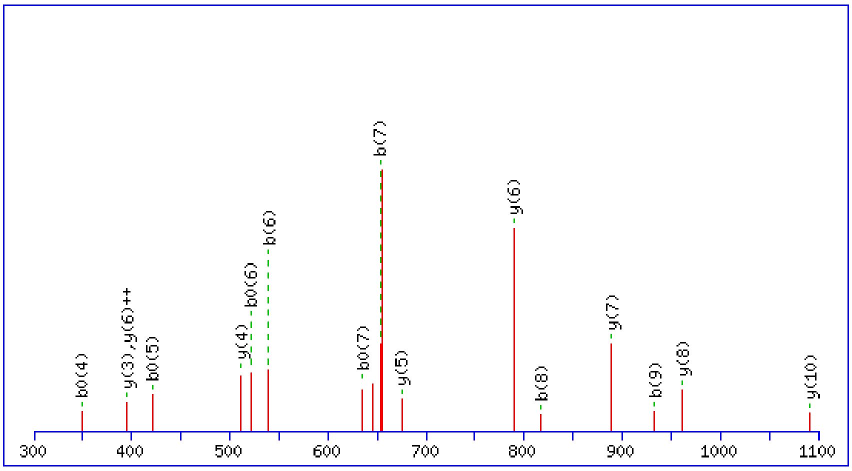
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFGAAVIYNNEK**
Found in **AT4G35100.1** in **TAIR_Arabidopsis**, Symbols: PIP3A, PIP2;7, SIMIP, PIP3 | PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel | chr4:16708677-16709963 FORWARD

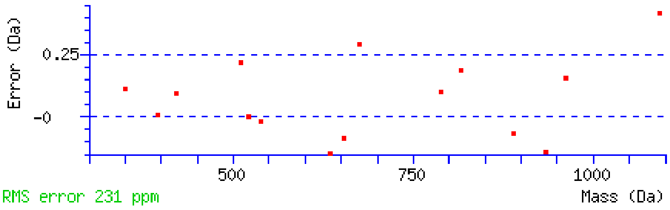
Match to Query 4703: 1326.597888 from(664.306220,2+) index(3879)
Title: Elution from: 36.374 to 36.374 scan no 4847 cid35.00 polarity:+
Data file D6h-2_3.mgf

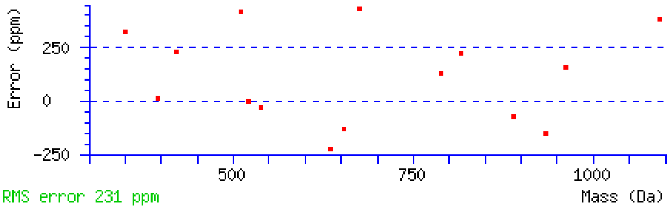
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1326.6014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 2.3e-007
Matches : 16/114 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	237.1018	119.0545			219.0912	110.0492	F	1239.5797	620.2935	1221.5561	611.2817	1221.5691	611.2882	11
3	295.1203	148.0638			277.1097	139.0585	G	***1091.5142***	546.2607	1073.4906	537.2489	1073.5036	537.2555	10
4	367.1544	184.0809			349.1439	175.0756	A	1033.4957	517.2515	1015.4721	508.2397	1015.4851	508.2462	9
5	439.1886	220.0979			421.1780	211.0926	A	***961.4616***	481.2344	943.4380	472.2226	943.4510	472.2291	8
6	**539.2540**	270.1307			521.2435	261.1254	V	***889.4274***	445.2173	871.4038	436.2056	871.4168	436.2121	7
7	**653.3351**	327.1712			635.3246	318.1659	I	***789.3620***	395.1846	771.3384	386.1728	771.3514	386.1793	6
8	**817.3955**	409.2014			799.3849	400.1961	Y	***675.2809***	338.1441	657.2573	329.1323	657.2703	329.1388	5
9	**933.4325**	467.2199	915.4089	458.2081	915.4219	458.2146	N	***511.2205***	256.1139	493.1969	247.1021	493.2099	247.1086	4
10	1049.4695	525.2384	1031.4459	516.2266	1031.4589	516.2331	N	***395.1835***	198.0954	377.1599	189.0836	377.1729	189.0901	3
11	1179.5091	590.2582	1161.4855	581.2464	1161.4986	581.2529	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SFGAAVIYNNEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G35100.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.0	1326.6014	-0.0036	SFGAAVIYNNEK
14.6	1326.5957	0.0021	LMRMQMRQGR
14.2	1326.5970	0.0009	KASTGSDKSSTNK
13.9	1326.6014	-0.0035	RAIYYDPETGK
13.2	1326.5974	0.0005	MMLDDYIAKSK
12.4	1326.5967	0.0012	LYWAGMSAERK
6.9	1326.6001	-0.0022	LDRFSCILCK
5.5	1326.6014	-0.0036	YNNYILEDLR
5.0	1326.5996	-0.0017	TRRDTSETSVR
4.5	1326.5978	0.0000	AMAKDKMSIGSR

AT4G35140.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGELIR**
Found in **AT4G35140.1** in **TAIR_Arabidopsis**, Symbols: | transducin family protein / WD-40 repeat family protein | chr4:16723878-16726482 REVERSE

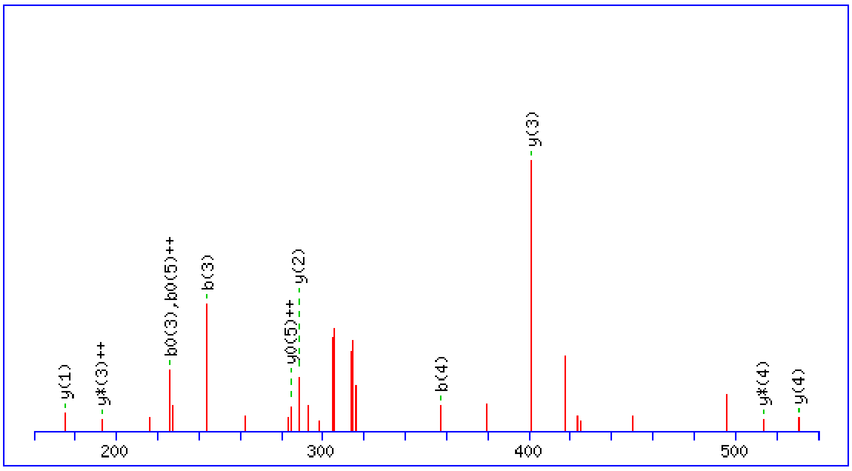
Match to Query 532: 643.364878 from(322.689715,2+) index(450)
Title: Elution from: 10.200 to 10.200 scan no 713 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 160 to 540 Da Full range

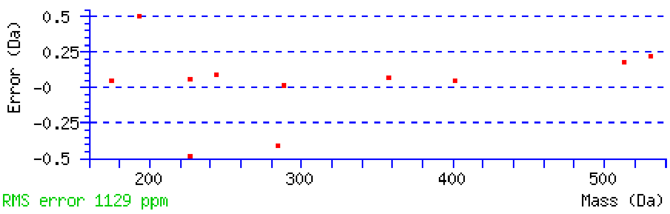
Label all possible matches ○ Label matches used for scoring ●

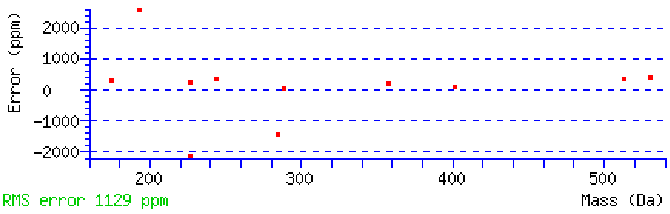
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 643.3653
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.039
Matches : 11/40 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							6
2	115.0502	58.0287			G	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	5
3	**244.0928**	122.5500	226.0822	113.5448	E	***530.3297***	265.6685	513.3031	257.1552	512.3191	256.6632	4
4	**357.1769**	179.0921	339.1663	170.0868	L	***401.2871***	201.1472	384.2605	192.6339			3
5	470.2609	235.6341	452.2504	226.6288	I	***288.2030***	144.6051	271.1765	136.0919			2
6					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GGELIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.5	643.3653	-0.0004	GGELIR
26.1	643.3653	-0.0004	NEIIR
26.1	643.3653	-0.0004	NEILR

AT4G35140.1

26.1	643.3653	-0.0004	NELLR
21.5	643.3653	-0.0004	GGLIER
21.5	643.3653	-0.0004	INIER
21.5	643.3653	-0.0004	INLER
21.5	643.3653	-0.0004	LNIER
21.5	643.3653	-0.0004	LNLER
21.5	643.3653	-0.0004	NILER

AT4G35250.1

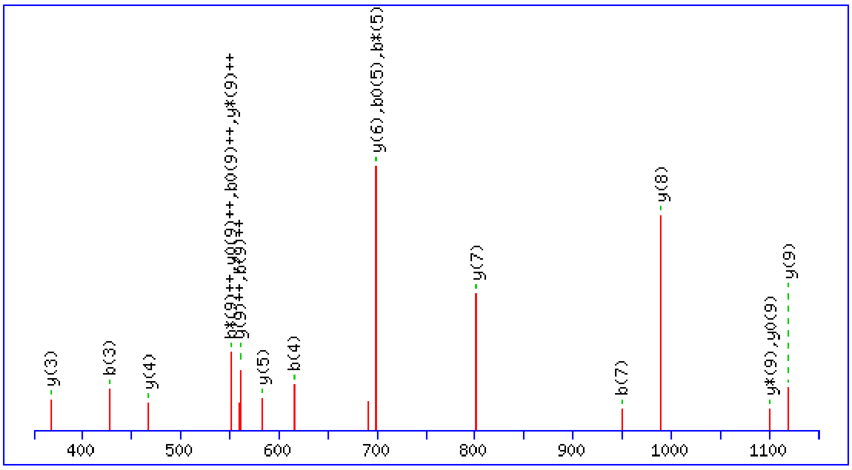
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFQWTNDVADR**
Found in **AT4G35250.1** in **TAIR_Arabidopsis**, Symbols: | vestitone reductase-related | chr4:16771406-16773274 REVERSE

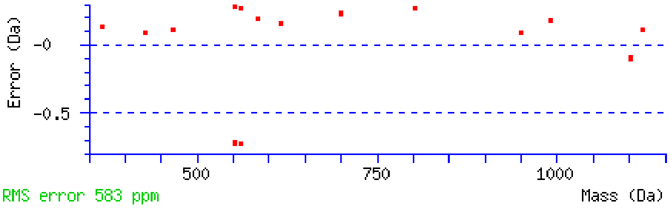
Match to Query 5920: 1414.587158 from(708.300855,2+) index(7125)
Title: Elution from: 61.842 to 61.842 scan no 9044 cid35.00 polarity:+
Data file D12h-1_1.mgf

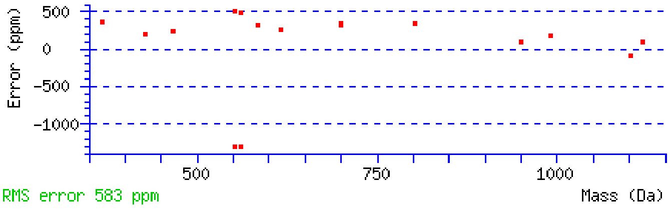
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1414.5860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.2e-006
Matches : 20/106 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							11
2	297.1382	149.0727					F	1267.5278	634.2676	1249.5043	625.2558	1249.5173	625.2623	10
3	**427.1908**	214.0990	409.1672	205.0873			Q	***1119.4624***	560.2348	1101.4388	551.2230	1101.4518	551.2295	9
4	**615.2642**	308.1357	597.2406	299.1239			W	***989.4097***	495.2085	971.3862	486.1967	971.3992	486.2032	8
5	717.3089	359.1581	699.2853	350.1463	699.2984	350.1528	T	***801.3364***	401.1718	783.3128	392.1600	783.3258	392.1665	7
6	833.3459	417.1766	815.3223	408.1648	815.3353	408.1713	N	***699.2916***	350.1495	681.2681	341.1377	681.2811	341.1442	6
7	**949.3699**	475.1886	931.3463	466.1768	931.3593	466.1833	D	***583.2546***	292.1310	565.2311	283.1192	565.2441	283.1257	5
8	1049.4353	525.2213	1031.4118	516.2095	1031.4248	516.2160	V	***467.2307***	234.1190	449.2071	225.1072	449.2201	225.1137	4
9	1121.4695	561.2384	1103.4459	552.2266	1103.4589	552.2331	A	***367.1652***	184.0862	349.1416	175.0745	349.1547	175.0810	3
10	1237.4935	619.2504	1219.4699	610.2386	1219.4829	610.2451	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FFQWTNDVADR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G35250.1

Score	Mr(calc)	Delta	Sequence
64.8	1414.5860	0.0012	FFQWTNDVADR
16.2	1414.5905	-0.0033	TGGAQMSRMVSEK
11.9	1414.5838	0.0034	SVDGYSSGWVNAR
5.2	1414.5831	0.0041	DMESMVKKMER
4.3	1414.5851	0.0021	AARCFMNSKHR
4.3	1414.5831	0.0041	QMGGMSGLQSLMK
4.3	1414.5831	0.0041	QMGGMSGLQSLMK
0.6	1414.5871	0.0000	GVMYTREEAEGR
0.1	1414.5880	-0.0009	MWKDRNLMCK
0.0	1414.5831	0.0041	DMESMVKKMER

Mascot: http://www.matrixscience.com/

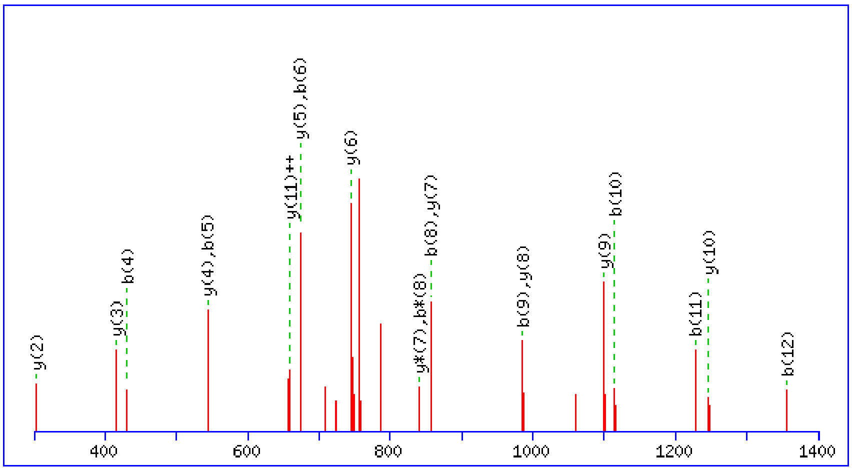
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPAFNQLAEQLQR**
Found in **AT4G35450.1** in **TAIR_Arabidopsis**, Symbols: AFT, AKR2A, AKR2 | AKR2 (ANKYRIN REPEAT-CONTAINING PROTEIN 2); protein binding | chr4:16839867-16841764 FORWARD

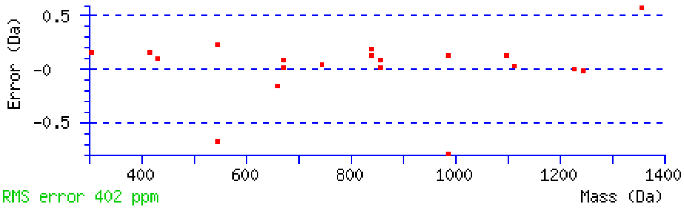
Match to Query 6146: 1528.767040 from(765.390796,2+) index(7294)
Title: Elution from: 67.235 to 67.235 scan no 9616 cid35.00 polarity:+
Data file D12h-2_2.mgf

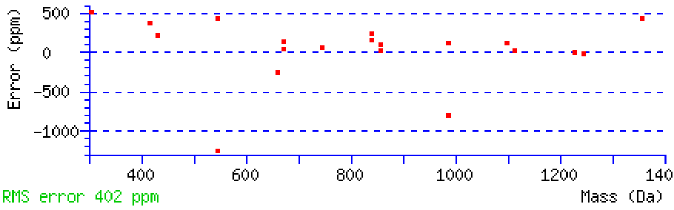
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1528.7634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 6.6e-009
Matches : 20/128 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							13
2	213.0870	107.0471			195.0764	98.0418	P	1414.7437	707.8755	1397.7172	699.3622	1396.7332	698.8702	12
3	284.1241	142.5657			266.1135	133.5604	A	1317.6910	659.3491	1300.6644	650.8359	1299.6804	650.3438	11
4	***431.1925***	216.0999			413.1819	207.0946	F	***1246.6539***	623.8306	1229.6273	615.3173	1228.6433	614.8253	10
5	***545.2354***	273.1214	528.2089	264.6081	527.2249	264.1161	N	***1099.5854***	550.2964	1082.5589	541.7831	1081.5749	541.2911	9
6	***673.2940***	337.1506	656.2675	328.6374	655.2835	328.1454	Q	***985.5425***	493.2749	968.5160	484.7616	967.5320	484.2696	8
7	786.3781	393.6927	769.3515	385.1794	768.3675	384.6874	L	***857.4839***	429.2456	840.4574	420.7323	839.4734	420.2403	7
8	***857.4152***	429.2112	840.3886	420.6980	839.4046	420.2060	A	***744.3999***	372.7036	727.3733	364.1903	726.3893	363.6983	6
9	***986.4578***	493.7325	969.4312	485.2193	968.4472	484.7272	E	***673.3628***	337.1850	656.3362	328.6717	655.3522	328.1797	5
10	***1114.5164***	557.7618	1097.4898	549.2485	1096.5058	548.7565	Q	***544.3202***	272.6637	527.2936	264.1504			4
11	***1227.6004***	614.3039	1210.5739	605.7906	1209.5899	605.2986	L	***416.2616***	208.6344	399.2350	200.1212			3
12	***1355.6590***	678.3331	1338.6325	669.8199	1337.6484	669.3279	Q	***303.1775***	152.0924	286.1510	143.5791			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DPAFNQLAEQLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G35450.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
87.5	1528.7634	0.0037	DPAFNQLAEQLQR
10.3	1528.7634	0.0037	QDKEWADLQAVAR
1.7	1528.7668	0.0003	LVMPSNGNGVKEER
0.6	1528.7668	0.0003	QSSMKIVEVAEHR

AT4G35460.1

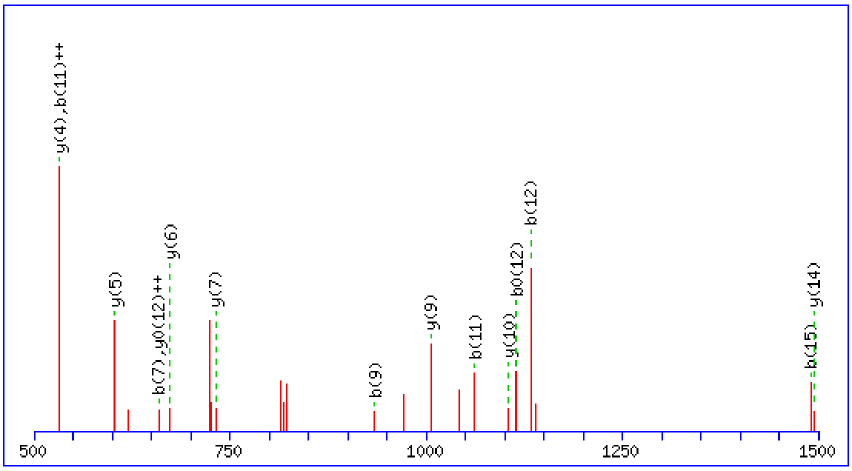
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GISACAVCDGAAPIFR**
Found in **AT4G35460.1** in **TAIR_Arabidopsis**, Symbols: TRB1, ATNTRB, NTRB, NTR1 | NTR1 (NADPH-dependent thioredoxin reductase 1) | chr4:16842223-16843745 FORWARD

Match to Query 7437: 1663.783882 from(832.899217,2+) index(6185)
Title: Elution from: 54.074 to 54.074 scan no 7938 cid35.00 polarity:+
Data file D6h-3_3.mgf

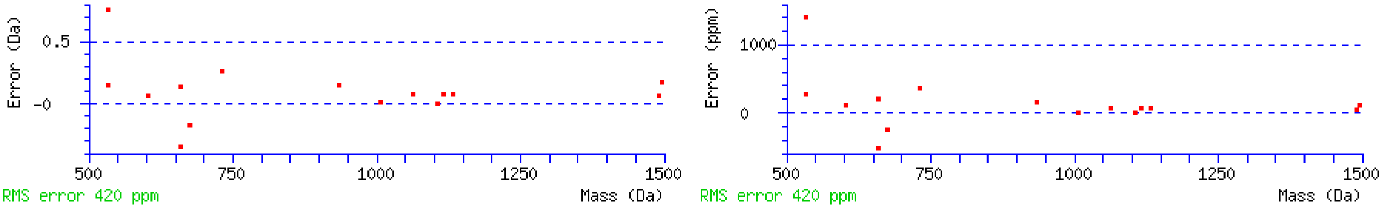
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1663.7811
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 4e-005
Matches : 15/132 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180			G							16
2	171.1128	86.0600			I	1607.7669	804.3871	1590.7403	795.8738	1589.7563	795.3818	15
3	258.1448	129.5761	240.1343	120.5708	S	***1494.6828***	747.8450	1477.6562	739.3318	1476.6722	738.8398	14
4	329.1819	165.0946	311.1714	156.0893	A	1407.6508	704.3290	1390.6242	695.8157	1389.6402	695.3237	13
5	489.2126	245.1099	471.2020	236.1047	C	1336.6137	668.8105	1319.5871	660.2972	1318.6031	659.8052	12
6	560.2497	280.6285	542.2391	271.6232	A	1176.5830	588.7951	1159.5565	580.2819	1158.5724	579.7899	11
7	**659.3181**	330.1627	641.3076	321.1574	V	***1105.5459***	553.2766	1088.5193	544.7633	1087.5353	544.2713	10
8	819.3488	410.1780	801.3382	401.1727	C	***1006.4775***	503.7424	989.4509	495.2291	988.4669	494.7371	9
9	**934.3757**	467.6915	916.3651	458.6862	D	846.4468	423.7271	829.4203	415.2138	828.4363	414.7218	8
10	991.3972	496.2022	973.3866	487.1969	G	***731.4199***	366.2136	714.3933	357.7003			7
11	**1062.4343**	531.7208	1044.4237	522.7155	A	***674.3984***	337.7028	657.3719	329.1896			6
12	**1133.4714**	567.2393	1115.4608	558.2341	A	***603.3613***	302.1843	586.3348	293.6710			5
13	1230.5242	615.7657	1212.5136	606.7604	P	***532.3242***	266.6657	515.2976	258.1525			4
14	1343.6082	672.3078	1325.5977	663.3025	I	435.2714	218.1394	418.2449	209.6261			3
15	**1490.6766**	745.8420	1472.6661	736.8367	F	322.1874	161.5973	305.1608	153.0840			2
16					R	175.1190	88.0631	158.0924	79.5498			1

AT4G35460.1



NCBI **BLAST** search of GISACAVCDGAAPIFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.6	1663.7811	0.0028	GISACAVCDGAAPIFR
4.6	1663.7835	0.0004	EELDKMLEENSRR
4.6	1663.7797	0.0042	LMTEEMEVAVEVER
3.5	1663.7835	0.0004	DVETASLRMDNLER

Mascot: http://www.matrixscience.com/

AT4G35630.1

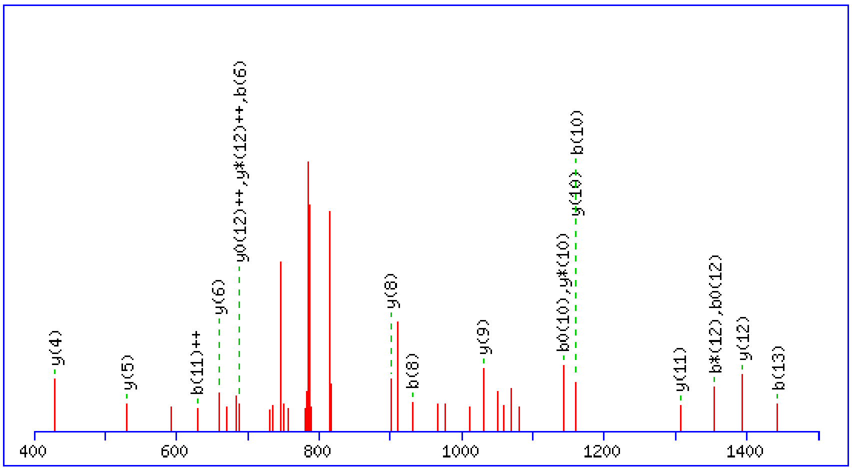
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPSFEELEQTPDAK**
Found in **AT4G35630.1** in **TAIR_Arabidopsis**, Symbols: PSAT | PSAT (phosphoserine aminotransferase); phosphoserine transaminase | chr4:16904210-16905502 FORWARD

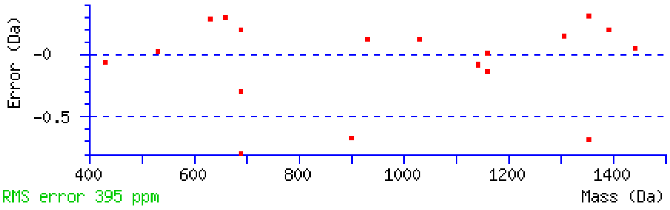
Match to Query 7612: 1588.762876 from(795.388714,2+) index(6484)
Title: Elution from: 56.585 to 56.585 scan no 8122 cid35.00 polarity:+
Data file 0-1_1.mgf

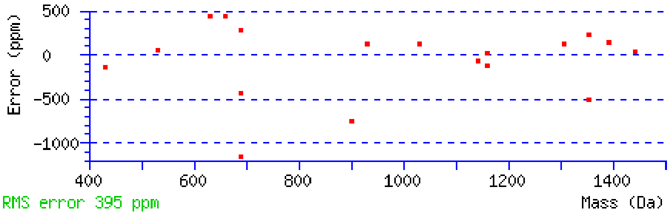
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1588.7621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.3e-005
Matches : 19/132 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							14
2	197.1285	99.0679					P	1490.7009	745.8541	1473.6744	737.3408	1472.6904	736.8488	13
3	284.1605	142.5839			266.1499	133.5786	S	***1393.6482***	697.3277	1376.6216	688.8144	1375.6376	688.3224	12
4	431.2289	216.1181			413.2183	207.1128	F	***1306.6161***	653.8117	1289.5896	645.2984	1288.6056	644.8064	11
5	560.2715	280.6394			542.2609	271.6341	E	***1159.5477***	580.2775	1142.5212	571.7642	1141.5372	571.2722	10
6	**689.3141**	345.1607			671.3035	336.1554	E	***1030.5051***	515.7562	1013.4786	507.2429	1012.4946	506.7509	9
7	802.3981	401.7027			784.3876	392.6974	L	***901.4625***	451.2349	884.4360	442.7216	883.4520	442.2296	8
8	**931.4407**	466.2240			913.4302	457.2187	E	788.3785	394.6929	771.3519	386.1796	770.3679	385.6876	7
9	1059.4993	530.2533	1042.4728	521.7400	1041.4888	521.2480	Q	***659.3359***	330.1716	642.3093	321.6583	641.3253	321.1663	6
10	**1160.5470**	580.7771	1143.5204	572.2639	1142.5364	571.7719	T	***531.2773***	266.1423	514.2508	257.6290	513.2667	257.1370	5
11	1257.5998	629.3035	1240.5732	620.7902	1239.5892	620.2982	P	***430.2296***	215.6185	413.2031	207.1052	412.2191	206.6132	4
12	1372.6267	686.8170	1355.6002	678.3037	1354.6161	677.8117	D	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
13	**1443.6638**	722.3355	1426.6373	713.8223	1425.6533	713.3303	A	218.1499	109.5786	201.1234	101.0653			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VPSFEELEQTPDAK

AT4G35630.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.8	1588.7621	0.0008	VPSFEELEQTPDAK

AT4G35690.1

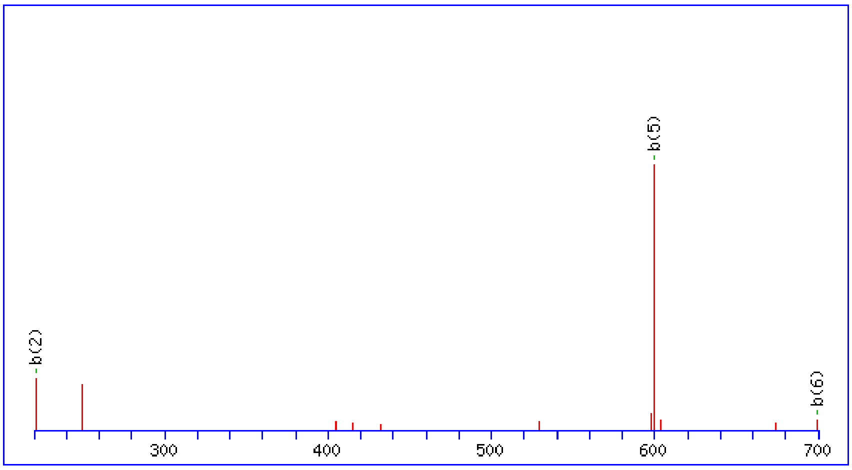
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSNMLVK**
Found in **AT4G35690.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35710.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22786.1); contains InterPro domain Protein of unknown function DUF241, plant (InterPro:IPR004320) | chr4:16

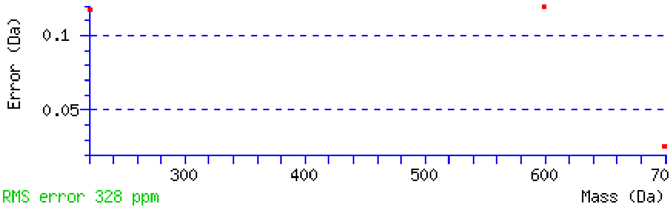
Match to Query 1253: 846.382384 from(424.198468,2+) index(4662)
Title: Elution from: 42.523 to 42.523 scan no 5863 cid35.00 polarity:+
Data file C7-1_2.mgf

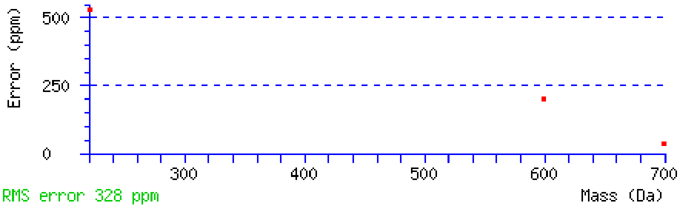
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 220 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 846.3822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.041
Matches : 3/88 fragment ions using 5 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	133.0448	67.0260					**M**							**7**
2	***221.0739***	111.0406			203.0633	102.0353	**S**	715.3519	358.1796	697.3283	349.1678	697.3414	349.1743	**6**
3	337.1109	169.0591	319.0873	160.0473	319.1003	160.0538	**N**	627.3229	314.1651	609.2993	305.1533			**5**
4	485.1433	243.0753	467.1197	234.0635	467.1327	234.0700	**M**	511.2859	256.1466	493.2623	247.1348			**4**
5	***599.2244***	300.1158	581.2008	291.1040	581.2138	291.1106	**L**	363.2534	182.1303	345.2298	173.1186			**3**
6	***699.2898***	350.1486	681.2663	341.1368	681.2793	341.1433	**V**	249.1723	125.0898	231.1487	116.0780			**2**
7							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MSNMLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis

AT4G35690.1

21.4	846.3822	0.0002	MSNMLVK	Oxidation M4 92.78%
16.5	846.3815	0.0009	SRCWVK	
11.8	846.3837	-0.0013	FVFMHR	
10.3	846.3810	0.0014	FVWMEK	
10.3	846.3822	0.0002	MSNMLVK	Oxidation M1 7.22%
10.3	846.3822	0.0002	MVVMTNK	
6.2	846.3822	0.0002	NLMMAVK	
4.7	846.3840	-0.0016	SRKSDDK	
4.7	846.3840	-0.0016	SRSATADK	
4.7	846.3835	-0.0011	VFTEESK	

AT4G35830.1

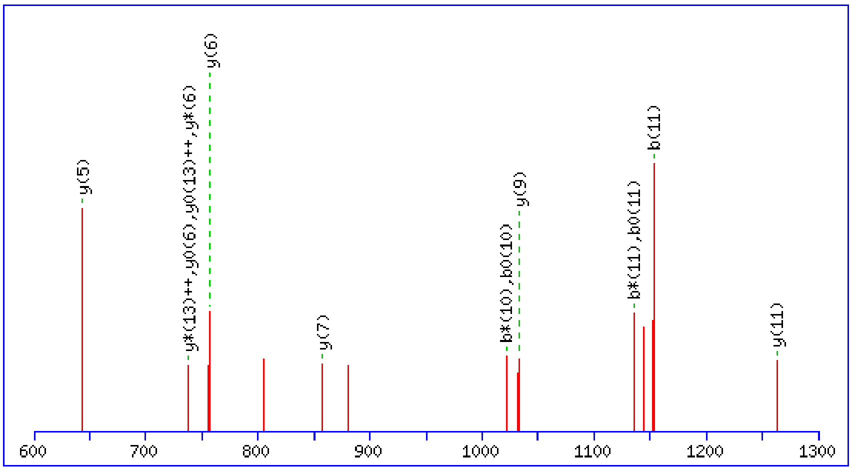
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVAEVVQSSVLPDMFK**
Found in **AT4G35830.1** in **TAIR_Arabidopsis**, Symbols: | aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO) | chr4:16973011-16977953 REVERSE

Match to Query 8496: 1794.838918 from(898.426735,2+) index(9158)
Title: Elution from: 82.218 to 82.218 scan no 12385 cid35.00 polarity:+
Data file 0-3_2.mgf

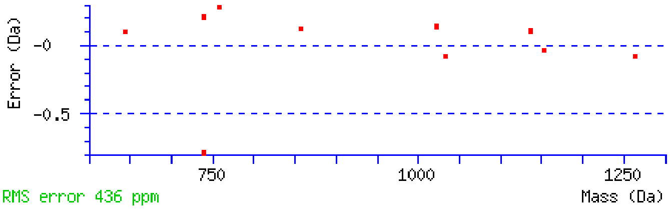
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

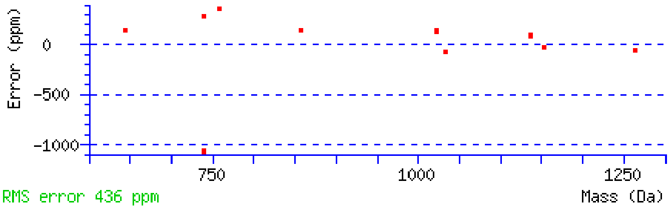


Monoisotopic mass of neutral peptide Mr(calc): 1794.8434
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.02
Matches : 14/162 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							16
2	231.1124	116.0598			213.1018	107.0545	V	1665.8111	833.4092	1647.7875	824.3974	1647.8005	824.4039	15
3	303.1465	152.0769			285.1359	143.0716	A	1565.7456	783.3764	1547.7220	774.3647	1547.7351	774.3712	14
4	433.1861	217.0967			415.1756	208.0914	E	1493.7115	747.3594	1475.6879	738.3476	1475.7009	738.3541	13
5	533.2516	267.1294			515.2410	258.1241	V	1363.6718	682.3396	1345.6483	673.3278	1345.6613	673.3343	12
6	633.3170	317.1622			615.3065	308.1569	V	***1263.6064***	632.3068	1245.5828	623.2950	1245.5958	623.3016	11
7	763.3697	382.1885	745.3461	373.1767	745.3591	373.1832	Q	1163.5409	582.2741	1145.5174	573.2623	1145.5304	573.2688	10
8	851.3987	426.2030	833.3752	417.1912	833.3882	417.1977	S	***1033.4883***	517.2478	1015.4647	508.2360	1015.4777	508.2425	9
9	939.4278	470.2175	921.4042	461.2057	921.4172	461.2123	S	945.4592	473.2333	927.4356	464.2215	927.4487	464.2280	8
10	1039.4932	520.2503	1021.4697	511.2385	1021.4827	511.2450	V	***857.4302***	429.2187	839.4066	420.2069	839.4196	420.2134	7
11	1153.5743	577.2908	1135.5508	568.2790	1135.5638	568.2855	L	***757.3647***	379.1860	739.3411	370.1742	739.3542	370.1807	6
12	1251.6241	626.3157	1233.6006	617.3039	1233.6136	617.3104	P	***643.2836***	322.1454	625.2600	313.1337	625.2731	313.1402	5
13	1367.6481	684.3277	1349.6245	675.3159	1349.6376	675.3224	D	545.2338	273.1205	527.2102	264.1088	527.2233	264.1153	4
14	1499.6856	750.3465	1481.6621	741.3347	1481.6751	741.3412	M	429.2098	215.1086	411.1863	206.0968			3
15	1647.7511	824.3792	1629.7275	815.3674	1629.7405	815.3739	F	297.1723	149.0898	279.1487	140.0780			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT4G35830.1





NCBI **BLAST** search of EVAEVVQSSVLPDMFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.5	1794.8434	-0.0045	EVAEVVQSSVLPDMFK
4.9	1794.8391	-0.0002	MDPVPVRCLLNSISR
2.1	1794.8365	0.0025	KGSMPLISKDIPCDAK
1.4	1794.8414	-0.0024	MCNETRILPVHYLK

Mascot: http://www.matrixscience.com/

AT4G35870.1

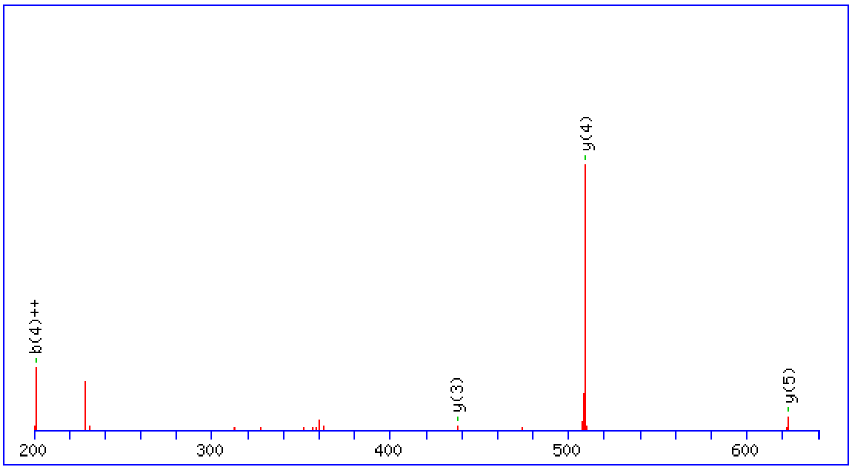
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLAVWK**
Found in **AT4G35870.1** in **TAIR_Arabidopsis**, Symbols: | similar to early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] (TAIR:AT3G21620.1); similar to hypothetical protein OsI_009692 [Oryza sativa (indica cultivar-group)] (GB:EAY88459.1); similar to un

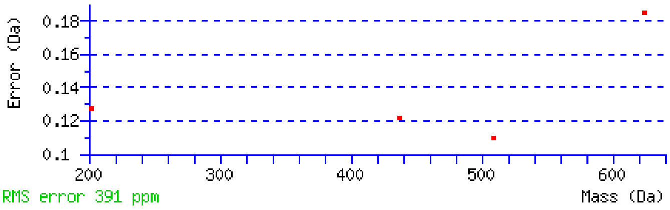
Match to Query 732: 736.435132 from(369.224842,2+) index(4168)
Title: Elution from: 38.882 to 38.882 scan no 5232 cid35.00 polarity:+
Data file D12h-3_2.mgf

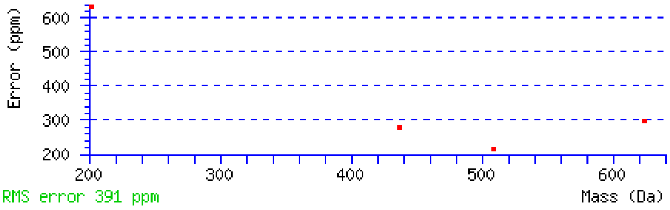
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 640 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 736.4348
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.003
Matches : 4/30 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	115.0884	58.0478	L					6
2	229.1695	115.0884	L	*623.3610*	312.1841	605.3374	303.1723	5
3	301.2036	151.1054	A	*509.2799*	255.1436	491.2563	246.1318	4
4	401.2691	201.1382	V	*437.2457*	219.1265	419.2221	210.1147	3
5	589.3425	295.1749	W	337.1803	169.0938	319.1567	160.0820	2
6			K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LLAVWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.6	736.4348	0.0004	LLAVWK
24.8	736.4348	0.0004	LIAWVK

AT4G35870.1

12.7	736.4348	0.0004	LILGWK
11.9	736.4348	0.0004	ILWLGK
11.9	736.4352	-0.0001	LIRPAR
11.9	736.4348	0.0004	LLLWGK
11.9	736.4348	0.0004	LLWIGK

AT4G35930.1

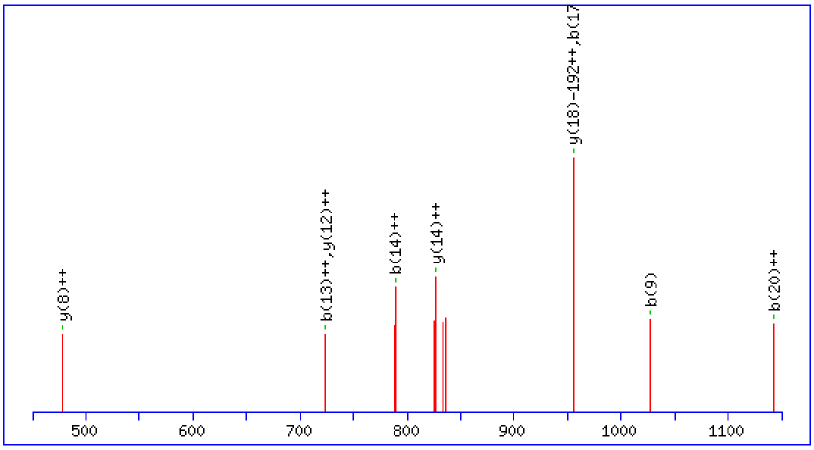
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSPLMLSPMGIVMQNTLLRTPK**
Found in **AT4G35930.1** in **TAIR_Arabidopsis**, Symbols: | Identical to F-box protein At4g35930 [Arabidopsis Thaliana] (GB:Q5XF11;GB:O65630); similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT1G61340.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN71843.1); similar to u

Match to Query 10179: 2531.245407 from(844.755745,3+) index(8491)
Title: Elution from: 76.034 to 76.034 scan no 11383 cid35.00 polarity:+
Data file D12h-3_2.mgf

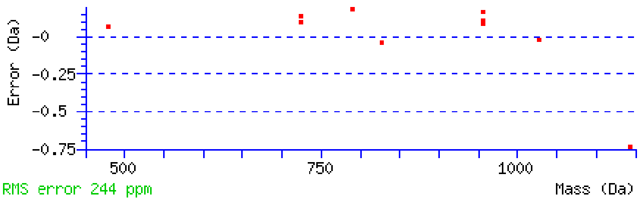
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

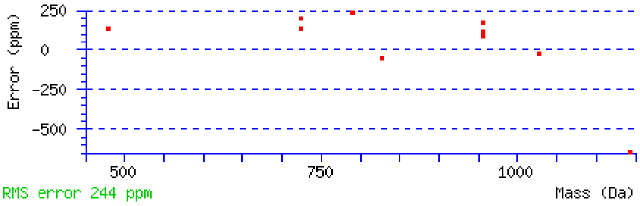


Monoisotopic mass of neutral peptide Mr(calc): 2531.2513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.0041
Matches : 10/420 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							22
2	219.1254	110.0663	201.1018	101.0545	201.1148	101.0610	S	2402.1695	1201.5884	2384.1459	1192.5766	2384.1589	1192.5831	21
3	317.1752	159.0912	299.1516	150.0794	299.1646	150.0859	P	2314.1404	1157.5738	2296.1168	1148.5620	2296.1298	1148.5686	20
4	431.2563	216.1318	413.2327	207.1200	413.2457	207.1265	L	2216.0906	1108.5489	2198.0670	1099.5371	2198.0800	1099.5437	19
5	579.2887	290.1480	561.2651	281.1362	561.2781	281.1427	M	2102.0095	1051.5084	2083.9859	1042.4966	2083.9989	1042.5031	18
6	693.3698	347.1885	675.3462	338.1767	675.3592	338.1833	L	1953.9771	977.4922	1935.9535	968.4804	1935.9665	968.4869	17
7	781.3989	391.2031	763.3753	382.1913	763.3883	382.1978	S	1839.8960	920.4516	1821.8724	911.4398	1821.8854	911.4463	16
8	879.4487	440.2280	861.4251	431.2162	861.4381	431.2227	P	1751.8669	876.4371	1733.8433	867.4253	1733.8563	867.4318	15
9	1027.4811	514.2442	1009.4575	505.2324	1009.4705	505.2389	M	1653.8171	827.4122	1635.7935	818.4004	1635.8065	818.4069	14
10	1085.4996	543.2534	1067.4760	534.2416	1067.4890	534.2482	G	1505.7847	753.3960	1487.7611	744.3842	1487.7741	744.3907	13
11	1199.5807	600.2940	1181.5571	591.2822	1181.5701	591.2887	I	1447.7662	724.3867	1429.7426	715.3749	1429.7556	715.3814	12
12	1299.6461	650.3267	1281.6226	641.3149	1281.6356	641.3214	V	1333.6851	667.3462	1315.6615	658.3344	1315.6745	658.3409	11
13	1447.6786	***724.3429***	1429.6550	715.3311	1429.6680	715.3376	M	1233.6196	617.3135	1215.5960	608.3017	1215.6091	608.3082	10
14	1577.7312	***789.3693***	1559.7076	780.3575	1559.7207	780.3640	Q	1085.5872	543.2972	1067.5636	534.2854	1067.5766	534.2920	9
15	1693.7682	847.3878	1675.7446	838.3760	1675.7577	838.3825	N	955.5345	478.2709	937.5110	469.2591	937.5240	469.2656	8
16	1795.8129	898.4101	1777.7894	889.3983	1777.8024	889.4048	T	839.4975	420.2524	821.4740	411.2406	821.4870	411.2471	7
17	1909.8940	***955.4507***	1891.8705	946.4389	1891.8835	946.4454	L	737.4528	369.2301	719.4293	360.2183	719.4423	360.2248	6
18	2023.9751	1012.4912	2005.9516	1003.4794	2005.9646	1003.4859	L	623.3717	312.1895	605.3482	303.1777	605.3612	303.1842	5
19	2184.0644	1092.5358	2166.0408	1083.5240	2166.0538	1083.5305	R	509.2906	255.1490	491.2671	246.1372	491.2801	246.1437	4
20	2286.1091	***1143.5582***	2268.0855	1134.5464	2268.0985	1134.5529	T	349.2014	175.1043	331.1778	166.0925	331.1908	166.0990	3
21	2384.1589	1192.5831	2366.1353	1183.5713	2366.1483	1183.5778	P	247.1567	124.0820	229.1331	115.0702			2
22							K	149.1069	75.0571	131.0833	66.0453			1

AT4G35930.1





NCBI **BLAST** search of KSPLMLSPMGIVMQNTLLRTPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.1	2531.2513	-0.0058	KSPLMLSPMGIVMQNTLLRTPK
8.1	2531.2451	0.0003	VETGMIKPGMVVTFAPTGLTTEVK
8.0	2531.2526	-0.0072	LSFLPELMESVKRAALEGAAEVK
4.0	2531.2438	0.0016	LEHFSKTTGKLVWNLTVSHFR
2.7	2531.2396	0.0058	AEIDAANMKVALGKYEEAIDILK
2.5	2531.2415	0.0039	EWKPKSNQKPVGHNPGVIGTPTK

Mascot: http://www.matrixscience.com/

AT4G36080.1

Mascot Search Results

Peptide View

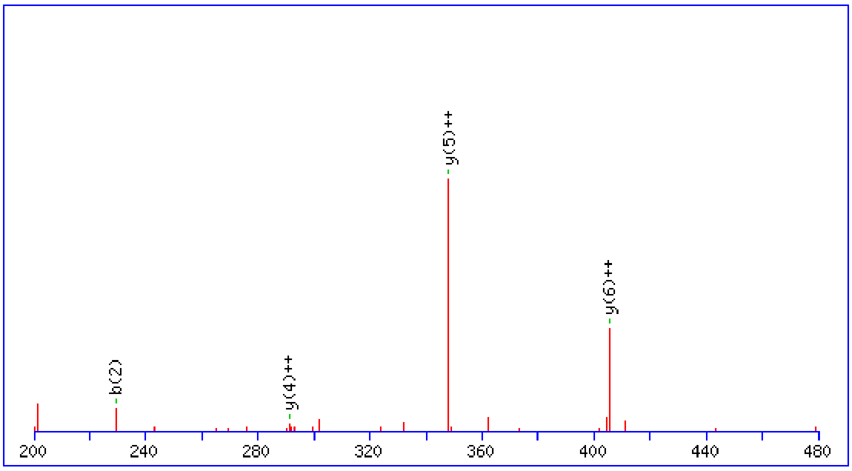
MS/MS Fragmentation of **LILHLFR**
Found in **AT4G36080.1** in **TAIR_Arabidopsis**, Symbols: | FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein | chr4:17059999-17077631 REVERSE

Match to Query 1963: 922.538046 from(308.519958,3+) index(667)
Title: Elution from: 11.542 to 11.542 scan no 953 cid35.00 polarity:+
Data file D1d-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

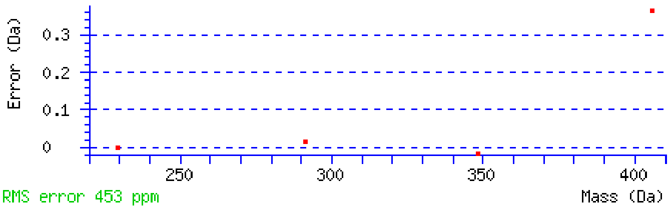
Or, Plot from 200 to 480 Da Full range

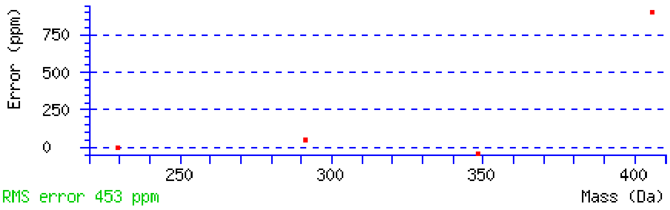
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 922.5397
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 16 **Expect:** 0.039
Matches : 4/36 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	115.0884	58.0478	L					7
2	229.1695	115.0884	I	809.4659	405.2366	791.4423	396.2248	6
3	343.2506	172.1289	L	695.3848	348.1960	677.3612	339.1842	5
4	483.3006	242.1539	H	581.3037	291.1555	563.2801	282.1437	4
5	597.3817	299.1945	L	441.2536	221.1305	423.2301	212.1187	3
6	745.4471	373.2272	F	327.1725	164.0899	309.1490	155.0781	2
7			R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of LILHLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.0	922.5397	-0.0016	LILHLFR
13.5	922.5374	0.0006	ILPRGNLK

AT4G36080.1

13.5	922.5374	0.0006	LLARPNVK
13.5	922.5374	0.0006	LLGKPLNR
3.3	922.5374	0.0006	KPLPTRAK
0.1	922.5374	0.0006	RKLPTPAK

AT4G36520.1

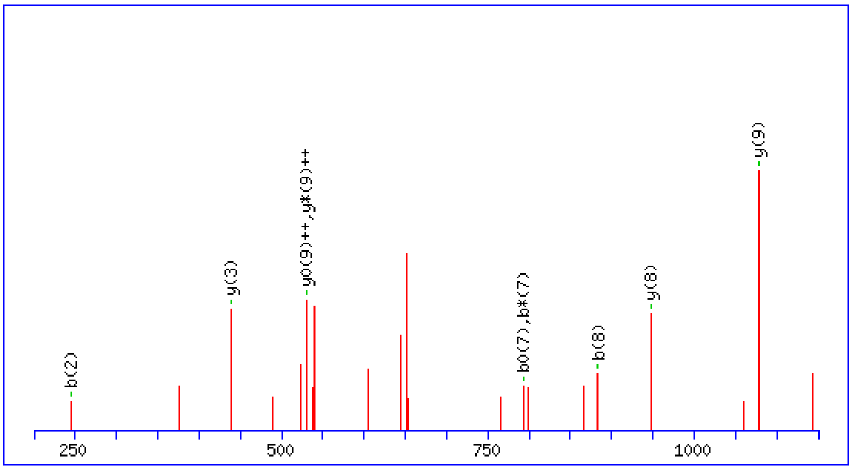
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEKACAEAREK**
Found in **AT4G36520.1** in **TAIR_Arabidopsis**, Symbols: | trichohyalin-related | chr4:17230592-17235438 REVERSE

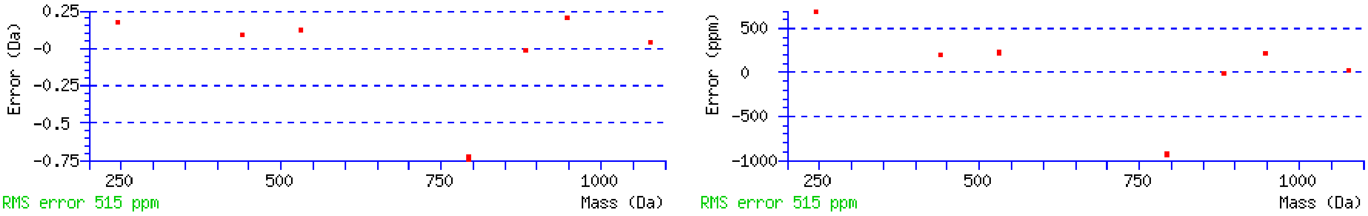
Match to Query 4804: 1320.608944 from(661.311748,2+) index(2810)
Title: Elution from: 30.178 to 30.178 scan no 3551 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1320.6050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.028
Matches : 9/112 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							11
2	**245.1280**	123.0676			227.1174	114.0624	E	1207.5312	604.2692	1189.5076	595.2574	1189.5206	595.2640	10
3	375.2170	188.1122	357.1935	179.1004	357.2065	179.1069	K	***1077.4916***	539.2494	1059.4680	530.2376	1059.4810	530.2441	9
4	447.2512	224.1292	429.2276	215.1174	429.2406	215.1239	A	***947.4025***	474.2049	929.3790	465.1931	929.3920	465.1996	8
5	609.2759	305.1416	591.2523	296.1298	591.2653	296.1363	C	875.3684	438.1878	857.3448	429.1760	857.3578	429.1826	7
6	681.3101	341.1587	663.2865	332.1469	663.2995	332.1534	A	713.3437	357.1755	695.3201	348.1637	695.3331	348.1702	6
7	811.3497	406.1785	793.3261	397.1667	793.3391	397.1732	E	641.3095	321.1584	623.2859	312.1466	623.2990	312.1531	5
8	**883.3838**	442.1956	865.3602	433.1838	865.3733	433.1903	A	511.2699	256.1386	493.2463	247.1268	493.2593	247.1333	4
9	1043.4731	522.2402	1025.4495	513.2284	1025.4625	513.2349	R	***439.2358***	220.1215	421.2122	211.1097	421.2252	211.1162	3
10	1173.5127	587.2600	1155.4891	578.2482	1155.5021	578.2547	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
11							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of LEKACAEAREK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G36520.1

Score	Mr(calc)	Delta	Sequence
25.5	1320.6050	0.0039	LEKACAEAREK
8.5	1320.6050	0.0039	LESLKQGMENR
6.1	1320.6120	-0.0031	KEEKEDPLYR
5.8	1320.6124	-0.0035	IENDTKEAARR
4.7	1320.6099	-0.0010	LRRSFMGYTR
3.8	1320.6120	-0.0031	LFENLREEEK
3.5	1320.6106	-0.0017	CKQLMELVER
2.6	1320.6061	0.0028	LKPGHYWYDK
1.8	1320.6099	-0.0010	SCNGLLHRFAK
1.6	1320.6120	-0.0030	ELTVVFAEENR

Mascot: http://www.matrixscience.com/

AT4G37170.1

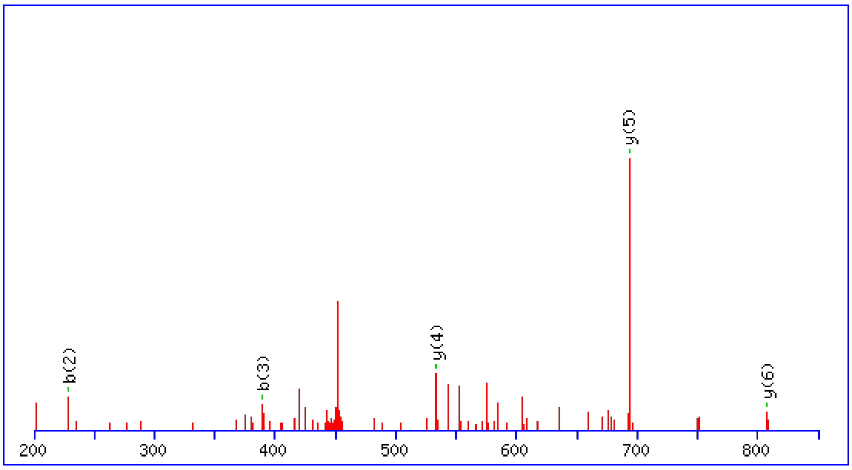
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLRMYAK**
Found in **AT4G37170.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr4:17498574-17500649 REVERSE

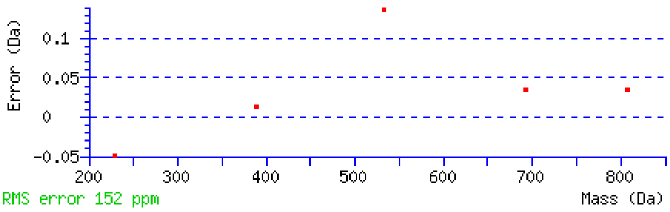
Match to Query 1502: 920.477910 from(461.246231,2+) index(3260)
Title: Elution from: 34.872 to 34.872 scan no 4188 cid35.00 polarity:+
Data file D1d-2_2.mgf

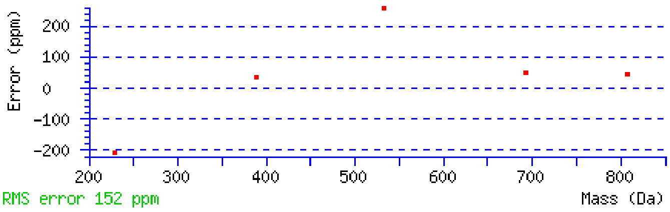
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 920.4780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.01
Matches : 5/68 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	115.0884	58.0478			L					7
2	**229.1695**	115.0884			L	***807.4042***	404.2057	789.3806	395.1939	6
3	**389.2587**	195.1330	371.2351	186.1212	R	***693.3231***	347.1652	675.2995	338.1534	5
4	537.2912	269.1492	519.2676	260.1374	M	***533.2338***	267.1205	515.2102	258.1088	4
5	701.3515	351.1794	683.3279	342.1676	Y	385.2014	193.1043	367.1778	184.0925	3
6	773.3857	387.1965	755.3621	378.1847	A	221.1410	111.0741	203.1174	102.0624	2
7					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LLRMYAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	920.4780	-0.0001	LLRMYAK

AT4G37170.1

Mascot: http://www.matrixscience.com/

AT4G37300.1

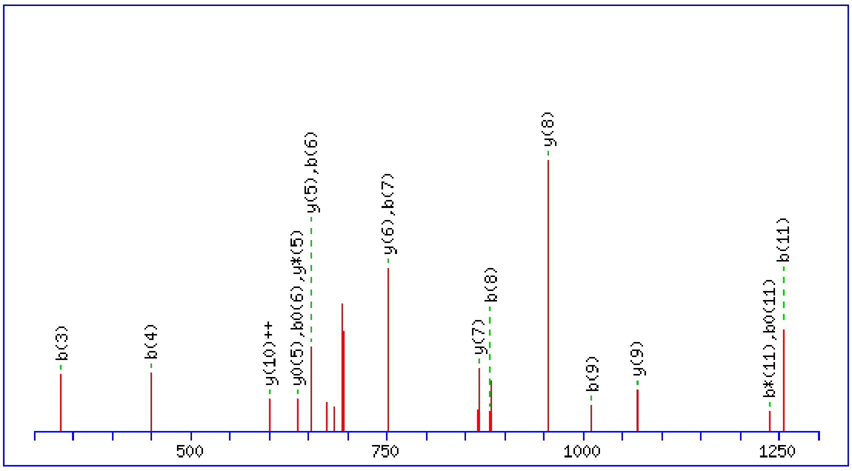
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDEISDPEQQIK**
Found in **AT4G37300.1** in **TAIR_Arabidopsis**, Symbols: MEE59 | MEE59 (maternal effect embryo arrest 59) | chr4:17554799-17555492 FORWARD

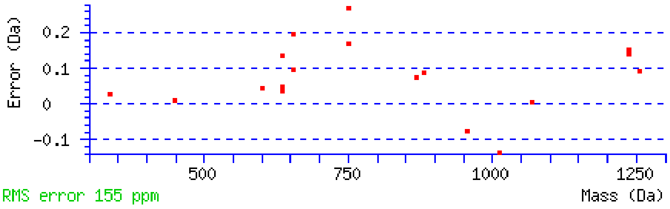
Match to Query 5400: 1402.600940 from(702.307746,2+) index(2503)
Title: Elution from: 27.590 to 27.590 scan no 3200 cid35.00 polarity:+
Data file 0-1_2.mgf

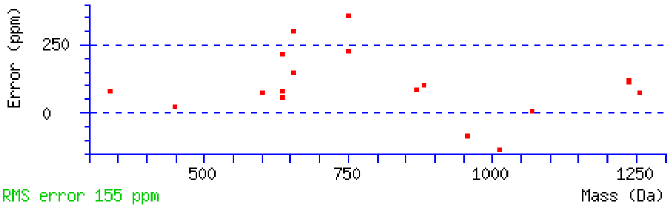
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1402.6022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 7.5e-006
Matches : 18/108 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	205.0603	103.0338			187.0498	94.0285	D	1315.5804	658.2939	1297.5569	649.2821	1297.5699	649.2886	11
3	***335.0999***	168.0536			317.0894	159.0483	E	1199.5565	600.2819	1181.5329	591.2701	1181.5459	591.2766	10
4	***449.1810***	225.0942			431.1705	216.0889	I	**1069.5168**	535.2621	1051.4933	526.2503	1051.5063	526.2568	9
5	537.2101	269.1087			519.1995	260.1034	S	**955.4357**	478.2215	937.4122	469.2097	937.4252	469.2162	8
6	***653.2341***	327.1207			635.2235	318.1154	D	**867.4067**	434.2070	849.3831	425.1952	849.3961	425.2017	7
7	***751.2839***	376.1456			733.2733	367.1403	P	**751.3827**	376.1950	733.3591	367.1832	733.3721	367.1897	6
8	***881.3235***	441.1654			863.3129	432.1601	E	**653.3329**	327.1701	635.3093	318.1583	635.3223	318.1648	5
9	***1011.3762***	506.1917	993.3526	497.1799	993.3656	497.1864	Q	523.2933	262.1503	505.2697	253.1385			4
10	1141.4288	571.2180	1123.4052	562.2062	1123.4182	562.2128	Q	393.2406	197.1239	375.2170	188.1122			3
11	***1255.5099***	628.2586	1237.4863	619.2468	1237.4993	619.2533	I	263.1880	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SDEISDPEQQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G37300.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.6	1402.6022	-0.0013	SDEISDPEQQIK
10.5	1402.6045	-0.0035	EEQELAPFDPSK
8.0	1402.6022	-0.0013	ENEISKEDAEPK
3.5	1402.6002	0.0008	SNCHLLEENIR
0.5	1402.6024	-0.0015	LDYAKEHHMNK
0.2	1402.6049	-0.0039	DSQHIDEKASQK

AT4G37910.1

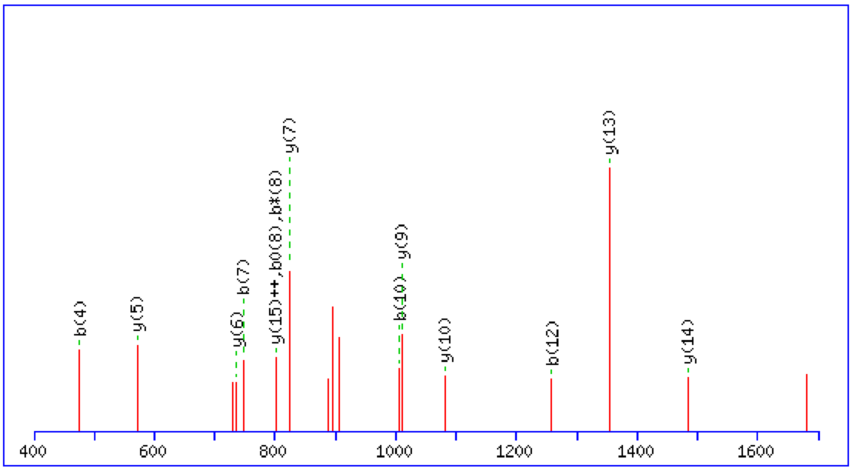
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IINEPTAAALSYGMNNK**
Found in **AT4G37910.1** in **TAIR_Arabidopsis**, Symbols: MTHSC70-1 | MTHSC70-1 (mitochondrial heat shock protein 70-1); ATP binding / unfolded protein binding | chr4:17825362-17828093 REVERSE

Match to Query 8727: 1826.832968 from(914.423760,2+) index(5998)
Title: Elution from: 52.866 to 52.866 scan no 7588 cid35.00 polarity:+
Data file D12h-1_2.mgf

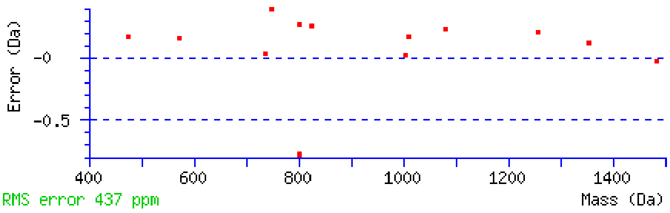
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

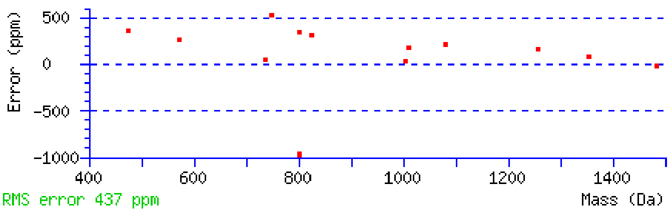


Monoisotopic mass of neutral peptide Mr(calc): 1826.8359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.1e-005
Matches : 14/170 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							17
2	229.1695	115.0884					I	1713.7621	857.3847	1695.7385	848.3729	1695.7515	848.3794	16
3	345.2065	173.1069	327.1829	164.0951			N	1599.6810	800.3441	1581.6574	791.3323	1581.6704	791.3389	15
4	**475.2461**	238.1267	457.2225	229.1149	457.2355	229.1214	E	***1483.6440***	742.3256	1465.6204	733.3138	1465.6334	733.3204	14
5	573.2959	287.1516	555.2723	278.1398	555.2853	278.1463	P	***1353.6044***	677.3058	1335.5808	668.2940	1335.5938	668.3005	13
6	675.3406	338.1739	657.3170	329.1622	657.3300	329.1687	T	1255.5546	628.2809	1237.5310	619.2691	1237.5440	619.2756	12
7	**747.3748**	374.1910	729.3512	365.1792	729.3642	365.1857	A	1153.5099	577.2586	1135.4863	568.2468	1135.4993	568.2533	11
8	819.4089	410.2081	801.3853	401.1963	801.3983	401.2028	A	***1081.4757***	541.2415	1063.4521	532.2297	1063.4651	532.2362	10
9	891.4431	446.2252	873.4195	437.2134	873.4325	437.2199	A	***1009.4416***	505.2244	991.4180	496.2126	991.4310	496.2191	9
10	**1005.5242**	503.2657	987.5006	494.2539	987.5136	494.2604	L	937.4074	469.2073	919.3838	460.1956	919.3968	460.2021	8
11	1093.5532	547.2802	1075.5296	538.2685	1075.5427	538.2750	S	***823.3263***	412.1668	805.3027	403.1550	805.3157	403.1615	7
12	**1257.6136**	629.3104	1239.5900	620.2986	1239.6030	620.3051	Y	***735.2973***	368.1523	717.2737	359.1405			6
13	1315.6321	658.3197	1297.6085	649.3079	1297.6215	649.3144	G	***571.2369***	286.1221	553.2133	277.1103			5
14	1447.6696	724.3384	1429.6460	715.3266	1429.6590	715.3332	M	513.2184	257.1128	495.1948	248.1010			4
15	1563.7066	782.3569	1545.6830	773.3451	1545.6960	773.3517	N	381.1809	191.0941	363.1573	182.0823			3
16	1679.7436	840.3754	1661.7200	831.3636	1661.7330	831.3702	N	265.1439	133.0756	247.1203	124.0638			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT4G37910.1





NCBI **BLAST** search of IINEPTAAALSYGMNNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.3	1826.8359	-0.0030	IINEPTAAALSYGMNNK
3.3	1826.8381	-0.0052	IIVDGVMAHYEELFR
2.1	1826.8299	0.0031	FPETLDLAPYVSGGSEK

Mascot: http://www.matrixscience.com/

AT4G37930.1

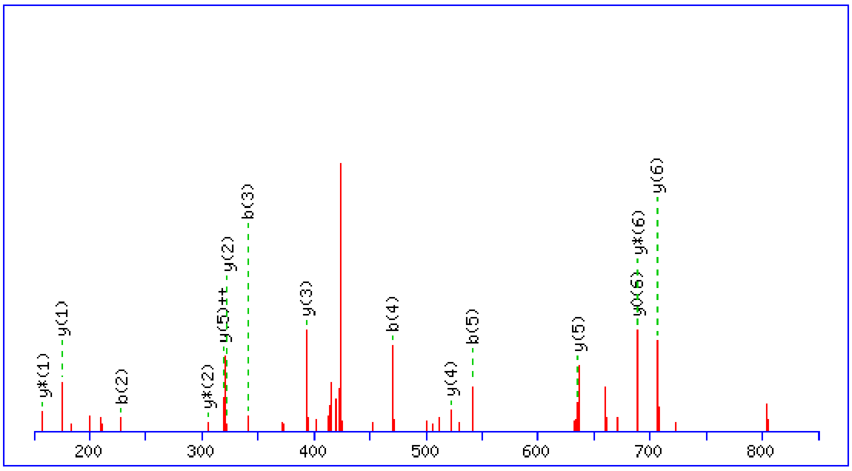
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RALEAFR**
Found in **AT4G37930.1** in **TAIR_Arabidopsis**, Symbols: STM, SHMT1, SHM1 | SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); glycine hydroxymethyltransferase/ poly(U) binding | chr4:17831885-17834736 REVERSE

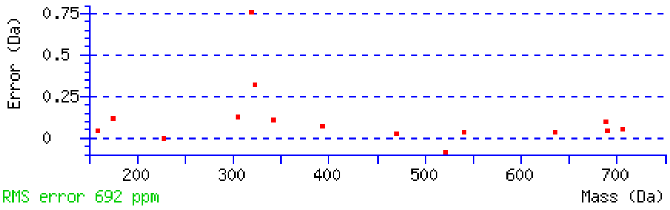
Match to Query 1330: 861.482366 from(431.748459,2+) index(1007)
Title: Elution from: 16.090 to 16.090 scan no 1430 cid35.00 polarity:+
Data file D6h-1_3.mgf

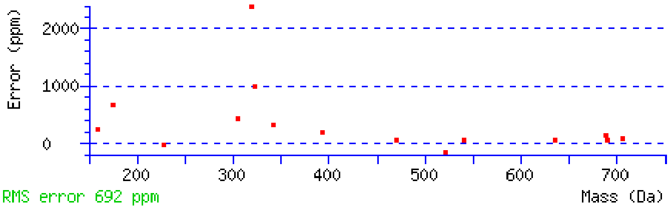
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 861.4821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00041
Matches : 16/60 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							7
2	**228.1455**	114.5764	211.1190	106.0631			A	***706.3883***	353.6978	689.3617	345.1845	688.3777	344.6925	6
3	**341.2296**	171.1184	324.2030	162.6051			L	***635.3511***	318.1792	618.3246	309.6659	617.3406	309.1739	5
4	**470.2722**	235.6397	453.2456	227.1264	452.2616	226.6344	E	***522.2671***	261.6372	505.2405	253.1239	504.2565	252.6319	4
5	**541.3093**	271.1583	524.2827	262.6450	523.2987	262.1530	A	***393.2245***	197.1159	376.1979	188.6026			3
6	**688.3777**	344.6925	671.3511	336.1792	670.3671	335.6872	F	***322.1874***	161.5973	305.1608	153.0840			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of RALEAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.2	861.4821	0.0003	RALEAFR
27.8	861.4821	0.0003	ARIEAFR

AT4G37930.1

13.3	861.4821	0.0003	KVNAGFAR
8.1	861.4821	0.0003	GFNKALGR
6.6	861.4821	0.0003	GLRDVFR
4.7	861.4821	0.0003	RFPSLSR
0.5	861.4821	0.0003	RGFEVVR
0.5	861.4821	0.0003	RLDGFVR
0.5	861.4821	0.0003	RVFDGLR
0.4	861.4821	0.0003	GFQGGIKR

AT4G37980.1

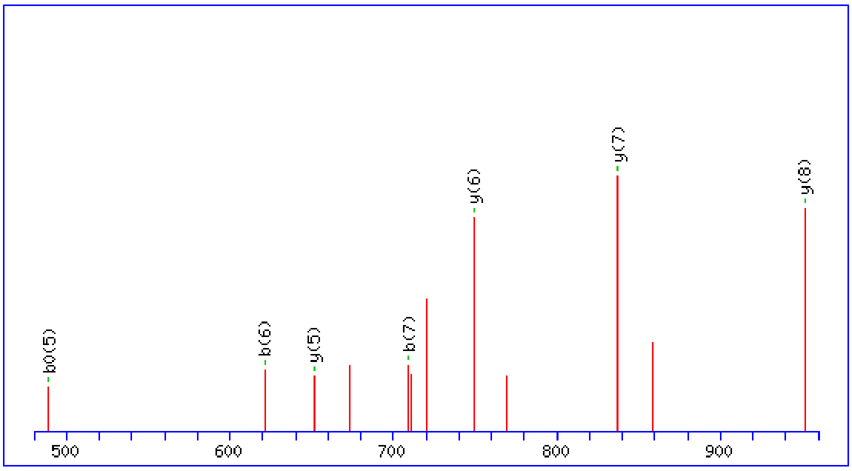
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DESGILSPFSFSR**
Found in **AT4G37980.1** in **TAIR_Arabidopsis**, Symbols: ELI3-1 | ELI3-1 (ELICITOR-ACTIVATED GENE 3); binding / catalytic/ oxidoreductase/ zinc ion binding | chr4:17852664-17854296 FORWARD

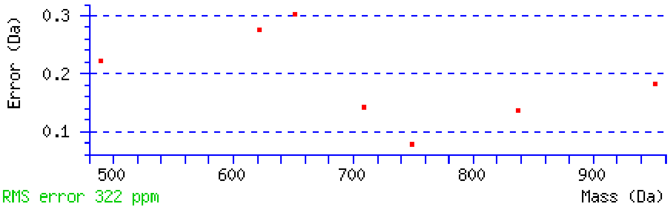
Match to Query 6005: 1456.640620 from(729.327586,2+) index(9376)
Title: Elution from: 83.794 to 83.794 scan no 12649 cid35.00 polarity:+
Data file C7-2_2.mgf

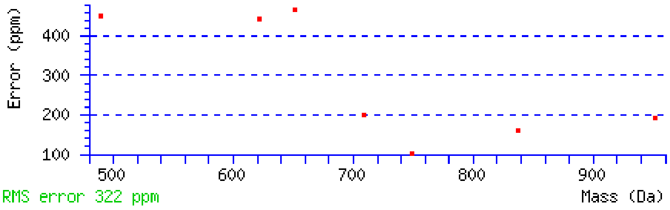
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 480 to 960 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1456.6411
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0087
Matches : 7/118 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							13
2	247.0709	124.0391	229.0603	115.0338	E	1341.6244	671.3158	1323.6008	662.3040	1323.6138	662.3105	12
3	335.0999	168.0536	317.0894	159.0483	S	1211.5847	606.2960	1193.5612	597.2842	1193.5742	597.2907	11
4	393.1184	197.0629	375.1079	188.0576	G	1123.5557	562.2815	1105.5321	553.2697	1105.5451	553.2762	10
5	507.1995	254.1034	489.1890	245.0981	I	1065.5372	533.2722	1047.5136	524.2604	1047.5266	524.2669	9
6	**621.2806**	311.1440	603.2701	302.1387	L	***951.4561***	476.2317	933.4325	467.2199	933.4455	467.2264	8
7	**709.3097**	355.1585	691.2991	346.1532	S	***837.3750***	419.1911	819.3514	410.1793	819.3644	410.1858	7
8	807.3595	404.1834	789.3489	395.1781	P	***749.3459***	375.1766	731.3223	366.1648	731.3353	366.1713	6
9	955.4250	478.2161	937.4144	469.2108	F	***651.2961***	326.1517	633.2725	317.1399	633.2856	317.1464	5
10	1043.4540	522.2306	1025.4435	513.2254	S	503.2307	252.1190	485.2071	243.1072	485.2201	243.1137	4
11	1191.5195	596.2634	1173.5089	587.2581	F	415.2016	208.1044	397.1780	199.0926	397.1910	199.0992	3
12	1279.5485	640.2779	1261.5380	631.2726	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
13					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of DESGILSPFSFSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT4G37980.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.6	1456.6411	-0.0004	DESGILSPFSFSR
6.8	1456.6363	0.0043	VFFTTMSPTHTR
3.4	1456.6444	-0.0038	EDVAKNMAKYEK
1.8	1456.6388	0.0018	ELSGEEALVNDHK

AT4G38410.1

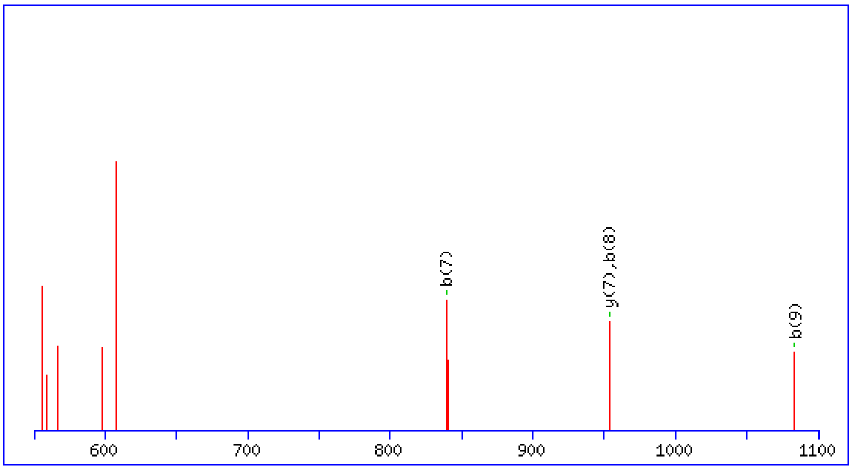
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCGMFDFLKK**
Found in **AT4G38410.1** in **TAIR_Arabidopsis**, Symbols: | dehydrin, putative | chr4:17981019-17981598 FORWARD

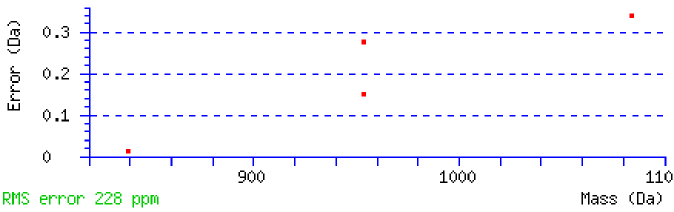
Match to Query 4154: 1230.515108 from(616.264830,2+) index(3828)
Title: Elution from: 35.354 to 35.354 scan no 4789 cid35.00 polarity:+
Data file 0-2_3.mgf

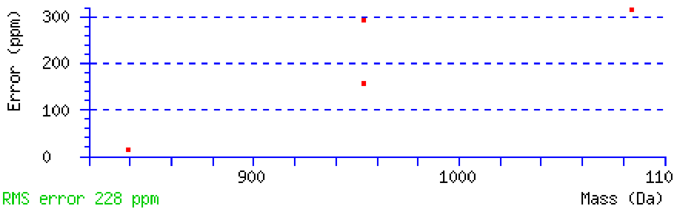
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1230.5187
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.025
Matches : 4/114 fragment ions using 4 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							10
2	221.0505	111.0289					C	1173.5075	587.2574	1155.4839	578.2456	1155.4970	578.2521	9
3	279.0690	140.0381					G	1011.4828	506.2450	993.4592	497.2333	993.4723	497.2398	8
4	427.1014	214.0544					M	953.4643	477.2358	935.4407	468.2240	935.4538	468.2305	7
5	575.1669	288.0871					F	805.4319	403.2196	787.4083	394.2078	787.4213	394.2143	6
6	691.1909	346.0991			673.1803	337.0938	D	657.3664	329.1869	639.3428	320.1751	639.3559	320.1816	5
7	***839.2563***	420.1318			821.2457	411.1265	F	541.3425	271.1749	523.3189	262.1631			4
8	***953.3374***	477.1723			935.3268	468.1671	L	393.2770	197.1421	375.2534	188.1303			3
9	***1083.4264***	542.2169	1065.4029	533.2051	1065.4159	533.2116	K	279.1959	140.1016	261.1723	131.0898			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GCGMFDFLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G38410.1

Score	Mr(calc)	Delta	Sequence
20.8	1230.5187	-0.0036	GCGMFDFLKK
19.7	1230.5136	0.0015	MQHQGPSREK
5.5	1230.5165	-0.0014	FRESMKMEK
5.5	1230.5136	0.0015	MAQNHQTQQK
5.5	1230.5131	0.0020	MSRAFYADEK
5.5	1230.5132	0.0020	NPMYTYREK
4.3	1230.5132	0.0020	SHTSWMLDPK
3.7	1230.5132	0.0020	NCYNFSLTAK
2.9	1230.5170	-0.0018	MSSCSRTRTK
2.3	1230.5154	-0.0003	GNAYWVYMSK

AT4G38500.1

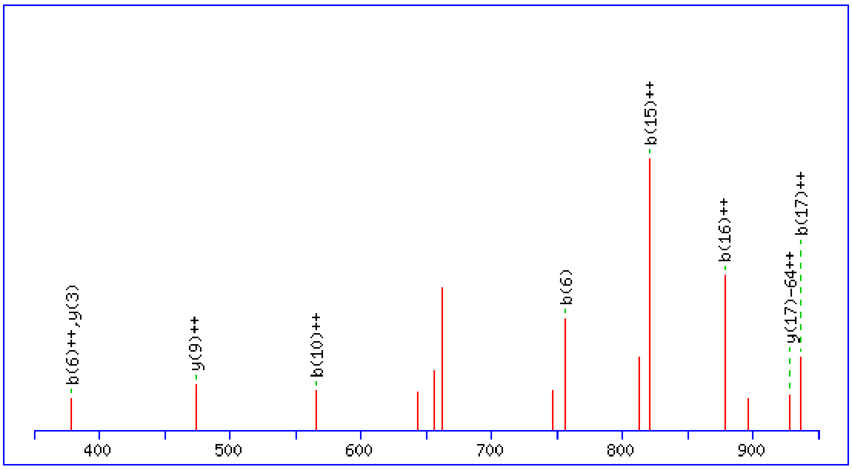
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VHCGFMPRGGAEMSSLDK**
Found in **AT4G38500.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G28240.1); similar to Os06g0724300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001058611.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47423.1); similar to

Match to Query 9855: 2018.812545 from(673.944791,3+) index(6945)
Title: Elution from: 60.302 to 60.302 scan no 8872 cid35.00 polarity:+
Data file D6h-1_1.mgf

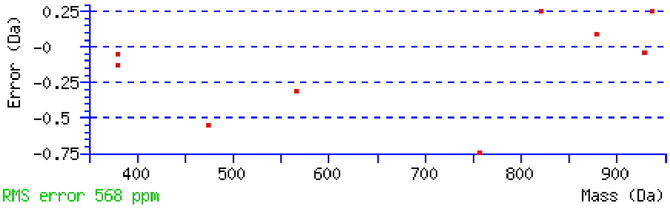
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

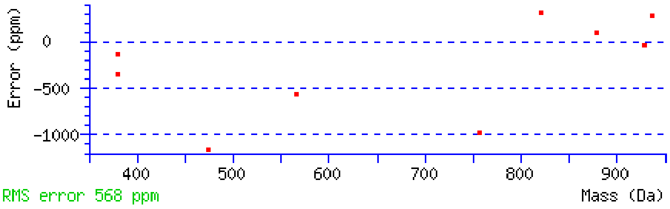


Monoisotopic mass of neutral peptide Mr(calc): 2018.8067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.011
Matches : 9/252 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							18
2	241.1227	121.0650					H	1919.7485	960.3779	1901.7250	951.3661	1901.7380	951.3726	17
3	403.1475	202.0774					C	1779.6985	890.3529	1761.6749	881.3411	1761.6880	881.3476	16
4	461.1660	231.0866					G	1617.6738	809.3405	1599.6502	800.3287	1599.6632	800.3353	15
5	609.2314	305.1193					F	1559.6553	780.3313	1541.6317	771.3195	1541.6447	771.3260	14
6	757.2638	***379.1356***					M	1411.5899	706.2986	1393.5663	697.2868	1393.5793	697.2933	13
7	855.3136	428.1605					P	1263.5574	632.2823	1245.5338	623.2706	1245.5469	623.2771	12
8	1015.4029	508.2051	997.3793	499.1933			R	1165.5076	583.2574	1147.4840	574.2457	1147.4971	574.2522	11
9	1073.4214	537.2143	1055.3978	528.2025			G	1005.4184	503.2128	987.3948	494.2010	987.4078	494.2075	10
10	1131.4399	***566.2236***	1113.4163	557.2118			G	947.3999	474.2036	929.3763	465.1918	929.3893	465.1983	9
11	1203.4740	602.2407	1185.4505	593.2289			A	889.3814	445.1943	871.3578	436.1825	871.3708	436.1890	8
12	1333.5137	667.2605	1315.4901	658.2487	1315.5031	658.2552	E	817.3472	409.1773	799.3236	400.1655	799.3367	400.1720	7
13	1465.5512	733.2792	1447.5276	724.2674	1447.5406	724.2739	M	687.3076	344.1574	669.2840	335.1456	669.2970	335.1522	6
14	1553.5803	777.2938	1535.5567	768.2820	1535.5697	768.2885	S	555.2701	278.1387	537.2465	269.1269	537.2595	269.1334	5
15	1641.6093	***821.3083***	1623.5857	812.2965	1623.5987	812.3030	S	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
16	1755.6904	***878.3488***	1737.6668	869.3371	1737.6798	869.3436	L	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
17	1871.7144	***936.3608***	1853.6908	927.3490	1853.7038	927.3556	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
18							K	149.1069	75.0571	131.0833	66.0453			1

AT4G38500.1





NCBI **BLAST** search of VHCGFMPRGGAEMSSLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
24.0	2018.8067	0.0058	VHCGFMPRGGAEMSSLDK	Oxidation M6 98.65%
22.4	2018.8121	0.0004	SMKDCGSPIADEMIGDIK	
15.2	2018.8101	0.0025	ITNDDDDDIDFAFEIGGK	
11.8	2018.8170	-0.0045	QIGPGMFQQMTEQVCDK	
11.1	2018.8114	0.0011	SPLYSQMESGTCHQKDK	
5.4	2018.8065	0.0060	MNLCGDSEILKEDDNTK	
5.4	2018.8067	0.0058	VHCGFMPRGGAEMSSLDK	Oxidation M13 1.35%
3.8	2018.8105	0.0020	GLDQTHKSEEAETGHDEL	
3.3	2018.8097	0.0029	NMEMEKAIEFYMRMK	
3.0	2018.8155	-0.0029	EKNEWSDGWNSNGGGTKK	

AT4G38510.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVVQVFEGTSGIDNK**
Found in **AT4G38510.1** in **TAIR_Arabidopsis**, Symbols: | (VACUOLAR ATP SYNTHASE SUBUNIT B2); hydrogen ion transporting ATP synthase, rotational mechanism | chr4:18011149-18014783 REVERSE

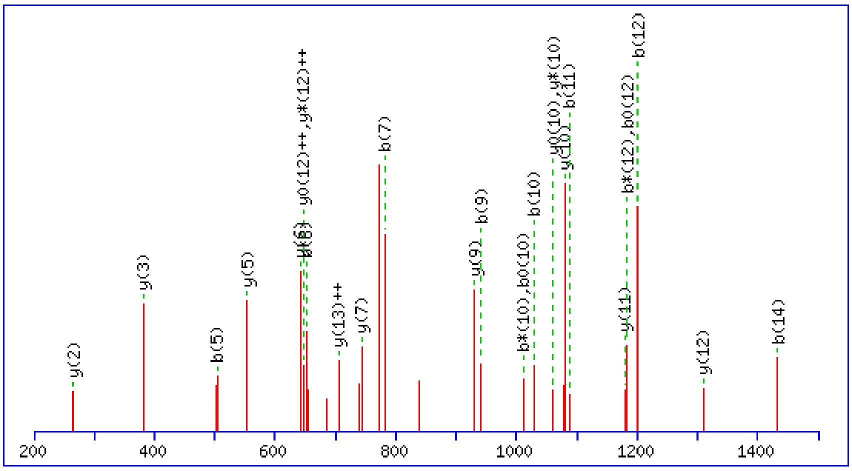
Match to Query 6644: 1580.736526 from(791.375539,2+) index(5037)
Title: Elution from: 46.645 to 46.645 scan no 6450 cid35.00 polarity:+
Data file D12h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

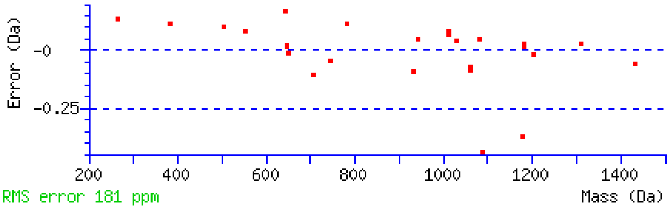
Label all possible matches ○ Label matches used for scoring ●

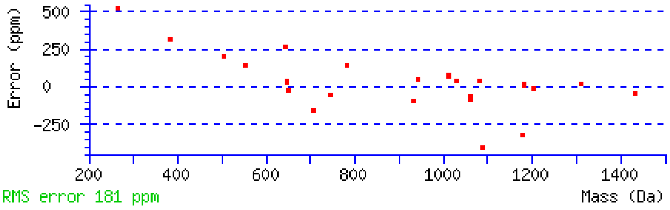
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1580.7406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 5e-010
Matches : 26/146 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							15
2	173.1069	87.0571					V	1509.7138	755.3605	1491.6902	746.3487	1491.7032	746.3553	14
3	273.1723	137.0898					V	1409.6483	705.3278	1391.6248	696.3160	1391.6378	696.3225	13
4	403.2250	202.1161	385.2014	193.1043			Q	***1309.5829***	655.2951	1291.5593	646.2833	1291.5723	646.2898	12
5	***503.2904***	252.1488	485.2668	243.1371			V	***1179.5302***	590.2688	1161.5067	581.2570	1161.5197	581.2635	11
6	***651.3559***	326.1816	633.3323	317.1698			F	***1079.4648***	540.2360	1061.4412	531.2242	1061.4542	531.2308	10
7	***781.3955***	391.2014	763.3719	382.1896	763.3849	382.1961	E	***931.3993***	466.2033	913.3758	457.1915	913.3888	457.1980	9
8	839.4140	420.2106	821.3904	411.1988	821.4034	411.2054	G	801.3597	401.1835	783.3361	392.1717	783.3492	392.1782	8
9	***941.4587***	471.2330	923.4351	462.2212	923.4481	462.2277	T	***743.3412***	372.1742	725.3176	363.1625	725.3307	363.1690	7
10	***1029.4878***	515.2475	1011.4642	506.2357	1011.4772	506.2422	S	***641.2965***	321.1519	623.2729	312.1401	623.2859	312.1466	6
11	***1087.5063***	544.2568	1069.4827	535.2450	1069.4957	535.2515	G	***553.2674***	277.1374	535.2439	268.1256	535.2569	268.1321	5
12	***1201.5874***	601.2973	1183.5638	592.2855	1183.5768	592.2920	I	495.2489	248.1281	477.2254	239.1163	477.2384	239.1228	4
13	1317.6113	659.3093	1299.5878	650.2975	1299.6008	650.3040	D	***381.1678***	191.0876	363.1443	182.0758	363.1573	182.0823	3
14	***1433.6483***	717.3278	1415.6248	708.3160	1415.6378	708.3225	N	***265.1439***	133.0756	247.1203	124.0638			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT4G38510.1

NCBI **BLAST** search of AVVQVFEGTSGIDNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
102.8	1580.7406	-0.0041	AVVQVFEGTSGIDNK
6.7	1580.7407	-0.0042	LLNSESQAYSLPNK
5.2	1580.7337	0.0028	CSEIVLKNERGEK
5.2	1580.7384	-0.0019	AGRSSESDLLALTDK
3.5	1580.7337	0.0028	MTKNIASDNVPLSR
3.1	1580.7333	0.0033	MTKEFAEELNLPK
2.9	1580.7393	-0.0028	EMRILMVGLDNSGK
2.4	1580.7406	-0.0041	DTIFAVNEQLTNAK
2.3	1580.7337	0.0029	VDEGMQLLREISR
1.3	1580.7380	-0.0014	EKTLEFAEELTEK

AT4G38680.1

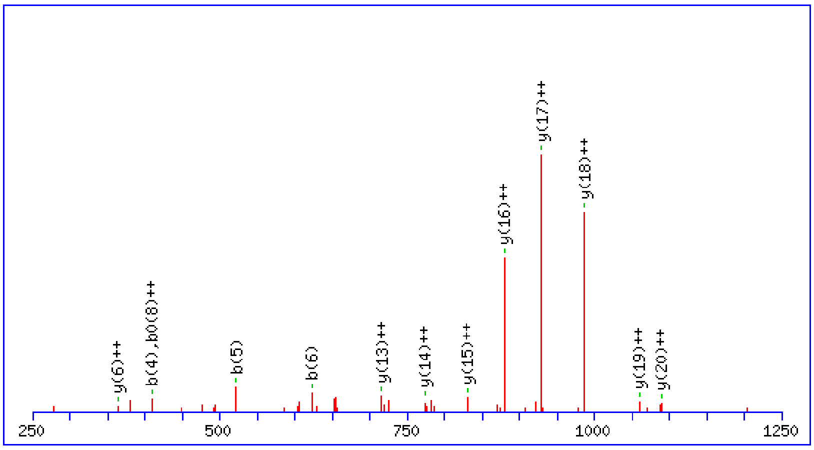
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGFITPDDGGDDLFVHQSSIR**
Found in **AT4G38680.1** in **TAIR_Arabidopsis**, Symbols: CSDP2, GRP2 | CSDP2/GRP2 (COLD SHOCK DOMAIN PROTEIN 2, GLYCINE RICH PROTEIN 2); nucleic acid binding | chr4:18072234-18072845 REVERSE

Match to Query 9870: 2379.115335 from(794.045721,3+) index(8806)
Title: Elution from: 79.570 to 79.570 scan no 12091 cid35.00 polarity:+
Data file D12h-3_3.mgf

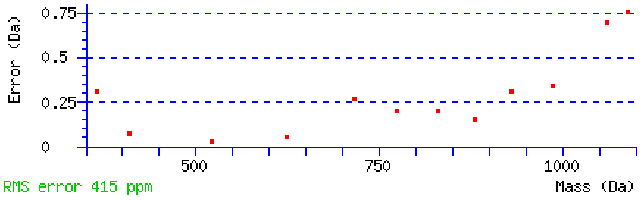
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

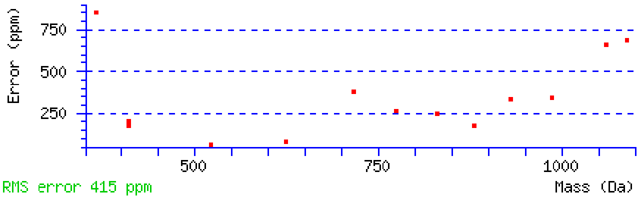


Monoisotopic mass of neutral peptide Mr(calc): 2379.1132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 2.1e-005
Matches : 13/204 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							22
2	205.0972	103.0522					F	2323.0990	1162.0531	2306.0724	1153.5398	2305.0884	1153.0478	21
3	262.1186	131.5629					G	2176.0305	1088.5189	2159.0040	1080.0056	2158.0200	1079.5136	20
4	**409.1870**	205.0972					F	2119.0091	1060.0082	2101.9825	1051.4949	2100.9985	1051.0029	19
5	**522.2711**	261.6392					I	1971.9407	986.4740	1954.9141	977.9607	1953.9301	977.4687	18
6	**623.3188**	312.1630			605.3082	303.1577	T	1858.8566	929.9319	1841.8300	921.4187	1840.8460	920.9267	17
7	720.3715	360.6894			702.3610	351.6841	P	1757.8089	879.4081	1740.7824	870.8948	1739.7984	870.4028	16
8	835.3985	418.2029			817.3879	409.1976	D	1660.7562	830.8817	1643.7296	822.3684	1642.7456	821.8764	15
9	950.4254	475.7164			932.4149	466.7111	D	1545.7292	773.3682	1528.7027	764.8550	1527.7186	764.3630	14
10	1007.4469	504.2271			989.4363	495.2218	G	1430.7023	715.8548	1413.6757	707.3415	1412.6917	706.8495	13
11	1064.4684	532.7378			1046.4578	523.7325	G	1373.6808	687.3440	1356.6543	678.8308	1355.6702	678.3388	12
12	1179.4953	590.2513			1161.4847	581.2460	D	1316.6593	658.8333	1299.6328	650.3200	1298.6488	649.8280	11
13	1294.5222	647.7648			1276.5117	638.7595	D	1201.6324	601.3198	1184.6058	592.8066	1183.6218	592.3146	10
14	1407.6063	704.3068			1389.5957	695.3015	L	1086.6055	543.8064	1069.5789	535.2931	1068.5949	534.8011	9
15	1554.6747	777.8410			1536.6642	768.8357	F	973.5214	487.2643	956.4948	478.7511	955.5108	478.2591	8
16	1653.7431	827.3752			1635.7326	818.3699	V	826.4530	413.7301	809.4264	405.2169	808.4424	404.7248	7
17	1790.8020	895.9047			1772.7915	886.8994	H	727.3846	364.1959	710.3580	355.6826	709.3740	355.1906	6
18	1918.8606	959.9339	1901.8341	951.4207	1900.8501	950.9287	Q	590.3257	295.6665	573.2991	287.1532	572.3151	286.6612	5
19	2005.8926	1003.4500	1988.8661	994.9367	1987.8821	994.4447	S	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
20	2092.9247	1046.9660	2075.8981	1038.4527	2074.9141	1037.9607	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2206.0087	1103.5080	2188.9822	1094.9947	2187.9982	1094.5027	I	288.2030	144.6051	271.1765	136.0919			2
22							R	175.1190	88.0631	158.0924	79.5498			1

AT4G38680.1





NCBI **BLAST** search of GFGFITPDDGGDDLFVHQSSIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.6	2379.1132	0.0021	GFGFITPDDGGDDLFVHQSSIR
4.1	2379.1167	-0.0014	MPSYEPVLTEFFWDMVTKK
1.4	2379.1214	-0.0061	GFGYPGPTTMMQMPAFSLPPPR
1.1	2379.1106	0.0047	EWGFFYVTNHGVSRDMYKK
0.3	2379.1129	0.0024	AMMLETVAAVPGMVGGMLLHCK

Mascot: http://www.matrixscience.com/

AT4G38740.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSSSGKPTKPVVVADCGQLS**
Found in **AT4G38740.1** in **TAIR_Arabidopsis**, Symbols: ROC1 | ROC1 (rotamase CyP 1); peptidyl-prolyl cis-trans isomerase | chr4:18083614-18084132 REVERSE

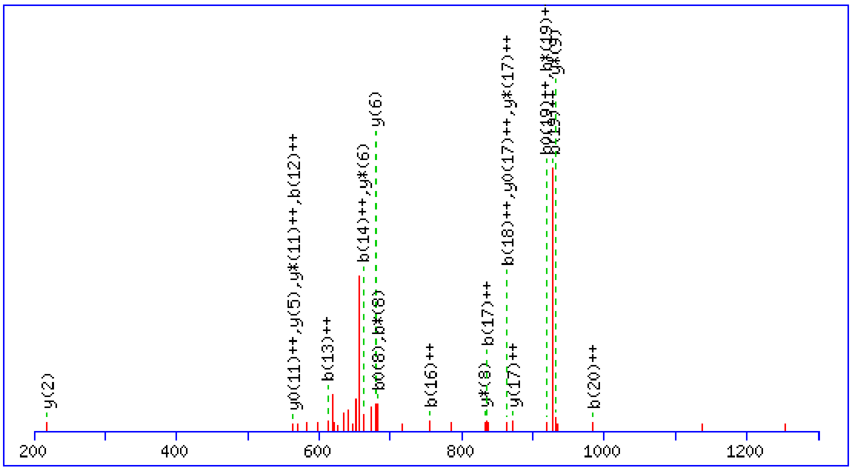
Match to Query 9676: 2072.052624 from(691.691484,3+) index(2277)
Title: Elution from: 26.905 to 26.905 scan no 2958 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

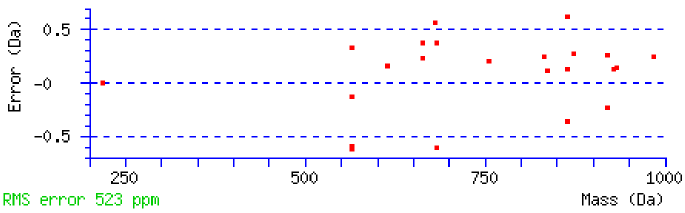
Show Y-axis ☐

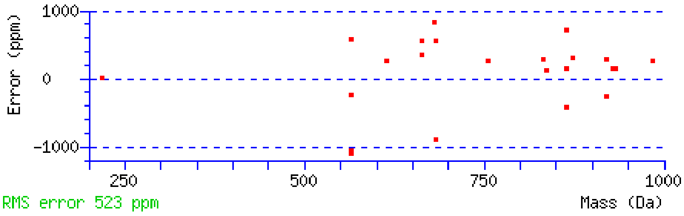


Monoisotopic mass of neutral peptide Mr(calc): 2072.0572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0022
Matches : 23/220 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							21
2	157.0972	79.0522					G	1973.9961	987.5017	1956.9695	978.9884	1955.9855	978.4964	20
3	244.1292	122.5682			226.1186	113.5629	S	1916.9746	958.9909	1899.9481	950.4777	1898.9640	949.9857	19
4	331.1612	166.0842			313.1506	157.0790	S	1829.9426	915.4749	1812.9160	906.9617	1811.9320	906.4696	18
5	418.1932	209.6003			400.1827	200.5950	S	1742.9105	871.9589	1725.8840	863.4456	1724.9000	862.9536	17
6	475.2147	238.1110			457.2041	229.1057	G	1655.8785	828.4429	1638.8520	819.9296	1637.8680	819.4376	16
7	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	K	1598.8571	799.9322	1581.8305	791.4189	1580.8465	790.9269	15
8	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	P	1470.7621	735.8847	1453.7355	727.3714	1452.7515	726.8794	14
9	801.4101	401.2087	784.3836	392.6954	783.3995	392.2034	T	1373.7093	687.3583	1356.6828	678.8450	1355.6988	678.3530	13
10	929.5051	465.2562	912.4785	456.7429	911.4945	456.2509	K	1272.6617	636.8345	1255.6351	628.3212	1254.6511	627.8292	12
11	1026.5578	513.7826	1009.5313	505.2693	1008.5473	504.7773	P	1144.5667	572.7870	1127.5401	564.2737	1126.5561	563.7817	11
12	1125.6262	***563.3168***	1108.5997	554.8035	1107.6157	554.3115	V	1047.5139	524.2606	1030.4874	515.7473	1029.5034	515.2553	10
13	1224.6947	***612.8510***	1207.6681	604.3377	1206.6841	603.8457	V	948.4455	474.7264	931.4190	466.2131	930.4349	465.7211	9
14	1323.7631	***662.3852***	1306.7365	653.8719	1305.7525	653.3799	V	849.3771	425.1922	832.3505	416.6789	831.3665	416.1869	8
15	1394.8002	697.9037	1377.7736	689.3905	1376.7896	688.8985	A	750.3087	375.6580	733.2821	367.1447	732.2981	366.6527	7
16	1509.8271	***755.4172***	1492.8006	746.9039	1491.8166	746.4119	D	**679.2716**	340.1394	662.2450	331.6261	661.2610	331.1341	6
17	1669.8578	***835.4325***	1652.8312	826.9193	1651.8472	826.4272	C	**564.2446**	282.6259	547.2181	274.1127	546.2341	273.6207	5
18	1726.8792	***863.9433***	1709.8527	855.4300	1708.8687	854.9380	G	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	4
19	1854.9378	***927.9726***	1837.9113	919.4593	1836.9273	918.9673	Q	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
20	1968.0219	***984.5146***	1950.9953	976.0013	1950.0113	975.5093	L	**219.1339**	110.0706			201.1234	101.0653	2
21							S	106.0499	53.5286			88.0393	44.5233	1

AT4G38740.1





NCBI **BLAST** search of VGSSSGKPTKPVVVADCGQLS
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.3	2072.0572	-0.0046	VGSSSGKPTKPVVVADCGQLS
3.0	2072.0547	-0.0020	SMFSNLTFNNIIRMLAGK

Mascot: http://www.matrixscience.com/

AT4G38780.1

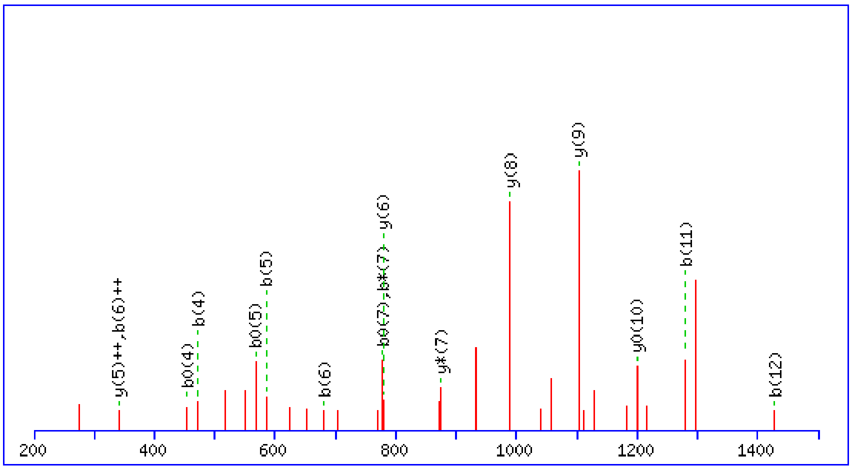
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RAEDIPLVAEWFK**
Found in **AT4G38780.1** in **TAIR_Arabidopsis**, Symbols: | splicing factor, putative | chr4:18101432-18111023 REVERSE

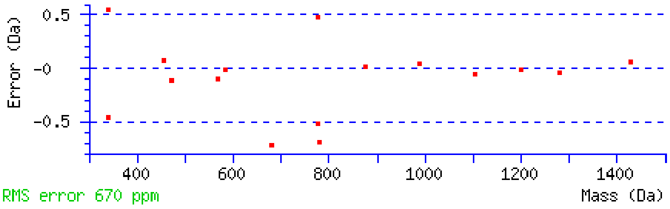
Match to Query 6830: 1572.829384 from(787.421968,2+) index(5121)
Title: Elution from: 46.347 to 46.347 scan no 6463 cid35.00 polarity:+
Data file D6h-1_3.mgf

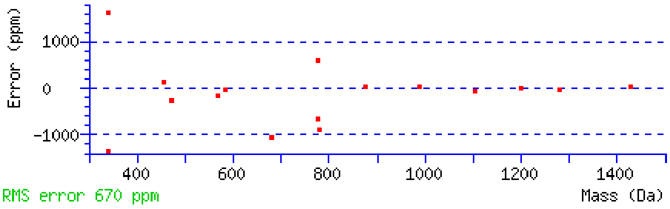
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1572.8300
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.044
Matches : 16/134 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							13
2	228.1455	114.5764	211.1190	106.0631			A	1417.7362	709.3717	1400.7096	700.8585	1399.7256	700.3665	12
3	357.1881	179.0977	340.1615	170.5844	339.1775	170.0924	E	1346.6991	673.8532	1329.6725	665.3399	1328.6885	664.8479	11
4	***472.2150***	236.6112	455.1885	228.0979	454.2045	227.6059	D	1217.6565	609.3319	1200.6299	600.8186	1199.6459	600.3266	10
5	***585.2991***	293.1532	568.2726	284.6399	567.2885	284.1479	I	**1102.6295**	551.8184	1085.6030	543.3051	1084.6190	542.8131	9
6	***682.3519***	341.6796	665.3253	333.1663	664.3413	332.6743	P	**989.5455**	495.2764	972.5189	486.7631	971.5349	486.2711	8
7	795.4359	398.2216	778.4094	389.7083	777.4254	389.2163	L	892.4927	446.7500	875.4662	438.2367	874.4822	437.7447	7
8	894.5043	447.7558	877.4778	439.2425	876.4938	438.7505	V	**779.4087**	390.2080	762.3821	381.6947	761.3981	381.2027	6
9	965.5415	483.2744	948.5149	474.7611	947.5309	474.2691	A	680.3402	340.6738	663.3137	332.1605	662.3297	331.6685	5
10	1094.5841	547.7957	1077.5575	539.2824	1076.5735	538.7904	E	609.3031	305.1552	592.2766	296.6419	591.2926	296.1499	4
11	***1280.6634***	640.8353	1263.6368	632.3220	1262.6528	631.8300	W	480.2605	240.6339	463.2340	232.1206			3
12	***1427.7318***	714.3695	1410.7052	705.8563	1409.7212	705.3642	F	294.1812	147.5942	277.1547	139.0810			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RAEDIPLVAEWFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT4G38780.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.1	1572.8300	-0.0006	RAEDIPLVAEWFK
4.1	1572.8293	0.0001	AKQLRAEIEQMEK
1.0	1572.8269	0.0025	KGHYVHLVSKMMK

AT4G38970.1

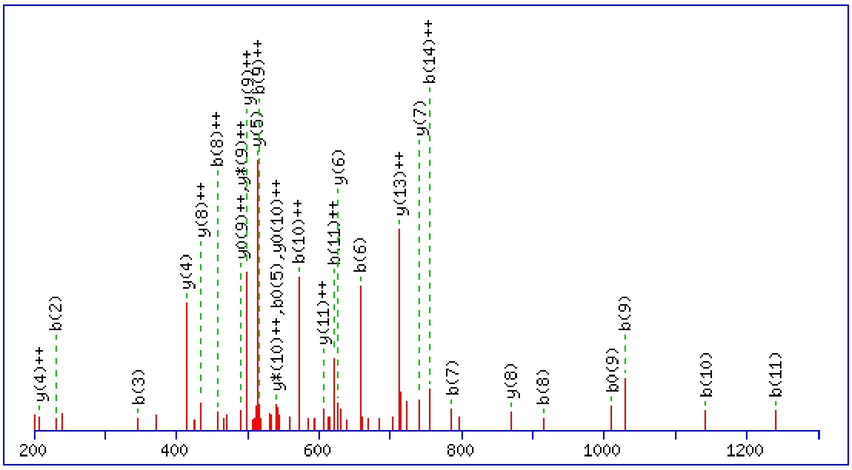
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVDVLVEQNIVPGIK**
Found in **AT4G38970.1** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr4:18163708-18165653 REVERSE

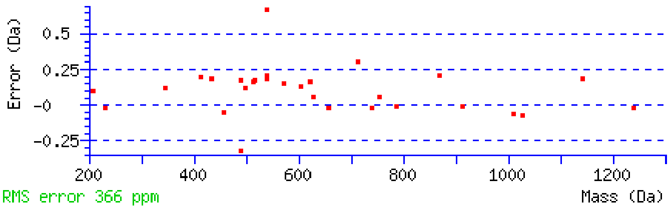
Match to Query 7982: 1652.918307 from(551.980045,3+) index(9159)
Title: Elution from: 81.554 to 81.554 scan no 12234 cid35.00 polarity:+
Data file 0-2_1.mgf

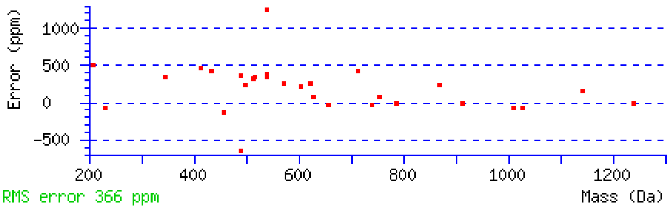
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1652.9171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 4.4e-006
Matches : 29/134 fragment ions using 36 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							15
2	***231.1162***	116.0617					V	1522.8839	761.9456	1505.8574	753.4323	1504.8734	752.9403	14
3	***346.1431***	173.5752			328.1326	164.5699	D	1423.8155	712.4114	1406.7890	703.8981	1405.8049	703.4061	13
4	445.2115	223.1094			427.2010	214.1041	V	1308.7886	654.8979	1291.7620	646.3846	1290.7780	645.8926	12
5	558.2956	279.6514			540.2850	270.6462	L	1209.7201	605.3637	1192.6936	596.8504	1191.7096	596.3584	11
6	***657.3640***	329.1856			639.3534	320.1804	V	1096.6361	548.8217	1079.6095	540.3084	1078.6255	539.8164	10
7	***786.4066***	393.7069			768.3960	384.7017	E	997.5677	499.2875	980.5411	490.7742	979.5571	490.2822	9
8	***914.4652***	**457.7362**	897.4386	449.2230	896.4546	448.7309	Q	**868.5251**	434.7662	851.4985	426.2529			8
9	***1028.5081***	**514.7577**	1011.4816	506.2444	1010.4975	505.7524	N	**740.4665**	370.7369	723.4400	362.2236			7
10	***1141.5922***	**571.2997**	1124.5656	562.7864	1123.5816	562.2944	I	**626.4236**	313.7154	609.3970	305.2022			6
11	***1240.6606***	**620.8339**	1223.6340	612.3207	1222.6500	611.8286	V	**513.3395**	257.1734	496.3130	248.6601			5
12	1337.7134	669.3603	1320.6868	660.8470	1319.7028	660.3550	P	**414.2711**	207.6392	397.2445	199.1259			4
13	1394.7348	697.8710	1377.7083	689.3578	1376.7242	688.8658	G	317.2183	159.1128	300.1918	150.5995			3
14	1507.8189	**754.4131**	1490.7923	745.8998	1489.8083	745.4078	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of MVDVLVEQNIVPGIK

AT4G38970.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.9	1652.9171	0.0012	MVDVLVEQNIVPGIK
4.0	1652.9144	0.0039	SRGNMGPKPTPLKVR
1.0	1652.9210	-0.0027	VTAIKVALSSGTQNHK

AT4G39170.1

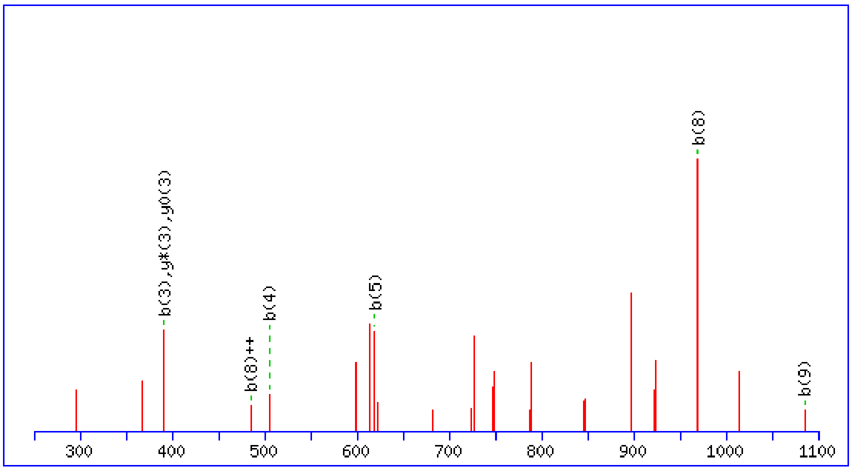
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEELLAYIDR**
Found in **AT4G39170.1** in **TAIR_Arabidopsis**, Symbols: | SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative | chr4:18240881-18243615 FORWARD

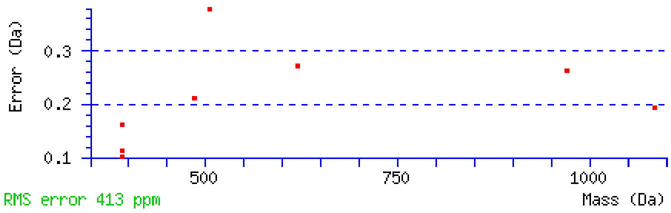
Match to Query 4744: 1262.591544 from(632.303048,2+) index(5224)
Title: Elution from: 47.019 to 47.019 scan no 6537 cid35.00 polarity:+
Data file C7-2_1.mgf

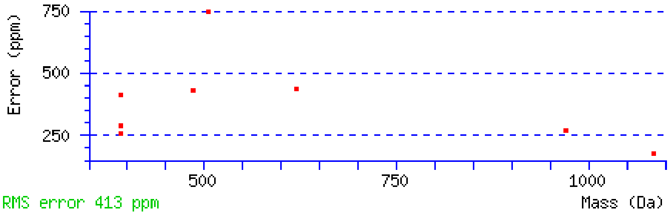
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1262.5935
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.034
Matches : 8/104 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			**Q**							**10**
2	261.0996	131.0534	243.0760	122.0416	243.0890	122.0481	**E**	1133.5481	567.2777	1115.5246	558.2659	1115.5376	558.2724	**9**
3	***391.1392***	196.0732	373.1156	187.0614	373.1286	187.0679	**E**	1003.5085	502.2579	985.4849	493.2461	985.4979	493.2526	**8**
4	***505.2203***	253.1138	487.1967	244.1020	487.2097	244.1085	**L**	873.4689	437.2381	855.4453	428.2263	855.4583	428.2328	**7**
5	***619.3014***	310.1543	601.2778	301.1425	601.2908	301.1490	**L**	759.3878	380.1975	741.3642	371.1857	741.3772	371.1922	**6**
6	691.3355	346.1714	673.3119	337.1596	673.3250	337.1661	**A**	645.3067	323.1570	627.2831	314.1452	627.2961	314.1517	**5**
7	855.3959	428.2016	837.3723	419.1898	837.3853	419.1963	**Y**	573.2725	287.1399	555.2489	278.1281	555.2620	278.1346	**4**
8	***969.4770***	485.2421	951.4534	476.2303	951.4664	476.2369	**I**	409.2122	205.1097	391.1886	196.0979	391.2016	196.1044	**3**
9	***1085.5010***	543.2541	1067.4774	534.2423	1067.4904	534.2488	**D**	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	**2**
10							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of QEELLAYIDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G39170.1

Score	Mr(calc)	Delta	Sequence
24.0	1262.5935	-0.0019	QEELLAYIDR
8.6	1262.5892	0.0023	LNADQRPRMK
5.4	1262.5880	0.0035	QRDGAPFLWR
4.6	1262.5939	-0.0024	EVKEERSVNR
3.1	1262.5939	-0.0024	NRDTSVLIGDR
2.5	1262.5921	-0.0006	SMKVPCEIIR
2.2	1262.5892	0.0023	MSETRPVPRR
0.3	1262.5888	0.0028	FMTLNPGTVPR
0.3	1262.5921	-0.0006	LLCIMVGDGVR
0.3	1262.5892	0.0023	MVRSNKQEPR

Mascot: http://www.matrixscience.com/

AT4G39260.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VITVNEAQSR**
Found in **AT4G39260.1** in **TAIR_Arabidopsis**, Symbols: GR-RBP8, ATGRP8, CCR1 | ATGRP8/GR-RBP8 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 1, GLYCINE-RICH PROTEIN 8); RNA binding | chr4:18274160-18274952 REVERSE

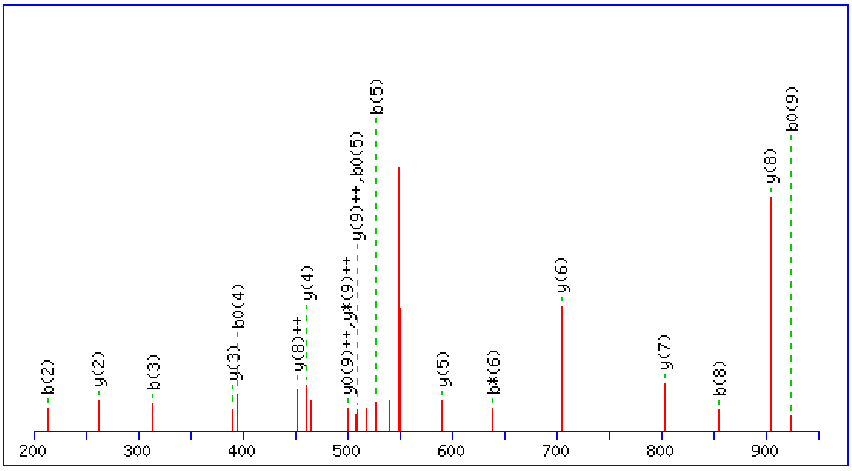
Match to Query 3711: 1115.591926 from(558.803239,2+) index(1058)
Title: Elution from: 17.243 to 17.243 scan no 1519 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 950 Da Full range

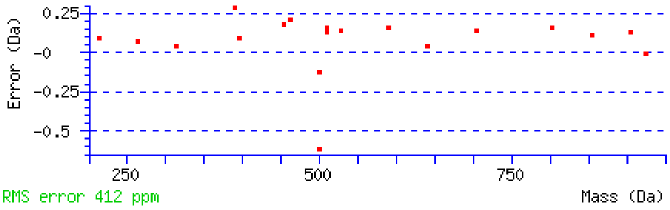
Label all possible matches ○ Label matches used for scoring ●

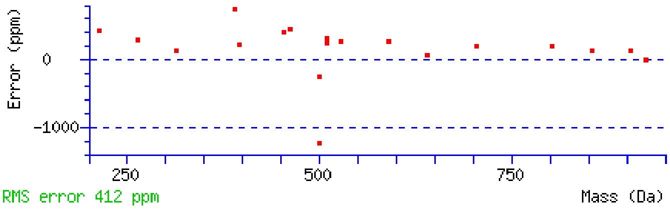
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1115.5935
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.9e-006
Matches : 19/94 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							10
2	**213.1598**	107.0835					I	1017.5323	509.2698	1000.5058	500.7565	999.5218	500.2645	9
3	**314.2074**	157.6074			296.1969	148.6021	T	***904.4483***	452.7278	887.4217	444.2145	886.4377	443.7225	8
4	413.2758	207.1416			395.2653	198.1363	V	***803.4006***	402.2039	786.3741	393.6907	785.3900	393.1987	7
5	**527.3188**	264.1630	510.2922	255.6498	509.3082	255.1577	N	***704.3322***	352.6697	687.3056	344.1565	686.3216	343.6645	6
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	E	***590.2893***	295.6483	573.2627	287.1350	572.2787	286.6430	5
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	A	***461.2467***	231.1270	444.2201	222.6137	443.2361	222.1217	4
8	**855.4571**	428.2322	838.4305	419.7189	837.4465	419.2269	Q	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	3
9	942.4891	471.7482	925.4625	463.2349	924.4785	462.7429	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VITVNEAQSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G39260.1

Score	Mr(calc)	Delta	Sequence
65.1	1115.5935	-0.0015	VITVNEAQSR
3.1	1115.5935	-0.0015	LVSNLSQAER
1.0	1115.5935	-0.0015	LTVSIAADNGR
0.6	1115.5935	-0.0015	GSLINLEQSR

AT4G39330.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDWGYSYYPVVPGHEIVGIATK**
Found in **AT4G39330.1** in **TAIR_Arabidopsis**, Symbols: | mannitol dehydrogenase, putative | chr4:18291262-18292766 FORWARD

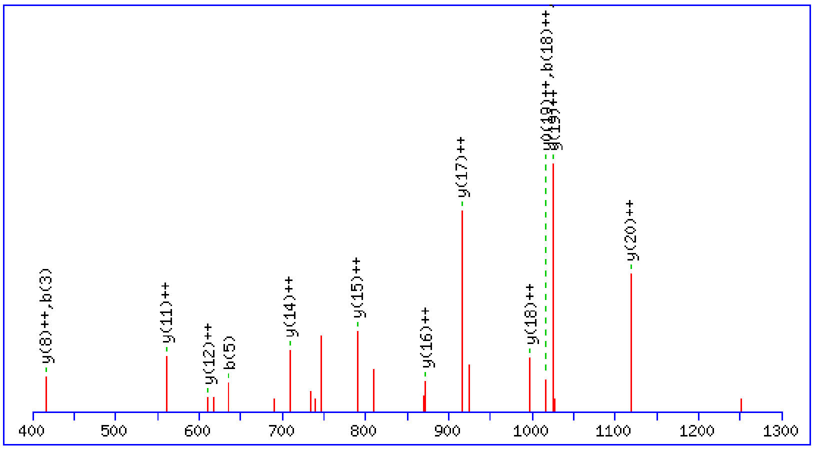
Match to Query 10205: 2464.199775 from(822.407201,3+) index(8487)
Title: Elution from: 75.016 to 75.016 scan no 11358 cid35.00 polarity:+
Data file C7-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

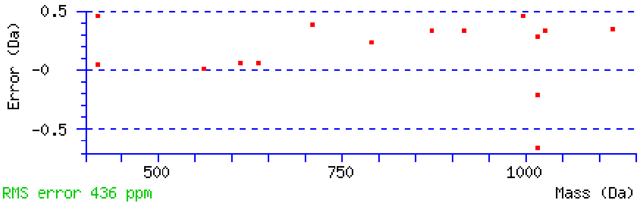
Show Y-axis ☐

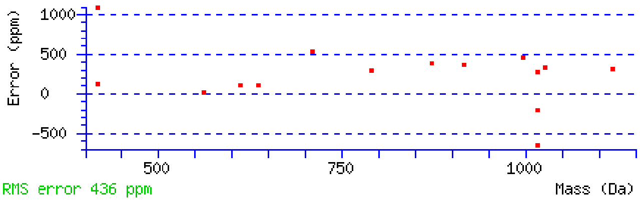


Monoisotopic mass of neutral peptide Mr(calc): 2464.2063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 6.9e-008
Matches : 15/248 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155			N							22
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	D	2351.1707	1176.0890	2334.1441	1167.5757	2333.1601	1167.0837	21
3	**416.1565**	208.5819	399.1299	200.0686	398.1459	199.5766	W	2236.1437	1118.5755	2219.1172	1110.0622	2218.1332	1109.5702	20
4	473.1779	237.0926	456.1514	228.5793	455.1674	228.0873	G	2050.0644	1025.5358	2033.0379	1017.0226	2032.0538	1016.5306	19
5	**636.2413**	318.6243	619.2147	310.1110	618.2307	309.6190	Y	1993.0429	997.0251	1976.0164	988.5118	1975.0324	988.0198	18
6	723.2733	362.1403	706.2467	353.6270	705.2627	353.1350	S	1829.9796	915.4934	1812.9531	906.9802	1811.9690	906.4882	17
7	886.3366	443.6719	869.3101	435.1587	868.3260	434.6667	Y	1742.9476	871.9774	1725.9210	863.4642	1724.9370	862.9721	16
8	1049.3999	525.2036	1032.3734	516.6903	1031.3894	516.1983	Y	1579.8843	790.4458	1562.8577	781.9325	1561.8737	781.4405	15
9	1146.4527	573.7300	1129.4262	565.2167	1128.4421	564.7247	P	1416.8209	708.9141	1399.7944	700.4008	1398.8104	699.9088	14
10	1245.5211	623.2642	1228.4946	614.7509	1227.5106	614.2589	V	1319.7682	660.3877	1302.7416	651.8744	1301.7576	651.3824	13
11	1344.5895	672.7984	1327.5630	664.2851	1326.5790	663.7931	V	1220.6998	610.8535	1203.6732	602.3402	1202.6892	601.8482	12
12	1441.6423	721.3248	1424.6157	712.8115	1423.6317	712.3195	P	1121.6313	561.3193	1104.6048	552.8060	1103.6208	552.3140	11
13	1498.6638	749.8355	1481.6372	741.3222	1480.6532	740.8302	G	1024.5786	512.7929	1007.5520	504.2796	1006.5680	503.7876	10
14	1635.7227	818.3650	1618.6961	809.8517	1617.7121	809.3597	H	967.5571	484.2822	950.5306	475.7689	949.5465	475.2769	9
15	1764.7653	882.8863	1747.7387	874.3730	1746.7547	873.8810	E	830.4982	415.7527	813.4716	407.2395	812.4876	406.7475	8
16	1877.8493	939.4283	1860.8228	930.9150	1859.8388	930.4230	I	701.4556	351.2314	684.4291	342.7182	683.4450	342.2262	7
17	1976.9177	988.9625	1959.8912	980.4492	1958.9072	979.9572	V	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	6
18	2033.9392	1017.4732	2016.9127	1008.9600	2015.9286	1008.4680	G	489.3031	245.1552	472.2766	236.6419	471.2926	236.1499	5
19	2147.0233	1074.0153	2129.9967	1065.5020	2129.0127	1065.0100	I	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
20	2218.0604	1109.5338	2201.0338	1101.0206	2200.0498	1100.5285	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
21	2319.1081	1160.0577	2302.0815	1151.5444	2301.0975	1151.0524	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
22							K	147.1128	74.0600	130.0863	65.5468			1

AT4G39330.1





NCBI **BLAST** search of NDWGYSYYPVVPGHEIVGIATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
77.8	2464.2063	-0.0065	NDWGYSYYPVVPGHEIVGIATK

Mascot: http://www.matrixscience.com/

AT4G39730.1

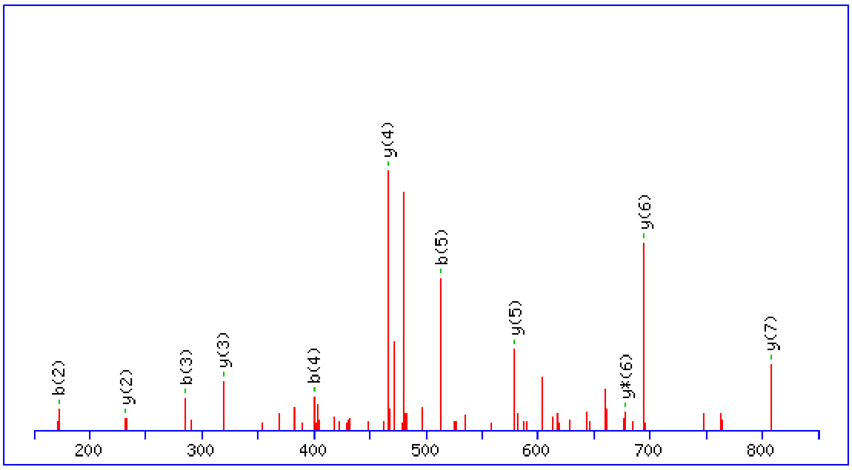
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNLDIFSGR**
Found in **AT4G39730.1** in **TAIR_Arabidopsis**, Symbols: | lipid-associated family protein | chr4:18432944-18433575 FORWARD

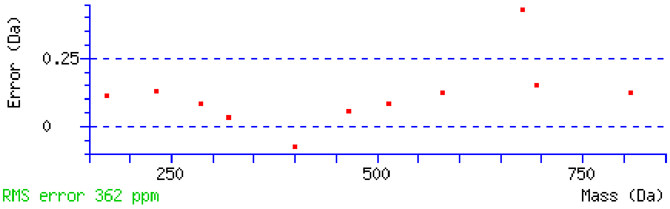
Match to Query 2286: 977.492040 from(489.753296,2+) index(5332)
Title: Elution from: 46.597 to 46.597 scan no 6696 cid35.00 polarity:+
Data file C7-2_3.mgf

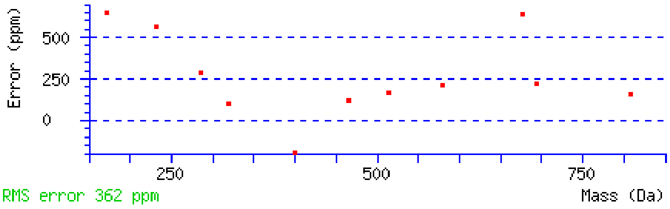
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 977.4930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.1e-006
Matches : 11/84 fragment ions using 13 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							9
2	**172.0717**	86.5395	155.0451	78.0262			N	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	8
3	**285.1557**	143.0815	268.1292	134.5682			L	***807.4359***	404.2216	790.4094	395.7083	789.4254	395.2163	7
4	**400.1827**	200.5950	383.1561	192.0817	382.1721	191.5897	D	***694.3519***	347.6796	677.3253	339.1663	676.3413	338.6743	6
5	**513.2667**	257.1370	496.2402	248.6237	495.2562	248.1317	I	***579.3249***	290.1661	562.2984	281.6528	561.3144	281.1608	5
6	660.3352	330.6712	643.3086	322.1579	642.3246	321.6659	F	***466.2409***	233.6241	449.2143	225.1108	448.2303	224.6188	4
7	747.3672	374.1872	730.3406	365.6740	729.3566	365.1819	S	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	3
8	804.3886	402.6980	787.3621	394.1847	786.3781	393.6927	G	***232.1404***	116.5738	215.1139	108.0606			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GNLDIFSGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.7	977.4930	-0.0010	GNLDIFSGR

AT4G39730.1

5.1	977.4930	-0.0010	DVQEKFGR

Mascot: http://www.matrixscience.com/

AT4G39800.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSFNGEEIYAPFK**
Found in **AT4G39800.1** in **TAIR_Arabidopsis**, Symbols: MI-1-P SYNTHASE | MI-1-P SYNTHASE (Myo-inositol-1-phosphate synthase); inositol-3-phosphate synthase | chr4:18469653-18471887 REVERSE

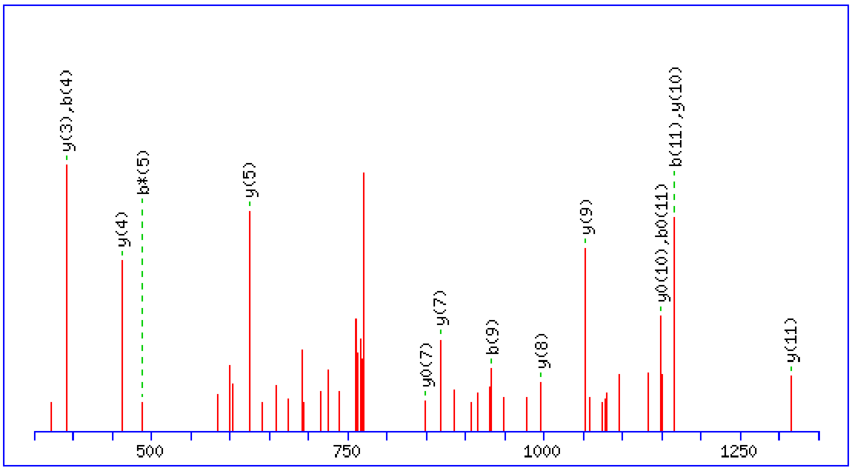
Match to Query 6798: 1556.750816 from(779.382684,2+) index(7285)
Title: Elution from: 65.173 to 65.173 scan no 9565 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1350 Da Full range

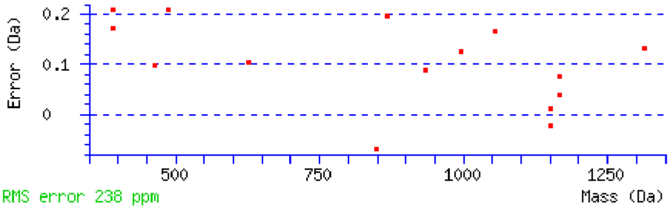
Label all possible matches ○ Label matches used for scoring ●

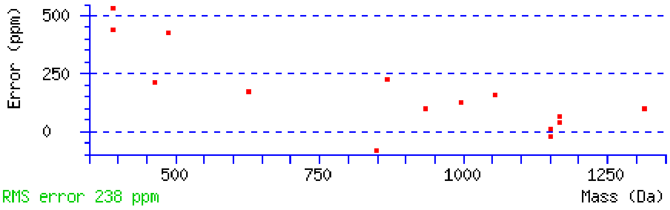
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1556.7511
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 2.1e-007
Matches : 15/132 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							14
2	157.0972	79.0522					G	1458.6900	729.8486	1441.6634	721.3353	1440.6794	720.8433	13
3	244.1292	122.5682			226.1186	113.5629	S	1401.6685	701.3379	1384.6420	692.8246	1383.6579	692.3326	12
4	**391.1976**	196.1024			373.1870	187.0972	F	***1314.6365***	657.8219	1297.6099	649.3086	1296.6259	648.8166	11
5	505.2405	253.1239	488.2140	244.6106	487.2300	244.1186	N	***1167.5681***	584.2877	1150.5415	575.7744	1149.5575	575.2824	10
6	562.2620	281.6346	545.2354	273.1214	544.2514	272.6293	G	***1053.5251***	527.2662	1036.4986	518.7529	1035.5146	518.2609	9
7	691.3046	346.1559	674.2780	337.6427	673.2940	337.1506	E	***996.5037***	498.7555	979.4771	490.2422	978.4931	489.7502	8
8	820.3472	410.6772	803.3206	402.1640	802.3366	401.6719	E	***867.4611***	434.2342	850.4345	425.7209	849.4505	425.2289	7
9	**933.4312**	467.2193	916.4047	458.7060	915.4207	458.2140	I	738.4185	369.7129	721.3919	361.1996			6
10	1096.4946	548.7509	1079.4680	540.2376	1078.4840	539.7456	Y	***625.3344***	313.1709	608.3079	304.6576			5
11	**1167.5317**	584.2695	1150.5051	575.7562	1149.5211	575.2642	A	***462.2711***	231.6392	445.2445	223.1259			4
12	1264.5844	632.7959	1247.5579	624.2826	1246.5739	623.7906	P	***391.2340***	196.1206	374.2074	187.6074			3
13	1411.6529	706.3301	1394.6263	697.8168	1393.6423	697.3248	F	294.1812	147.5942	277.1547	139.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VGSFNGEEIYAPFK

AT4G39800.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.8	1556.7511	-0.0003	VGSFNGEEIYAPFK

Mascot: http://www.matrixscience.com/

AT4G39980.1

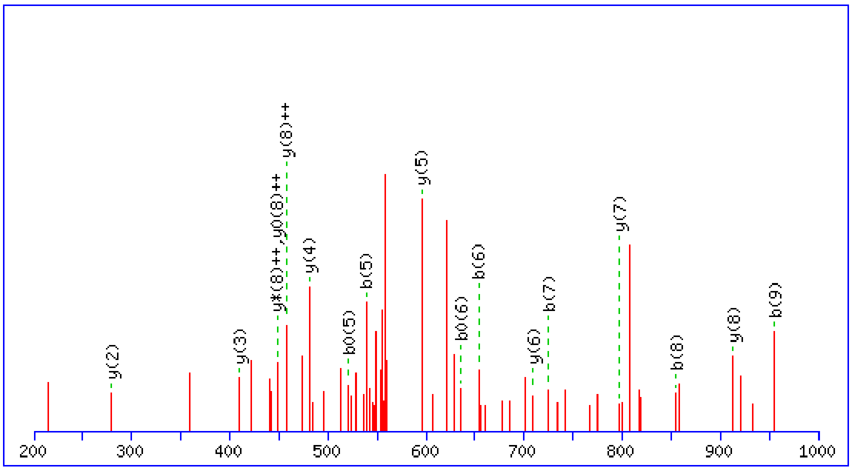
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFDSILAEVR**
Found in **AT4G39980.1** in **TAIR_Arabidopsis**, Symbols: DHS1 | DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1); 3-deoxy-7-phosphoheptulonate synthase | chr4:18539648-18541826 FORWARD

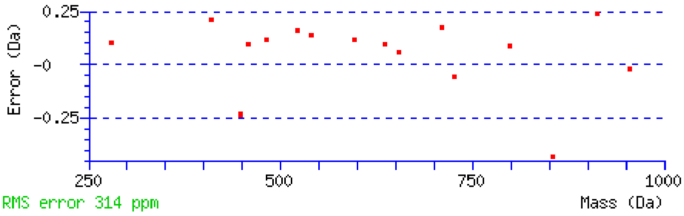
Match to Query 3635: 1132.552524 from(567.283538,2+) index(7448)
Title: Elution from: 66.034 to 66.034 scan no 9767 cid35.00 polarity:+
Data file D12h-3_2.mgf

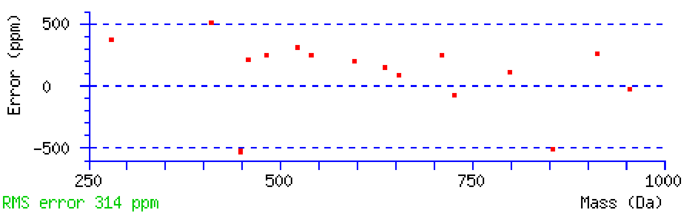
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1132.5539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.021
Matches : 17/82 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244			A							10
2	221.1069	111.0571			F	1061.5270	531.2671	1043.5034	522.2553	1043.5164	522.2619	9
3	337.1309	169.0691	319.1203	160.0638	D	***913.4616***	457.2344	895.4380	448.2226	895.4510	448.2291	8
4	425.1599	213.0836	407.1494	204.0783	S	***797.4376***	399.2224	779.4140	390.2106	779.4270	390.2171	7
5	**539.2410**	270.1241	521.2304	261.1189	I	***709.4085***	355.2079	691.3849	346.1961	691.3980	346.2026	6
6	**653.3221**	327.1647	635.3115	318.1594	L	***595.3274***	298.1673	577.3038	289.1556	577.3169	289.1621	5
7	**725.3563**	363.1818	707.3457	354.1765	A	***481.2463***	241.1268	463.2227	232.1150	463.2358	232.1215	4
8	**855.3959**	428.2016	837.3853	419.1963	E	***409.2122***	205.1097	391.1886	196.0979	391.2016	196.1044	3
9	**955.4613**	478.2343	937.4508	469.2290	V	***279.1725***	140.0899	261.1490	131.0781			2
10					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AFDSILAEVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT4G39980.1

Score	Mr(calc)	Delta	Sequence
27.6	1132.5539	-0.0013	AFDSILAEVR
10.6	1132.5539	-0.0013	EFKAVIEER
8.9	1132.5539	-0.0013	EEVKEAIFR
8.5	1132.5539	-0.0013	LLADAESVFR
5.2	1132.5539	-0.0013	EILSFLDQR
4.8	1132.5516	0.0009	ISKDAGGSEKK
4.5	1132.5539	-0.0013	IADAAEKFGAK
3.8	1132.5539	-0.0013	TGDFPKSLQK
3.3	1132.5539	-0.0013	YIAGQNEVVK
3.0	1132.5543	-0.0018	RNTVKNQEK

AT5G01410.1

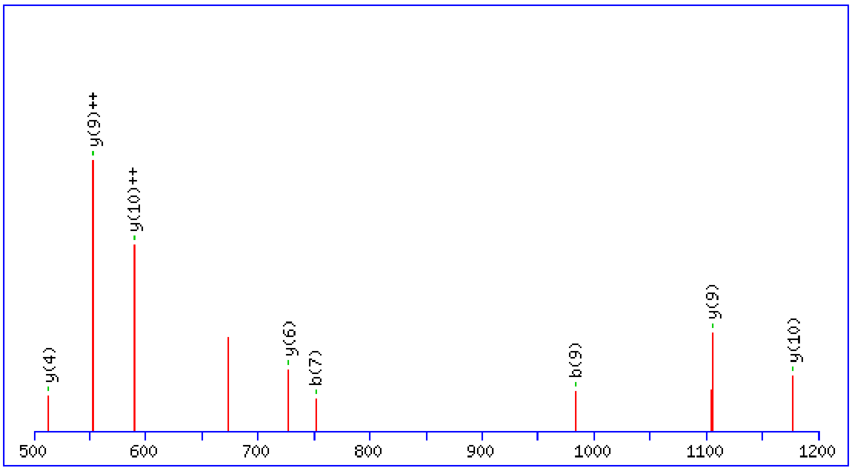
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAAPYDLVMQTK**
Found in **AT5G01410.1** in **TAIR_Arabidopsis**, Symbols: ATPDX1.3, RSR4, PDX1.3, PDX1 | PDX1 (PYRIDOXINE BIOSYNTHESIS 1.3); protein heterodimerization/ protein homodimerization | chr5:172575-173504 REVERSE

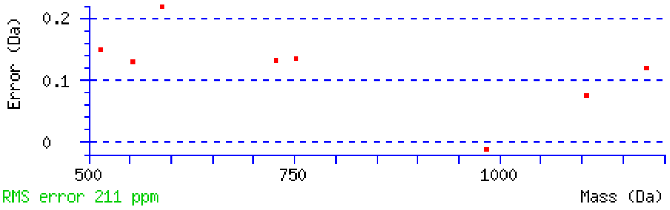
Match to Query 5426: 1362.665356 from(682.339954,2+) index(7390)
Title: Elution from: 65.120 to 65.120 scan no 9564 cid35.00 polarity:+
Data file 0-2_1.mgf

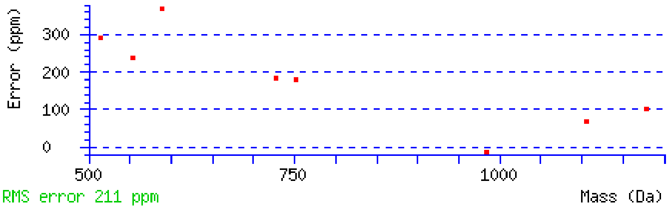
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1362.6646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0029
Matches : 8/102 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							12
2	187.1225	94.0649					A	1249.5907	625.2990	1231.5672	616.2872	1231.5802	616.2937	11
3	259.1567	130.0820					A	***1177.5566***	589.2819	1159.5330	580.2701	1159.5460	580.2767	10
4	357.2065	179.1069					P	***1105.5224***	553.2649	1087.4989	544.2531	1087.5119	544.2596	9
5	521.2668	261.1371					Y	1007.4726	504.2400	989.4491	495.2282	989.4621	495.2347	8
6	637.2908	319.1490			619.2802	310.1438	D	843.4123	422.2098	825.3887	413.1980	825.4017	413.2045	7
7	***751.3719***	376.1896			733.3613	367.1843	L	***727.3883***	364.1978	709.3647	355.1860	709.3777	355.1925	6
8	851.4374	426.2223			833.4268	417.2170	V	613.3072	307.1572	595.2836	298.1454	595.2966	298.1520	5
9	***983.4749***	492.2411			965.4643	483.2358	M	***513.2418***	257.1245	495.2182	248.1127	495.2312	248.1192	4
10	1113.5275	557.2674	1095.5039	548.2556	1095.5170	548.2621	Q	381.2042	191.1058	363.1807	182.0940	363.1937	182.1005	3
11	1215.5722	608.2898	1197.5487	599.2780	1197.5617	599.2845	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LAAPYDLVMQTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G01410.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.4	1362.6646	0.0008	LAAPYDLVMQTK
6.2	1362.6623	0.0030	AIETELMERLK
4.7	1362.6650	0.0004	LAMERLAQIER
2.9	1362.6638	0.0015	ALTTWGRWVEK

AT5G01530.1

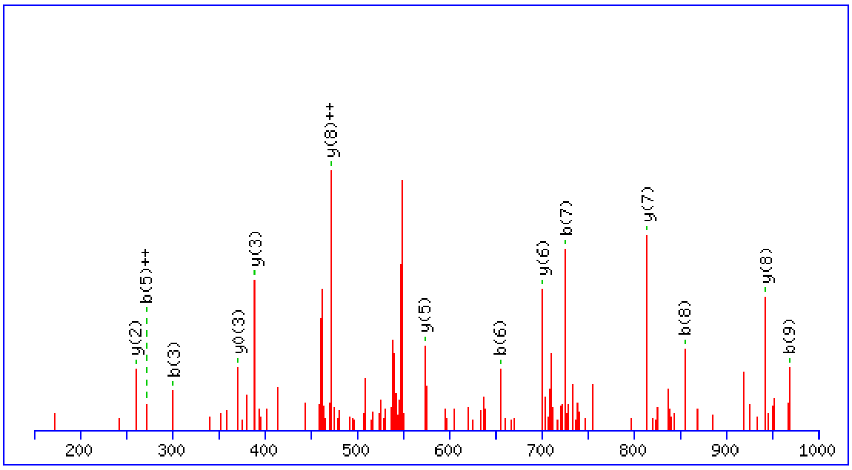
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAQLQLAEIK**
Found in **AT5G01530.1** in **TAIR_Arabidopsis**, Symbols: | chlorophyll A-B binding protein CP29 (LHCB4) | chr5:209083-210242 FORWARD

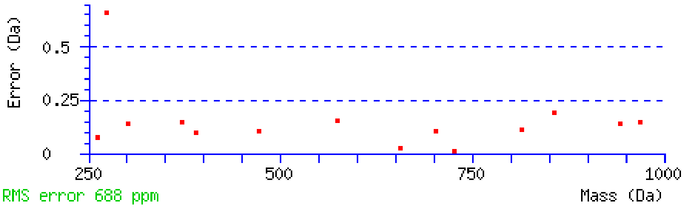
Match to Query 2897: 1113.636256 from(557.825404,2+) index(3802)
Title: Elution from: 38.263 to 38.263 scan no 4910 cid35.00 polarity:+
Data file D1d-1_3.mgf

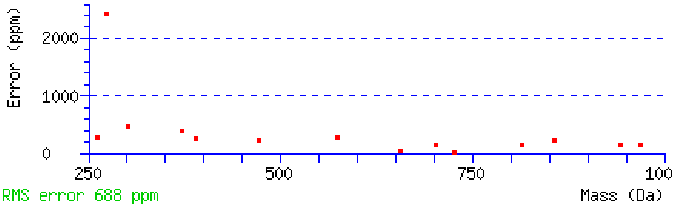
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1113.6393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 4.1e-006
Matches : 14/100 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	173.0921	87.0497			155.0815	78.0444	A	1013.5990	507.3031	996.5724	498.7899	995.5884	498.2978	9
3	***301.1506***	151.0790	284.1241	142.5657	283.1401	142.0737	Q	***942.5619***	471.7846	925.5353	463.2713	924.5513	462.7793	8
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	L	***814.5033***	407.7553	797.4767	399.2420	796.4927	398.7500	7
5	542.2933	271.6503	525.2667	263.1370	524.2827	262.6450	Q	***701.4192***	351.2132	684.3927	342.7000	683.4087	342.2080	6
6	***655.3774***	328.1923	638.3508	319.6790	637.3668	319.1870	L	***573.3606***	287.1840	556.3341	278.6707	555.3501	278.1787	5
7	***726.4145***	363.7109	709.3879	355.1976	708.4039	354.7056	A	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
8	***855.4571***	428.2322	838.4305	419.7189	837.4465	419.2269	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	***968.5411***	484.7742	951.5146	476.2609	950.5306	475.7689	I	***260.1969***	130.6021	243.1703	122.0888			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TAQLQLAEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G01530.1

60.9	1113.6393	-0.0031	TAQLQLAEIK
11.2	1113.6368	-0.0006	MKFAPKAPPK
10.2	1113.6393	-0.0031	LDANIQSILK
6.8	1113.6393	-0.0031	NINALLDTLK
3.8	1113.6393	-0.0031	LQKELQDLK
3.8	1113.6393	-0.0031	LKQDQLIEK
1.2	1113.6394	-0.0031	LTLSGDKVPGK

AT5G01730.1

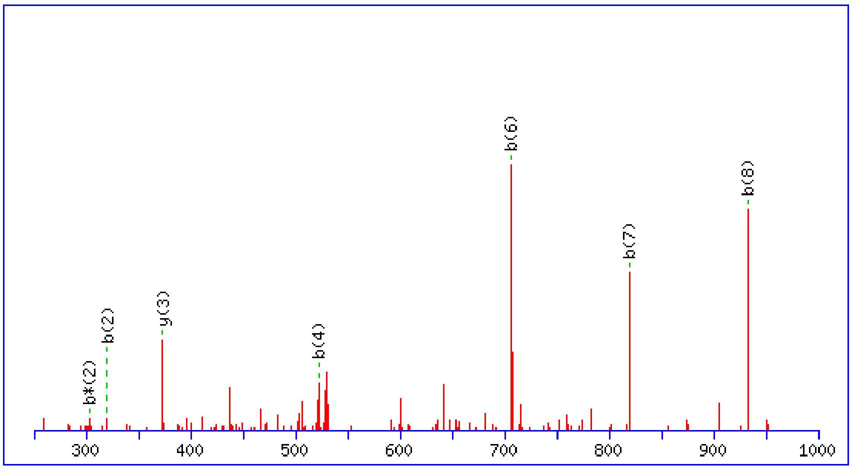
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RYSDPSLLK**
Found in **AT5G01730.1** in **TAIR_Arabidopsis**, Symbols: ATSCAR4, WAVE3 | WAVE3 | chr5:273016-277558 REVERSE

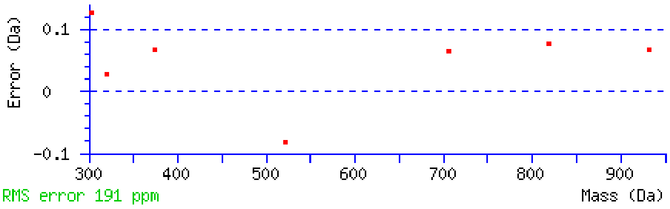
Match to Query 3406: 1077.582572 from(539.798562,2+) index(2101)
Title: Elution from: 23.828 to 23.828 scan no 2702 cid35.00 polarity:+
Data file D1d-3_1.mgf

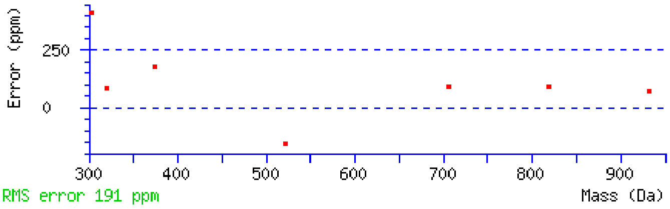
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1077.5818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.013
Matches : 7/86 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							9
2	***320.1717***	160.5895	303.1452	152.0762			Y	922.4880	461.7477	905.4615	453.2344	904.4775	452.7424	8
3	407.2037	204.1055	390.1772	195.5922	389.1932	195.1002	S	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	7
4	***522.2307***	261.6190	505.2041	253.1057	504.2201	252.6137	D	672.3927	336.7000	655.3661	328.1867	654.3821	327.6947	6
5	619.2835	310.1454	602.2569	301.6321	601.2729	301.1401	P	557.3657	279.1865	540.3392	270.6732	539.3552	270.1812	5
6	***706.3155***	353.6614	689.2889	345.1481	688.3049	344.6561	S	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
7	***819.3995***	410.2034	802.3730	401.6901	801.3890	401.1981	L	373.2809	187.1441	356.2544	178.6308			3
8	***932.4836***	466.7454	915.4571	458.2322	914.4730	457.7402	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RYSDPSLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.6	1077.5818	0.0007	RYSDPSLLK

AT5G01730.1

25.3	1077.5818	0.0008	YREAADLIK
7.9	1077.5852	-0.0026	QSSKKMELK
7.5	1077.5818	0.0007	SVNAFDLKGK
6.3	1077.5852	-0.0026	ACASSLKTLK
4.5	1077.5852	-0.0026	SNMKVATSIK
3.3	1077.5852	-0.0026	SSSGCLIVKK
2.3	1077.5818	0.0007	ENVLIHEPK
2.2	1077.5852	-0.0026	RLMTETAIK
2.1	1077.5818	0.0007	LGFETDRLK

AT5G01940.1

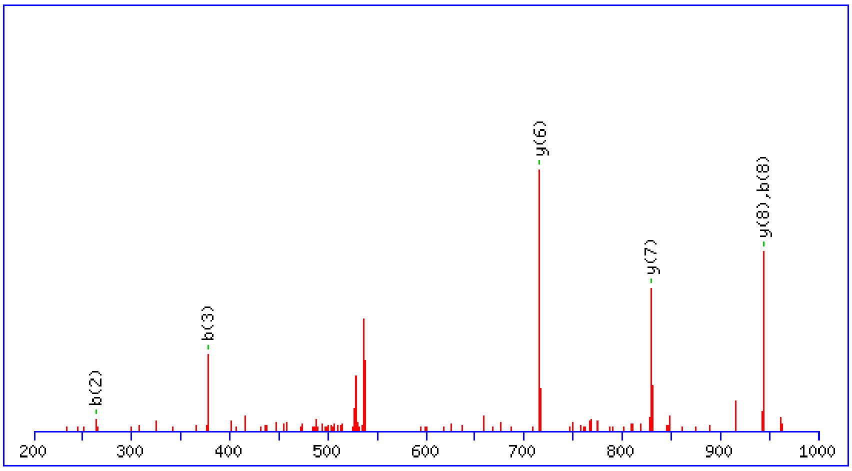
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLLAQMETK**
Found in **AT5G01940.1** in **TAIR_Arabidopsis**, Symbols: | eukaryotic translation initiation factor 2B family protein / eIF-2B family protein | chr5:363591-364766 REVERSE

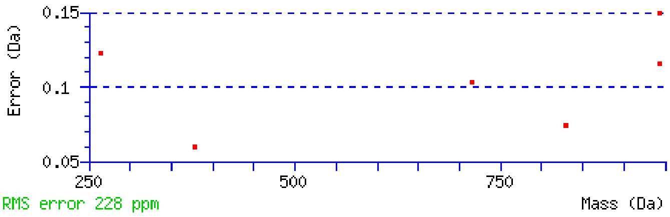
Match to Query 3482: 1090.536440 from(546.275496,2+) index(2067)
Title: Elution from: 24.636 to 24.636 scan no 2681 cid35.00 polarity:+
Data file 0-1_1.mgf

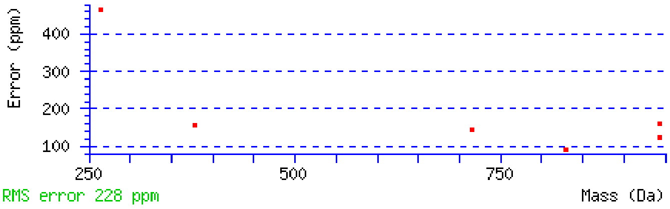
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1090.5359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.029
Matches : 6/74 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							9
2	***263.1538***	132.0805					L	***943.4777***	472.2425	925.4541	463.2307	925.4672	463.2372	8
3	***377.2349***	189.1211					L	***829.3966***	415.2020	811.3730	406.1902	811.3861	406.1967	7
4	449.2691	225.1382					A	***715.3155***	358.1614	697.2919	349.1496	697.3050	349.1561	6
5	579.3217	290.1645	561.2981	281.1527			Q	643.2814	322.1443	625.2578	313.1325	625.2708	313.1390	5
6	711.3592	356.1833	693.3357	347.1715			M	513.2287	257.1180	495.2052	248.1062	495.2182	248.1127	4
7	841.3989	421.2031	823.3753	412.1913	823.3883	412.1978	E	381.1912	191.0992	363.1676	182.0875	363.1807	182.0940	3
8	***943.4436***	472.2254	925.4200	463.2136	925.4330	463.2201	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FLLAQMETK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G01940.1

25.0	1090.5359	0.0006	FLLAQMETK
23.7	1090.5386	-0.0021	YRCPQLLK
22.5	1090.5337	0.0028	EMLKEKSSK
22.5	1090.5359	0.0006	EYMQGVLIK
22.5	1090.5359	0.0005	LYEAACLLK
18.2	1090.5386	-0.0021	TRGMLGWLK
13.0	1090.5337	0.0027	AMSLLSNSLK
11.3	1090.5393	-0.0028	KLVMMSIDK
10.0	1090.5393	-0.0028	KLVMMSIDK
7.7	1090.5359	0.0005	NLMFLADIK

AT5G01950.1

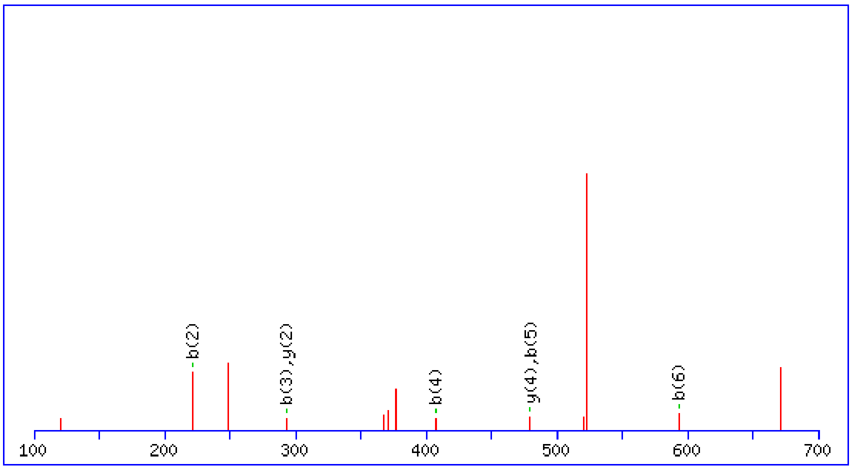
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAALALR**
Found in **AT5G01950.1** in **TAIR_Arabidopsis**, Symbols: | ATP binding / kinase/ protein serine/threonine kinase | chr5:365037-369529 REVERSE

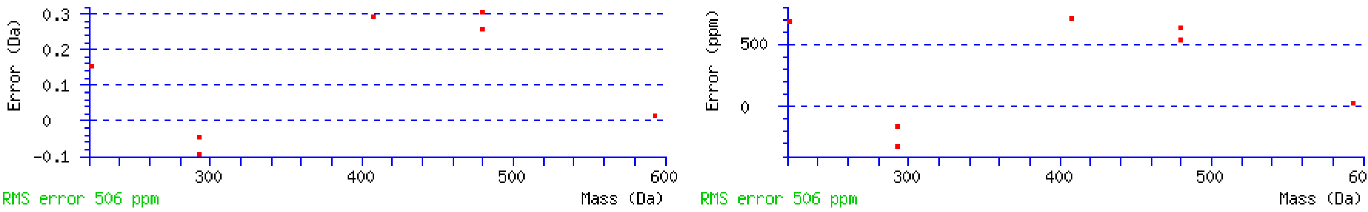
Match to Query 813: 770.430560 from(386.222556,2+) index(4562)
Title: Elution from: 41.559 to 41.559 scan no 5738 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.4299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0063
Matches : 7/36 fragment ions using 14 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	149.0727	75.0400	F					7
2	*221.1069*	111.0571	A	623.3717	312.1895	605.3482	303.1777	6
3	*293.1410*	147.0741	A	551.3376	276.1724	533.3140	267.1606	5
4	*407.2221*	204.1147	L	**479.3034**	240.1554	461.2799	231.1436	4
5	*479.2563*	240.1318	A	365.2223	183.1148	347.1988	174.1030	3
6	*593.3374*	297.1723	L	**293.1882**	147.0977	275.1646	138.0859	2
7			R	179.1071	90.0572	161.0835	81.0454	1



NCBI **BLAST** search of FAALALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.1	770.4299	0.0007	FAALALR
30.9	770.4299	0.0007	VFNILR
28.9	770.4299	0.0007	AFALLAR

AT5G01950.1

18.2	770.4299	0.0007	FVLNLR
9.2	770.4299	0.0007	ALAAFLR
9.1	770.4299	0.0007	VLNFIR
6.8	770.4299	0.0007	FKPTIR

AT5G02010.1

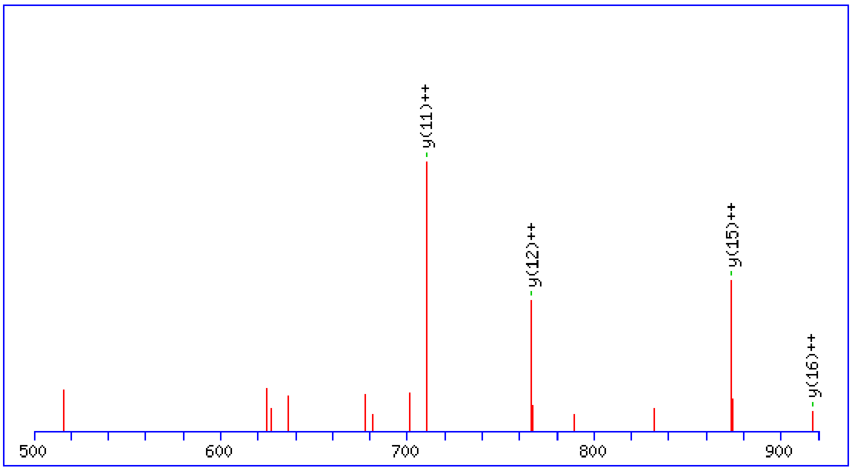
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSPGGLQENSRKQLQHK**
Found in **AT5G02010.1** in **TAIR_Arabidopsis**, Symbols: ATROPGEF7, ROPGEF7 | ATROPGEF7/ROPGEF7 (KINASE PARTNER PROTEIN-LIKE); Rho guanyl-nucleotide exchange factor/ | chr5:383490-385695 FORWARD

Match to Query 9095: 1932.930744 from(645.317524,3+) index(5562)
Title: Elution from: 52.856 to 52.856 scan no 7198 cid35.00 polarity:+
Data file D1d-1_1.mgf

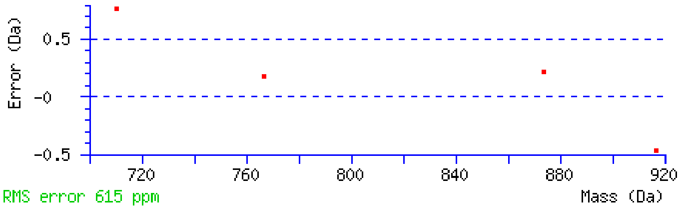
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 920 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

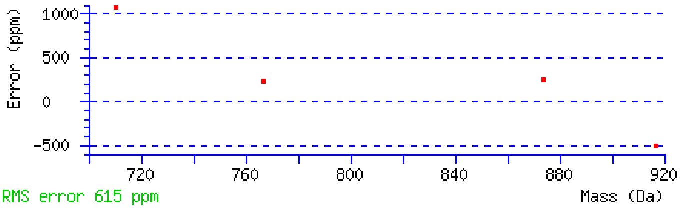


Monoisotopic mass of neutral peptide Mr(calc): 1932.9350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0082
Matches : 4/164 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							17
2	189.1018	95.0545			171.0912	86.0492	S	1833.8769	917.4421	1815.8533	908.4303	1815.8663	908.4368	16
3	287.1516	144.0794			269.1410	135.0741	P	1745.8478	873.4275	1727.8242	864.4157	1727.8372	864.4223	15
4	345.1701	173.0887			327.1595	164.0834	G	1647.7980	824.4026	1629.7744	815.3908	1629.7874	815.3974	14
5	403.1886	202.0979			385.1780	193.0926	G	1589.7795	795.3934	1571.7559	786.3816	1571.7689	786.3881	13
6	517.2697	259.1385			499.2591	250.1332	L	1531.7610	766.3841	1513.7374	757.3723	1513.7504	757.3789	12
7	647.3223	324.1648	629.2987	315.1530	629.3118	315.1595	Q	1417.6799	709.3436	1399.6563	700.3318	1399.6693	700.3383	11
8	777.3620	389.1846	759.3384	380.1728	759.3514	380.1793	E	1287.6273	644.3173	1269.6037	635.3055	1269.6167	635.3120	10
9	893.3990	447.2031	875.3754	438.1913	875.3884	438.1978	N	1157.5876	579.2975	1139.5640	570.2857	1139.5771	570.2922	9
10	981.4280	491.2176	963.4044	482.2059	963.4175	482.2124	S	1041.5506	521.2790	1023.5270	512.2672	1023.5401	512.2737	8
11	1141.5173	571.2623	1123.4937	562.2505	1123.5067	562.2570	R	953.5216	477.2644	935.4980	468.2526			7
12	1271.6063	636.3068	1253.5827	627.2950	1253.5957	627.3015	K	793.4323	397.2198	775.4087	388.2080			6
13	1401.6590	701.3331	1383.6354	692.3213	1383.6484	692.3278	Q	663.3433	332.1753	645.3197	323.1635			5
14	1515.7400	758.3737	1497.7165	749.3619	1497.7295	749.3684	L	533.2906	267.1490	515.2671	258.1372			4
15	1645.7927	823.4000	1627.7691	814.3882	1627.7821	814.3947	Q	419.2095	210.1084	401.1860	201.0966			3
16	1785.8427	893.4250	1767.8191	884.4132	1767.8321	884.4197	H	289.1569	145.0821	271.1333	136.0703			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT5G02010.1





NCBI **BLAST** search of VSPGGLQENSRKQLQHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.7	1932.9350	-0.0043	VSPGGLQENSRKQLQHK
4.9	1932.9272	0.0036	NINTAFAKMGYPGTVSIK
2.0	1932.9319	-0.0012	SPINSSGSLSDVLFFSKK
1.1	1932.9353	-0.0046	DAPLGIVSQSPNIMDLVK
0.9	1932.9324	-0.0016	VSADKHENSPGIKVGVSGK
0.9	1932.9299	0.0009	VSFAERPSFKIGACIAR
0.8	1932.9306	0.0002	KGSFKMLNIDGNMISLK
0.4	1932.9297	0.0011	VKLGVEDVEVDNPNAVSK

Mascot: http://www.matrixscience.com/

AT5G02490.1

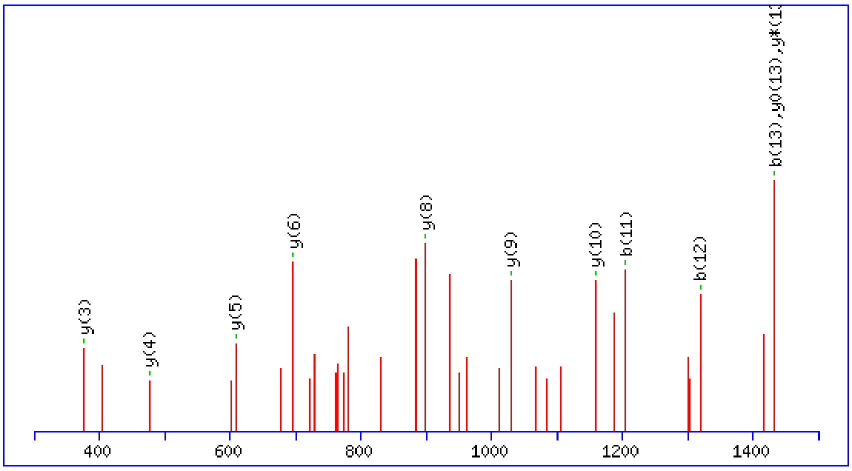
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFAAEEISSMVLIK**
Found in **AT5G02490.1** in **TAIR_Arabidopsis**, Symbols: | heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2) | chr5:550294-552563 REVERSE

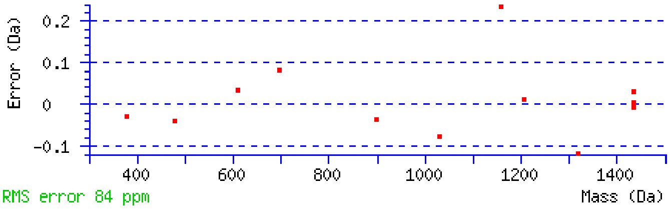
Match to Query 6764: 1580.769408 from(791.391980,2+) index(9343)
Title: Elution from: 85.640 to 85.640 scan no 12991 cid35.00 polarity:+
Data file 0-3_3.mgf

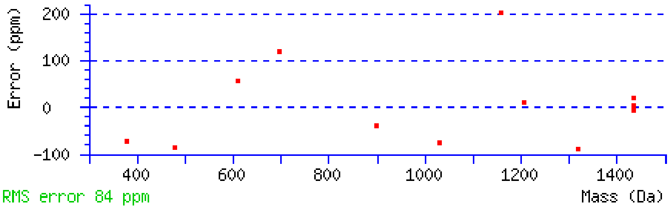
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1580.7696
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 1.3e-006
Matches : 12/138 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							14
2	279.1254	140.0663	261.1018	131.0545			F	1451.7243	726.3658	1433.7007	717.3540	1433.7137	717.3605	13
3	351.1595	176.0834	333.1359	167.0716			A	1303.6588	652.3330	1285.6352	643.3213	1285.6483	643.3278	12
4	423.1937	212.1005	405.1701	203.0887			A	1231.6247	616.3160	1213.6011	607.3042	1213.6141	607.3107	11
5	553.2333	277.1203	535.2097	268.1085	535.2227	268.1150	E	***1159.5905***	580.2989	1141.5669	571.2871	1141.5800	571.2936	10
6	683.2729	342.1401	665.2493	333.1283	665.2624	333.1348	E	***1029.5509***	515.2791	1011.5273	506.2673	1011.5403	506.2738	9
7	797.3540	399.1807	779.3304	390.1689	779.3435	390.1754	I	***899.5113***	450.2593	881.4877	441.2475	881.5007	441.2540	8
8	885.3831	443.1952	867.3595	434.1834	867.3725	434.1899	S	785.4302	393.2187	767.4066	384.2069	767.4196	384.2134	7
9	973.4122	487.2097	955.3886	478.1979	955.4016	478.2044	S	***697.4011***	349.2042	679.3775	340.1924	679.3905	340.1989	6
10	1105.4497	553.2285	1087.4261	544.2167	1087.4391	544.2232	M	***609.3720***	305.1897	591.3485	296.1779			5
11	**1205.5151**	603.2612	1187.4915	594.2494	1187.5046	594.2559	V	***477.3345***	239.1709	459.3109	230.1591			4
12	**1319.5962**	660.3017	1301.5726	651.2900	1301.5857	651.2965	L	***377.2691***	189.1382	359.2455	180.1264			3
13	**1433.6773**	717.3423	1415.6537	708.3305	1415.6668	708.3370	I	263.1880	132.0976	245.1644	123.0858			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QFAAEEISSMVLIK

AT5G02490.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.5	1580.7696	-0.0002	QFAAEEISSMVLIK
15.1	1580.7730	-0.0036	DAKLMDEVMKLLK
13.0	1580.7667	0.0027	NRVSFQGLSTDPLK
12.9	1580.7667	0.0027	NLQGTNIFEEIRK
9.8	1580.7723	-0.0029	TASFIMKNHGSLLK
8.5	1580.7710	-0.0016	LRMKLMGPLNNMK
6.5	1580.7723	-0.0029	IMASGKYANTLHLK
4.9	1580.7663	0.0031	DGSLFVLDPSKPYK
4.6	1580.7730	-0.0036	MLMVTDVQDIIKK
3.1	1580.7701	-0.0007	MLRSGKELEEVVR

AT5G02500.1

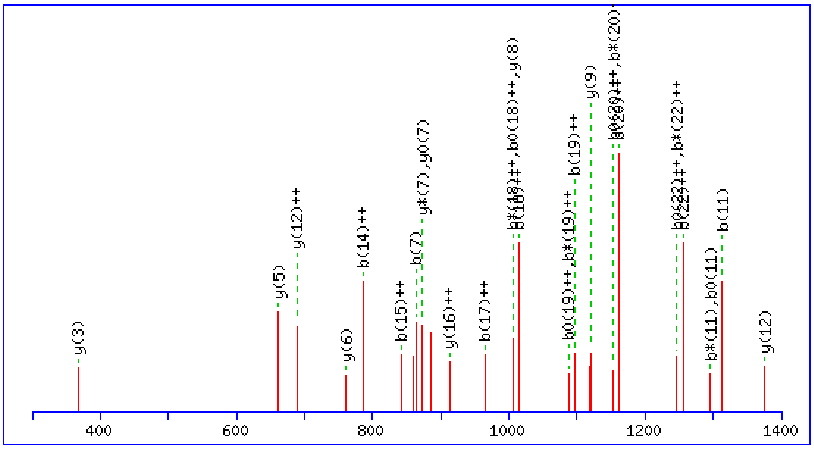
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQVFSTYSDNQPGVLIQVYEGER**
Found in **AT5G02500.1** in **TAIR_Arabidopsis**, Symbols: HSP70-1, AT-HSC70-1, HSC70, HSC70-1 | HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding | chr5:554053-556332 REVERSE

Match to Query 10893: 2687.173887 from(896.731905,3+) index(9303)
Title: Elution from: 84.341 to 84.341 scan no 12579 cid35.00 polarity:+
Data file 0-3_1.mgf

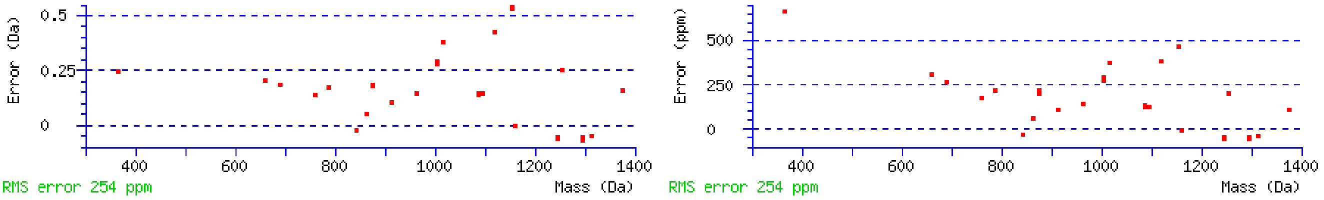
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2687.1719
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 5e-006
Matches : 29/260 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							23
2	261.0996	131.0534	243.0760	122.0416	243.0890	122.0481	Q	2558.1396	1279.5734	2540.1160	1270.5617	2540.1291	1270.5682	22
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	V	2428.0870	1214.5471	2410.0634	1205.5353	2410.0764	1205.5418	21
4	509.2304	255.1189	491.2069	246.1071	491.2199	246.1136	F	2328.0215	1164.5144	2309.9979	1155.5026	2310.0110	1155.5091	20
5	597.2595	299.1334	579.2359	290.1216	579.2489	290.1281	S	2179.9561	1090.4817	2161.9325	1081.4699	2161.9455	1081.4764	19
6	699.3042	350.1558	681.2806	341.1440	681.2937	341.1505	T	2091.9270	1046.4671	2073.9034	1037.4554	2073.9164	1037.4619	18
7	**863.3646**	432.1859	845.3410	423.1741	845.3540	423.1807	Y	1989.8823	995.4448	1971.8587	986.4330	1971.8717	986.4395	17
8	951.3937	476.2005	933.3701	467.1887	933.3831	467.1952	S	1825.8219	913.4146	1807.7984	904.4028	1807.8114	904.4093	16
9	1067.4176	534.2125	1049.3940	525.2007	1049.4071	525.2072	D	1737.7929	869.4001	1719.7693	860.3883	1719.7823	860.3948	15
10	1183.4546	592.2310	1165.4310	583.2192	1165.4441	583.2257	N	1621.7689	811.3881	1603.7453	802.3763	1603.7583	802.3828	14
11	**1313.5073**	657.2573	1295.4837	648.2455	1295.4967	648.2520	Q	1505.7319	753.3696	1487.7083	744.3578	1487.7213	744.3643	13
12	1411.5571	706.2822	1393.5335	697.2704	1393.5465	697.2769	P	***1375.6793***	688.3433	1357.6557	679.3315	1357.6687	679.3380	12
13	1469.5756	735.2914	1451.5520	726.2796	1451.5650	726.2861	G	1277.6295	639.3184	1259.6059	630.3066	1259.6189	630.3131	11
14	1569.6410	***785.3241***	1551.6174	776.3124	1551.6305	776.3189	V	1219.6110	610.3091	1201.5874	601.2973	1201.6004	601.3038	10
15	1683.7221	***842.3647***	1665.6985	833.3529	1665.7116	833.3594	L	***1119.5455***	560.2764	1101.5219	551.2646	1101.5349	551.2711	9
16	1797.8032	899.4052	1779.7796	890.3935	1779.7927	890.4000	I	***1005.4644***	503.2358	987.4408	494.2240	987.4538	494.2306	8
17	1927.8559	***964.4316***	1909.8323	955.4198	1909.8453	955.4263	Q	891.3833	446.1953	873.3597	437.1835	873.3727	437.1900	7
18	2027.9213	***1014.4643***	2009.8977	1005.4525	2009.9107	1005.4590	V	***761.3307***	381.1690	743.3071	372.1572	743.3201	372.1637	6
19	2191.9817	***1096.4945***	2173.9581	1087.4827	2173.9711	1087.4892	Y	***661.2652***	331.1362	643.2416	322.1245	643.2546	322.1310	5
20	2322.0213	***1161.5143***	2303.9977	1152.5025	2304.0107	1152.5090	E	497.2048	249.1061	479.1813	240.0943	479.1943	240.1008	4
21	2380.0398	1190.5235	2362.0162	1181.5117	2362.0292	1181.5183	G	***367.1652***	184.0862	349.1416	175.0745	349.1547	175.0810	3
22	2510.0794	***1255.5434***	2492.0558	1246.5316	2492.0689	1246.5381	E	309.1467	155.0770	291.1231	146.0652	291.1362	146.0717	2
23							R	179.1071	90.0572	161.0835	81.0454			1

AT5G02500.1



NCBI **BLAST** search of EQVFSTYSDNQPGVLIQVYEGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.2	2687.1719	0.0020	EQVFSTYSDNQPGVLIQVYEGER
4.3	2687.1706	0.0033	DCILEVRAGTGGEEASLFAMDIFR
1.1	2687.1683	0.0056	DISEKVALGMASTGGKGGGEVMYDQR
0.8	2687.1670	0.0069	NIDEVNHDKPNWRSDARIEWR
0.8	2687.1757	-0.0018	DSREVFGEQTSLKIDGIQTNTCR
0.1	2687.1784	-0.0045	AYTKWVAEMAQGLSTGVPWIMCK

Mascot: http://www.matrixscience.com/

AT5G02790.1

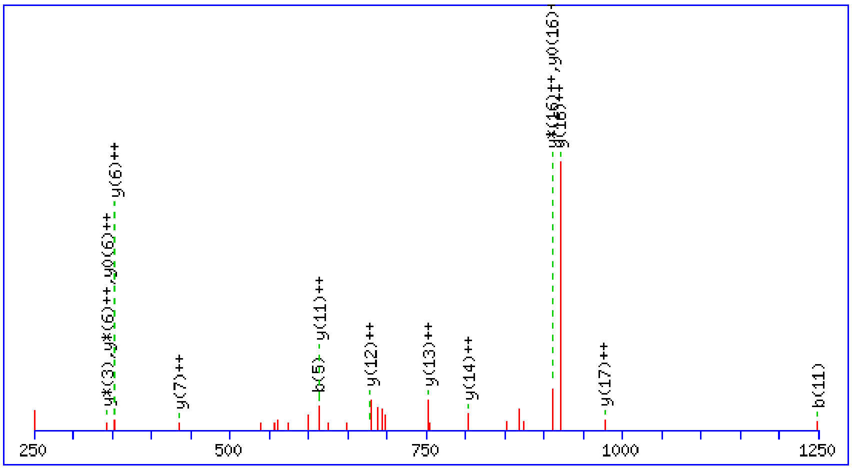
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLDNTFEGPSLYPEDHAK**
Found in **AT5G02790.1** in **TAIR_Arabidopsis**, Symbols: | In2-1 protein, putative | chr5:632875-634856 FORWARD

Match to Query 9790: 2116.886823 from(706.636217,3+) index(6424)
Title: Elution from: 56.395 to 56.395 scan no 8129 cid35.00 polarity:+
Data file C7-3_1.mgf

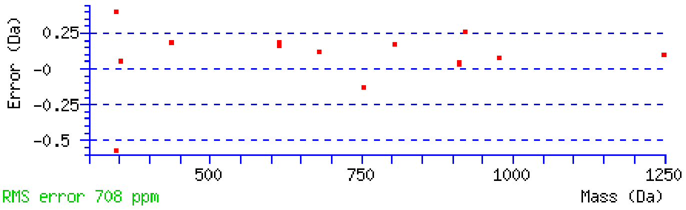
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

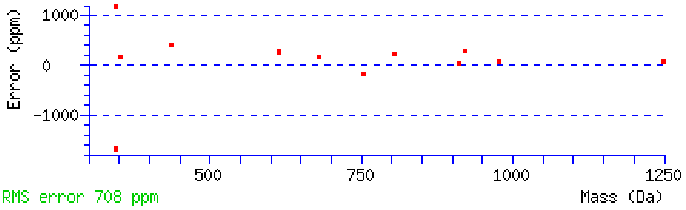


Monoisotopic mass of neutral peptide Mr(calc): 2116.8882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 8.2e-005
Matches : 15/188 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							18
2	279.1487	140.0780					L	1953.8351	977.4212	1935.8115	968.4094	1935.8246	968.4159	17
3	395.1727	198.0900			377.1622	189.0847	D	1839.7540	920.3807	1821.7304	911.3689	1821.7435	911.3754	16
4	511.2097	256.1085	493.1861	247.0967	493.1991	247.1032	N	1723.7301	862.3687	1705.7065	853.3569	1705.7195	853.3634	15
5	**613.2544**	307.1309	595.2308	298.1191	595.2439	298.1256	T	1607.6931	804.3502	1589.6695	795.3384	1589.6825	795.3449	14
6	761.3199	381.1636	743.2963	372.1518	743.3093	372.1583	F	1505.6483	753.3278	1487.6248	744.3160	1487.6378	744.3225	13
7	891.3595	446.1834	873.3359	437.1716	873.3489	437.1781	E	1357.5829	679.2951	1339.5593	670.2833	1339.5723	670.2898	12
8	949.3780	475.1926	931.3544	466.1808	931.3674	466.1874	G	1227.5433	614.2753	1209.5197	605.2635	1209.5327	605.2700	11
9	1047.4278	524.2175	1029.4042	515.2057	1029.4172	515.2123	P	1169.5248	585.2660	1151.5012	576.2542	1151.5142	576.2607	10
10	1135.4569	568.2321	1117.4333	559.2203	1117.4463	559.2268	S	1071.4750	536.2411	1053.4514	527.2293	1053.4644	527.2358	9
11	**1249.5380**	625.2726	1231.5144	616.2608	1231.5274	616.2673	L	983.4459	492.2266	965.4223	483.2148	965.4353	483.2213	8
12	1413.5983	707.3028	1395.5747	698.2910	1395.5878	698.2975	Y	869.3648	435.1860	851.3412	426.1743	851.3542	426.1808	7
13	1511.6481	756.3277	1493.6245	747.3159	1493.6376	747.3224	P	705.3044	353.1559	687.2809	344.1441	687.2939	344.1506	6
14	1641.6878	821.3475	1623.6642	812.3357	1623.6772	812.3422	E	607.2546	304.1310	589.2311	295.1192	589.2441	295.1257	5
15	1757.7117	879.3595	1739.6881	870.3477	1739.7012	870.3542	D	477.2150	239.1111	459.1914	230.0994	459.2045	230.1059	4
16	1897.7617	949.3845	1879.7382	940.3727	1879.7512	940.3792	H	361.1910	181.0992	343.1675	172.0874			3
17	1969.7959	985.4016	1951.7723	976.3898	1951.7853	976.3963	A	221.1410	111.0741	203.1174	102.0624			2
18							K	149.1069	75.0571	131.0833	66.0453			1

AT5G02790.1





NCBI **BLAST** search of YLDNTFEGPSLYPEDHAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.2	2116.8882	-0.0014	YLDNTFEGPSLYPEDHAK
7.1	2116.8902	-0.0034	VSYSNKSMTPFCADTMKK
5.0	2116.8873	-0.0005	CNTQMVIPHLTENYGASR
3.8	2116.8827	0.0041	QWNDVTNTVWWQDFPR
3.4	2116.8869	-0.0000	LHPPFPMMAPHESTEDVK
3.2	2116.8873	-0.0004	DRLGCFNLSIDGHAECVK
2.4	2116.8812	0.0056	NFGVTSFHSICGDAPDIEK
2.3	2116.8907	-0.0038	MLSQRDMGKMISSGSAFGR
2.0	2116.8899	-0.0031	QQPPGPRMPDGTRGFSMGR
2.0	2116.8871	-0.0003	KATCETSLKHTETSDEEK

Mascot: http://www.matrixscience.com/

AT5G02870.1

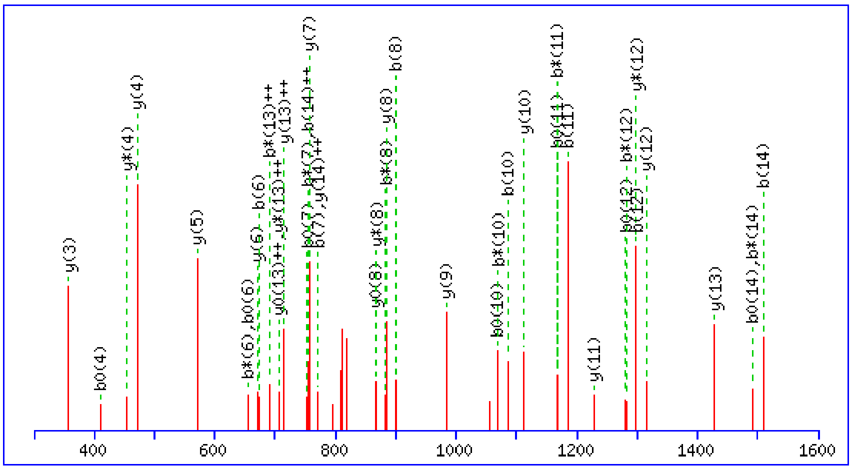
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IINSDEVQSVVNPIK**
Found in **AT5G02870.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L4/L1 (RPL4D) | chr5:657828-659524 FORWARD

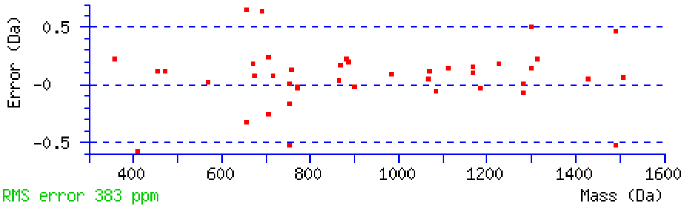
Match to Query 7095: 1653.892350 from(827.953451,2+) index(5662)
Title: Elution from: 52.814 to 52.814 scan no 7362 cid35.00 polarity:+
Data file D1d-1_3.mgf

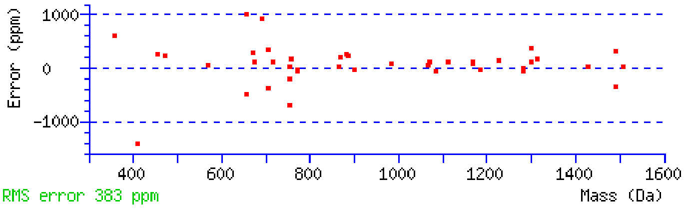
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1653.8937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 3.9e-011
Matches : 42/146 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							15
2	227.1754	114.0913					I	1541.8170	771.4121	1524.7904	762.8988	1523.8064	762.4068	14
3	341.2183	171.1128	324.1918	162.5995			N	***1428.7329***	714.8701	1411.7063	706.3568	1410.7223	705.8648	13
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	***1314.6900***	657.8486	1297.6634	649.3353	1296.6794	648.8433	12
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	D	***1227.6579***	614.3326	1210.6314	605.8193	1209.6474	605.3273	11
6	**672.3199**	336.6636	655.2933	328.1503	654.3093	327.6583	E	***1112.6310***	556.8191	1095.6045	548.3059	1094.6204	547.8139	10
7	**771.3883**	386.1978	754.3618	377.6845	753.3777	377.1925	V	***983.5884***	492.2978	966.5619	483.7846	965.5778	483.2926	9
8	**899.4469**	450.2271	882.4203	441.7138	881.4363	441.2218	Q	***884.5200***	442.7636	867.4934	434.2504	866.5094	433.7584	8
9	986.4789	493.7431	969.4524	485.2298	968.4683	484.7378	S	***756.4614***	378.7343	739.4349	370.2211	738.4509	369.7291	7
10	**1085.5473**	543.2773	1068.5208	534.7640	1067.5368	534.2720	V	***669.4294***	335.2183	652.4028	326.7051			6
11	**1184.6157**	592.8115	1167.5892	584.2982	1166.6052	583.8062	V	***570.3610***	285.6841	553.3344	277.1709			5
12	**1298.6587**	649.8330	1281.6321	641.3197	1280.6481	640.8277	N	***471.2926***	236.1499	454.2660	227.6366			4
13	1395.7114	698.3594	1378.6849	689.8461	1377.7009	689.3541	P	***357.2496***	179.1285	340.2231	170.6152			3
14	**1508.7955**	754.9014	1491.7689	746.3881	1490.7849	745.8961	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IINSDEVQSVVNPIK

AT5G02870.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.4	1653.8937	-0.0014	IINSDEVQSVVNPIK
9.8	1653.8878	0.0045	GWLNSSLPWIEPKK

AT5G03250.1

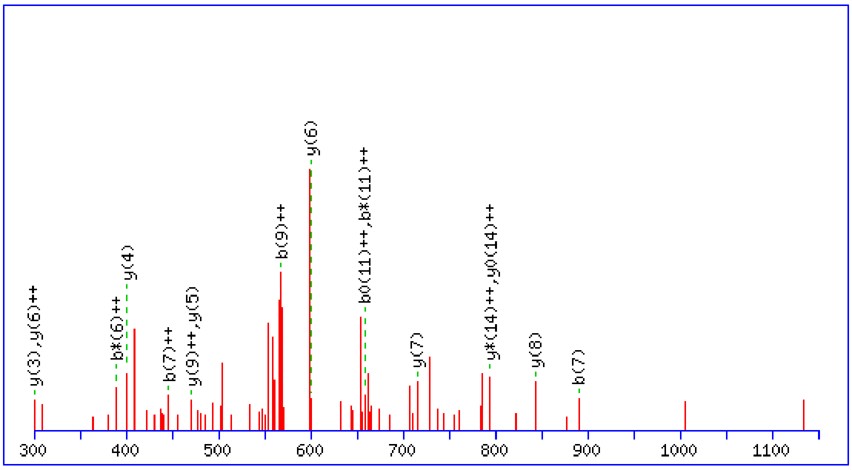
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSECCKPKDQATPAI**
Found in **AT5G03250.1** in **TAIR_Arabidopsis**, Symbols: | phototropic-responsive NPH3 family protein | chr5:774590-776854 FORWARD

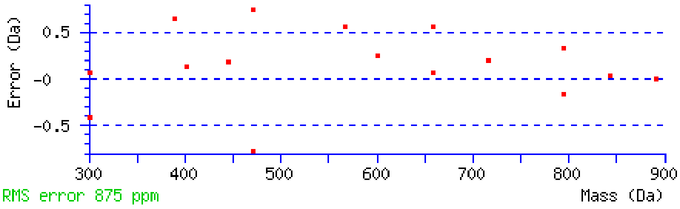
Match to Query 7998: 1731.833265 from(578.285031,3+) index(4935)
Title: Elution from: 44.995 to 44.995 scan no 6212 cid35.00 polarity:+
Data file C7-1_3.mgf

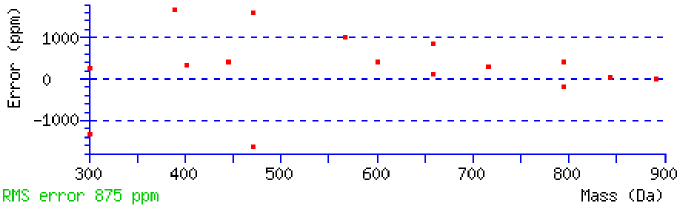
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1731.8284
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.045
Matches : 16/150 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							15
2	216.1343	108.5708	199.1077	100.0575	198.1237	99.5655	S	1604.7407	802.8740	1587.7142	794.3607	1586.7301	793.8687	14
3	345.1769	173.0921	328.1503	164.5788	327.1663	164.0868	E	1517.7087	759.3580	1500.6821	750.8447	1499.6981	750.3527	13
4	505.2075	253.1074	488.1810	244.5941	487.1969	244.1021	C	1388.6661	694.8367	1371.6395	686.3234	1370.6555	685.8314	12
5	665.2382	333.1227	648.2116	324.6094	647.2276	324.1174	C	1228.6354	614.8214	1211.6089	606.3081	1210.6249	605.8161	11
6	793.3331	397.1702	776.3066	388.6569	775.3226	388.1649	K	1068.6048	534.8060	1051.5782	526.2928	1050.5942	525.8007	10
7	890.3859	**445.6966**	873.3593	437.1833	872.3753	436.6913	P	940.5098	470.7586	923.4833	462.2453	922.4993	461.7533	9
8	1018.4808	509.7441	1001.4543	501.2308	1000.4703	500.7388	K	***843.4571***	422.2322	826.4305	413.7189	825.4465	413.2269	8
9	1133.5078	**567.2575**	1116.4812	558.7443	1115.4972	558.2523	D	***715.3621***	358.1847	698.3355	349.6714	697.3515	349.1794	7
10	1261.5664	631.2868	1244.5398	622.7735	1243.5558	622.2815	Q	***600.3352***	300.6712	583.3086	292.1579	582.3246	291.6659	6
11	1332.6035	666.8054	1315.5769	658.2921	1314.5929	657.8001	A	***472.2766***	236.6419			454.2660	227.6366	5
12	1433.6512	717.3292	1416.6246	708.8159	1415.6406	708.3239	T	***401.2395***	201.1234			383.2289	192.1181	4
13	1530.7039	765.8556	1513.6774	757.3423	1512.6934	756.8503	P	***300.1918***	150.5995					3
14	1601.7410	801.3742	1584.7145	792.8609	1583.7305	792.3689	A	203.1390	102.0731					2
15							I	132.1019	66.5546					1





NCBI **BLAST** search of KSECCKPKDQATPAI

AT5G03250.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.0	1731.8284	0.0049	KSECCKPKDQATPAI
8.0	1731.8322	0.0011	MDEARQAAKNGLEQR

AT5G03290.1

{MATRIX SCIENCE} Mascot Search Results

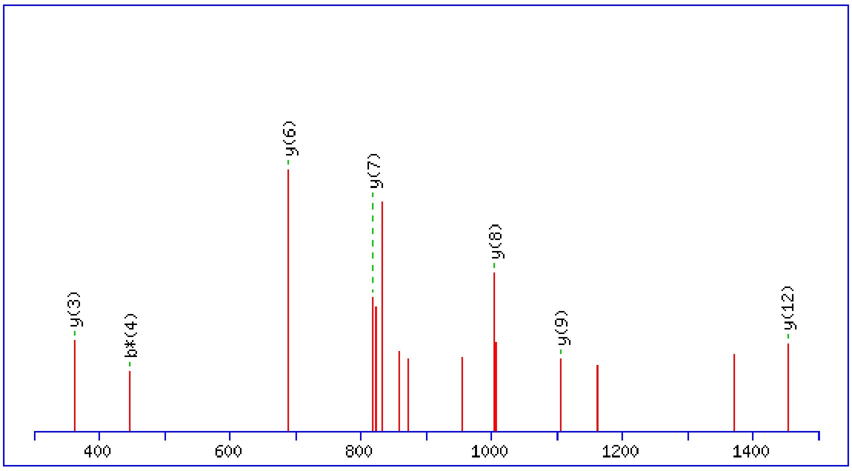
Peptide View

MS/MS Fragmentation of **TQSFLTWESLESVR**
Found in **AT5G03290.1** in **TAIR_Arabidopsis**, Symbols: | isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative | chr5:794042-795938 FORWARD

Match to Query 8023: 1681.834000 from(841.924276,2+) index(9143)
Title: Elution from: 80.768 to 80.768 scan no 12290 cid35.00 polarity:+
Data file D1d-3_2.mgf

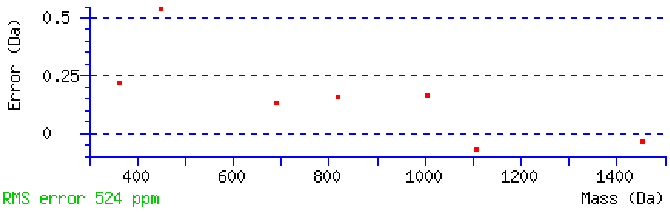
Click mouse within plot area to zoom in by factor of two about that point

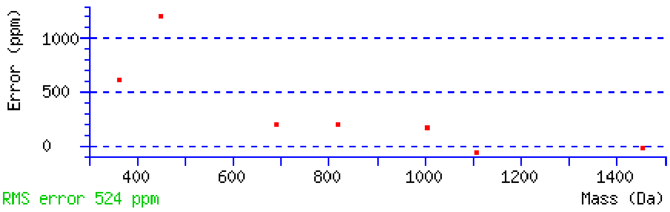
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1681.8311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00096
Matches : 7/150 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**14**
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	**Q**	1581.7907	791.3990	1564.7642	782.8857	1563.7802	782.3937	**13**
3	317.1456	159.0764	300.1190	150.5631	299.1350	150.0711	**S**	***1453.7322***	727.3697	1436.7056	718.8564	1435.7216	718.3644	**12**
4	464.2140	232.6106	447.1874	224.0974	446.2034	223.6053	**F**	1366.7001	683.8537	1349.6736	675.3404	1348.6896	674.8484	**11**
5	577.2980	289.1527	560.2715	280.6394	559.2875	280.1474	**L**	1219.6317	610.3195	1202.6052	601.8062	1201.6212	601.3142	**10**
6	678.3457	339.6765	661.3192	331.1632	660.3352	330.6712	**T**	***1106.5477***	553.7775	1089.5211	545.2642	1088.5371	544.7722	**9**
7	864.4250	432.7162	847.3985	424.2029	846.4145	423.7109	**W**	***1005.5000***	503.2536	988.4734	494.7404	987.4894	494.2483	**8**
8	993.4676	497.2375	976.4411	488.7242	975.4571	488.2322	**E**	***819.4207***	410.2140	802.3941	401.7007	801.4101	401.2087	**7**
9	1080.4997	540.7535	1063.4731	532.2402	1062.4891	531.7482	**S**	***690.3781***	345.6927	673.3515	337.1794	672.3675	336.6874	**6**
10	1193.5837	597.2955	1176.5572	588.7822	1175.5732	588.2902	**L**	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	**5**
11	1322.6263	661.8168	1305.5998	653.3035	1304.6157	652.8115	**E**	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	**4**
12	1409.6583	705.3328	1392.6318	696.8195	1391.6478	696.3275	**S**	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	**3**
13	1508.7268	754.8670	1491.7002	746.3537	1490.7162	745.8617	**V**	274.1874	137.5973	257.1608	129.0840			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TQSFLTWESLESVR

AT5G03290.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.3	1681.8311	0.0029	TQSFLTWESLESVR
5.6	1681.8345	-0.0005	KTGEFSNSEAIAMGIK
0.0	1681.8383	-0.0043	RYTNVSTAGTIQESR

AT5G03300.1

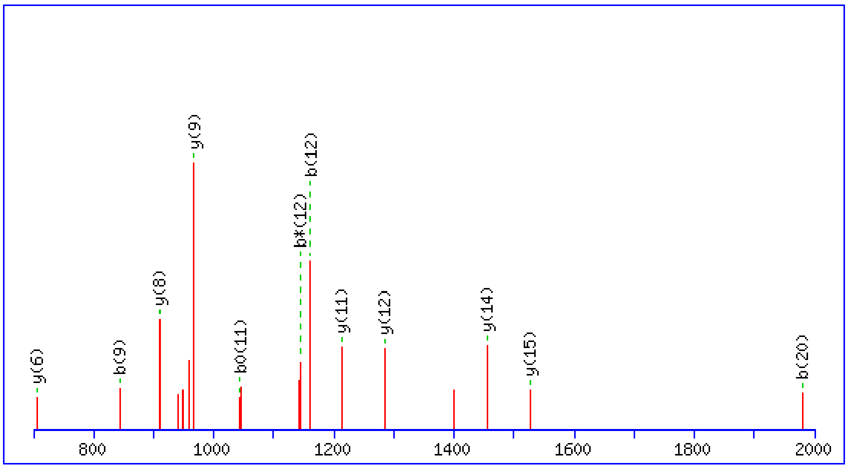
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVDTNGAGDAFVGGFMSQLVK**
Found in **AT5G03300.1** in **TAIR_Arabidopsis**, Symbols: ADK2 | ADK2 (ADENOSINE KINASE 2); kinase | chr5:796572-798996 FORWARD

Match to Query 9682: 2125.050326 from(1063.532439,2+) index(10565)
Title: Elution from: 101.936 to 101.936 scan no 15156 cid35.00 polarity:+
Data file 0-1_2.mgf

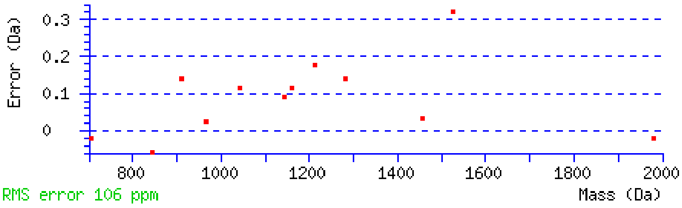
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 700 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

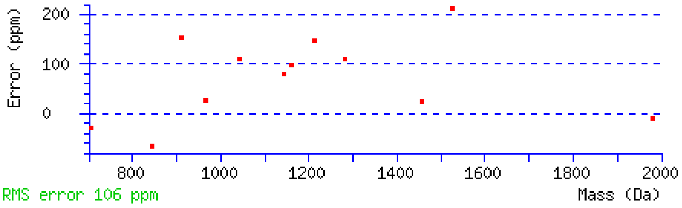


Monoisotopic mass of neutral peptide Mr(calc): 2125.0514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.8e-005
Matches : 12/220 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							21
2	213.1598	107.0835					V	2012.9746	1006.9909	1995.9481	998.4777	1994.9640	997.9857	20
3	328.1867	164.5970			310.1761	155.5917	D	1913.9062	957.4567	1896.8796	948.9435	1895.8956	948.4515	19
4	429.2344	215.1208			411.2238	206.1155	T	1798.8792	899.9433	1781.8527	891.4300	1780.8687	890.9380	18
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	N	1697.8316	849.4194	1680.8050	840.9061	1679.8210	840.4141	17
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	G	1583.7886	792.3980	1566.7621	783.8847	1565.7781	783.3927	16
7	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	A	***1526.7672***	763.8872	1509.7406	755.3740	1508.7566	754.8819	15
8	728.3573	364.6823	711.3308	356.1690	710.3468	355.6770	G	***1455.7301***	728.3687	1438.7035	719.8554	1437.7195	719.3634	14
9	**843.3843**	422.1958	826.3577	413.6825	825.3737	413.1905	D	1398.7086	699.8579	1381.6821	691.3447	1380.6980	690.8527	13
10	914.4214	457.7143	897.3949	449.2011	896.4108	448.7091	A	***1283.6817***	642.3445	1266.6551	633.8312	1265.6711	633.3392	12
11	1061.4898	531.2485	1044.4633	522.7353	1043.4793	522.2433	F	***1212.6445***	606.8259	1195.6180	598.3126	1194.6340	597.8206	11
12	**1160.5582**	580.7828	1143.5317	572.2695	1142.5477	571.7775	V	1065.5761	533.2917	1048.5496	524.7784	1047.5656	524.2864	10
13	1217.5797	609.2935	1200.5531	600.7802	1199.5691	600.2882	G	***966.5077***	483.7575	949.4812	475.2442	948.4972	474.7522	9
14	1274.6012	637.8042	1257.5746	629.2909	1256.5906	628.7989	G	***909.4863***	455.2468	892.4597	446.7335	891.4757	446.2415	8
15	1421.6696	711.3384	1404.6430	702.8251	1403.6590	702.3331	F	852.4648	426.7360	835.4382	418.2228	834.4542	417.7307	7
16	1552.7101	776.8587	1535.6835	768.3454	1534.6995	767.8534	M	***705.3964***	353.2018	688.3698	344.6886	687.3858	344.1965	6
17	1639.7421	820.3747	1622.7155	811.8614	1621.7315	811.3694	S	574.3559	287.6816	557.3293	279.1683	556.3453	278.6763	5
18	1767.8007	884.4040	1750.7741	875.8907	1749.7901	875.3987	Q	487.3239	244.1656	470.2973	235.6523			4
19	1880.8847	940.9460	1863.8582	932.4327	1862.8742	931.9407	L	359.2653	180.1363	342.2387	171.6230			3
20	**1979.9531**	990.4802	1962.9266	981.9669	1961.9426	981.4749	V	246.1812	123.5942	229.1547	115.0810			2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT5G03300.1





NCBI **BLAST** search of LVDTNGAGDAFVGGFMSQLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.1	2125.0514	-0.0011	LVDTNGAGDAFVGGFMSQLVK
3.2	2125.0448	0.0055	MAYPERSLIVDPRSGFCK
0.5	2125.0552	-0.0049	ALRLDTGNYSWGSEATTRK

Mascot: http://www.matrixscience.com/

AT5G03340.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDLFLVR**
Found in **AT5G03340.1** in **TAIR_Arabidopsis**, Symbols: | (Cell division control protein 48 homolog E); ATPase | chr5:810090-813132 REVERSE

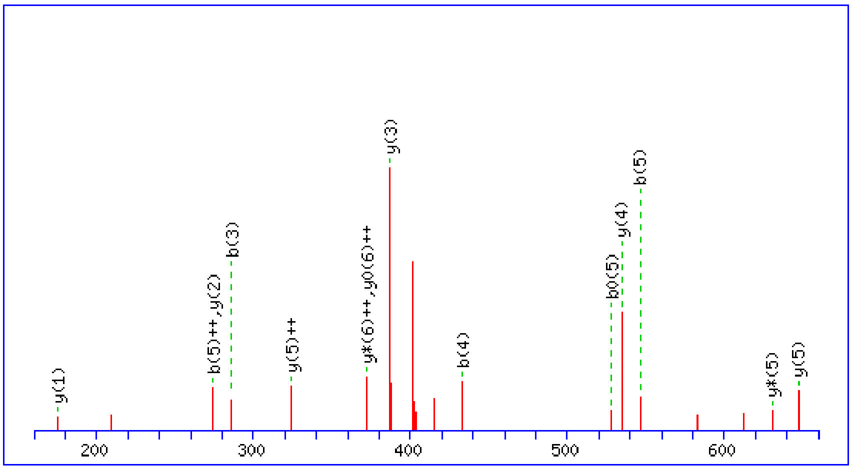
Match to Query 1192: 818.465446 from(410.239999,2+) index(6018)
Title: Elution from: 52.792 to 52.792 scan no 7487 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 160 to 660 Da Full range

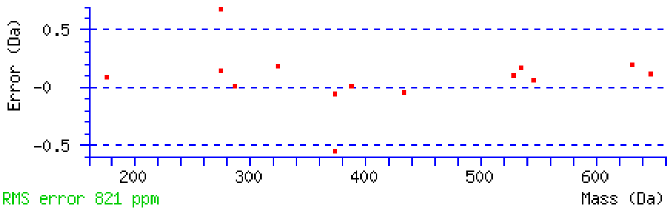
Label all possible matches ○ Label matches used for scoring ●

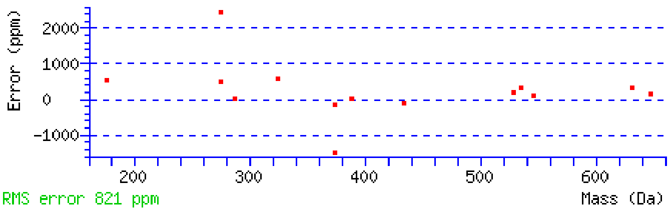
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 818.4650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00012
Matches : 14/48 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							7
2	173.0557	87.0315	155.0451	78.0262	D	762.4509	381.7291	745.4243	373.2158	744.4403	372.7238	6
3	**286.1397**	143.5735	268.1292	134.5682	L	***647.4239***	324.2156	630.3974	315.7023			5
4	**433.2082**	217.1077	415.1976	208.1024	F	***534.3398***	267.6736	517.3133	259.1603			4
5	**546.2922**	273.6498	528.2817	264.6445	L	***387.2714***	194.1394	370.2449	185.6261			3
6	645.3606	323.1840	627.3501	314.1787	V	***274.1874***	137.5973	257.1608	129.0840			2
7					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GDLFLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.3	818.4650	0.0004	GDLFLVR
13.4	818.4650	0.0004	FGDLLVR
0.4	818.4650	0.0004	GLVEFVR

AT5G03340.1

Mascot: http://www.matrixscience.com/

AT5G03530.1

Mascot Search Results

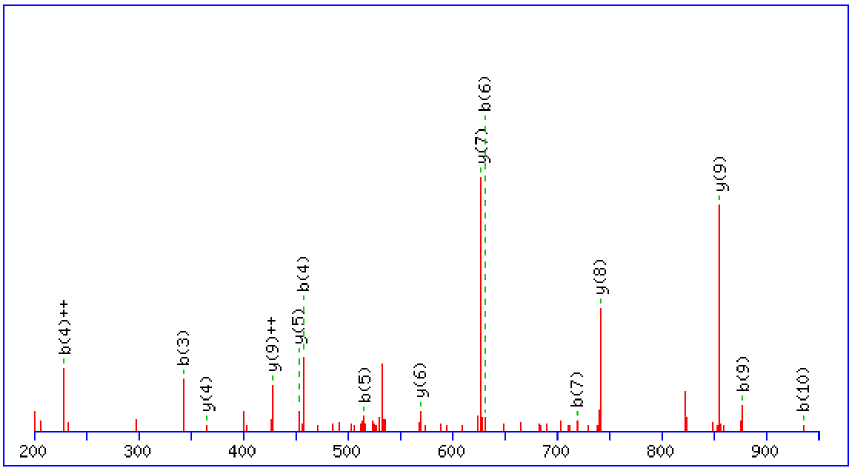
Peptide View

MS/MS Fragmentation of **ILLIGDSGVGK**
Found in **AT5G03530.1** in **TAIR_Arabidopsis**, Symbols: AtRab18B, AtRABC2a, ATRAB, ATRAB ALPHA | ATRAB ALPHA (Arabidopsis Rab GTPase homolog C2a); GTP binding | chr5:885740-887060 REVERSE

Match to Query 3209: 1082.597426 from(542.305989,2+) index(5747)
Title: Elution from: 51.404 to 51.404 scan no 7337 cid35.00 polarity:+
Data file 0-2_2.mgf

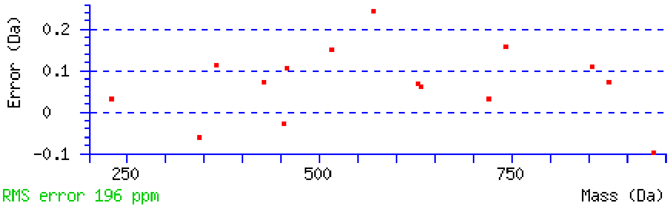
Click mouse within plot area to zoom in by factor of two about that point

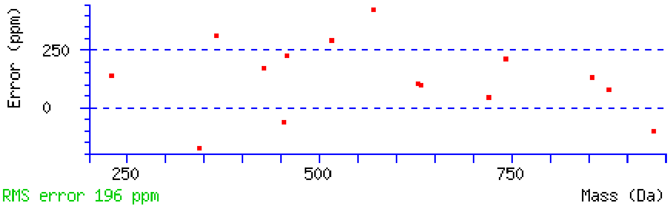
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1082.5980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.9e-006
Matches : 16/82 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							11
2	***229.1695***	115.0884			L	969.5242	485.2657	951.5006	476.2539	951.5136	476.2604	10
3	***343.2506***	172.1289			L	**855.4431**	428.2252	837.4195	419.2134	837.4325	419.2199	9
4	***457.3317***	229.1695			I	**741.3620**	371.1846	723.3384	362.1728	723.3514	362.1793	8
5	***515.3502***	258.1787			G	**627.2809**	314.1441	609.2573	305.1323	609.2703	305.1388	7
6	***631.3741***	316.1907	613.3636	307.1854	D	**569.2624**	285.1348	551.2388	276.1230	551.2518	276.1295	6
7	***719.4032***	360.2052	701.3926	351.2000	S	**453.2384**	227.1228	435.2148	218.1110	435.2278	218.1175	5
8	777.4217	389.2145	759.4111	380.2092	G	**365.2093**	183.1083	347.1857	174.0965			4
9	***877.4872***	439.2472	859.4766	430.2419	V	307.1908	154.0990	289.1672	145.0873			3
10	***935.5057***	468.2565	917.4951	459.2512	G	207.1254	104.0663	189.1018	95.0545			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ILLIGDSGVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G03530.1

Score	Mr(calc)	Delta	Sequence
61.0	1082.5980	-0.0005	IILLGDSGVGK
61.0	1082.5980	-0.0005	ILLIGDSGVGK
61.0	1082.5980	-0.0005	LLLIGDSGVGK
25.1	1082.5980	-0.0005	LILLDETVR
2.6	1082.6006	-0.0032	VRANTLLPGK
1.2	1082.5980	-0.0005	LLDQVVEKK
1.0	1082.5980	-0.0006	ILKLVEDNK

AT5G03630.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGAFLEGGSPEENNAIAK**
Found in **AT5G03630.1** in **TAIR_Arabidopsis**, Symbols: ATMDAR2 | ATMDAR2; monodehydroascorbate reductase (NADH) | chr5:922377-924615 REVERSE

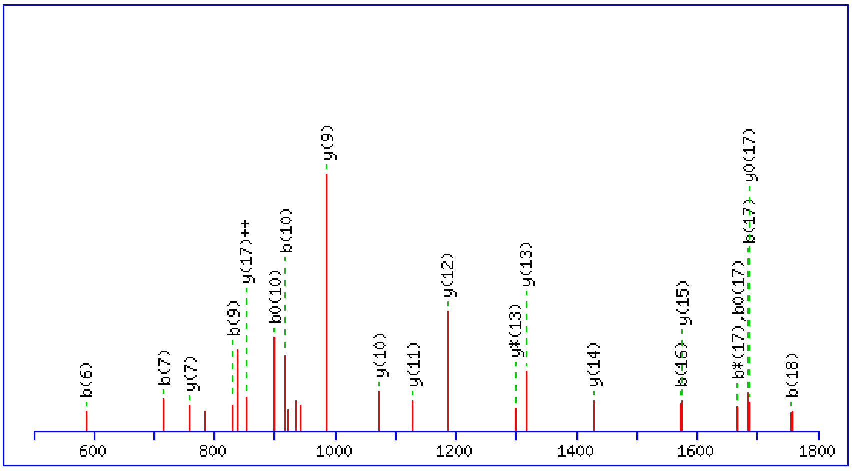
Match to Query 8783: 1900.949396 from(951.481974,2+) index(5622)
Title: Elution from: 50.061 to 50.061 scan no 7128 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

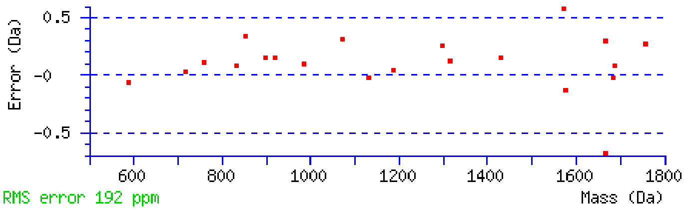
Show Y-axis ☐

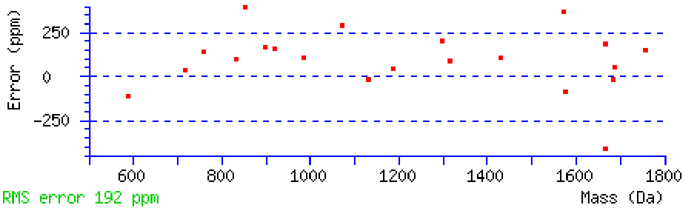


Monoisotopic mass of neutral peptide Mr(calc): 1900.9530
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 5.9e-007
Matches : 21/166 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							19
2	199.1441	100.0757					V	1802.8919	901.9496	1785.8654	893.4363	1784.8814	892.9443	18
3	256.1656	128.5864					G	1703.8235	852.4154	1686.7970	843.9021	1685.8129	843.4101	17
4	327.2027	164.1050					A	1646.8020	823.9047	1629.7755	815.3914	1628.7915	814.8994	16
5	474.2711	237.6392					F	***1575.7649***	788.3861	1558.7384	779.8728	1557.7544	779.3808	15
6	***587.3552***	294.1812					L	***1428.6965***	714.8519	1411.6700	706.3386	1410.6859	705.8466	14
7	***716.3978***	358.7025			698.3872	349.6972	E	***1315.6124***	658.3099	1298.5859	649.7966	1297.6019	649.3046	13
8	773.4192	387.2132			755.4087	378.2080	G	***1186.5699***	593.7886	1169.5433	585.2753	1168.5593	584.7833	12
9	***830.4407***	415.7240			812.4301	406.7187	G	***1129.5484***	565.2778	1112.5218	556.7646	1111.5378	556.2726	11
10	***917.4727***	459.2400			899.4621	450.2347	S	***1072.5269***	536.7671	1055.5004	528.2538	1054.5164	527.7618	10
11	1014.5255	507.7664			996.5149	498.7611	P	***985.4949***	493.2511	968.4684	484.7378	967.4843	484.2458	9
12	1143.5681	572.2877			1125.5575	563.2824	E	888.4421	444.7247	871.4156	436.2114	870.4316	435.7194	8
13	1272.6107	636.8090			1254.6001	627.8037	E	***759.3995***	380.2034	742.3730	371.6901	741.3890	371.1981	7
14	1386.6536	693.8304	1369.6270	685.3172	1368.6430	684.8251	N	630.3569	315.6821	613.3304	307.1688			6
15	1500.6965	750.8519	1483.6700	742.3386	1482.6859	741.8466	N	516.3140	258.6606	499.2875	250.1474			5
16	***1571.7336***	786.3705	1554.7071	777.8572	1553.7231	777.3652	A	402.2711	201.6392	385.2445	193.1259			4
17	***1684.8177***	842.9125	1667.7911	834.3992	1666.8071	833.9072	I	331.2340	166.1206	314.2074	157.6074			3
18	***1755.8548***	878.4310	1738.8283	869.9178	1737.8442	869.4258	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT5G03630.1





NCBI **BLAST** search of VVGAFLEGGSPEENNAIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.8	1900.9530	-0.0036	VVGAFLEGGSPEENNAIAK

Mascot: http://www.matrixscience.com/

AT5G03690.2

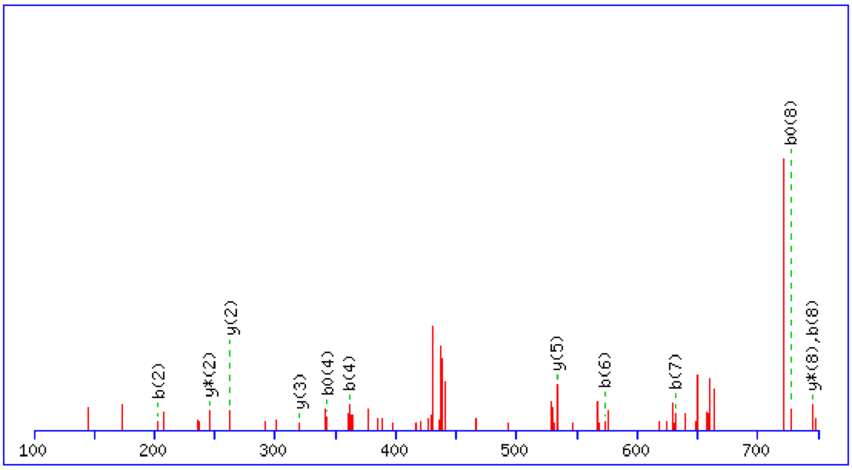
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAGVLPGIK**
Found in **AT5G03690.2** in **TAIR_Arabidopsis**, Symbols: | fructose-bisphosphate aldolase, putative | chr5:963388-964981 REVERSE

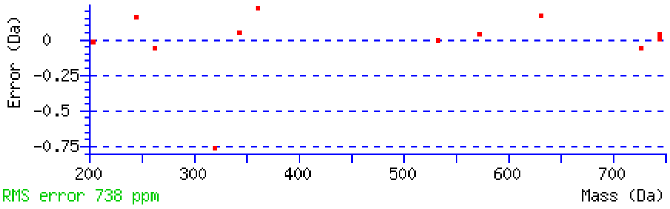
Match to Query 1486: 892.485666 from(447.250109,2+) index(4681)
Title: Elution from: 43.193 to 43.193 scan no 5900 cid35.00 polarity:+
Data file D6h-1_2.mgf

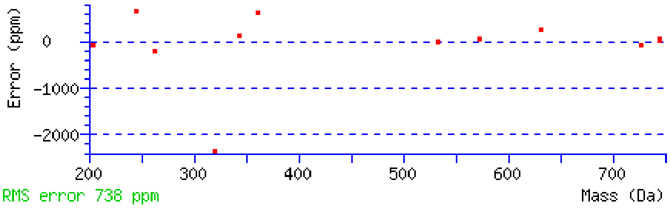
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 892.4878
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.048
Matches : 12/64 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	131.0469	66.0271	113.0363	57.0218	E					9
2	***203.0811***	102.0442	185.0705	93.0389	A	763.4555	382.2314	745.4319	373.2196	8
3	261.0996	131.0534	243.0890	122.0481	G	691.4213	346.2143	673.3977	337.2025	7
4	***361.1650***	181.0861	343.1544	172.0809	V	633.4028	317.2050	615.3792	308.1933	6
5	475.2461	238.1267	457.2355	229.1214	L	**533.3374**	267.1723	515.3138	258.1605	5
6	***573.2959***	287.1516	555.2853	278.1463	P	419.2563	210.1318	401.2327	201.1200	4
7	***631.3144***	316.1608	613.3038	307.1556	G	**321.2065**	161.1069	303.1829	152.0951	3
8	***745.3955***	373.2014	727.3849	364.1961	I	**263.1880**	132.0976	245.1644	123.0858	2
9					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of EAGVLPGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.6	892.4878	-0.0021	EAGVLPGIK

AT5G03690.2

12.0	892.4878	-0.0022	LGNLEIPK
3.5	892.4878	-0.0022	NLPELGLK
2.1	892.4878	-0.0022	ELLINPGK

AT5G04050.1

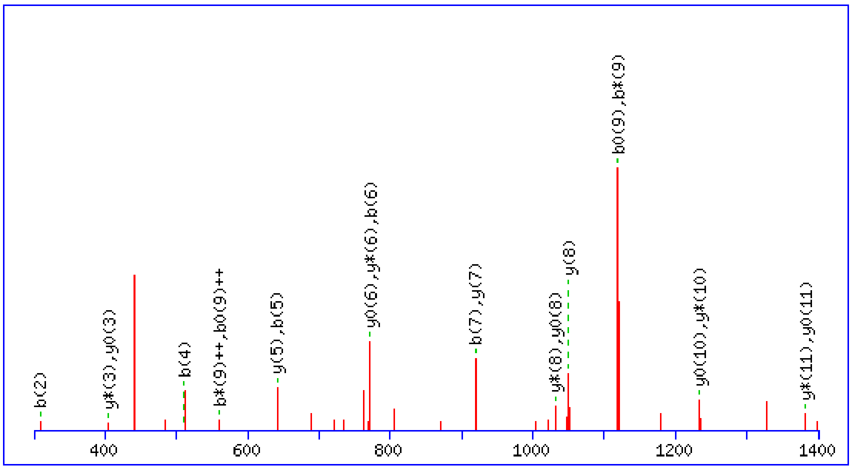
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RFSIEEMGREIR**
Found in **AT5G04050.1** in **TAIR_Arabidopsis**, Symbols: | maturase-related | chr5:1096091-1097794 FORWARD

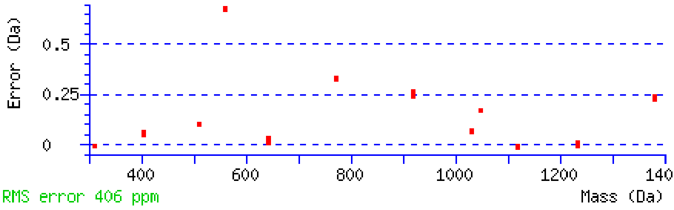
Match to Query 6748: 1558.701170 from(780.357861,2+) index(7919)
Title: Elution from: 70.265 to 70.265 scan no 10465 cid35.00 polarity:+
Data file 0-1_3.mgf

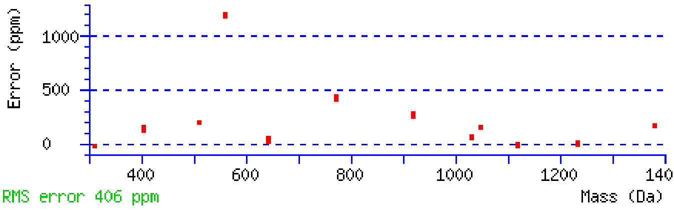
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1558.7048
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0026
Matches : 23/190 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							12
2	***309.1620***	155.0846	291.1384	146.0728			F	1399.6229	700.3151	1381.5993	691.3033	1381.6123	691.3098	11
3	397.1910	199.0992	379.1675	190.0874	379.1805	190.0939	S	1251.5574	626.2823	1233.5338	617.2706	1233.5469	617.2771	10
4	***511.2721***	256.1397	493.2486	247.1279	493.2616	247.1344	I	1163.5284	582.2678	1145.5048	573.2560	1145.5178	573.2625	9
5	***641.3118***	321.1595	623.2882	312.1477	623.3012	312.1542	E	**1049.4473**	525.2273	1031.4237	516.2155	1031.4367	516.2220	8
6	***771.3514***	386.1793	753.3278	377.1675	753.3408	377.1741	E	**919.4076**	460.2075	901.3840	451.1957	901.3971	451.2022	7
7	***919.3838***	460.1956	901.3602	451.1838	901.3733	451.1903	M	789.3680	395.1876	771.3444	386.1758	771.3574	386.1824	6
8	977.4023	489.2048	959.3787	480.1930	959.3918	480.1995	G	**641.3356**	321.1714	623.3120	312.1596	623.3250	312.1661	5
9	1137.4916	569.2494	1119.4680	560.2376	1119.4810	560.2441	R	583.3171	292.1622	565.2935	283.1504	565.3065	283.1569	4
10	1267.5312	634.2692	1249.5076	625.2574	1249.5206	625.2640	E	423.2278	212.1175	405.2042	203.1058	405.2173	203.1123	3
11	***1381.6123***	691.3098	1363.5887	682.2980	1363.6017	682.3045	I	293.1882	147.0977	275.1646	138.0859			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RFSIEEMGREIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G04050.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.9	1558.7048	-0.0037	RFSIEEMGREIR
17.4	1558.6974	0.0037	CGSLSCAEKIFLR
6.7	1558.7000	0.0012	TEMKAKLSASSSER
6.3	1558.6992	0.0019	DRSYAEANSIQKR
6.1	1558.6974	0.0038	ECGFGVTGMVSIKR
6.1	1558.7014	-0.0003	YAAREADFIAQAGR
5.2	1558.7019	-0.0007	RAKPNGEAHAEQAR
2.5	1558.6992	0.0019	QSLLEHQTPANGSR
1.7	1558.7048	-0.0037	SPHLIRNEGKCDL
0.6	1558.7010	0.0002	WAYVGGFTEEKQK

AT5G04140.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGLQVLGWR**
Found in **AT5G04140.1** in **TAIR_Arabidopsis**, Symbols: GLU1, GLS1, GLUS | GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1); glutamate synthase (ferredoxin) | chr5:1130032-1138187 FORWARD

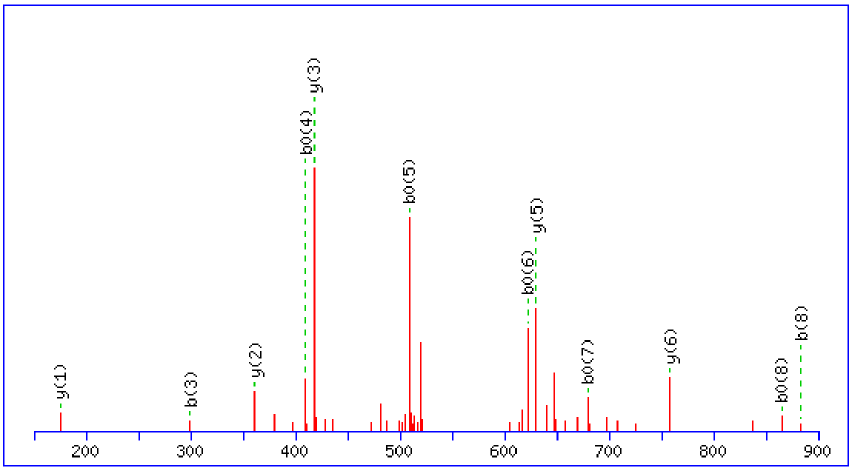
Match to Query 2923: 1056.571888 from(529.293220,2+) index(7098)
Title: Elution from: 63.398 to 63.398 scan no 9276 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

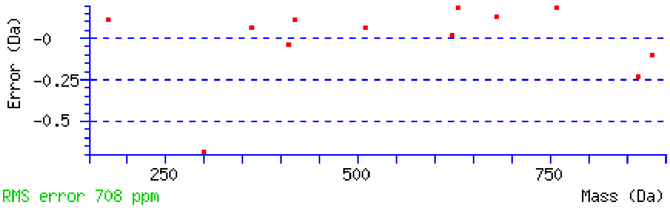
Label all possible matches ○ Label matches used for scoring ●

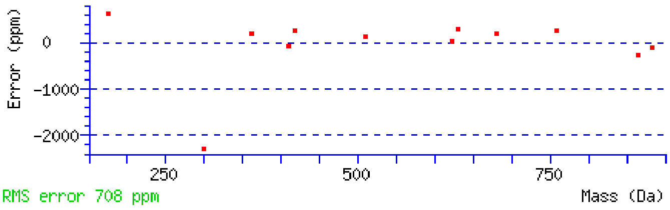
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.5716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 4.3e-005
Matches : 12/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.0499	65.5286			112.0393	56.5233	E					9
2	187.0713	94.0393			169.0608	85.0340	G	928.5363	464.7718	911.5098	456.2585	8
3	**300.1554**	150.5813			282.1448	141.5761	L	871.5148	436.2611	854.4883	427.7478	7
4	428.2140	214.6106	411.1874	206.0974	**410.2034**	205.6053	Q	***758.4308***	379.7190	741.4042	371.2058	6
5	527.2824	264.1448	510.2558	255.6316	**509.2718**	255.1396	V	***630.3722***	315.6897	613.3457	307.1765	5
6	640.3665	320.6869	623.3399	312.1736	**622.3559**	311.6816	L	531.3038	266.1555	514.2772	257.6423	4
7	697.3879	349.1976	680.3614	340.6843	**679.3774**	340.1923	G	***418.2197***	209.6135	401.1932	201.1002	3
8	**883.4672**	442.2373	866.4407	433.7240	**865.4567**	433.2320	W	***361.1983***	181.1028	344.1717	172.5895	2
9							R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of EGLQVLGWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G04140.1

46.7	1056.5716	0.0003	EGLQVLGWR
0.0	1056.5716	0.0003	LLWNIENR

Mascot: http://www.matrixscience.com/

AT5G04360.1

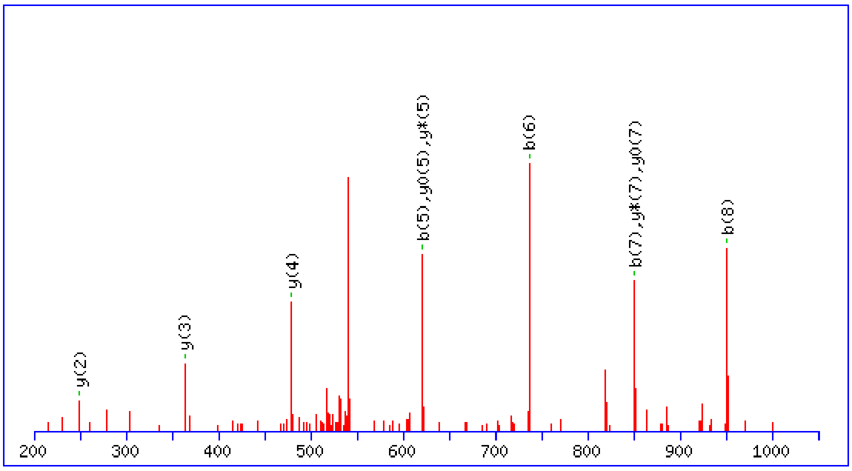
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLDIRDLVK**
Found in **AT5G04360.1** in **TAIR_Arabidopsis**, Symbols: ATPU1, ATLDA | ATLDA/ATPU1 (PULLULANASE 1); alpha-amylase/ limit dextrinase | chr5:1221567-1228400 FORWARD

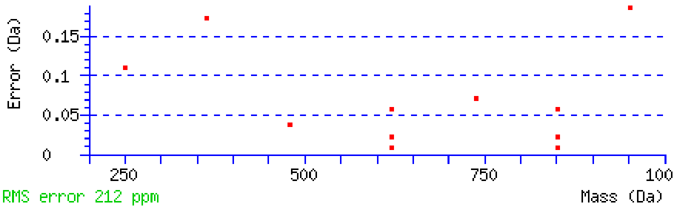
Match to Query 2901: 1098.567608 from(550.291080,2+) index(2218)
Title: Elution from: 27.464 to 27.464 scan no 2919 cid35.00 polarity:+
Data file D1d-2_2.mgf

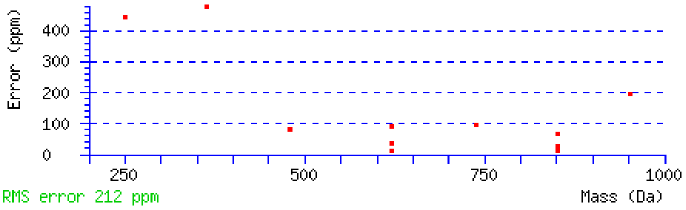
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1098.5695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00077
Matches : 11/82 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	**D**							**9**
2	231.1124	116.0598			213.1018	107.0545	**L**	983.5528	492.2801	965.5292	483.2683	965.5423	483.2748	**8**
3	347.1363	174.0718			329.1258	165.0665	**D**	869.4717	435.2395	851.4481	426.2277	851.4612	426.2342	**7**
4	461.2174	231.1124			443.2069	222.1071	**I**	753.4477	377.2275	735.4242	368.2157	735.4372	368.2222	**6**
5	***621.3067***	311.1570	603.2831	302.1452	603.2961	302.1517	**R**	639.3667	320.1870	621.3431	311.1752	621.3561	311.1817	**5**
6	***737.3307***	369.1690	719.3071	360.1572	719.3201	360.1637	**D**	**479.2774**	240.1423	461.2538	231.1305	461.2668	231.1371	**4**
7	***851.4118***	426.2095	833.3882	417.1977	833.4012	417.2042	**L**	**363.2534**	182.1303	345.2298	173.1186			**3**
8	***951.4772***	476.2422	933.4536	467.2304	933.4666	467.2370	**V**	**249.1723**	125.0898	231.1487	116.0780			**2**
9							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of DLDIRDLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G04360.1

37.4	1098.5695	-0.0019	DLDIRDLVK
21.5	1098.5695	-0.0019	IKEENNVLK
18.9	1098.5648	0.0028	RPNMLDVLK
6.3	1098.5695	-0.0019	KASDAPEIKK
4.3	1098.5695	-0.0019	ATDTVIKGPGK
3.5	1098.5695	-0.0019	TIVKASEPNK
2.0	1098.5670	0.0006	VLFPAKMHK
0.6	1098.5695	-0.0019	LQEINKDVK
0.2	1098.5695	-0.0019	LILSDGQNVK
0.2	1098.5695	-0.0019	SVLGTGSPAAVK

AT5G04430.1

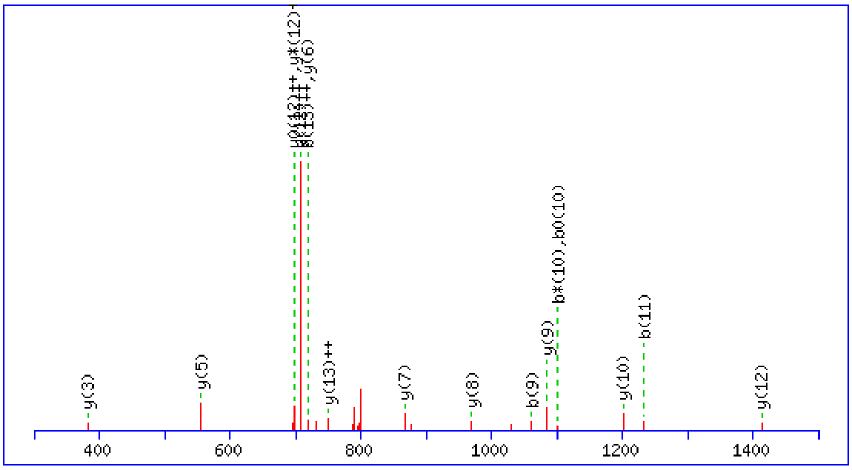
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISPLDNTFYGLSDR**
Found in **AT5G04430.1** in **TAIR_Arabidopsis**, Symbols: | KH domain-containing protein NOVA, putative | chr5:1250603-1253524 REVERSE

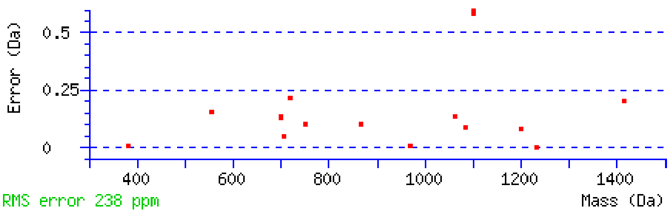
Match to Query 7329: 1614.724568 from(808.369560,2+) index(8095)
Title: Elution from: 71.234 to 71.234 scan no 10612 cid35.00 polarity:+
Data file D12h-1_2.mgf

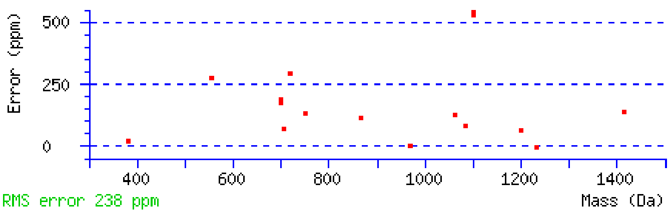
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1614.7250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.9e-007
Matches : 17/142 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**I**							**14**
2	203.1174	102.0624			185.1069	93.0571	**S**	1501.6512	751.3292	1483.6276	742.3174	1483.6406	742.3240	**13**
3	301.1672	151.0873			283.1567	142.0820	**P**	***1413.6221***	707.3147	1395.5985	698.3029	1395.6116	698.3094	**12**
4	415.2483	208.1278			397.2378	199.1225	**L**	1315.5723	658.2898	1297.5487	649.2780	1297.5618	649.2845	**11**
5	531.2723	266.1398			513.2617	257.1345	**D**	***1201.4912***	601.2493	1183.4676	592.2375	1183.4807	592.2440	**10**
6	647.3093	324.1583	629.2857	315.1465	629.2987	315.1530	**N**	***1085.4673***	543.2373	1067.4437	534.2255	1067.4567	534.2320	**9**
7	749.3540	375.1807	731.3304	366.1689	731.3435	366.1754	**T**	***969.4303***	485.2188	951.4067	476.2070	951.4197	476.2135	**8**
8	897.4195	449.2134	879.3959	440.2016	879.4089	440.2081	**F**	***867.3855***	434.1964	849.3620	425.1846	849.3750	425.1911	**7**
9	**1061.4798**	531.2436	1043.4563	522.2318	1043.4693	522.2383	**Y**	***719.3201***	360.1637	701.2965	351.1519	701.3095	351.1584	**6**
10	1119.4983	560.2528	1101.4748	551.2410	1101.4878	551.2475	**G**	***555.2597***	278.1335	537.2361	269.1217	537.2492	269.1282	**5**
11	**1233.5794**	617.2934	1215.5559	608.2816	1215.5689	608.2881	**L**	497.2412	249.1243	479.2176	240.1125	479.2307	240.1190	**4**
12	1321.6085	661.3079	1303.5849	652.2961	1303.5979	652.3026	**S**	***383.1601***	192.0837	365.1365	183.0719	365.1496	183.0784	**3**
13	1437.6325	719.3199	1419.6089	710.3081	1419.6219	710.3146	**D**	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	**2**
14							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of ISPLDNTFYGLSDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G04430.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.9	1614.7250	-0.0004	ISPLDNTFYGLSDR
5.9	1614.7232	0.0014	SIDGSVRTDRETTR
4.8	1614.7227	0.0018	VTSFTSGGVVDGDSLR
1.7	1614.7284	-0.0038	LSPDADPVVHMSVSK
1.7	1614.7277	-0.0031	INARREPGYEFDK

AT5G04590.1

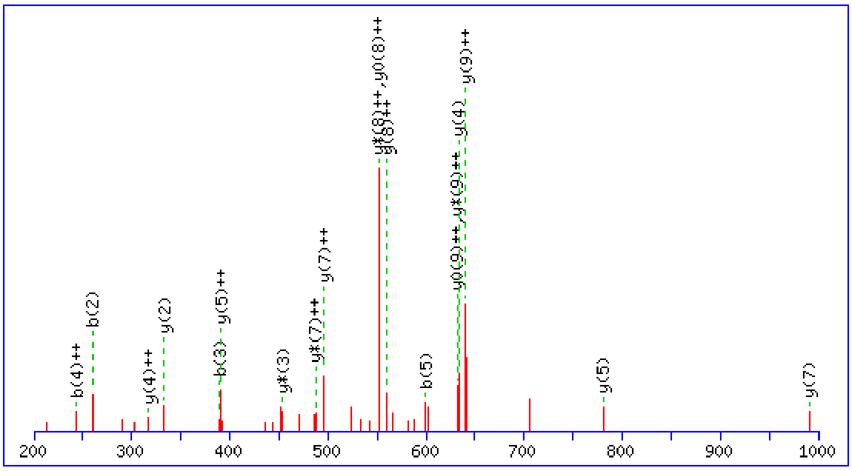
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCEPLFYHWK**
Found in **AT5G04590.1** in **TAIR_Arabidopsis**, Symbols: SIR | SIR (sulfite reductase); sulfite reductase (ferredoxin) | chr5:1319405-1322299 FORWARD

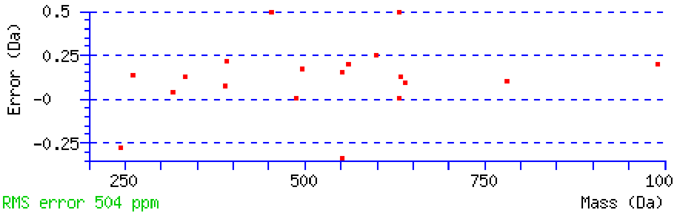
Match to Query 5691: 1377.651207 from(460.224345,3+) index(6448)
Title: Elution from: 56.209 to 56.209 scan no 8187 cid35.00 polarity:+
Data file D6h-1_1.mgf

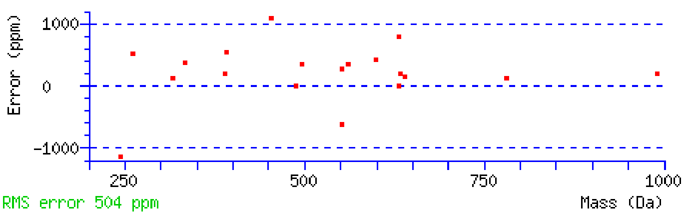
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1377.6540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.00091
Matches : 19/72 fragment ions using 24 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415			**V**							**10**
2	**260.1063**	130.5568			**C**	1279.5928	640.3001	1262.5663	631.7868	1261.5823	631.2948	**9**
3	**389.1489**	195.0781	371.1384	186.0728	**E**	1119.5622	560.2847	1102.5356	551.7715	1101.5516	551.2795	**8**
4	486.2017	243.6045	468.1911	234.5992	**P**	***990.5196***	495.7634	973.4931	487.2502			**7**
5	**599.2858**	300.1465	581.2752	291.1412	**L**	893.4668	447.2371	876.4403	438.7238			**6**
6	746.3542	373.6807	728.3436	364.6754	**F**	***780.3828***	390.6950	763.3562	382.1817			**5**
7	909.4175	455.2124	891.4069	446.2071	**Y**	***633.3144***	317.1608	616.2878	308.6475			**4**
8	1046.4764	523.7418	1028.4659	514.7366	**H**	470.2510	235.6292	453.2245	227.1159			**3**
9	1232.5557	616.7815	1214.5452	607.7762	**W**	***333.1921***	167.0997	316.1656	158.5864			**2**
10					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VCEPLFYHWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G04590.1

Score	Mr(calc)	Delta	Sequence
34.8	1377.6540	-0.0028	VCEPLFYHWK
1.4	1377.6525	-0.0013	VSDWSIVDSGSAR
1.1	1377.6493	0.0019	VSMAMSPSQRPR
1.0	1377.6519	-0.0007	EMDIIAALDEMK

AT5G04870.1

{MATRIX SCIENCE} Mascot Search Results

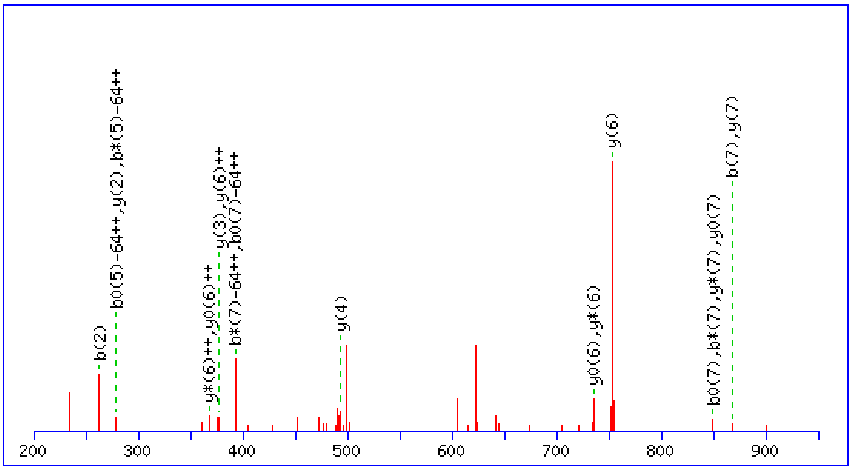
Peptide View

MS/MS Fragmentation of **MLVRDPKK**
Found in **AT5G04870.1** in **TAIR_Arabidopsis**, Symbols: AK1, ATCPK1, CPK1 | CPK1 (calcium-dependent protein kinase isoform AK1); calmodulin-dependent protein kinase/ kinase | chr5:1417016-1419878 REVERSE

Match to Query 2139: 1014.532552 from(508.273552,2+) index(5918)
Title: Elution from: 55.326 to 55.326 scan no 7658 cid35.00 polarity:+
Data file D12h-2_2.mgf

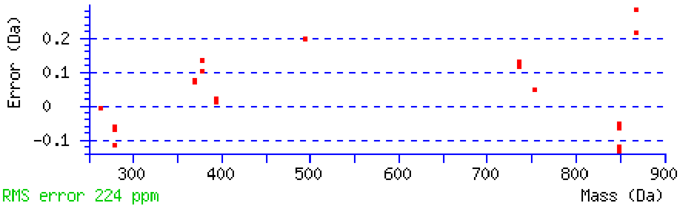
Click mouse within plot area to zoom in by factor of two about that point

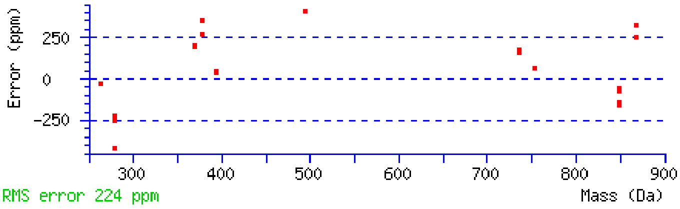
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1014.5306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.027
Matches : 20/92 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0397	75.0235					M							8
2	**263.1208**	132.0640					L	*867.5055*	434.2564	849.4819	425.2446	849.4949	425.2511	7
3	363.1863	182.0968					V	*753.4244*	377.2158	735.4008	368.2040	735.4138	368.2105	6
4	523.2755	262.1414	505.2519	253.1296			R	653.3589	327.1831	635.3354	318.1713	635.3484	318.1778	5
5	639.2995	320.1534	621.2759	311.1416	621.2889	311.1481	D	*493.2697*	247.1385	475.2461	238.1267	475.2591	238.1332	4
6	737.3493	369.1783	719.3257	360.1665	719.3387	360.1730	P	*377.2457*	189.1265	359.2221	180.1147			3
7	**867.4383**	434.2228	849.4147	425.2110	849.4278	425.2175	K	*279.1959*	140.1016	261.1723	131.0898			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MLVRDPKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G04870.1

23.8	1014.5306	0.0019	MLVRDPKK
21.7	1014.5354	-0.0028	ETNIASKLK
21.7	1014.5354	-0.0028	LGSGSVDKIK
21.7	1014.5306	0.0019	RDMVIQLK
14.4	1014.5306	0.0019	TMARPVSIK
11.8	1014.5306	0.0019	KMLVRDPK
8.9	1014.5306	0.0019	VQLQQKMK
8.1	1014.5306	0.0019	QQLVMIVR
7.9	1014.5306	0.0019	NVLRMLEK
7.6	1014.5306	0.0019	LGAKPCKTK

AT5G04950.1

MATRIX SCIENCE

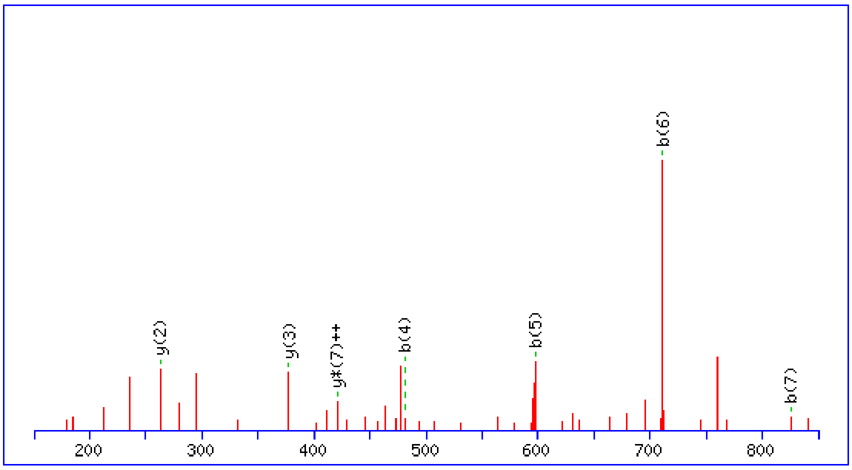
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMRANLIK**
Found in **AT5G04950.1** in **TAIR_Arabidopsis**, Symbols: | nicotianamine synthase, putative | chr5:1457877-1458839 REVERSE

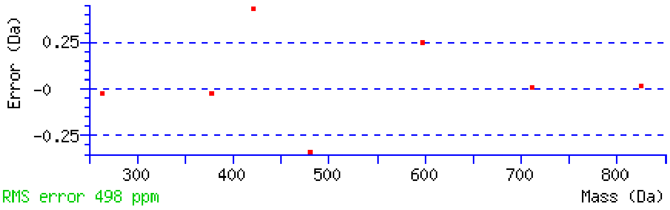
Match to Query 2220: 972.482304 from(487.248428,2+) index(5597)
Title: Elution from: 50.313 to 50.313 scan no 7133 cid35.00 polarity:+
Data file D6h-1_3.mgf

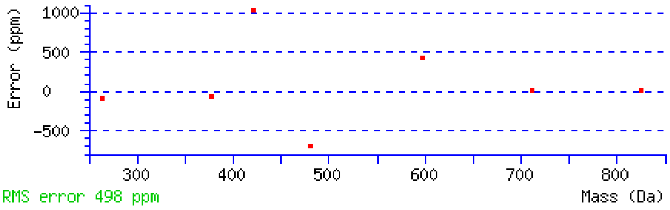
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.037
Matches : 7/66 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	117.0313	59.0193			99.0207	50.0140	D					8
2	249.0688	125.0380			231.0582	116.0327	M	857.4670	429.2371	839.4434	420.2253	7
3	409.1580	205.0827	391.1344	196.0709	391.1475	196.0774	R	725.4295	363.2184	707.4059	354.2066	6
4	***481.1922***	241.0997	463.1686	232.0879	463.1816	232.0944	A	565.3402	283.1737	547.3166	274.1620	5
5	***597.2292***	299.1182	579.2056	290.1064	579.2186	290.1129	N	493.3061	247.1567	475.2825	238.1449	4
6	***711.3103***	356.1588	693.2867	347.1470	693.2997	347.1535	L	**377.2691**	189.1382	359.2455	180.1264	3
7	***825.3914***	413.1993	807.3678	404.1875	807.3808	404.1940	I	**263.1880**	132.0976	245.1644	123.0858	2
8							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of DMRANLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.8	972.4837	-0.0014	DMRANLIK
24.3	972.4810	0.0013	MAEDKILK

AT5G04950.1

22.0	972.4810	0.0013	EDMKSLIK
22.0	972.4810	0.0013	KMEDALIK
22.0	972.4837	-0.0014	MELRIGNK
18.1	972.4799	0.0024	LFEEWLK
17.3	972.4810	0.0013	MLSEGAVLK
16.1	972.4810	0.0013	MKESLLDK
10.5	972.4832	-0.0009	MLVFDPVK
10.5	972.4837	-0.0014	MSHKVSKK

AT5G05170.1

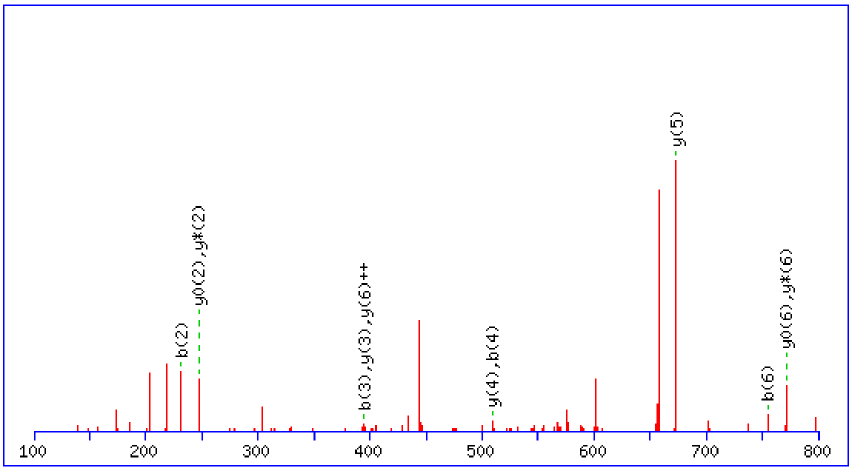
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDYLKDK**
Found in **AT5G05170.1** in **TAIR_Arabidopsis**, Symbols: CESA3, IXR1, ATCESA3, ATH-B, CEV1 | CESA3 (CELLULOSE SYNTHASE 3); cellulose synthase/ transferase, transferring glycosyl groups | chr5:1530402-1535091 REVERSE

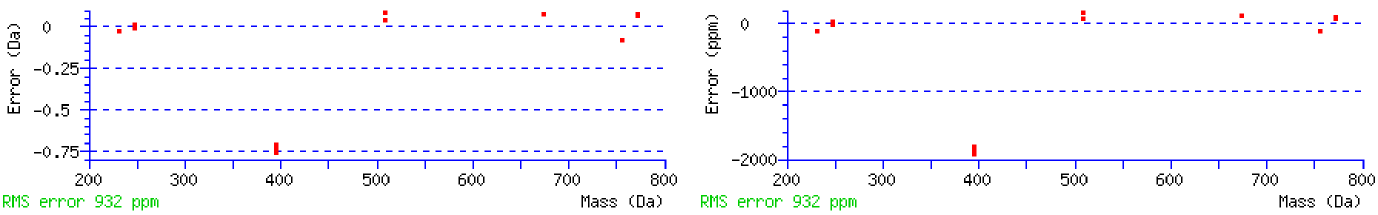
Match to Query 1547: 902.457256 from(452.235904,2+) index(5429)
Title: Elution from: 48.556 to 48.556 scan no 6916 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 902.4591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.034
Matches : 12/60 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							7
2	***231.1124***	116.0598			213.1018	107.0545	D	789.3853	395.1963	771.3617	386.1845	771.3748	386.1910	6
3	***395.1727***	198.0900			377.1622	189.0847	Y	**673.3613**	337.1843	655.3378	328.1725	655.3508	328.1790	5
4	***509.2538***	255.1305			491.2433	246.1253	L	**509.3010**	255.1541	491.2774	246.1423	491.2904	246.1488	4
5	639.3428	320.1751	621.3193	311.1633	621.3323	311.1698	K	**395.2199**	198.1136	377.1963	189.1018	377.2093	189.1083	3
6	***755.3668***	378.1871	737.3432	369.1753	737.3563	369.1818	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
7							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of IDYLKDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.5	902.4591	-0.0019	IDYLKDK
13.7	902.4591	-0.0019	VKYELDK

AT5G05170.1

12.4	902.4548	0.0024	NLARCKK
6.3	902.4548	0.0024	RGREIMK
5.2	902.4578	-0.0005	MEMKKVK
4.9	902.4591	-0.0019	DKYELVK
3.5	902.4591	-0.0019	DALTSFIK
3.5	902.4591	-0.0019	TVAYDVVK
2.5	902.4591	-0.0019	DLEVKYK
1.3	902.4591	-0.0019	IEGVYSVK

AT5G05400.1

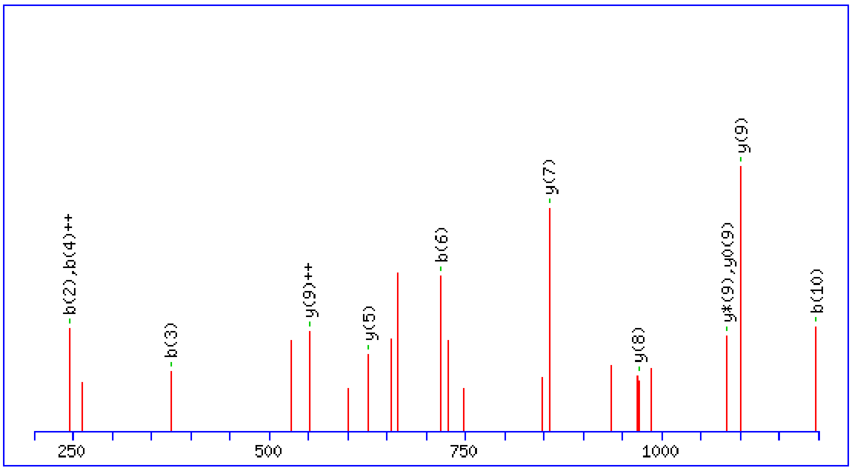
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKEINIKSCPK**
Found in **AT5G05400.1** in **TAIR_Arabidopsis**, Symbols: | disease resistance protein (CC-NBS-LRR class), putative | chr5:1597746-1600370 REVERSE

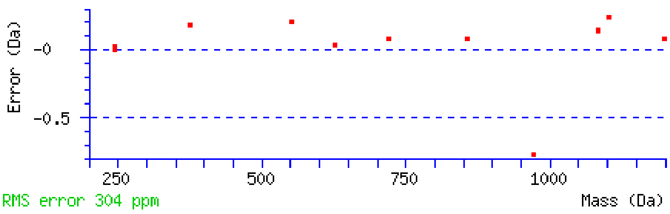
Match to Query 4565: 1344.701660 from(673.358106,2+) index(10119)
Title: Elution from: 99.990 to 99.990 scan no 14715 cid35.00 polarity:+
Data file D1d-2_2.mgf

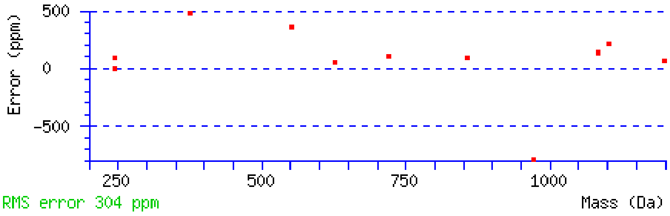
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1344.7012
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.026
Matches : 12/108 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					**L**							**11**
2	***245.1774***	123.0923	227.1538	114.0805			**K**	1231.6273	616.3173	1213.6038	607.3055	1213.6168	607.3120	**10**
3	***375.2170***	188.1122	357.1935	179.1004	357.2065	179.1069	**E**	***1101.5383***	551.2728	1083.5147	542.2610	1083.5277	542.2675	**9**
4	489.2981	245.1527	471.2746	236.1409	471.2876	236.1474	**I**	***971.4987***	486.2530	953.4751	477.2412	953.4881	477.2477	**8**
5	605.3351	303.1712	587.3115	294.1594	587.3246	294.1659	**N**	***857.4176***	429.2124	839.3940	420.2006	839.4070	420.2071	**7**
6	***719.4162***	360.2118	701.3926	351.2000	701.4057	351.2065	**I**	741.3806	371.1939	723.3570	362.1821	723.3700	362.1886	**6**
7	849.5053	425.2563	831.4817	416.2445	831.4947	416.2510	**K**	***627.2995***	314.1534	609.2759	305.1416	609.2889	305.1481	**5**
8	937.5343	469.2708	919.5107	460.2590	919.5238	460.2655	**S**	497.2105	249.1089	479.1869	240.0971	479.1999	240.1036	**4**
9	1099.5590	550.2832	1081.5355	541.2714	1081.5485	541.2779	**C**	409.1814	205.0943	391.1578	196.0825			**3**
10	***1197.6088***	599.3081	1179.5853	590.2963	1179.5983	590.3028	**P**	247.1567	124.0820	229.1331	115.0702			**2**
11							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of LKEINIKSCPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G05400.1

Score	Mr(calc)	Delta	Sequence
23.0	1344.7012	0.0005	LKEINIKSCPK
7.8	1344.6978	0.0039	LKPNTQYIPQK
3.9	1344.7034	-0.0017	EIYLGVMHKIK
3.1	1344.6978	0.0039	LEGLEGLPKFAR
1.7	1344.7034	-0.0017	KIWCAVIAIEK
1.7	1344.7034	-0.0017	KIWCAVIALEK
1.0	1344.7012	0.0005	QIVELPIMRSK
1.0	1344.7012	0.0005	SPGGLGLIKSLCK
0.7	1344.7012	0.0005	EIEVTMKPKVR

AT5G05540.1

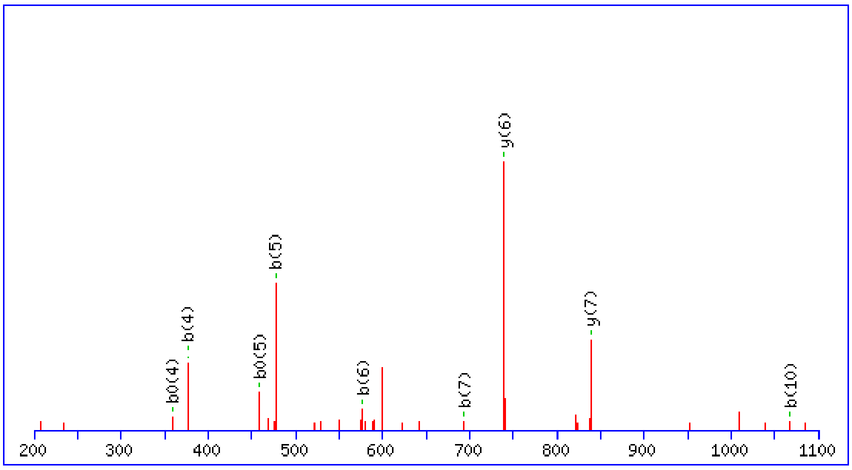
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATISVVDIQEK**
Found in **AT5G05540.1** in **TAIR_Arabidopsis**, Symbols: | exonuclease family protein | chr5:1636420-1638760 FORWARD

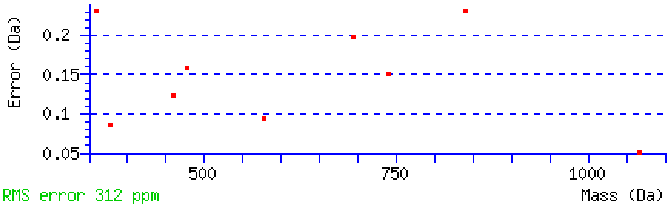
Match to Query 4516: 1214.619026 from(608.316789,2+) index(1791)
Title: Elution from: 21.999 to 21.999 scan no 2345 cid35.00 polarity:+
Data file D6h-1_1.mgf

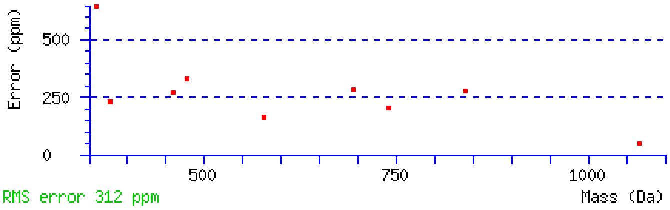
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1214.6169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.006
Matches : 9/100 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							11
2	175.0861	88.0467			157.0756	79.0414	T	1143.5900	572.2986	1125.5664	563.2868	1125.5794	563.2934	10
3	289.1672	145.0873			271.1567	136.0820	I	1041.5453	521.2763	1023.5217	512.2645	1023.5347	512.2710	9
4	*377.1963*	189.1018			359.1857	180.0965	S	927.4642	464.2357	909.4406	455.2239	909.4536	455.2304	8
5	*477.2617*	239.1345			459.2512	230.1292	V	**839.4351**	420.2212	821.4115	411.2094	821.4246	411.2159	7
6	*577.3272*	289.1672			559.3166	280.1620	V	**739.3697**	370.1885	721.3461	361.1767	721.3591	361.1832	6
7	*693.3512*	347.1792			675.3406	338.1739	D	639.3042	320.1558	621.2806	311.1440	621.2937	311.1505	5
8	807.4323	404.2198			789.4217	395.2145	I	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	4
9	937.4849	469.2461	919.4613	460.2343	919.4744	460.2408	Q	409.1991	205.1032	391.1756	196.0914	391.1886	196.0979	3
10	*1067.5246*	534.2659	1049.5010	525.2541	1049.5140	525.2606	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ATISVVDIQEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G05540.1

Score	Mr(calc)	Delta	Sequence
31.1	1214.6169	0.0022	ATISVVDIQEK
30.8	1214.6195	-0.0005	RTGSIVDVPAGK
15.0	1214.6218	-0.0027	KTLEHLQFGK
12.2	1214.6196	-0.0005	KNQASKAIDPK
5.8	1214.6195	-0.0005	LRDALNEQLK
2.8	1214.6195	-0.0005	VRVDLNELNK
2.7	1214.6169	0.0021	LSAISIAEAEAK
2.4	1214.6225	-0.0035	EIETMKPLVK
1.8	1214.6169	0.0022	DTKEEGVAIIK
1.7	1214.6169	0.0022	AVETASVSTIPK

AT5G05920.1

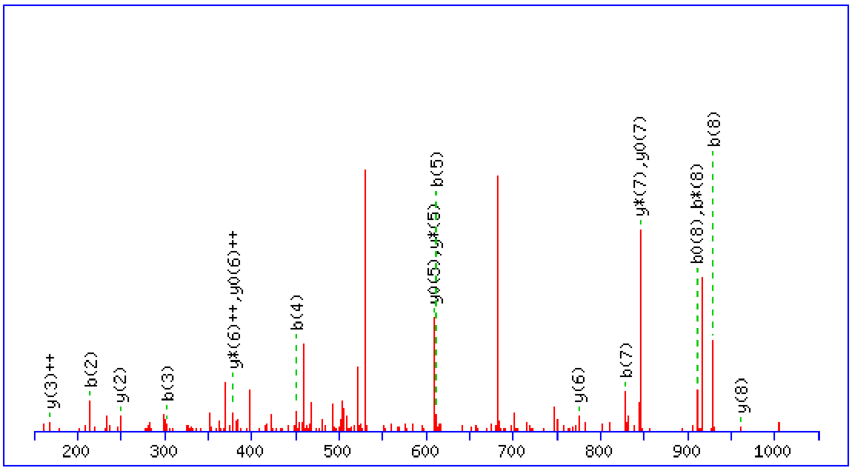
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPSFRESVK**
Found in **AT5G05920.1** in **TAIR_Arabidopsis**, Symbols: EDA22, DHS | DHS (embryo sac development arrest 22) | chr5:1777782-1779700 REVERSE

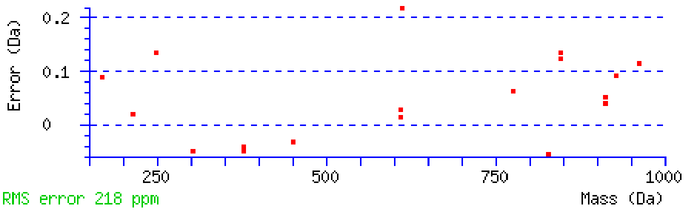
Match to Query 3054: 1076.501338 from(539.257945,2+) index(2768)
Title: Elution from: 28.326 to 28.326 scan no 3430 cid35.00 polarity:+
Data file 0-3_2.mgf

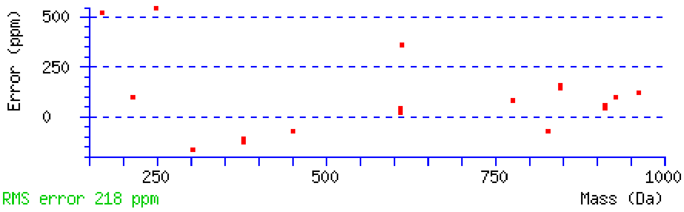
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1076.5043
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.016
Matches : 18/88 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							9
2	***215.0941***	108.0507	197.0705	99.0389			P	**961.4746**	481.2409	943.4510	472.2291	943.4640	472.2356	8
3	***303.1231***	152.0652	285.0996	143.0534	285.1126	143.0599	S	863.4248	432.2160	845.4012	423.2042	845.4142	423.2107	7
4	***451.1886***	226.0979	433.1650	217.0861	433.1780	217.0926	F	**775.3957**	388.2015	757.3721	379.1897	757.3851	379.1962	6
5	***611.2778***	306.1426	593.2543	297.1308	593.2673	297.1373	R	627.3303	314.1688	609.3067	305.1570	609.3197	305.1635	5
6	741.3175	371.1624	723.2939	362.1506	723.3069	362.1571	E	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
7	***829.3465***	415.1769	811.3229	406.1651	811.3360	406.1716	S	337.2014	169.1043	319.1778	160.0925	319.1908	160.0990	3
8	***929.4120***	465.2096	911.3884	456.1978	911.4014	456.2043	V	**249.1723**	125.0898	231.1487	116.0780			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NPSFRESVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G05920.1

27.2	1076.5043	-0.0030	NPSFRESVK
11.5	1076.5016	-0.0003	SASEVVFAEK
9.3	1076.5038	-0.0025	DDPAFYVLK
8.2	1076.5003	0.0011	AMKVENMVK
6.2	1076.4995	0.0018	RAVWMVER
5.7	1076.5003	0.0011	AMKVENMVK
5.7	1076.5003	0.0011	IVSMAVMNGK
5.2	1076.5016	-0.0003	KDESDVVFK
4.4	1076.5002	0.0011	MVKTEICGK
4.3	1076.5002	0.0011	GKLMGVEGMK

AT5G05940.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENLVKSCAGIEK**
Found in **AT5G05940.1** in **TAIR_Arabidopsis**, Symbols: ATROPGEF5, ROPGEF5 | ATROPGEF5/ROPGEF5 (KINASE PARTNER PROTEIN-LIKE); Rho guanyl-nucleotide exchange factor/ | chr5:1786029-1788364 FORWARD

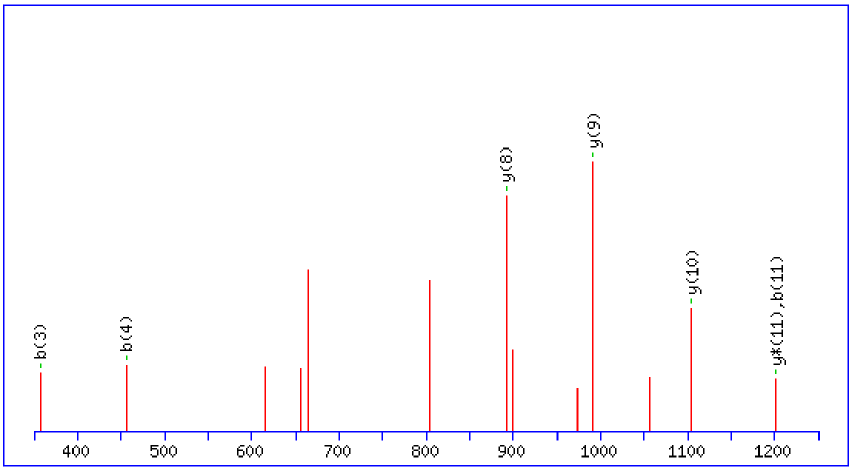
Match to Query 4971: 1346.687024 from(674.350788,2+) index(5521)
Title: Elution from: 50.385 to 50.385 scan no 6983 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1250 Da Full range

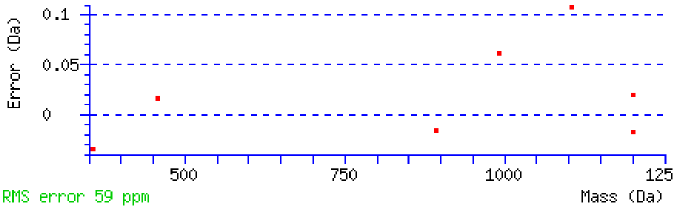
Label all possible matches ○ Label matches used for scoring ●

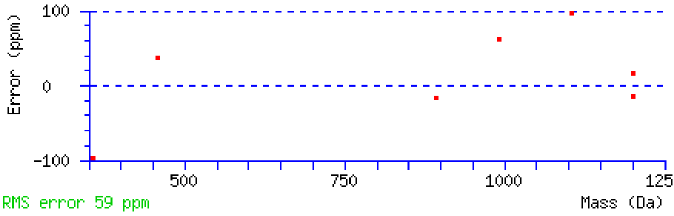
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1346.6864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.041
Matches : 7/128 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							12
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	N	1218.6511	609.8292	1201.6245	601.3159	1200.6405	600.8239	11
3	***357.1769***	179.0921	340.1503	170.5788	339.1663	170.0868	L	***1104.6082***	552.8077	1087.5816	544.2944	1086.5976	543.8024	10
4	***456.2453***	228.6263	439.2187	220.1130	438.2347	219.6210	V	***991.5241***	496.2657	974.4975	487.7524	973.5135	487.2604	9
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	K	***892.4557***	446.7315	875.4291	438.2182	874.4451	437.7262	8
6	671.3723	336.1898	654.3457	327.6765	653.3617	327.1845	S	764.3607	382.6840	747.3342	374.1707	746.3502	373.6787	7
7	831.4029	416.2051	814.3764	407.6918	813.3923	407.1998	C	677.3287	339.1680	660.3021	330.6547	659.3181	330.1627	6
8	902.4400	451.7237	885.4135	443.2104	884.4295	442.7184	A	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	5
9	959.4615	480.2344	942.4349	471.7211	941.4509	471.2291	G	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
10	1072.5456	536.7764	1055.5190	528.2631	1054.5350	527.7711	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	***1201.5881***	601.2977	1184.5616	592.7844	1183.5776	592.2924	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ENLVKSCAGIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G05940.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.8	1346.6864	0.0007	ENLVKSCAGIEK
12.7	1346.6904	-0.0034	LNELWVSMVEK
11.1	1346.6830	0.0040	ERFVQESDIPK
8.3	1346.6864	0.0006	KDMGPTKTDLGGK
2.0	1346.6864	0.0007	EVKLGCEEQKK
1.8	1346.6904	-0.0034	NFPPKEVMEIK
1.5	1346.6904	-0.0034	CGIAIEPSYPIK

AT5G06060.1

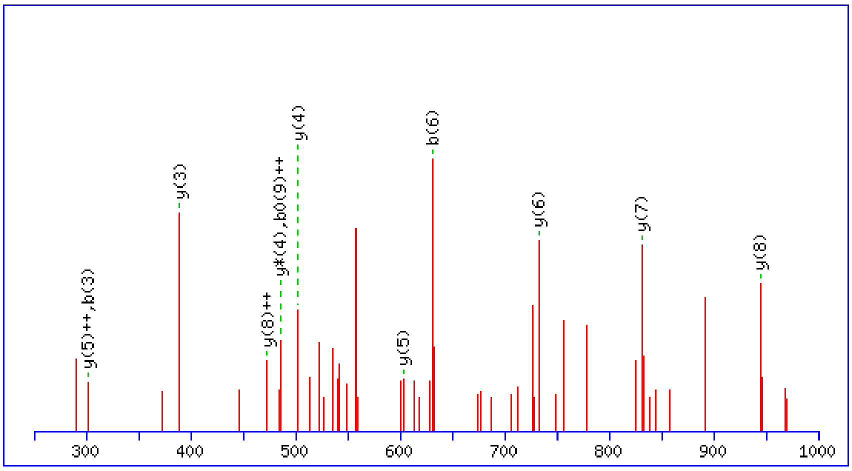
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSLVETLLEK**
Found in **AT5G06060.1** in **TAIR_Arabidopsis**, Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr5:1824067-1825834 REVERSE

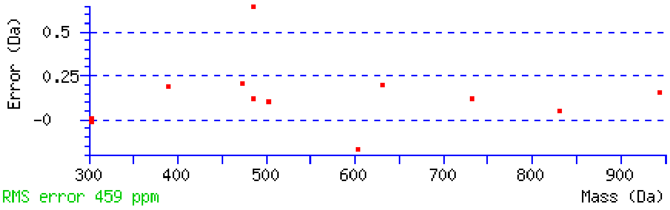
Match to Query 3604: 1131.636938 from(566.825745,2+) index(8290)
Title: Elution from: 74.078 to 74.078 scan no 11020 cid35.00 polarity:+
Data file D6h-1_2.mgf

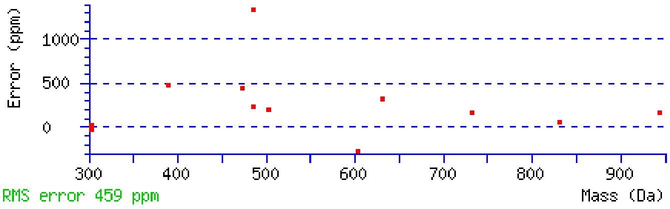
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1131.6387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0013
Matches : 12/88 fragment ions using 21 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	189.0870	95.0471	171.0764	86.0418	S	1031.5983	516.3028	1014.5718	507.7895	1013.5877	507.2975	9
3	**302.1710**	151.5892	284.1605	142.5839	L	***944.5663***	472.7868	927.5397	464.2735	926.5557	463.7815	8
4	401.2395	201.1234	383.2289	192.1181	V	***831.4822***	416.2447	814.4557	407.7315	813.4716	407.2395	7
5	530.2821	265.6447	512.2715	256.6394	E	***732.4138***	366.7105	715.3872	358.1973	714.4032	357.7053	6
6	**631.3297**	316.1685	613.3192	307.1632	T	***603.3712***	302.1892	586.3447	293.6760	585.3606	293.1840	5
7	744.4138	372.7105	726.4032	363.7053	L	***502.3235***	251.6654	485.2970	243.1521	484.3130	242.6601	4
8	857.4979	429.2526	839.4873	420.2473	L	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	986.5405	493.7739	968.5299	484.7686	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TSLVETLLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G06060.1

Score	Mr(calc)	Delta	Sequence
34.3	1131.6387	-0.0017	TSLVETLLEK
4.8	1131.6387	-0.0017	SSLLEITEIK

Mascot: http://www.matrixscience.com/

AT5G06290.1

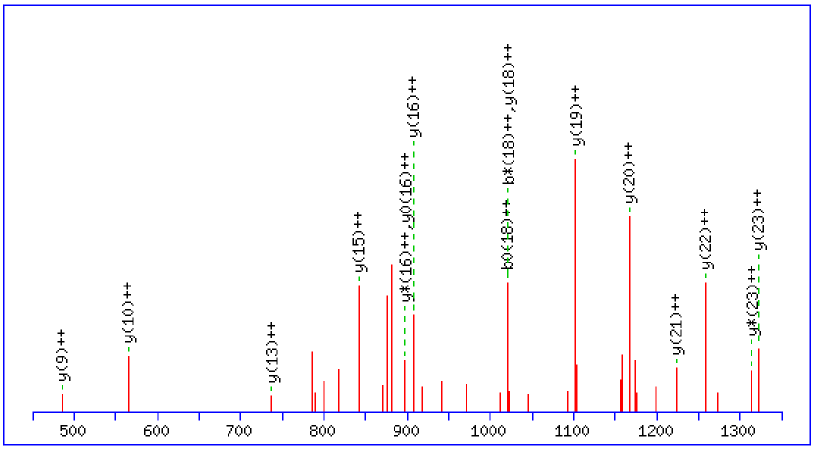
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLQALQYVQENPDEVCPAGWKPGEK**
Found in **AT5G06290.1** in **TAIR_Arabidopsis**, Symbols: 2-CYS PRX B | 2-cys peroxiredoxin, chloroplast, putative | chr5:1919381-1921212 FORWARD

Match to Query 11206: 2856.370200 from(953.130676,3+) index(7810)
Title: Elution from: 68.700 to 68.700 scan no 10137 cid35.00 polarity:+
Data file C7-2_1.mgf

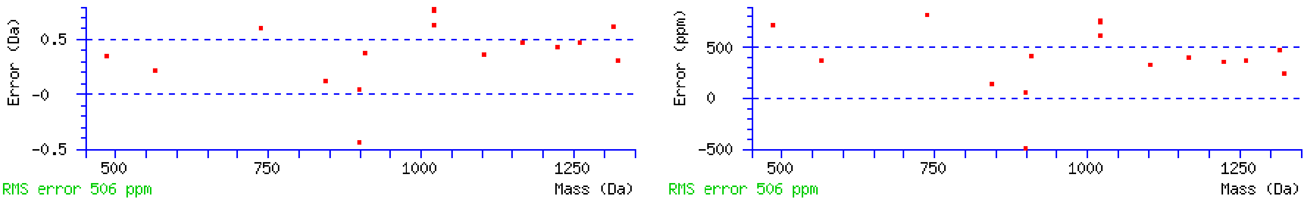
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2856.3752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 5.3e-009
Matches : 16/282 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							25
2	215.1390	108.0731			197.1285	99.0679	L	2756.3348	1378.6711	2739.3083	1370.1578	2738.3243	1369.6658	24
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	Q	2643.2508	1322.1290	2626.2242	1313.6158	2625.2402	1313.1237	23
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	A	2515.1922	1258.0997	2498.1657	1249.5865	2497.1816	1249.0945	22
5	527.3188	264.1630	510.2922	255.6498	509.3082	255.1577	L	2444.1551	1222.5812	2427.1285	1214.0679	2426.1445	1213.5759	21
6	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	Q	2331.0710	1166.0392	2314.0445	1157.5259	2313.0605	1157.0339	20
7	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	Y	2203.0124	1102.0099	2185.9859	1093.4966	2185.0019	1093.0046	19
8	917.5091	459.2582	900.4825	450.7449	899.4985	450.2529	V	2039.9491	1020.4782	2022.9226	1011.9649	2021.9386	1011.4729	18
9	1045.5677	523.2875	1028.5411	514.7742	1027.5571	514.2822	Q	1940.8807	970.9440	1923.8542	962.4307	1922.8701	961.9387	17
10	1174.6103	587.8088	1157.5837	579.2955	1156.5997	578.8035	E	1812.8221	906.9147	1795.7956	898.4014	1794.8116	897.9094	16
11	1288.6532	644.8302	1271.6266	636.3170	1270.6426	635.8250	N	1683.7795	842.3934	1666.7530	833.8801	1665.7690	833.3881	15
12	1385.7060	693.3566	1368.6794	684.8433	1367.6954	684.3513	P	1569.7366	785.3719	1552.7101	776.8587	1551.7260	776.3667	14
13	1500.7329	750.8701	1483.7064	742.3568	1482.7223	741.8648	D	1472.6838	736.8456	1455.6573	728.3323	1454.6733	727.8403	13
14	1629.7755	815.3914	1612.7489	806.8781	1611.7649	806.3861	E	1357.6569	679.3321	1340.6304	670.8188	1339.6463	670.3268	12
15	1728.8439	864.9256	1711.8174	856.4123	1710.8333	855.9203	V	1228.6143	614.8108	1211.5878	606.2975	1210.6037	605.8055	11
16	1888.8746	944.9409	1871.8480	936.4276	1870.8640	935.9356	C	1129.5459	565.2766	1112.5193	556.7633	1111.5353	556.2713	10
17	1985.9273	993.4673	1968.9008	984.9540	1967.9168	984.4620	P	969.5152	485.2613	952.4887	476.7480	951.5047	476.2560	9
18	2056.9644	1028.9859	2039.9379	1020.4726	2038.9539	1019.9806	A	872.4625	436.7349	855.4359	428.2216	854.4519	427.7296	8
19	2113.9859	1057.4966	2096.9594	1048.9833	2095.9753	1048.4913	G	801.4254	401.2163	784.3988	392.7030	783.4148	392.2110	7
20	2300.0652	1150.5362	2283.0387	1142.0230	2282.0546	1141.5310	W	744.4039	372.7056	727.3774	364.1923	726.3933	363.7003	6
21	2428.1602	1214.5837	2411.1336	1206.0705	2410.1496	1205.5784	K	558.3246	279.6659	541.2980	271.1527	540.3140	270.6606	5
22	2525.2129	1263.1101	2508.1864	1254.5968	2507.2024	1254.1048	P	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	4
23	2582.2344	1291.6208	2565.2079	1283.1076	2564.2238	1282.6156	G	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
24	2711.2770	1356.1421	2694.2504	1347.6289	2693.2664	1347.1369	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
25							K	147.1128	74.0600	130.0863	65.5468			1

AT5G06290.1



NCBI **BLAST** search of TLQALQYVQENPDEVCPAGWKPGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.1	2856.3752	-0.0050	TLQALQYVQENPDEVCPAGWKPGEK
6.0	2856.3752	-0.0050	TNFYEGIGLNTKEFDMHVIIETNR
0.8	2856.3679	0.0023	FEYNDDLQSGGQSVGGTQVLNHVAPPK

Mascot: http://www.matrixscience.com/

AT5G06460.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFLFR**
Found in **AT5G06460.1** in **TAIR_Arabidopsis**, Symbols: ATUBA2 | ATUBA2 (Arabidopsis thaliana ubiquitin activating enzyme 2); ubiquitin activating enzyme | chr5:1970240-1974383 FORWARD

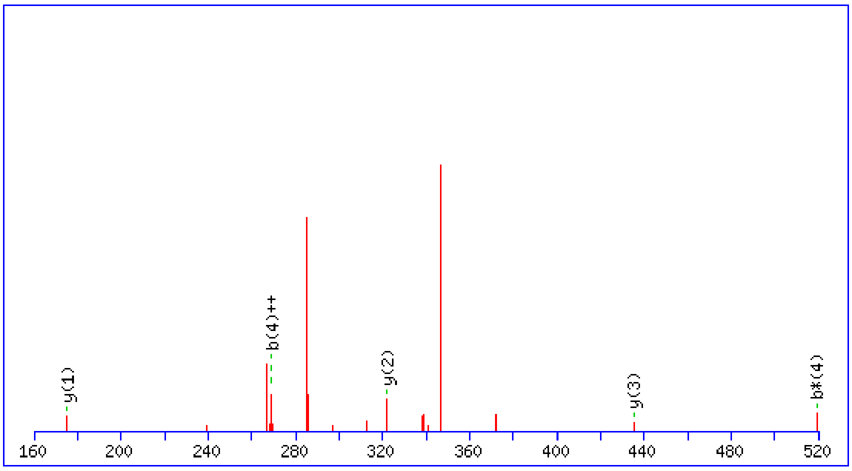
Match to Query 759: 709.390156 from(355.702354,2+) index(4821)
Title: Elution from: 43.621 to 43.621 scan no 5980 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 160 to 520 Da Full range

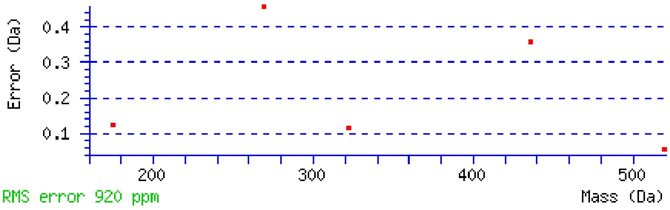
Label all possible matches ○ Label matches used for scoring ●

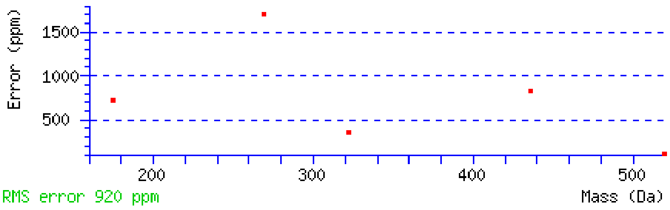
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 709.3911
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.042
Matches : 5/32 fragment ions using 10 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	129.0659	65.0366	112.0393	56.5233	**Q**					**5**
2	276.1343	138.5708	259.1077	130.0575	**F**	582.3398	291.6736	565.3133	283.1603	**4**
3	389.2183	195.1128	372.1918	186.5995	**L**	***435.2714***	218.1394	418.2449	209.6261	**3**
4	536.2867	268.6470	519.2602	260.1337	**F**	***322.1874***	161.5973	305.1608	153.0840	**2**
5					**R**	***175.1190***	88.0631	158.0924	79.5498	**1**





NCBI **BLAST** search of QFLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.8	709.3911	-0.0010	QFLFR
6.6	709.3911	-0.0010	FQFLR
6.6	709.3911	-0.0010	GFAFLR
6.6	709.3911	-0.0010	KFYPR

AT5G06460.1

2.5	709.3911	-0.0010	LQFFR
2.5	709.3911	-0.0010	QIFFR
1.2	709.3911	-0.0010	FFALGR

AT5G07020.1

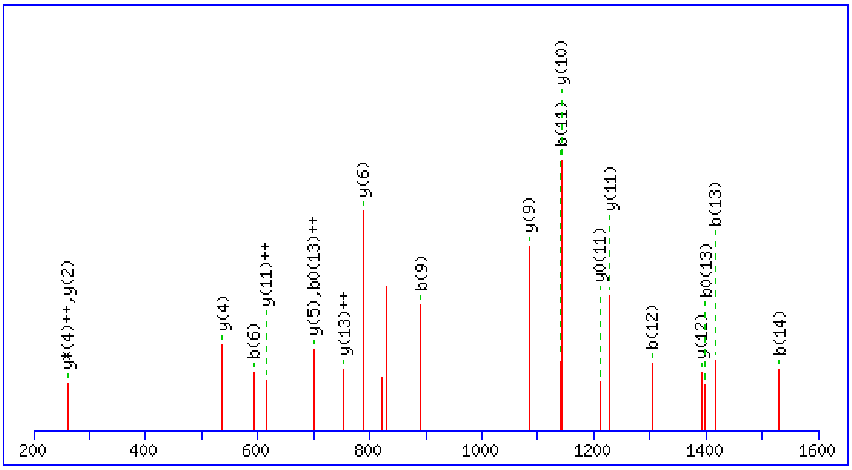
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVDYSGPSLSYYINK**
Found in **AT5G07020.1** in **TAIR_Arabidopsis**, Symbols: | proline-rich family protein | chr5:2180670-2182285 REVERSE

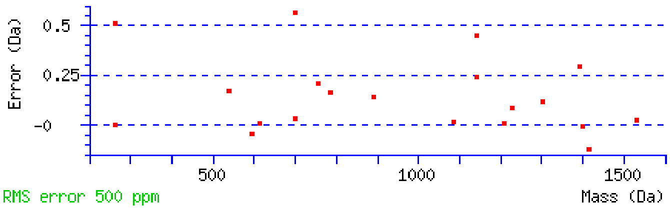
Match to Query 7621: 1675.807924 from(838.911238,2+) index(6781)
Title: Elution from: 59.524 to 59.524 scan no 8847 cid35.00 polarity:+
Data file 0-2_3.mgf

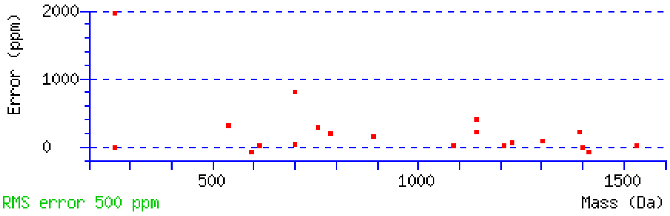
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1675.8093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90 **Expect:** 2.6e-009
Matches : 20/128 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							15
2	171.1128	86.0600					V	1605.7795	803.3934	1588.7530	794.8801	1587.7690	794.3881	14
3	286.1397	143.5735			268.1292	134.5682	D	1506.7111	753.8592	1489.6846	745.3459	1488.7005	744.8539	13
4	449.2031	225.1052			431.1925	216.0999	Y	***1391.6842***	696.3457	1374.6576	687.8324	1373.6736	687.3404	12
5	536.2351	268.6212			518.2245	259.6159	S	***1228.6208***	614.8141	1211.5943	606.3008	1210.6103	605.8088	11
6	***593.2566***	297.1319			575.2460	288.1266	G	***1141.5888***	571.2980	1124.5623	562.7848	1123.5782	562.2928	10
7	690.3093	345.6583			672.2988	336.6530	P	***1084.5673***	542.7873	1067.5408	534.2740	1066.5568	533.7820	9
8	777.3414	389.1743			759.3308	380.1690	S	987.5146	494.2609	970.4880	485.7477	969.5040	485.2556	8
9	***890.4254***	445.7164			872.4149	436.7111	L	900.4825	450.7449	883.4560	442.2316	882.4720	441.7396	7
10	977.4575	489.2324			959.4469	480.2271	S	***787.3985***	394.2029	770.3719	385.6896	769.3879	385.1976	6
11	***1140.5208***	570.7640			1122.5102	561.7587	Y	***700.3665***	350.6869	683.3399	342.1736			5
12	***1303.5841***	652.2957			1285.5735	643.2904	Y	***537.3031***	269.1552	520.2766	260.6419			4
13	***1416.6682***	708.8377			1398.6576	699.8324	I	374.2398	187.6235	357.2132	179.1103			3
14	***1530.7111***	765.8592	1513.6846	757.3459	1512.7005	756.8539	N	***261.1557***	131.0815	244.1292	122.5682			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AVDYSGPSLSYYINK

AT5G07020.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.2	1675.8093	-0.0014	AVDYSGPSLSYYINK
1.7	1675.8062	0.0017	MATCSLLPPPSFSPR

Mascot: http://www.matrixscience.com/

AT5G07030.1

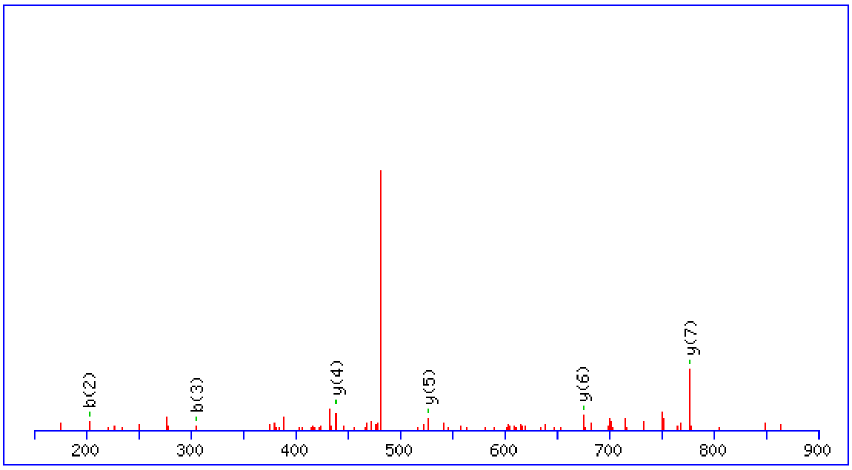
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLTFSGSLR**
Found in **AT5G07030.1** in **TAIR_Arabidopsis**, Symbols: | pepsin A | chr5:2183601-2185718 REVERSE

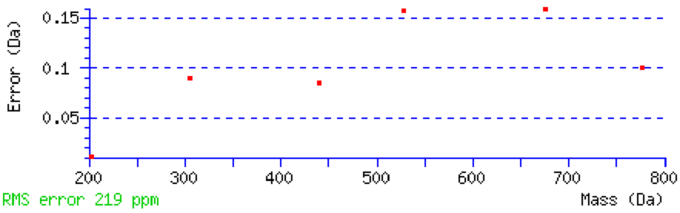
Match to Query 2250: 978.477188 from(490.245870,2+) index(3931)
Title: Elution from: 36.999 to 36.999 scan no 4907 cid35.00 polarity:+
Data file D12h-3_2.mgf

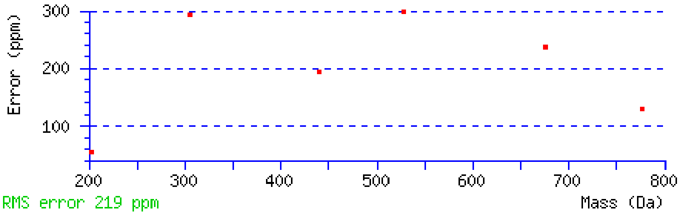
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 978.4779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.024
Matches : 6/76 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							9
2	**203.1174**	102.0624	185.1069	93.0571	L	891.4561	446.2317	873.4325	437.2199	873.4455	437.2264	8
3	**305.1622**	153.0847	287.1516	144.0794	T	***777.3750***	389.1911	759.3514	380.1793	759.3644	380.1858	7
4	453.2276	227.1174	435.2170	218.1122	F	***675.3303***	338.1688	657.3067	329.1570	657.3197	329.1635	6
5	541.2567	271.1320	523.2461	262.1267	S	***527.2648***	264.1360	509.2412	255.1243	509.2543	255.1308	5
6	599.2752	300.1412	581.2646	291.1359	G	***439.2358***	220.1215	421.2122	211.1097	421.2252	211.1162	4
7	687.3042	344.1558	669.2937	335.1505	S	381.2173	191.1123	363.1937	182.1005	363.2067	182.1070	3
8	801.3853	401.1963	783.3748	392.1910	L	293.1882	147.0977	275.1646	138.0859			2
9					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SLTFSGSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.6	978.4779	-0.0007	SLTFSGSLR

6.7	978.4779	-0.0007	TVHIPSGEK
3.6	978.4801	-0.0029	SLFEGFIR
3.2	978.4778	-0.0007	LIHQVDDK
1.6	978.4779	-0.0007	LIQAHEEK
1.2	978.4779	-0.0007	LYERTSAK
1.1	978.4778	-0.0007	YLQSTTVR

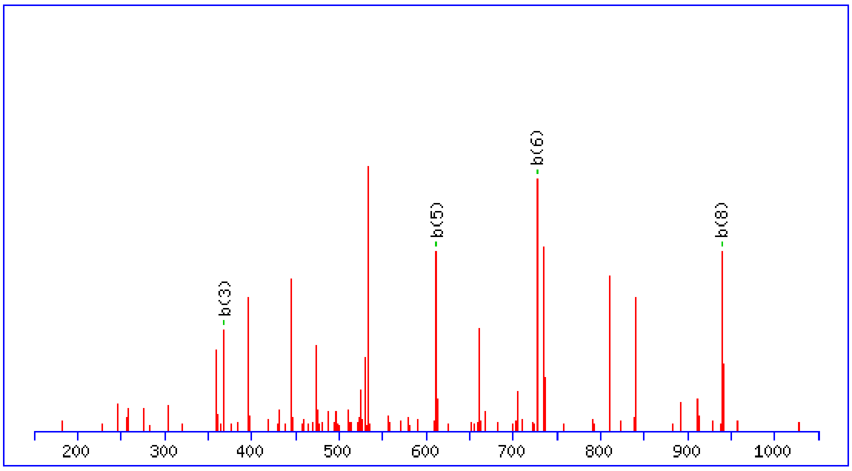
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPNMLDVLK**
Found in **AT5G07280.1** in **TAIR_Arabidopsis**, Symbols: EXS, EMS1 | EMS1 (EXCESS MICROSPOROCYTES1); kinase | chr5:2285089-2288667 FORWARD

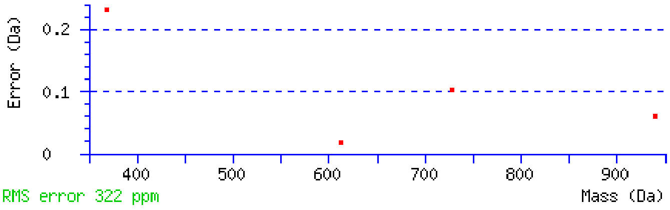
Match to Query 3155: 1084.605686 from(543.310119,2+) index(2493)
Title: Elution from: 26.398 to 26.398 scan no 3135 cid35.00 polarity:+
Data file C7-3_3.mgf

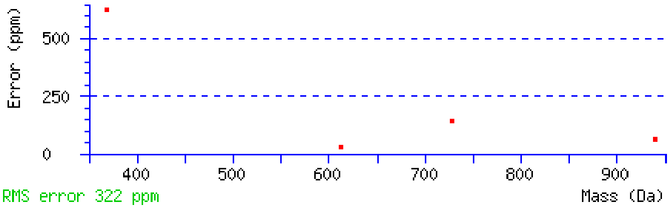
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1084.6063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.024
Matches : 4/80 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							9
2	254.1612	127.5842	237.1346	119.0709			P	929.5125	465.2599	912.4859	456.7466	911.5019	456.2546	8
3	*368.2041*	184.6057	351.1775	176.0924			N	832.4597	416.7335	815.4332	408.2202	814.4491	407.7282	7
4	499.2446	250.1259	482.2180	241.6126			M	718.4168	359.7120	701.3902	351.1988	700.4062	350.7067	6
5	*612.3286*	306.6680	595.3021	298.1547			L	587.3763	294.1918	570.3497	285.6785	569.3657	285.1865	5
6	*727.3556*	364.1814	710.3290	355.6681	709.3450	355.1761	D	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
7	826.4240	413.7156	809.3974	405.2024	808.4134	404.7103	V	359.2653	180.1363	342.2387	171.6230			3
8	*939.5080*	470.2577	922.4815	461.7444	921.4975	461.2524	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RPNMLDVLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G07280.1

19.3	1084.6063	-0.0006	RPNMLDVLK

Mascot: http://www.matrixscience.com/

AT5G07350.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPGAAEASIR**
Found in **AT5G07350.1** in **TAIR_Arabidopsis**, Symbols: | tudor domain-containing protein / nuclease family protein | chr5:2320345-2324893 REVERSE

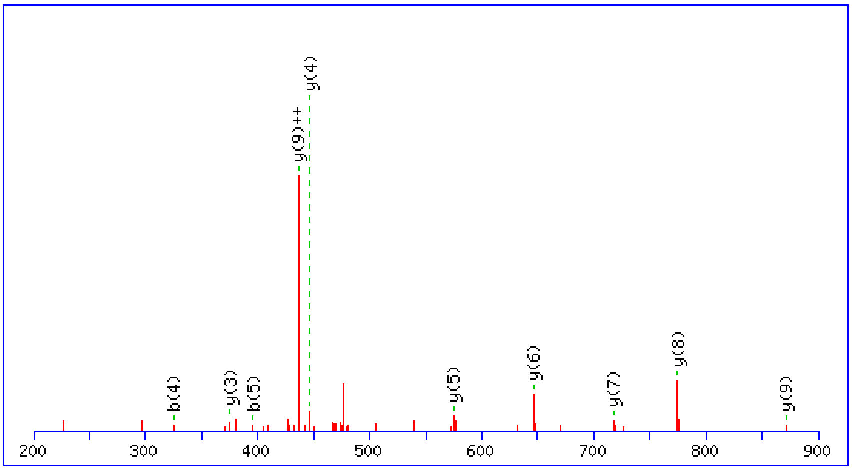
Match to Query 2193: 969.524508 from(485.769530,2+) index(1375)
Title: Elution from: 20.163 to 20.163 scan no 1922 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

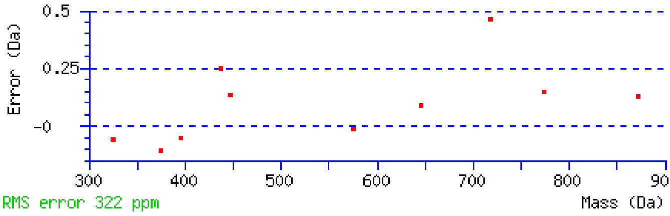
Label all possible matches ○ Label matches used for scoring ●

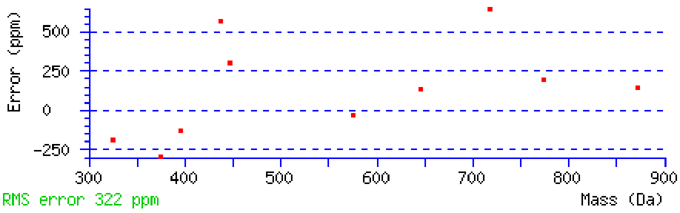
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 969.5243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 1.9e-005
Matches : 10/76 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							10
2	197.1285	99.0679			P	***871.4632***	436.2352	854.4367	427.7220	853.4526	427.2300	9
3	254.1499	127.5786			G	***774.4104***	387.7089	757.3839	379.1956	756.3999	378.7036	8
4	**325.1870**	163.0972			A	***717.3890***	359.1981	700.3624	350.6849	699.3784	350.1928	7
5	**396.2241**	198.6157			A	***646.3519***	323.6796	629.3253	315.1663	628.3413	314.6743	6
6	525.2667	263.1370	507.2562	254.1317	E	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
7	596.3039	298.6556	578.2933	289.6503	A	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
8	683.3359	342.1716	665.3253	333.1663	S	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	796.4199	398.7136	778.4094	389.7083	I	288.2030	144.6051	271.1765	136.0919			2
10					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VPGAAEASIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G07350.1

Score	Mr(calc)	Delta	Sequence
51.7	969.5243	0.0002	VPGAAEASIR

AT5G07390.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGFEHVR**
Found in **AT5G07390.1** in **TAIR_Arabidopsis**, Symbols: ATRBOHA | ATRBOHA (RESPIRATORY BURST OXIDASE HOMOLOG A); FAD binding / calcium ion binding / iron ion binding / oxidoreductase | chr5:2336064-2339729 REVERSE

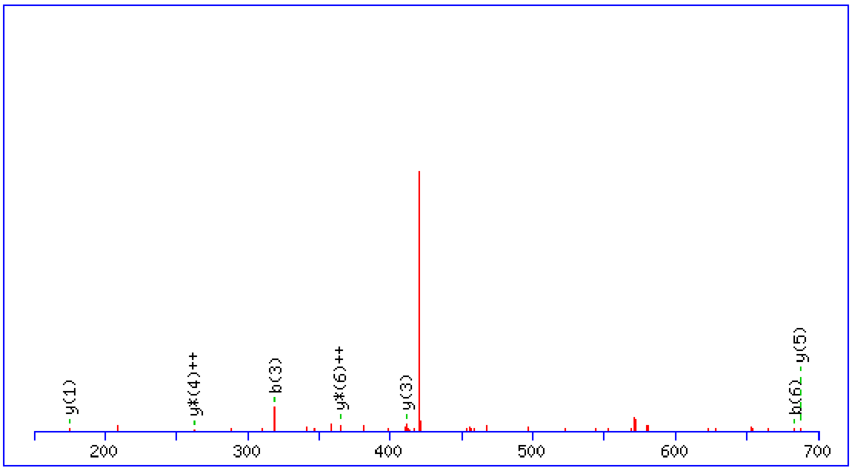
Match to Query 1411: 856.457544 from(429.236048,2+) index(2668)
Title: Elution from: 28.331 to 28.331 scan no 3351 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 700 Da Full range

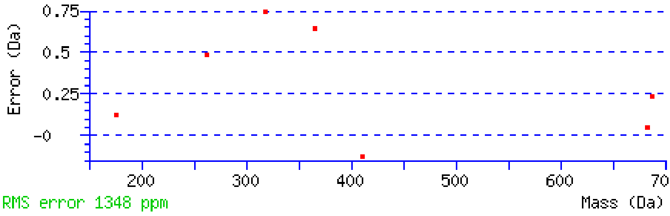
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

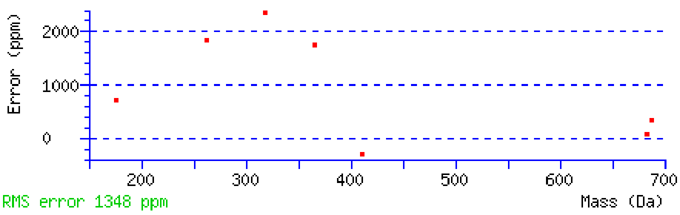


Monoisotopic mass of neutral peptide Mr(calc): 856.4555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 16 **Expect:** 0.049
Matches : 7/48 fragment ions using 17 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493			L							7
2	171.1128	86.0600			G	744.3787	372.6930	727.3522	364.1797	726.3682	363.6877	6
3	***318.1812***	159.5942			F	***687.3573***	344.1823	670.3307	335.6690	669.3467	335.1770	5
4	447.2238	224.1155	429.2132	215.1103	E	540.2889	270.6481	523.2623	262.1348	522.2783	261.6428	4
5	584.2827	292.6450	566.2722	283.6397	H	***411.2463***	206.1268	394.2197	197.6135			3
6	***683.3511***	342.1792	665.3406	333.1739	V	274.1874	137.5973	257.1608	129.0840			2
7					R	***175.1190***	88.0631	158.0924	79.5498			1



RMS error 1348 ppm



RMS error 1348 ppm

NCBI **BLAST** search of LGFEHVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.3	856.4555	0.0020	LGFEHVR
14.3	856.4555	0.0020	AVDLFHR

AT5G07390.1

11.1	856.4555	0.0020	EGVFHLR
10.4	856.4555	0.0020	EFGLHVR
10.4	856.4589	-0.0013	KLCPPSR
7.7	856.4555	0.0020	LGPQWTR
3.7	856.4555	0.0020	FHVDLAR
3.6	856.4555	0.0020	GLWQPTR
3.4	856.4555	0.0020	LFADVHR
3.3	856.4589	-0.0013	QVPINMR

AT5G07440.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVVFATEALLAEYGK**
Found in **AT5G07440.1** in **TAIR_Arabidopsis**, Symbols: GDH2 | GDH2 (GLUTAMATE DEHYDROGENASE 2); oxidoreductase | chr5:2356154-2358013 FORWARD

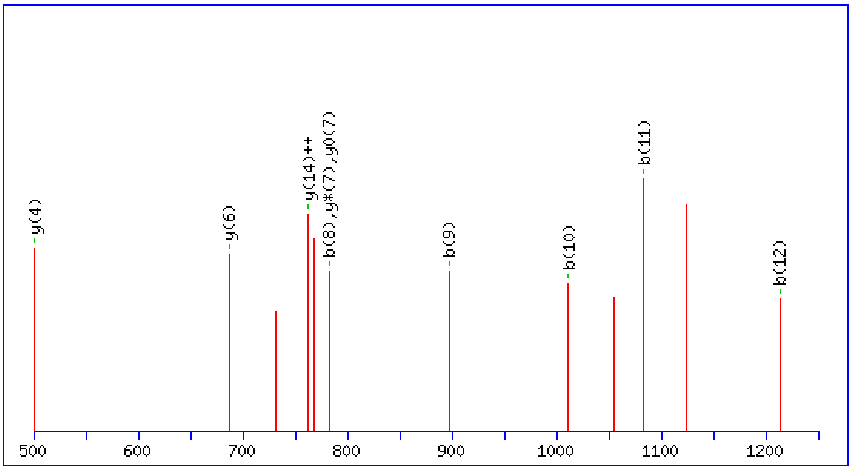
Match to Query 6570: 1582.780836 from(792.397694,2+) index(9200)
Title: Elution from: 88.160 to 88.160 scan no 12880 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1250 Da Full range

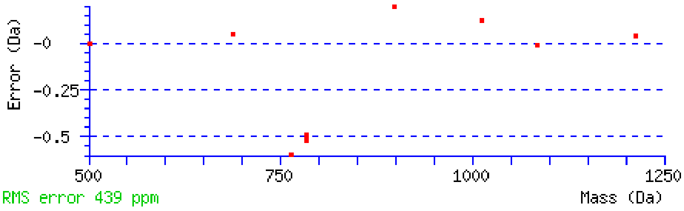
Label all possible matches ○ Label matches used for scoring ●

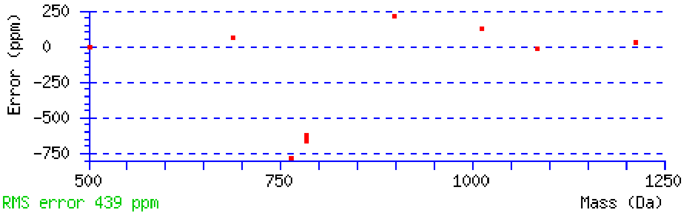
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1582.7819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0051
Matches : 10/124 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165			G							15
2	159.0912	80.0492			V	1525.7707	763.3890	1507.7471	754.3772	1507.7601	754.3837	14
3	259.1567	130.0820			V	1425.7052	713.3563	1407.6817	704.3445	1407.6947	704.3510	13
4	407.2221	204.1147			F	1325.6398	663.3235	1307.6162	654.3117	1307.6292	654.3183	12
5	479.2563	240.1318			A	1177.5744	589.2908	1159.5508	580.2790	1159.5638	580.2855	11
6	581.3010	291.1541	563.2904	282.1488	T	1105.5402	553.2737	1087.5166	544.2619	1087.5296	544.2685	10
7	711.3406	356.1739	693.3300	347.1687	E	1003.4955	502.2514	985.4719	493.2396	985.4849	493.2461	9
8	***783.3748***	392.1910	765.3642	383.1857	A	873.4559	437.2316	855.4323	428.2198	855.4453	428.2263	8
9	***897.4559***	449.2316	879.4453	440.2263	L	801.4217	401.2145	783.3981	392.2027	783.4111	392.2092	7
10	***1011.5370***	506.2721	993.5264	497.2668	L	**687.3406**	344.1739	669.3170	335.1622	669.3300	335.1687	6
11	***1083.5711***	542.2892	1065.5605	533.2839	A	573.2595	287.1334	555.2359	278.1216	555.2489	278.1281	5
12	***1213.6107***	607.3090	1195.6002	598.3037	E	**501.2254**	251.1163	483.2018	242.1045	483.2148	242.1110	4
13	1377.6711	689.3392	1359.6605	680.3339	Y	371.1857	186.0965	353.1622	177.0847			3
14	1435.6896	718.3484	1417.6790	709.3432	G	207.1254	104.0663	189.1018	95.0545			2
15					K	149.1069	75.0571	131.0833	66.0453			1





AT5G07440.1

NCBI **BLAST** search of GVVFATEALLAEYGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.8	1582.7819	-0.0011	GVVFATEALLAEYGK
0.9	1582.7776	0.0032	IHNQLIGVEKMHK
0.4	1582.7823	-0.0015	KEAVTKLTEANGFR
0.1	1582.7846	-0.0037	FRDFIPSILDVSR

AT5G08050.1

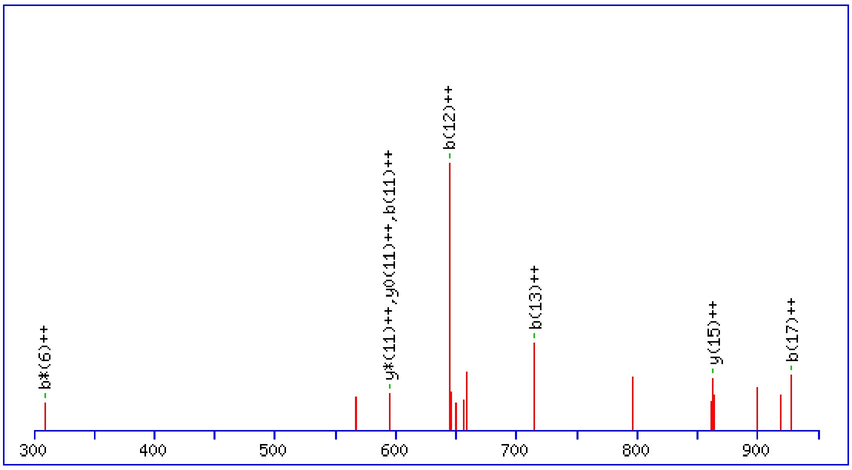
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAAKLICSSLTVHSMANK**
Found in **AT5G08050.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO62462.1); similar to unknown [Populus trichocarpa] (GB:ABK95457.1); contains InterPro domain Protein of unknown function DUF1118 (InterPro:IPR009500); contains InterPro domain U

Match to Query 9118: 2000.908368 from(667.976732,3+) index(7312)
Title: Elution from: 65.233 to 65.233 scan no 9599 cid35.00 polarity:+
Data file D6h-1_3.mgf

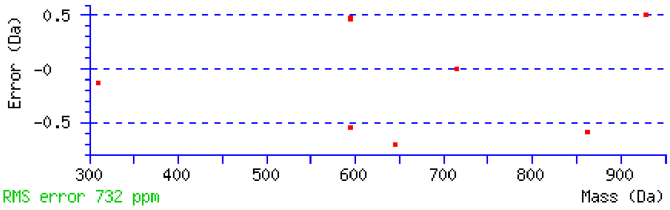
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

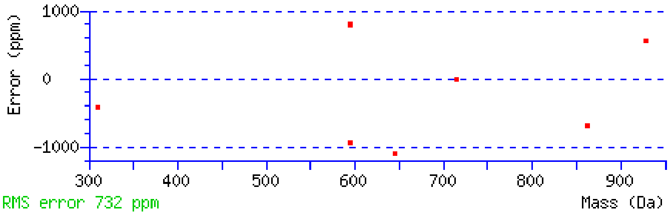


Monoisotopic mass of neutral peptide Mr(calc): 2000.9134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.031
Matches : 8/276 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							18
2	205.0789	103.0431					A	1869.8832	935.4452	1851.8596	926.4334	1851.8726	926.4399	17
3	277.1131	139.0602					A	1797.8490	899.4281	1779.8254	890.4164	1779.8385	890.4229	16
4	407.2021	204.1047	389.1785	195.0929			K	1725.8149	863.4111	1707.7913	854.3993	1707.8043	854.4058	15
5	521.2832	261.1453	503.2596	252.1335			L	1595.7258	798.3666	1577.7023	789.3548	1577.7153	789.3613	14
6	635.3643	318.1858	617.3407	309.1740			I	1481.6447	741.3260	1463.6212	732.3142	1463.6342	732.3207	13
7	797.3890	399.1982	779.3655	390.1864			C	1367.5636	684.2855	1349.5401	675.2737	1349.5531	675.2802	12
8	885.4181	443.2127	867.3945	434.2009	867.4075	434.2074	S	1205.5389	603.2731	1187.5153	594.2613	1187.5284	594.2678	11
9	973.4472	487.2272	955.4236	478.2154	955.4366	478.2219	S	1117.5099	559.2586	1099.4863	550.2468	1099.4993	550.2533	10
10	1087.5283	544.2678	1069.5047	535.2560	1069.5177	535.2625	L	1029.4808	515.2440	1011.4572	506.2322	1011.4702	506.2388	9
11	1189.5730	***595.2901***	1171.5494	586.2783	1171.5624	586.2848	T	915.3997	458.2035	897.3761	449.1917	897.3891	449.1982	8
12	1289.6384	***645.3229***	1271.6148	636.3111	1271.6279	636.3176	V	813.3550	407.1811	795.3314	398.1693	795.3444	398.1758	7
13	1429.6884	***715.3479***	1411.6649	706.3361	1411.6779	706.3426	H	713.2895	357.1484	695.2660	348.1366	695.2790	348.1431	6
14	1517.7175	759.3624	1499.6939	750.3506	1499.7069	750.3571	S	573.2395	287.1234	555.2159	278.1116	555.2290	278.1181	5
15	1665.7499	833.3786	1647.7264	824.3668	1647.7394	824.3733	M	485.2105	243.1089	467.1869	234.0971			4
16	1737.7841	869.3957	1719.7605	860.3839	1719.7735	860.3904	A	337.1780	169.0926	319.1544	160.0809			3
17	1853.8211	***927.4142***	1835.7975	918.4024	1835.8105	918.4089	N	265.1439	133.0756	247.1203	124.0638			2
18							K	149.1069	75.0571	131.0833	66.0453			1

AT5G08050.1





NCBI **BLAST** search of MAAKLICSSLTVHSMANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.3	2000.9134	-0.0051	MAAKLICSSLTVHSMANK
13.8	2000.9082	0.0001	MMWLCVIVILQDMGQK
13.8	2000.9082	0.0001	MMWLCVIVILQDMGQK
12.9	2000.9114	-0.0030	YYINERSSNFTEVTKK
10.8	2000.9026	0.0057	VLEHFDACDLVKMMKK
10.8	2000.9026	0.0057	VLEHFDACDLVKMMKK
9.1	2000.9114	-0.0030	GSTATSSLVALSSSFGFFGR
8.7	2000.9105	-0.0021	AMNEINAAARMRLAANEK
8.4	2000.9044	0.0039	VSPVPMKNGFGNESTREK
7.4	2000.9140	-0.0057	YQARVGDALPDSVDWRK

Mascot: http://www.matrixscience.com/

AT5G08280.1

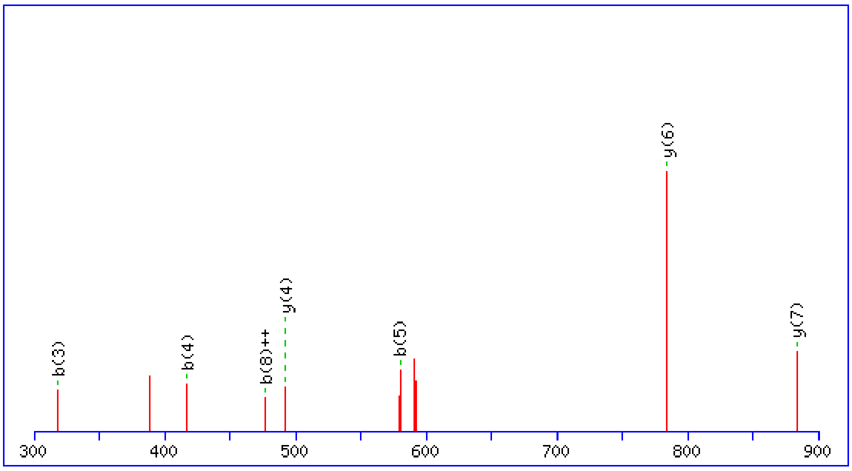
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPYVYEDMVK**
Found in **AT5G08280.1** in **TAIR_Arabidopsis**, Symbols: HEMC | HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase | chr5:2663764-2665597 REVERSE

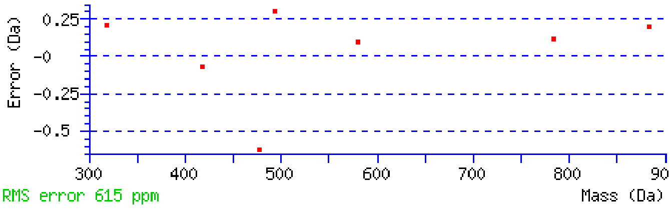
Match to Query 4404: 1199.553576 from(600.784064,2+) index(4895)
Title: Elution from: 43.460 to 43.460 scan no 6071 cid35.00 polarity:+
Data file D1d-3_1.mgf

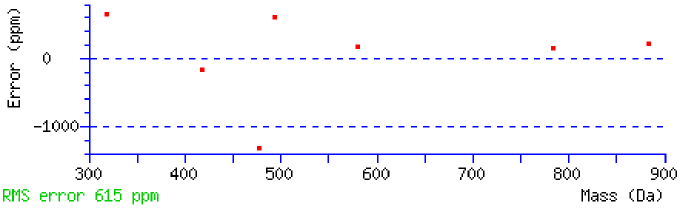
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1199.5533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0026
Matches : 7/74 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							10
2	155.0815	78.0444			P	1143.5391	572.2732	1126.5125	563.7599	1125.5285	563.2679	9
3	***318.1448***	159.5761			Y	1046.4863	523.7468	1029.4598	515.2335	1028.4757	514.7415	8
4	***417.2132***	209.1103			V	***883.4230***	442.2151	866.3964	433.7019	865.4124	433.2098	7
5	***580.2766***	290.6419			Y	***784.3546***	392.6809	767.3280	384.1676	766.3440	383.6756	6
6	709.3192	355.1632	691.3086	346.1579	E	621.2912	311.1493	604.2647	302.6360	603.2807	302.1440	5
7	824.3461	412.6767	806.3355	403.6714	D	***492.2486***	246.6280	475.2221	238.1147	474.2381	237.6227	4
8	955.3866	478.1969	937.3760	469.1917	M	377.2217	189.1145	360.1952	180.6012			3
9	1054.4550	527.7311	1036.4444	518.7259	V	246.1812	123.5942	229.1547	115.0810			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GPYVYEDMVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G08280.1

Score	Mr(calc)	Delta	Sequence
26.9	1199.5533	0.0003	GPYVYEDMVK

Mascot: http://www.matrixscience.com/

AT5G08300.1

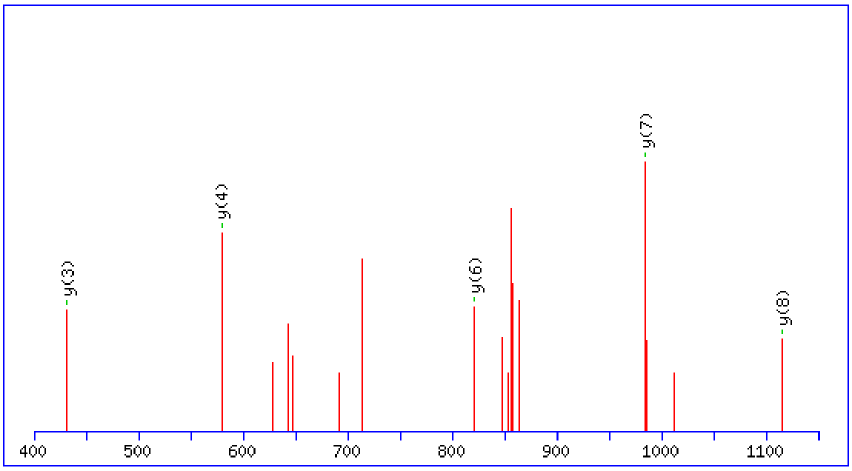
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGSAMYELFQER**
Found in **AT5G08300.1** in **TAIR_Arabidopsis**, Symbols: | succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative | chr5:2667580-2669673 FORWARD

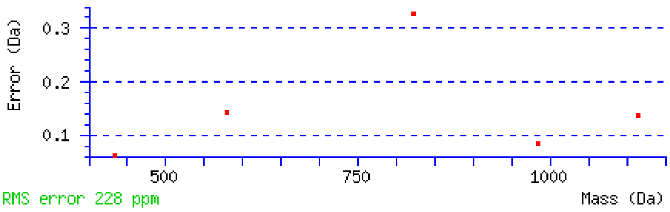
Match to Query 5537: 1442.685860 from(722.350206,2+) index(7723)
Title: Elution from: 67.167 to 67.167 scan no 10094 cid35.00 polarity:+
Data file D6h-3_3.mgf

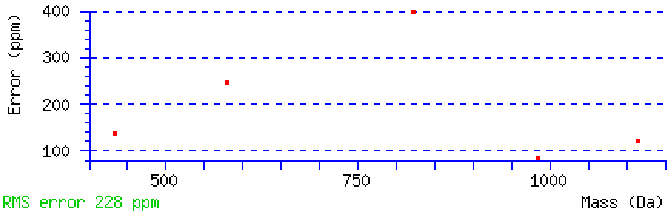
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1442.6864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00029
Matches : 5/108 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							12
2	171.1128	86.0600					G	1330.6096	665.8084	1313.5831	657.2952	1312.5990	656.8032	11
3	258.1448	129.5761			240.1343	120.5708	S	1273.5881	637.2977	1256.5616	628.7844	1255.5776	628.2924	10
4	329.1819	165.0946			311.1714	156.0893	A	1186.5561	593.7817	1169.5296	585.2684	1168.5456	584.7764	9
5	460.2224	230.6149			442.2119	221.6096	M	***1115.5190***	558.2631	1098.4925	549.7499	1097.5084	549.2579	8
6	623.2858	312.1465			605.2752	303.1412	Y	***984.4785***	492.7429	967.4520	484.2296	966.4680	483.7376	7
7	752.3284	376.6678			734.3178	367.6625	E	***821.4152***	411.2112	804.3886	402.6980	803.4046	402.2060	6
8	865.4124	433.2098			847.4019	424.2046	L	692.3726	346.6899	675.3461	338.1767	674.3620	337.6847	5
9	1012.4808	506.7441			994.4703	497.7388	F	***579.2885***	290.1479	562.2620	281.6346	561.2780	281.1426	4
10	1140.5394	570.7733	1123.5129	562.2601	1122.5288	561.7681	Q	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
11	1269.5820	635.2946	1252.5555	626.7814	1251.5714	626.2894	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IGSAMYELFQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G08300.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.9	1442.6864	-0.0005	IGSAMYELFQER
13.4	1442.6898	-0.0039	VTQMYMIASLDR

Mascot: http://www.matrixscience.com/

AT5G08450.1

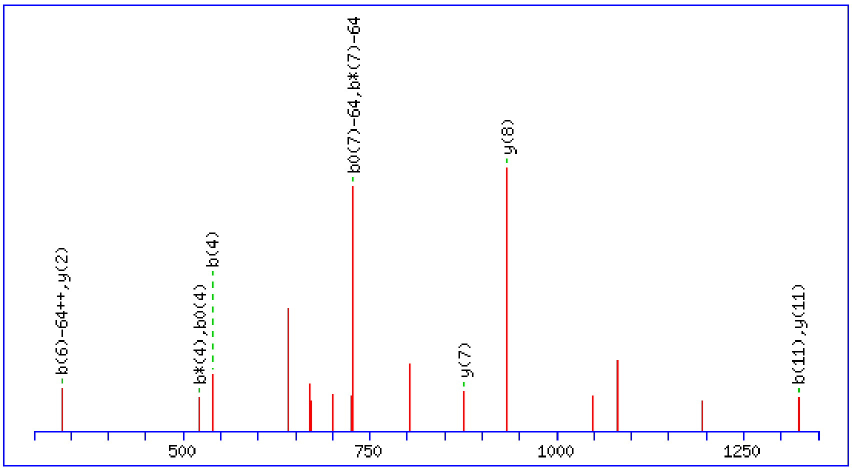
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEKEGHAHLAWK**
Found in **AT5G08450.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO67090.1); contains InterPro domain Histone deacetylation protein Rxt3 (InterPro:IPR013951) | chr5:2727971-2732573 REVERSE

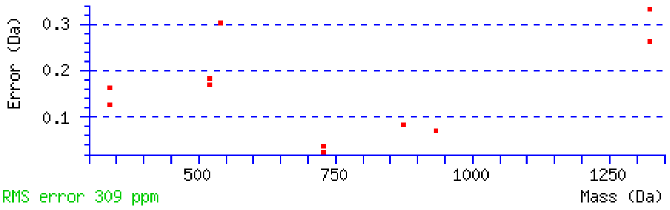
Match to Query 6243: 1470.637804 from(736.326178,2+) index(7077)
Title: Elution from: 62.677 to 62.677 scan no 9116 cid35.00 polarity:+
Data file D12h-3_1.mgf

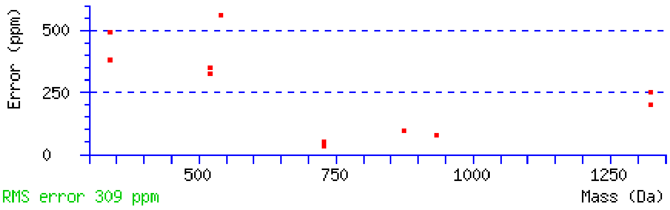
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1470.6416
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.039
Matches : 11/170 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0397	75.0235					M							12
2	279.0793	140.0433			261.0688	131.0380	E	***1323.6165***	662.3119	1305.5929	653.3001	1305.6059	653.3066	11
3	409.1684	205.0878	391.1448	196.0760	391.1578	196.0825	K	1193.5768	597.2921	1175.5533	588.2803	1175.5663	588.2868	10
4	**539.2080**	270.1076	521.1844	261.0958	521.1974	261.1024	E	1063.4878	532.2475	1045.4642	523.2358	1045.4773	523.2423	9
5	597.2265	299.1169	579.2029	290.1051	579.2159	290.1116	G	***933.4482***	467.2277	915.4246	458.2159			8
6	737.2765	369.1419	719.2529	360.1301	719.2660	360.1366	H	***875.4297***	438.2185	857.4061	429.2067			7
7	809.3107	405.1590	791.2871	396.1472	791.3001	396.1537	A	735.3797	368.1935	717.3561	359.1817			6
8	949.3607	475.1840	931.3371	466.1722	931.3501	466.1787	H	663.3455	332.1764	645.3219	323.1646			5
9	1063.4418	532.2245	1045.4182	523.2127	1045.4312	523.2192	L	523.2955	262.1514	505.2719	253.1396			4
10	1135.4759	568.2416	1117.4523	559.2298	1117.4654	559.2363	A	409.2144	205.1108	391.1908	196.0990			3
11	**1323.5493**	662.2783	1305.5257	653.2665	1305.5387	653.2730	W	***337.1803***	169.0938	319.1567	160.0820			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MEKEGHAHLAWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G08450.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.6	1470.6416	-0.0038	MEKEGHAHLAWK
9.1	1470.6401	-0.0023	STQAMGEAMKGVTK
8.8	1470.6401	-0.0023	MTDVELRNMVSK
5.2	1470.6401	-0.0023	STQAMGEAMKGVTK
4.8	1470.6389	-0.0011	MAKDFDVNSVWK
3.4	1470.6340	0.0038	AGLISEMESTFEK
3.0	1470.6421	-0.0043	SSRVREFHGMSR
3.0	1470.6392	-0.0014	SESESAASGSVSKTK
1.0	1470.6389	-0.0011	SNMLGEGGFGPVYK
1.0	1470.6401	-0.0023	AMDIAERKMTEK

AT5G08560.1

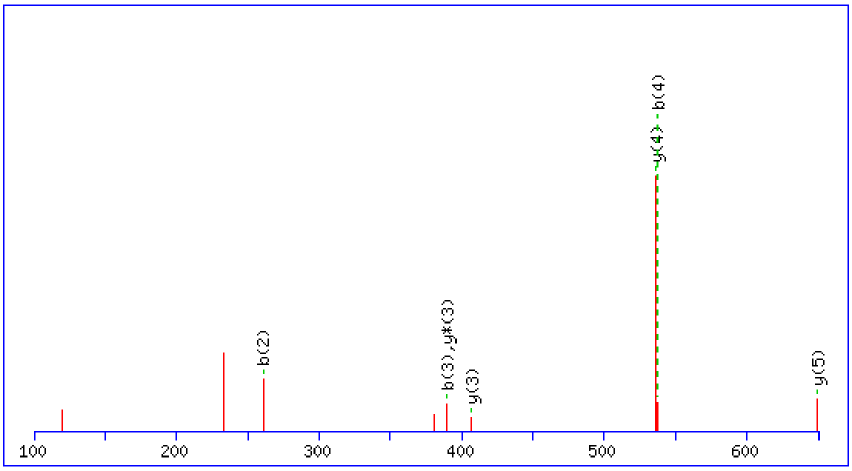
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLEFLK**
Found in **AT5G08560.1** in **TAIR_Arabidopsis**, Symbols: | transducin family protein / WD-40 repeat family protein | chr5:2771105-2773828 REVERSE

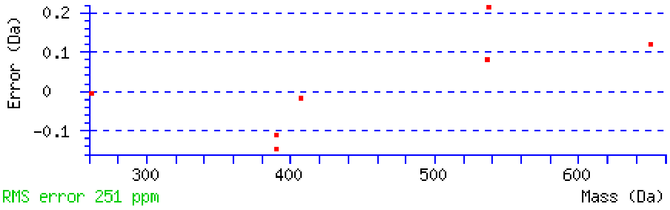
Match to Query 845: 795.453314 from(398.733933,2+) index(7057)
Title: Elution from: 65.196 to 65.196 scan no 9279 cid35.00 polarity:+
Data file D12h-2_1.mgf

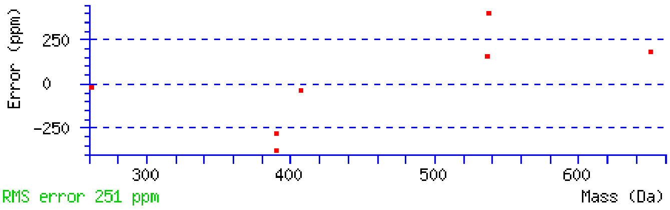
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 795.4531
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0014
Matches : 7/40 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415			F							6
2	***261.1598***	131.0835			L	***649.3919***	325.1996	632.3654	316.6863	631.3814	316.1943	5
3	***390.2023***	195.6048	372.1918	186.5995	E	***536.3079***	268.6576	519.2813	260.1443	518.2973	259.6523	4
4	***537.2708***	269.1390	519.2602	260.1337	F	***407.2653***	204.1363	390.2387	195.6230			3
5	650.3548	325.6811	632.3443	316.6758	L	260.1969	130.6021	243.1703	122.0888			2
6					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FLEFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.5	795.4531	0.0003	FLEFIK
28.5	795.4531	0.0003	FLEFLK
21.0	795.4531	0.0003	FLEIFK

AT5G08560.1

20.9	795.4531	0.0003	IFEFLK
5.0	795.4531	0.0003	LFFLEK

Mascot: http://www.matrixscience.com/

AT5G08660.1

Mascot Search Results

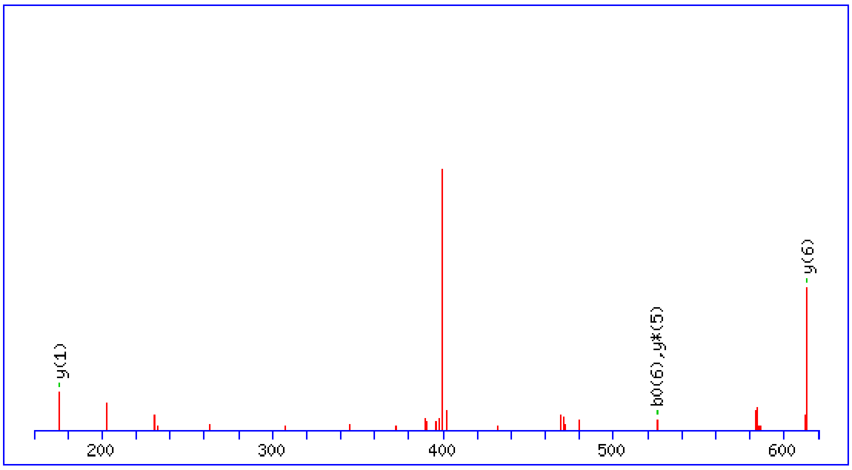
Peptide View

MS/MS Fragmentation of **SDARGGPR**
Found in **AT5G08660.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G34320.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82727.1); contains InterPro domain Protein of unknown function DUF668 (InterPro:IPR007700)

Match to Query 1178: 814.404608 from(408.209580,2+) index(1163)
Title: Elution from: 16.022 to 16.022 scan no 1560 cid35.00 polarity:+
Data file D1d-3_2.mgf

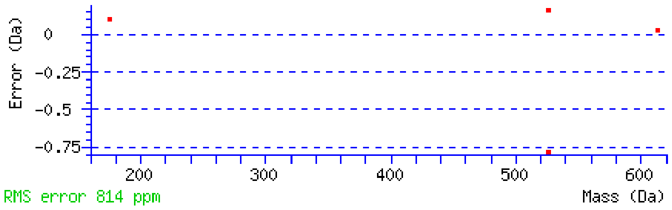
Click mouse within plot area to zoom in by factor of two about that point

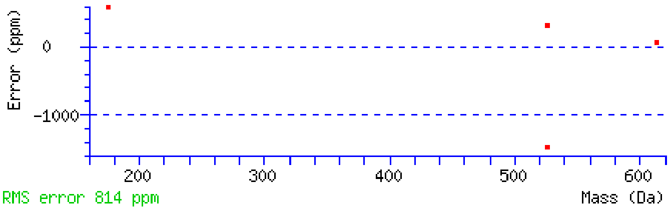
Or, Plot from 160 to 620 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 814.4046
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.042
Matches : 4/66 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							8
2	203.0662	102.0368			185.0557	93.0315	D	728.3798	364.6935	711.3533	356.1803	710.3692	355.6883	7
3	274.1034	137.5553			256.0928	128.5500	A	***613.3529***	307.1801	596.3263	298.6668			6
4	430.2045	215.6059	413.1779	207.0926	412.1939	206.6006	R	542.3158	271.6615	525.2892	263.1482			5
5	487.2259	244.1166	470.1994	235.6033	469.2154	235.1113	G	386.2146	193.6110	369.1881	185.0977			4
6	544.2474	272.6273	527.2209	264.1141	526.2368	263.6221	G	329.1932	165.1002	312.1666	156.5870			3
7	641.3002	321.1537	624.2736	312.6404	623.2896	312.1484	P	272.1717	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SDARGGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G08660.1

14.2	814.4046	0.0001	SDARGGPR
2.5	814.4046	0.0001	QNGNQVR

Mascot: http://www.matrixscience.com/

AT5G08670.1

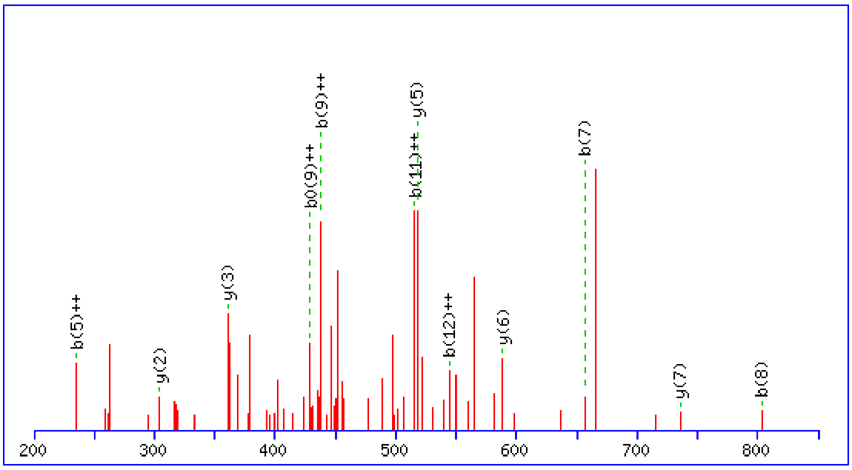
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHGGFSVFAGVGER**
Found in **AT5G08670.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase beta chain 1, mitochondrial | chr5:2818396-2821150 REVERSE

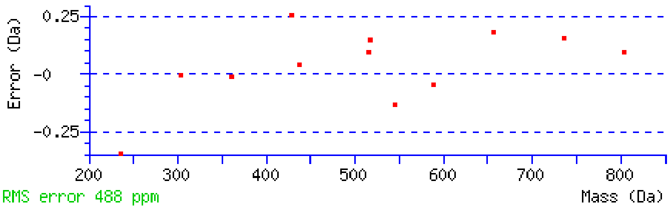
Match to Query 5431: 1389.679005 from(464.233611,3+) index(5111)
Title: Elution from: 46.912 to 46.912 scan no 6446 cid35.00 polarity:+
Data file 0-3_1.mgf

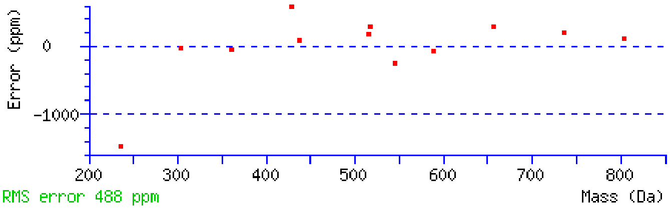
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1389.6790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0022
Matches : 12/118 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			**A**							**14**
2	209.1033	105.0553			**H**	1319.6491	660.3282	1302.6226	651.8149	1301.6385	651.3229	**13**
3	266.1248	133.5660			**G**	1182.5902	591.7987	1165.5636	583.2855	1164.5796	582.7935	**12**
4	323.1462	162.0768			**G**	1125.5687	563.2880	1108.5422	554.7747	1107.5582	554.2827	**11**
5	470.2146	***235.6110***			**F**	1068.5473	534.7773	1051.5207	526.2640	1050.5367	525.7720	**10**
6	557.2467	279.1270	539.2361	270.1217	**S**	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	**9**
7	**656.3151**	328.6612	638.3045	319.6559	**V**	834.4468	417.7271	817.4203	409.2138	816.4363	408.7218	**8**
8	**803.3835**	402.1954	785.3729	393.1901	**F**	***735.3784***	368.1928	718.3519	359.6796	717.3678	359.1876	**7**
9	874.4206	***437.7139***	856.4100	428.7087	**A**	***588.3100***	294.6586	571.2835	286.1454	570.2994	285.6534	**6**
10	931.4421	466.2247	913.4315	457.2194	**G**	***517.2729***	259.1401	500.2463	250.6268	499.2623	250.1348	**5**
11	1030.5105	***515.7589***	1012.4999	506.7536	**V**	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	**4**
12	1087.5320	***544.2696***	1069.5214	535.2643	**G**	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	**3**
13	1216.5745	608.7909	1198.5640	599.7856	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
14					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of AHGGFSVFAGVGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G08670.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.0	1389.6790	0.0000	AHGGFSVFAGVGER
0.5	1389.6776	0.0014	SSSSSEIGKSFFK
0.1	1389.6783	0.0007	DVAKRQSCSPSR

AT5G08680.1

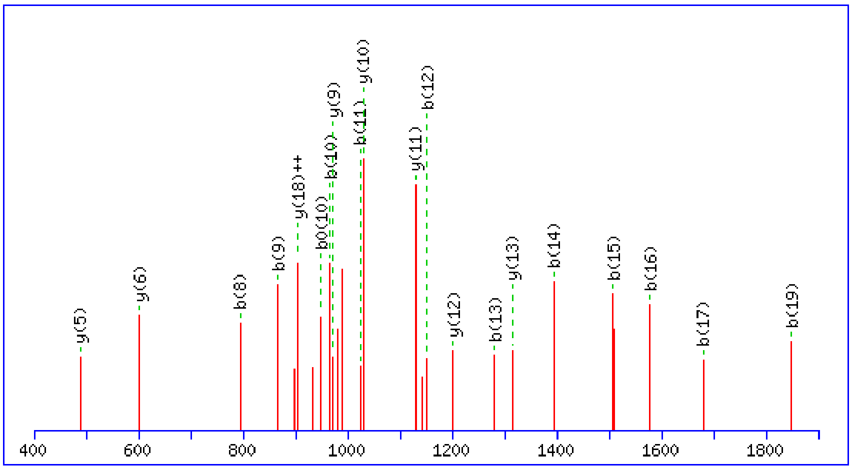
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAPALVDLATGQEILATGIK**
Found in **AT5G08680.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase beta chain, mitochondrial, putative | chr5:2821993-2824684 FORWARD

Match to Query 8884: 1995.089052 from(998.551802,2+) index(10146)
Title: Elution from: 98.355 to 98.355 scan no 14747 cid35.00 polarity:+
Data file D1d-2_3.mgf

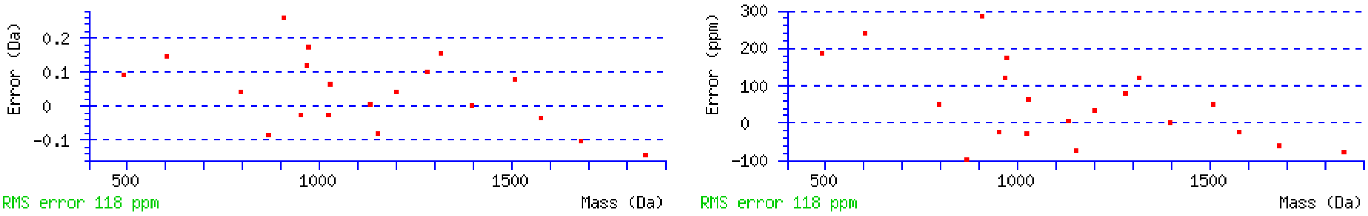
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1995.0888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90 **Expect:** 2.4e-009
Matches : 20/200 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							20
2	187.0713	94.0393			169.0608	85.0340	A	1881.0692	941.0382	1864.0426	932.5249	1863.0586	932.0329	19
3	284.1241	142.5657			266.1135	133.5604	P	1810.0320	905.5197	1793.0055	897.0064	1792.0215	896.5144	18
4	355.1612	178.0842			337.1506	169.0790	A	1712.9793	856.9933	1695.9527	848.4800	1694.9687	847.9880	17
5	468.2453	234.6263			450.2347	225.6210	L	1641.9422	821.4747	1624.9156	812.9614	1623.9316	812.4694	16
6	567.3137	284.1605			549.3031	275.1552	V	1528.8581	764.9327	1511.8316	756.4194	1510.8475	755.9274	15
7	682.3406	341.6740			664.3301	332.6687	D	1429.7897	715.3985	1412.7631	706.8852	1411.7791	706.3932	14
8	***795.4247***	398.2160			777.4141	389.2107	L	**1314.7627**	657.8850	1297.7362	649.3717	1296.7522	648.8797	13
9	***866.4618***	433.7345			848.4512	424.7293	A	**1201.6787**	601.3430	1184.6521	592.8297	1183.6681	592.3377	12
10	***967.5095***	484.2584			949.4989	475.2531	T	**1130.6416**	565.8244	1113.6150	557.3111	1112.6310	556.8191	11
11	***1024.5310***	512.7691			1006.5204	503.7638	G	**1029.5939**	515.3006	1012.5673	506.7873	1011.5833	506.2953	10
12	***1152.5895***	576.7984	1135.5630	568.2851	1134.5790	567.7931	Q	**972.5724**	486.7898	955.5459	478.2766	954.5619	477.7846	9
13	***1281.6321***	641.3197	1264.6056	632.8064	1263.6216	632.3144	E	844.5138	422.7606	827.4873	414.2473	826.5033	413.7553	8
14	***1394.7162***	697.8617	1377.6896	689.3485	1376.7056	688.8564	I	715.4713	358.2393	698.4447	349.7260	697.4607	349.2340	7
15	***1507.8003***	754.4038	1490.7737	745.8905	1489.7897	745.3985	L	**602.3872**	301.6972	585.3606	293.1840	584.3766	292.6919	6
16	***1578.8374***	789.9223	1561.8108	781.4090	1560.8268	780.9170	A	**489.3031**	245.1552	472.2766	236.6419	471.2926	236.1499	5
17	***1679.8850***	840.4462	1662.8585	831.9329	1661.8745	831.4409	T	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
18	1736.9065	868.9569	1719.8800	860.4436	1718.8959	859.9516	G	317.2183	159.1128	300.1918	150.5995			3
19	***1849.9906***	925.4989	1832.9640	916.9856	1831.9800	916.4936	I	260.1969	130.6021	243.1703	122.0888			2
20							K	147.1128	74.0600	130.0863	65.5468			1

AT5G08680.1



NCBI **BLAST** search of DAPALVDLATGQEILATGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.1	1995.0888	0.0002	DAPALVDLATGQEILATGIK
0.8	1995.0902	-0.0011	LHSAVLDTRSSVQWVVAK

Mascot: http://www.matrixscience.com/

AT5G08690.1

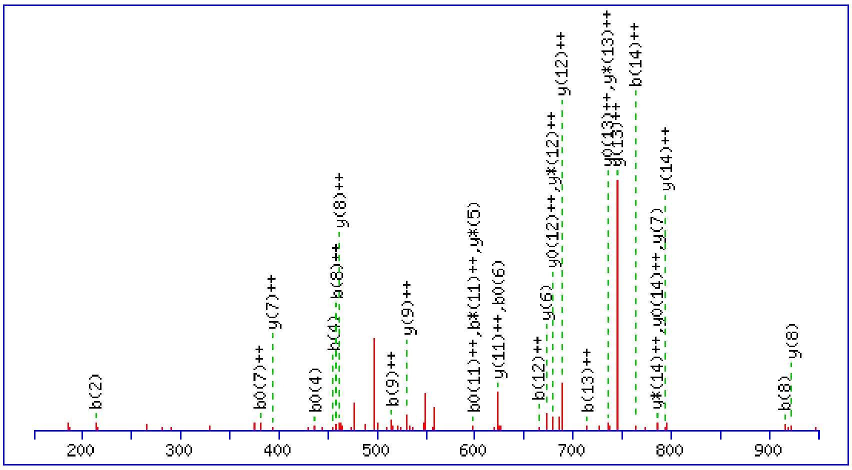
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLEVSHHLGQNVVR**
Found in **AT5G08690.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase beta chain 2, mitochondrial | chr5:2825740-2828353 FORWARD

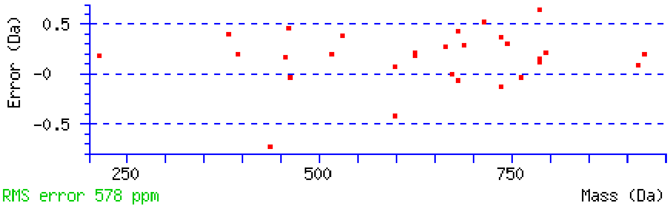
Match to Query 8137: 1698.949464 from(567.323764,3+) index(4092)
Title: Elution from: 37.550 to 37.550 scan no 5112 cid35.00 polarity:+
Data file C7-3_2.mgf

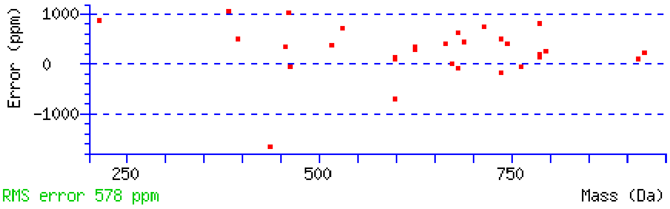
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1698.9529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0011
Matches : 30/124 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							15
2	**213.1598**	107.0835					V	1586.8762	793.9417	1569.8496	785.4284	1568.8656	784.9364	14
3	326.2438	163.6255					L	1487.8077	744.4075	1470.7812	735.8942	1469.7972	735.4022	13
4	**455.2864**	228.1468			437.2758	219.1416	E	1374.7237	687.8655	1357.6971	679.3522	1356.7131	678.8602	12
5	554.3548	277.6811			536.3443	268.6758	V	1245.6811	623.3442	1228.6545	614.8309	1227.6705	614.3389	11
6	641.3869	321.1971			623.3763	312.1918	S	1146.6127	573.8100	1129.5861	565.2967	1128.6021	564.8047	10
7	778.4458	389.7265			760.4352	380.7212	H	1059.5806	530.2940	1042.5541	521.7807			9
8	**915.5047**	***458.2560***			897.4941	449.2507	H	**922.5217**	461.7645	905.4952	453.2512			8
9	1028.5887	***514.7980***			1010.5782	505.7927	L	**785.4628**	393.2350	768.4363	384.7218			7
10	1085.6102	543.3087			1067.5996	534.3035	G	**672.3787**	336.6930	655.3522	328.1797			6
11	1213.6688	607.3380	1196.6422	598.8248	1195.6582	598.3327	Q	615.3573	308.1823	598.3307	299.6690			5
12	1327.7117	***664.3595***	1310.6852	655.8462	1309.7011	655.3542	N	487.2987	244.1530	470.2722	235.6397			4
13	1426.7801	***713.8937***	1409.7536	705.3804	1408.7696	704.8884	V	373.2558	187.1315	356.2292	178.6183			3
14	1525.8485	***763.4279***	1508.8220	754.9146	1507.8380	754.4226	V	274.1874	137.5973	257.1608	129.0840			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LVLEVSHHLGQNVVR

AT5G08690.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.9	1698.9529	-0.0035	LVLEVSHHLGQNVVR
1.9	1698.9491	0.0004	VLKLMGELHELVYR
1.6	1698.9451	0.0044	NIVAIVDACSLAGLRK
1.6	1698.9491	0.0004	LIPSFHEKLKMNVK
0.6	1698.9450	0.0044	QKPPERMASLTKGLK

AT5G09350.1

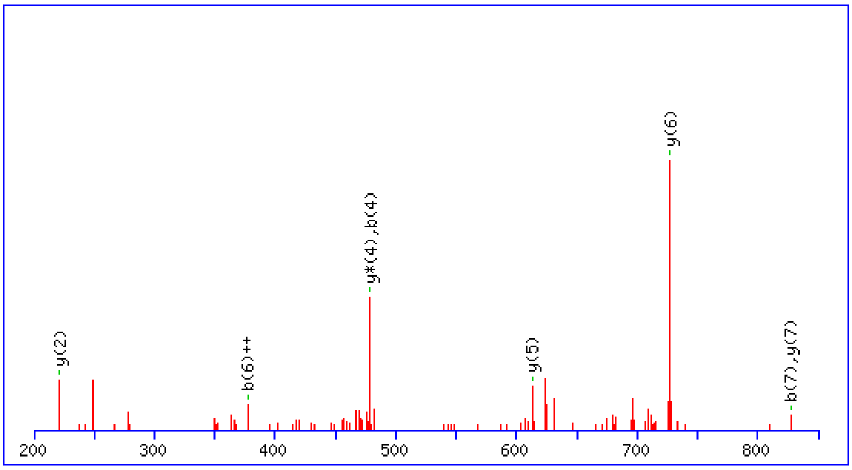
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVIDICAK**
Found in **AT5G09350.1** in **TAIR_Arabidopsis**, Symbols: | phosphatidylinositol 4-kinase, putative | chr5:2899366-2905611 REVERSE

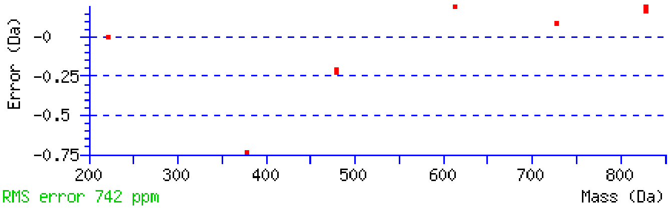
Match to Query 2376: 974.478214 from(488.246383,2+) index(1998)
Title: Elution from: 23.950 to 23.950 scan no 2593 cid35.00 polarity:+
Data file 0-2_1.mgf

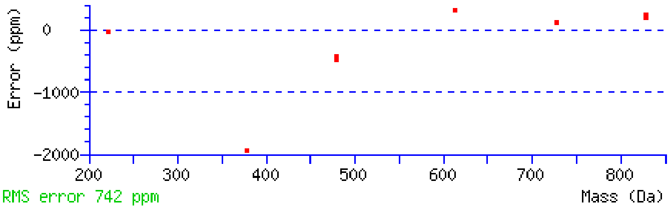
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 974.4755
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.013
Matches : 8/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400			F							8
2	249.1382	125.0727			V	***827.4174***	414.2123	809.3938	405.2005	809.4068	405.2070	7
3	363.2193	182.1133			I	***727.3519***	364.1796	709.3283	355.1678	709.3414	355.1743	6
4	**479.2433**	240.1253	461.2327	231.1200	D	***613.2708***	307.1390	595.2472	298.1273	595.2603	298.1338	5
5	593.3244	297.1658	575.3138	288.1605	I	497.2468	249.1271	479.2233	240.1153			4
6	755.3491	378.1782	737.3385	369.1729	C	383.1657	192.0865	365.1422	183.0747			3
7	**827.3832**	414.1952	809.3727	405.1900	A	***221.1410***	111.0741	203.1174	102.0624			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FVIDICAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.5	974.4755	0.0027	FVIDICAK
20.9	974.4807	-0.0025	SRTDEKVK

AT5G09350.1

16.1	974.4782	0.0000	MVIYHRK
13.8	974.4760	0.0022	GMREKNVK
13.8	974.4789	-0.0007	KMSEIMVK
12.4	974.4807	-0.0025	SRESSVAVK
10.4	974.4807	-0.0025	ASTLNKSNK
9.8	974.4807	-0.0025	RSEDSLKK
9.3	974.4807	-0.0025	VVSSTGERK
8.2	974.4807	-0.0025	DRTVESKK

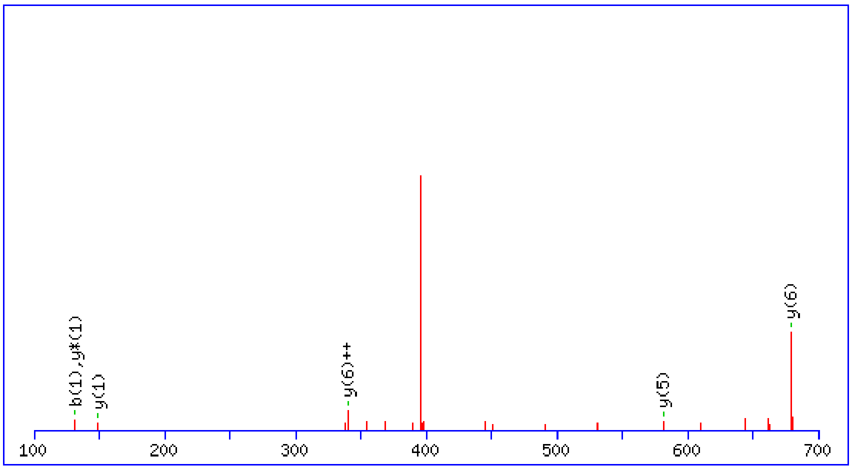
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPMALIK**
Found in **AT5G09500.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S15 (RPS15C) | chr5:2954045-2954851 REVERSE

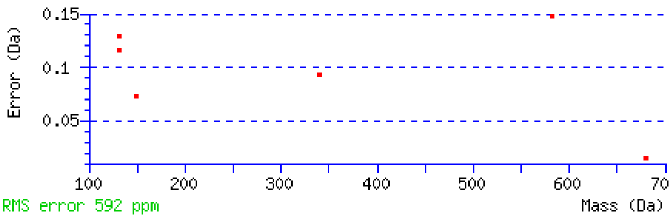
Match to Query 1117: 808.472414 from(405.243483,2+) index(880)
Title: Elution from: 14.726 to 14.726 scan no 1266 cid35.00 polarity:+
Data file D6h-1_1.mgf

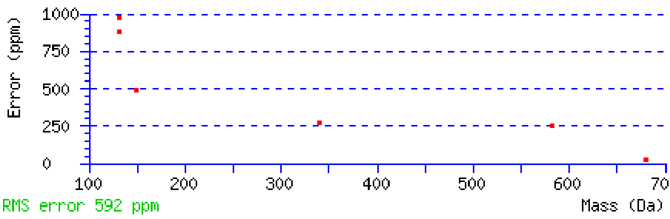
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 808.4723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 0.019
Matches : 6/48 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	131.0963	66.0518	113.0727	57.0400	K					7
2	229.1461	115.0767	211.1225	106.0649	P	*679.3905*	340.1989	661.3670	331.1871	6
3	361.1836	181.0955	343.1600	172.0837	M	*581.3407*	291.1740	563.3172	282.1622	5
4	433.2178	217.1125	415.1942	208.1007	A	449.3032	225.1552	431.2796	216.1435	4
5	547.2989	274.1531	529.2753	265.1413	L	377.2691	189.1382	359.2455	180.1264	3
6	661.3800	331.1936	643.3564	322.1818	I	263.1880	132.0976	245.1644	123.0858	2
7					K	*149.1069*	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of KPMALIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.1	808.4723	0.0001	KPMALIK
14.4	808.4723	0.0001	KLMIPAK
14.4	808.4723	0.0001	KMLLAPK

AT5G09500.1

5.7	808.4723	0.0001	KIMPALK

Mascot: http://www.matrixscience.com/

AT5G09590.1

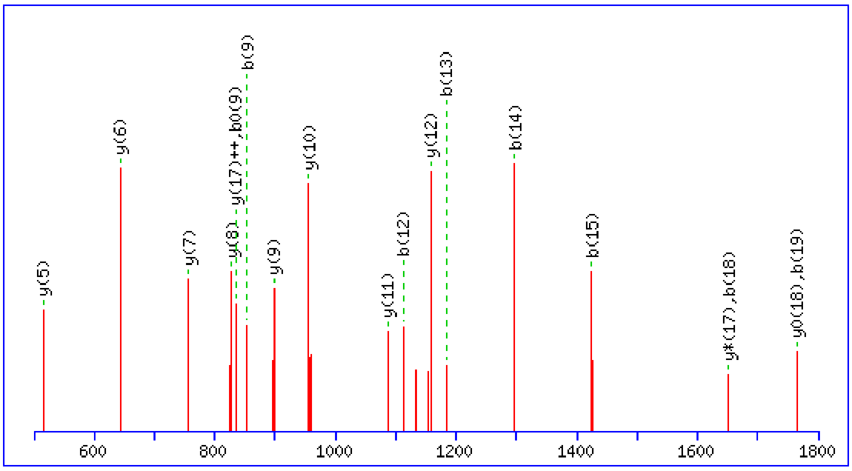
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNPDEAVAMGAALQGGILR**
Found in **AT5G09590.1** in **TAIR_Arabidopsis**, Symbols: HSC70-5, mtHSC70-2 | mtHSC70-2 (HEAT SHOCK PROTEIN 70); ATP binding / unfolded protein binding | chr5:2975722-2978509 FORWARD

Match to Query 9311: 1937.996912 from(970.005732,2+) index(9481)
Title: Elution from: 85.610 to 85.610 scan no 12918 cid35.00 polarity:+
Data file D6h-3_1.mgf

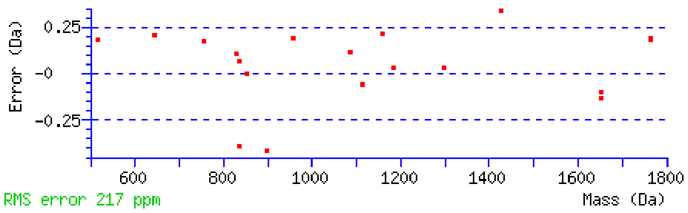
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

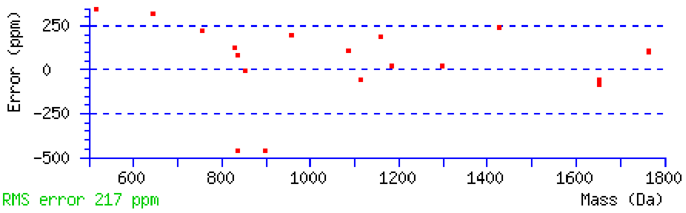


Monoisotopic mass of neutral peptide Mr(calc): 1937.9993
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 8e-007
Matches : 19/188 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							20
2	157.0972	79.0522					V	1881.9851	941.4962	1864.9586	932.9829	1863.9745	932.4909	19
3	271.1401	136.0737	254.1135	127.5604			N	1782.9167	891.9620	1765.8901	883.4487	1764.9061	882.9567	18
4	368.1928	184.6001	351.1663	176.0868			P	1668.8738	834.9405	1651.8472	826.4272	1650.8632	825.9352	17
5	483.2198	242.1135	466.1932	233.6003	465.2092	233.1082	D	1571.8210	786.4141	1554.7945	777.9009	1553.8104	777.4089	16
6	612.2624	306.6348	595.2358	298.1216	594.2518	297.6295	E	1456.7941	728.9007	1439.7675	720.3874	1438.7835	719.8954	15
7	683.2995	342.1534	666.2729	333.6401	665.2889	333.1481	A	1327.7515	664.3794	1310.7249	655.8661			14
8	782.3679	391.6876	765.3414	383.1743	764.3573	382.6823	V	1256.7144	628.8608	1239.6878	620.3475			13
9	***853.4050***	427.2061	836.3785	418.6929	835.3945	418.2009	A	***1157.6459***	579.3266	1140.6194	570.8133			12
10	984.4455	492.7264	967.4190	484.2131	966.4349	483.7211	M	***1086.6088***	543.8081	1069.5823	535.2948			11
11	1041.4670	521.2371	1024.4404	512.7238	1023.4564	512.2318	G	***955.5683***	478.2878	938.5418	469.7745			10
12	***1112.5041***	556.7557	1095.4775	548.2424	1094.4935	547.7504	A	***898.5469***	449.7771	881.5203	441.2638			9
13	***1183.5412***	592.2742	1166.5147	583.7610	1165.5306	583.2690	A	***827.5098***	414.2585	810.4832	405.7452			8
14	***1296.6253***	648.8163	1279.5987	640.3030	1278.6147	639.8110	L	***756.4726***	378.7400	739.4461	370.2267			7
15	***1424.6838***	712.8456	1407.6573	704.3323	1406.6733	703.8403	Q	***643.3886***	322.1979	626.3620	313.6847			6
16	1481.7053	741.3563	1464.6788	732.8430	1463.6947	732.3510	G	***515.3300***	258.1686	498.3035	249.6554			5
17	1538.7268	769.8670	1521.7002	761.3537	1520.7162	760.8617	G	458.3085	229.6579	441.2820	221.1446			4
18	***1651.8108***	826.4091	1634.7843	817.8958	1633.8003	817.4038	I	401.2871	201.1472	384.2605	192.6339			3
19	***1764.8949***	882.9511	1747.8683	874.4378	1746.8843	873.9458	L	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1

AT5G09590.1





NCBI **BLAST** search of GVNPDEAVAMGAALQGGILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.4	1937.9993	-0.0024	GVNPDEAVAMGAAIQGGILR
66.4	1937.9993	-0.0024	GVNPDEAVAMGAALQGGILR
2.4	1937.9973	-0.0003	KNTPHHPQDLQAFHLR
1.3	1938.0006	-0.0037	HASPIHLMSPVHGGGGRTK
0.2	1937.9993	-0.0024	EALAVAAAMEKGTTHPIGR

Mascot: http://www.matrixscience.com/

AT5G09650.1

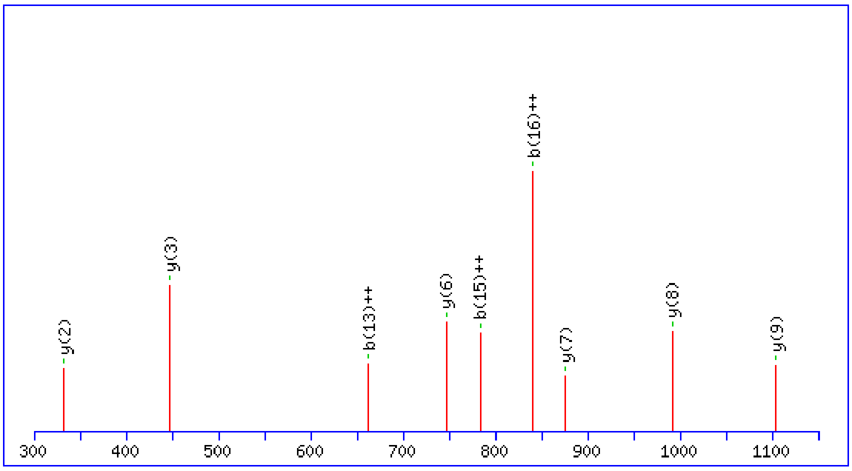
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IKPLAALAMIDEGELDWK**
Found in **AT5G09650.1** in **TAIR_Arabidopsis**, Symbols: ATPPA6 | ATPPA6 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 6); inorganic diphosphatase/ pyrophosphatase | chr5:2991332-2993118 REVERSE

Match to Query 8810: 2012.063169 from(671.694999,3+) index(9657)
Title: Elution from: 92.965 to 92.965 scan no 13802 cid35.00 polarity:+
Data file D1d-1_3.mgf

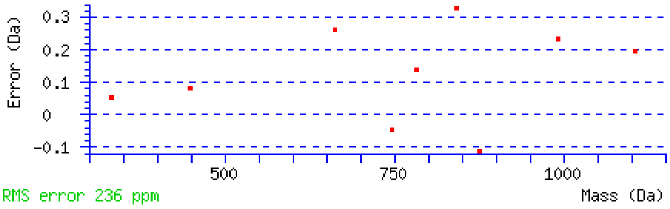
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

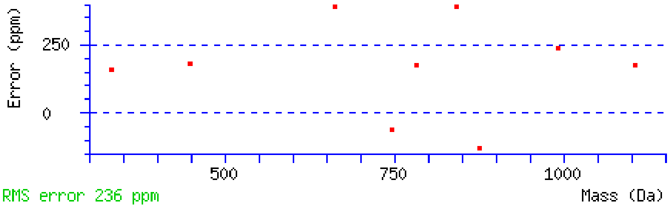


Monoisotopic mass of neutral peptide Mr(calc): 2012.0652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 8.4e-006
Matches : 9/178 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							18
2	242.1863	121.5968	225.1598	113.0835			K	1899.9885	950.4979	1882.9619	941.9846	1881.9779	941.4926	17
3	339.2391	170.1232	322.2125	161.6099			P	1771.8935	886.4504	1754.8670	877.9371	1753.8829	877.4451	16
4	452.3231	226.6652	435.2966	218.1519			L	1674.8407	837.9240	1657.8142	829.4107	1656.8302	828.9187	15
5	523.3602	262.1838	506.3337	253.6705			A	1561.7567	781.3820	1544.7301	772.8687	1543.7461	772.3767	14
6	594.3974	297.7023	577.3708	289.1890			A	1490.7196	745.8634	1473.6930	737.3501	1472.7090	736.8581	13
7	707.4814	354.2443	690.4549	345.7311			L	1419.6824	710.3449	1402.6559	701.8316	1401.6719	701.3396	12
8	778.5185	389.7629	761.4920	381.2496			A	1306.5984	653.8028	1289.5718	645.2896	1288.5878	644.7975	11
9	909.5590	455.2831	892.5325	446.7699			M	1235.5613	618.2843	1218.5347	609.7710	1217.5507	609.2790	10
10	1022.6431	511.8252	1005.6165	503.3119			I	***1104.5208***	552.7640	1087.4942	544.2508	1086.5102	543.7587	9
11	1137.6700	569.3387	1120.6435	560.8254	1119.6595	560.3334	D	***991.4367***	496.2220	974.4102	487.7087	973.4262	487.2167	8
12	1266.7126	633.8599	1249.6861	625.3467	1248.7021	624.8547	E	***876.4098***	438.7085	859.3832	430.1953	858.3992	429.7032	7
13	1323.7341	**662.3707**	1306.7075	653.8574	1305.7235	653.3654	G	***747.3672***	374.1872	730.3406	365.6740	729.3566	365.1819	6
14	1452.7767	726.8920	1435.7501	718.3787	1434.7661	717.8867	E	690.3457	345.6765	673.3192	337.1632	672.3352	336.6712	5
15	1565.8607	**783.4340**	1548.8342	774.9207	1547.8502	774.4287	L	561.3031	281.1552	544.2766	272.6419	543.2926	272.1499	4
16	1680.8877	**840.9475**	1663.8611	832.4342	1662.8771	831.9422	D	***448.2191***	224.6132	431.1925	216.0999	430.2085	215.6079	3
17	1866.9670	933.9871	1849.9405	925.4739	1848.9564	924.9819	W	***333.1921***	167.0997	316.1656	158.5864			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT5G09650.1





NCBI **BLAST** search of IKPLAALAMIDEGELDWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.1	2012.0652	-0.0020	IKPLAALAMIDEGELDWK

Mascot: http://www.matrixscience.com/

AT5G09660.1

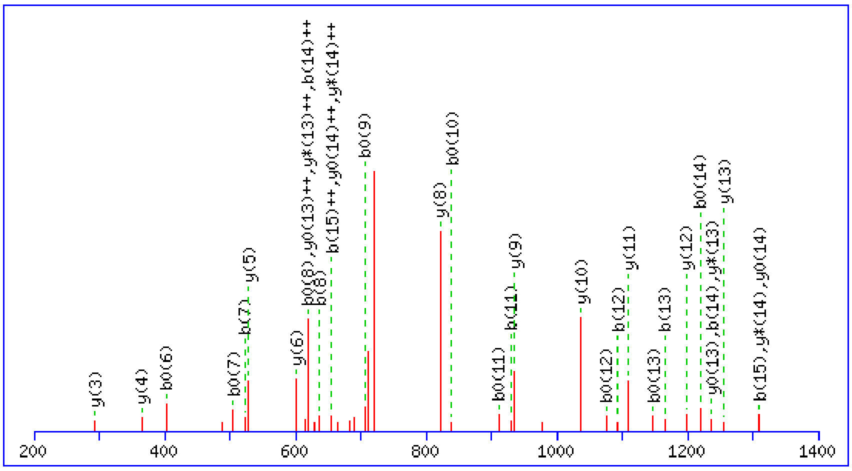
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGAGSATLSMAYAAAK**
Found in **AT5G09660.1** in **TAIR_Arabidopsis**, Symbols: PMDH2 | PMDH2 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 2); malate dehydrogenase | chr5:2993646-2995552 REVERSE

Match to Query 6168: 1456.659872 from(729.337212,2+) index(4805)
Title: Elution from: 43.873 to 43.873 scan no 6005 cid35.00 polarity:+
Data file C7-2_1.mgf

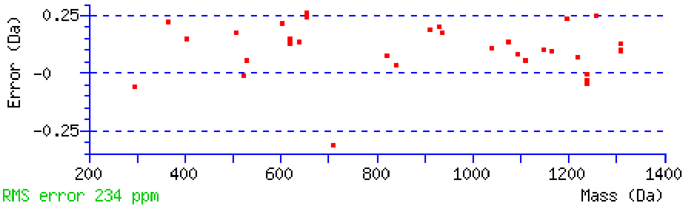
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

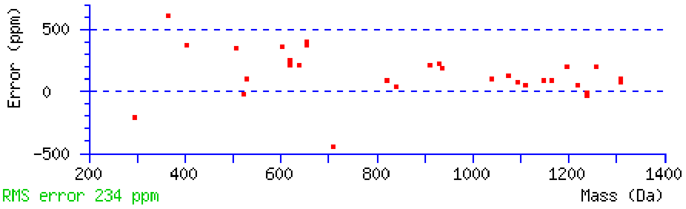


Monoisotopic mass of neutral peptide Mr(calc): 1456.6575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 101 **Expect:** 6e-010
Matches : 36/128 fragment ions using 33 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	73.0414	37.0244			A							16
2	131.0599	66.0336			G	1385.6306	693.3189	1367.6070	684.3071	1367.6200	684.3136	15
3	203.0941	102.0507			A	1327.6121	664.3097	1309.5885	655.2979	1309.6015	655.3044	14
4	261.1126	131.0599			G	***1255.5779***	628.2926	1237.5544	619.2808	1237.5674	619.2873	13
5	349.1416	175.0745	331.1311	166.0692	S	***1197.5594***	599.2834	1179.5359	590.2716	1179.5489	590.2781	12
6	421.1758	211.0915	403.1652	202.0862	A	***1109.5304***	555.2688	1091.5068	546.2570	1091.5198	546.2635	11
7	***523.2205***	262.1139	505.2099	253.1086	T	***1037.4962***	519.2518	1019.4726	510.2400	1019.4857	510.2465	10
8	***637.3016***	319.1544	619.2910	310.1492	L	***935.4515***	468.2294	917.4279	459.2176	917.4410	459.2241	9
9	725.3307	363.1690	707.3201	354.1637	S	***821.3704***	411.1888	803.3468	402.1771	803.3599	402.1836	8
10	857.3682	429.1877	839.3576	420.1824	M	733.3414	367.1743	715.3178	358.1625			7
11	***929.4023***	465.2048	911.3918	456.1995	A	***601.3038***	301.1556	583.2803	292.1438			6
12	***1093.4627***	547.2350	1075.4521	538.2297	Y	***529.2697***	265.1385	511.2461	256.1267			5
13	***1165.4968***	583.2521	1147.4863	574.2468	A	***365.2093***	183.1083	347.1857	174.0965			4
14	***1237.5310***	619.2691	1219.5204	610.2639	A	***293.1752***	147.0912	275.1516	138.0794			3
15	***1309.5651***	655.2862	1291.5546	646.2809	A	221.1410	111.0741	203.1174	102.0624			2
16					K	149.1069	75.0571	131.0833	66.0453			1

AT5G09660.1





NCBI **BLAST** search of AGAGSATLSMAYAAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.3	1456.6575	0.0024	AGAGSATLSMAYAAAK
3.3	1456.6635	-0.0036	MALCATTQRTIR
2.9	1456.6575	0.0024	ASNILLDADMHPK
2.7	1456.6574	0.0024	VYVGKDKESQCK
1.8	1456.6563	0.0036	FGAGYVSDTFLHK
1.4	1456.6575	0.0024	LDCESYVSLRAK
1.1	1456.6561	0.0038	GGKQMKCLGVMAK
1.0	1456.6631	-0.0032	CEASAYQKLLMK
0.3	1456.6635	-0.0036	MRLSITNMDGRK
0.1	1456.6624	-0.0025	IMWSQRDLAYR

Mascot: http://www.matrixscience.com/

AT5G09810.1

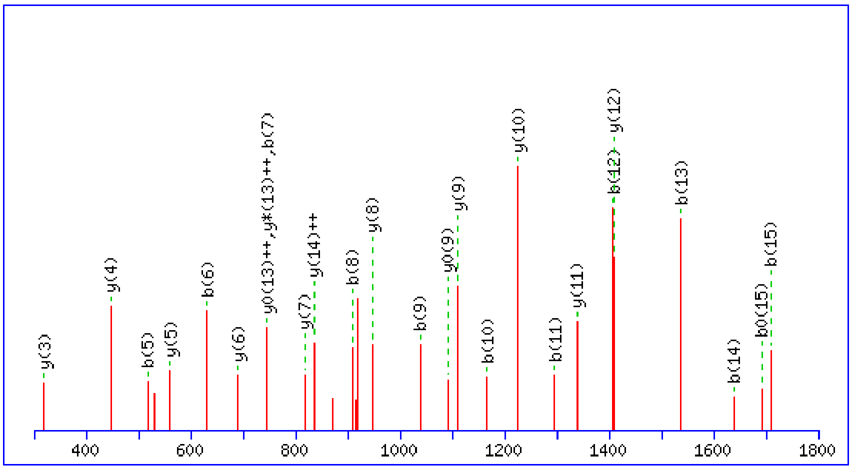
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAYVALDYEQELETAK**
Found in **AT5G09810.1** in **TAIR_Arabidopsis**, Symbols: ACT2/7, ACT7 | ACT7 (actin 7) | chr5:3052810-3054221 FORWARD

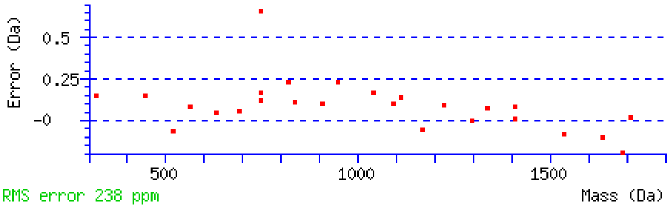
Match to Query 8912: 1854.924392 from(928.469472,2+) index(8350)
Title: Elution from: 73.175 to 73.175 scan no 10947 cid35.00 polarity:+
Data file C7-2_2.mgf

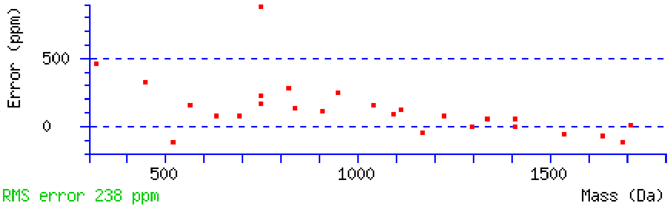
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1854.9251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 115 **Expect:** 9.4e-012
Matches : 26/146 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.0913	57.5493					L							16
2	185.1285	93.0679					A	1742.8483	871.9278	1725.8218	863.4145	1724.8378	862.9225	15
3	348.1918	174.5995					Y	1671.8112	836.4092	1654.7847	827.8960	1653.8006	827.4040	14
4	447.2602	224.1337					V	1508.7479	754.8776	1491.7213	746.3643	1490.7373	745.8723	13
5	***518.2973***	259.6523					A	***1409.6795***	705.3434	1392.6529	696.8301	1391.6689	696.3381	12
6	***631.3814***	316.1943					L	***1338.6424***	669.8248	1321.6158	661.3115	1320.6318	660.8195	11
7	***746.4083***	373.7078			728.3978	364.7025	D	***1225.5583***	613.2828	1208.5317	604.7695	1207.5477	604.2775	10
8	***909.4716***	455.2395			891.4611	446.2342	Y	***1110.5313***	555.7693	1093.5048	547.2560	1092.5208	546.7640	9
9	***1038.5142***	519.7608			1020.5037	510.7555	E	***947.4680***	474.2376	930.4415	465.7244	929.4575	465.2324	8
10	***1166.5728***	583.7900	1149.5463	575.2768	1148.5623	574.7848	Q	***818.4254***	409.7164	801.3989	401.2031	800.4149	400.7111	7
11	***1295.6154***	648.3113	1278.5889	639.7981	1277.6048	639.3061	E	***690.3668***	345.6871	673.3403	337.1738	672.3563	336.6818	6
12	***1408.6995***	704.8534	1391.6729	696.3401	1390.6889	695.8481	L	***561.3243***	281.1658	544.2977	272.6525	543.3137	272.1605	5
13	***1537.7421***	769.3747	1520.7155	760.8614	1519.7315	760.3694	E	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6185	4
14	***1638.7897***	819.8985	1621.7632	811.3852	1620.7792	810.8932	T	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	3
15	***1709.8269***	855.4171	1692.8003	846.9038	1691.8163	846.4118	A	218.1499	109.5786	201.1234	101.0653			2
16							K	147.1128	74.0600	130.0863	65.5468			1





AT5G09810.1

NCBI **BLAST** search of LAYVALDYEQELETAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
115.5	1854.9251	-0.0007	LAYVALDYEQELETAK

AT5G10170.1

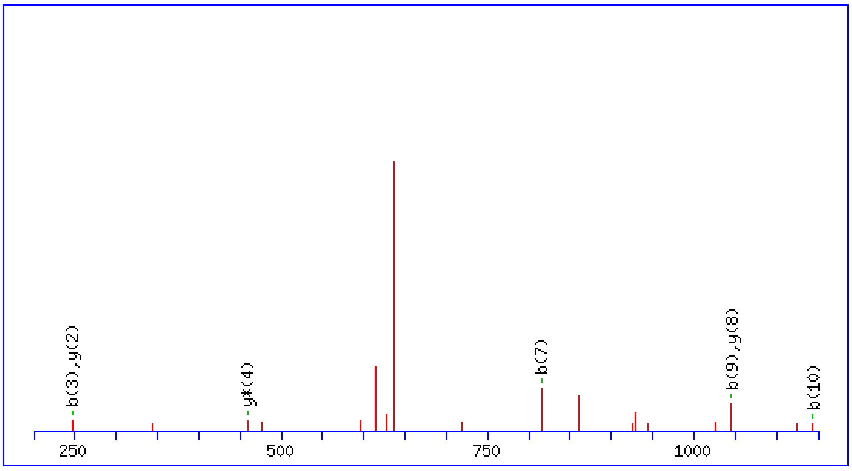
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGAFQWTVKPK**
Found in **AT5G10170.1** in **TAIR_Arabidopsis**, Symbols: | inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putative | chr5:3187539-3190162 REVERSE

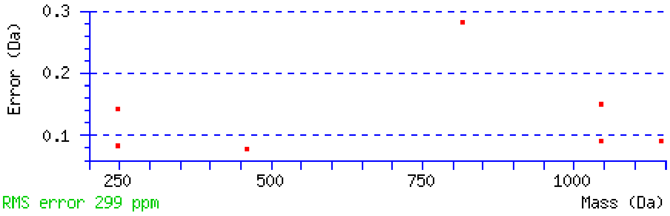
Match to Query 4886: 1290.631976 from(646.323264,2+) index(6234)
Title: Elution from: 54.877 to 54.877 scan no 7877 cid35.00 polarity:+
Data file C7-3_1.mgf

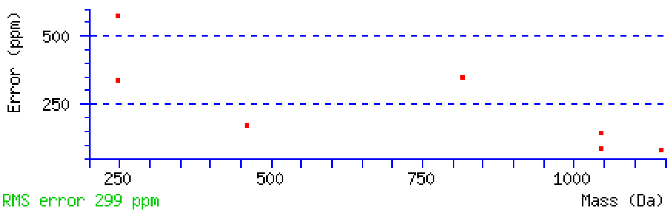
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1290.6297
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.012
Matches : 7/100 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							11
2	175.0628	88.0350	157.0392	79.0232			G	1175.6000	588.3036	1157.5764	579.2918	1157.5894	579.2984	10
3	***247.0969***	124.0521	229.0733	115.0403			A	1117.5815	559.2944	1099.5579	550.2826	1099.5709	550.2891	9
4	395.1624	198.0848	377.1388	189.0730			F	**1045.5473**	523.2773	1027.5238	514.2655	1027.5368	514.2720	8
5	525.2150	263.1111	507.1914	254.0994			Q	897.4819	449.2446	879.4583	440.2328	879.4713	440.2393	7
6	713.2884	357.1478	695.2648	348.1360			W	767.4293	384.2183	749.4057	375.2065	749.4187	375.2130	6
7	***815.3331***	408.1702	797.3095	399.1584	797.3225	399.1649	T	579.3559	290.1816	561.3323	281.1698	561.3453	281.1763	5
8	915.3986	458.2029	897.3750	449.1911	897.3880	449.1976	V	477.3112	239.1592	459.2876	230.1474			4
9	***1045.4876***	523.2474	1027.4640	514.2356	1027.4770	514.2422	K	377.2457	189.1265	359.2221	180.1147			3
10	***1143.5374***	572.2723	1125.5138	563.2605	1125.5268	563.2671	P	**247.1567**	124.0820	229.1331	115.0702			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NGAFQWTVKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G10170.1

Score	Mr(calc)	Delta	Sequence
29.1	1290.6297	0.0023	NGAFQWTVKPK
18.1	1290.6282	0.0038	DEEKKMGTLVK
16.1	1290.6331	-0.0011	MKLTWNKNPK
9.2	1290.6335	-0.0016	CRTLINRNPK
9.2	1290.6338	-0.0018	DEKAIMTMVIK
8.2	1290.6308	0.0011	IMNVQLGEKSR
6.4	1290.6331	-0.0011	FLPNMKEPRK
5.3	1290.6283	0.0036	WGRRPLLMVM
5.2	1290.6297	0.0023	WANYLRPDIK
4.4	1290.6297	0.0023	NELWWSKGKK

Mascot: http://www.matrixscience.com/

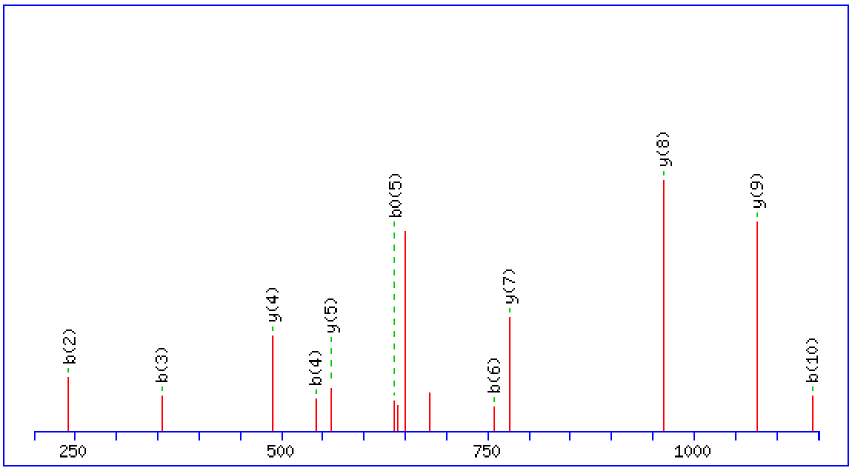
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQLWDTAGQER**
Found in **AT5G10260.1** in **TAIR_Arabidopsis**, Symbols: AtRABH1e | AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding | chr5:3219992-3221302 FORWARD

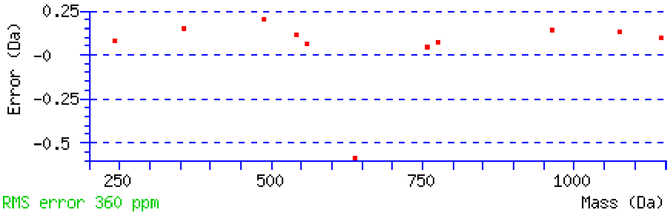
Match to Query 4705: 1315.652896 from(658.833724,2+) index(4787)
Title: Elution from: 43.105 to 43.105 scan no 6087 cid35.00 polarity:+
Data file D12h-3_3.mgf

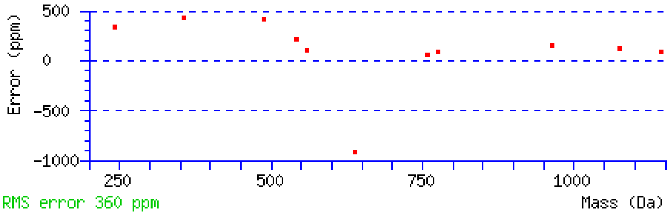
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1315.6521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 2.2e-005
Matches : 11/108 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	***242.1499***	121.5786	225.1234	113.0653			Q	1203.5753	602.2913	1186.5487	593.7780	1185.5647	593.2860	10
3	***355.2340***	178.1206	338.2074	169.6074			L	***1075.5167***	538.2620	1058.4902	529.7487	1057.5061	529.2567	9
4	***541.3133***	271.1603	524.2867	262.6470			W	***962.4326***	481.7200	945.4061	473.2067	944.4221	472.7147	8
5	656.3402	328.6738	639.3137	320.1605	638.3297	319.6685	D	***776.3533***	388.6803	759.3268	380.1670	758.3428	379.6750	7
6	***757.3879***	379.1976	740.3614	370.6843	739.3774	370.1923	T	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	6
7	828.4250	414.7162	811.3985	406.2029	810.4145	405.7109	A	***560.2787***	280.6430	543.2522	272.1297	542.2681	271.6377	5
8	885.4465	443.2269	868.4199	434.7136	867.4359	434.2216	G	***489.2416***	245.1244	472.2150	236.6112	471.2310	236.1191	4
9	1013.5051	507.2562	996.4785	498.7429	995.4945	498.2509	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
10	***1142.5477***	571.7775	1125.5211	563.2642	1124.5371	562.7722	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LQLWDTAGQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G10260.1

Score	Mr(calc)	Delta	Sequence
53.3	1315.6521	0.0008	LQIWDTAGQER
53.3	1315.6521	0.0008	LQLWDTAGQER
0.2	1315.6529	-0.0000	TCVKPLCPWR

Mascot: http://www.matrixscience.com/

AT5G10320.1

Mascot Search Results

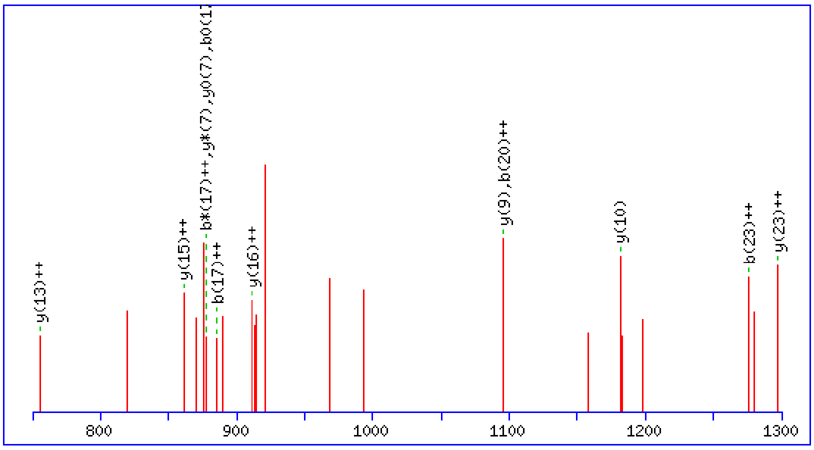
Peptide View

MS/MS Fragmentation of **SLELDDEATTPLNTISAECQNSCVK**
Found in **AT5G10320.1** in **TAIR_Arabidopsis**, Symbols: | similar to 80A08_29 [Brassica rapa subsp. pekinensis] (GB:AAZ67614.1) | chr5:3244181-3246604 REVERSE

Match to Query 10282: 2794.258335 from(932.426721,3+) index(9707)
Title: Elution from: 91.321 to 91.321 scan no 13760 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

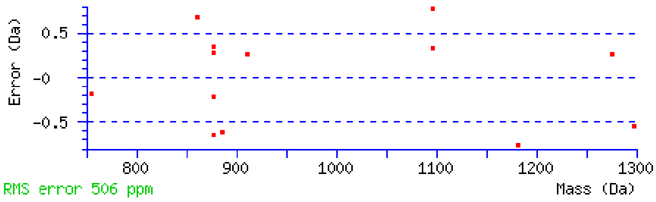
Or, Plot from 750 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

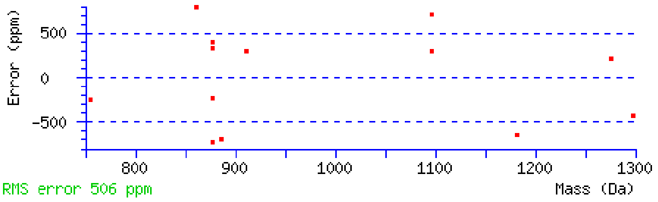


Monoisotopic mass of neutral peptide Mr(calc): 2794.2637
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 0.044
Matches : 13/258 fragment ions using 22 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	201.1234	101.0653			183.1128	92.0600	L	2708.2390	1354.6231	2691.2124	1346.1098	2690.2284	1345.6178	24
3	330.1660	165.5866			312.1554	156.5813	E	2595.1549	1298.0811	2578.1283	1289.5678	2577.1443	1289.0758	23
4	443.2500	222.1287			425.2395	213.1234	L	2466.1123	1233.5598	2449.0857	1225.0465	2448.1017	1224.5545	22
5	558.2770	279.6421			540.2664	270.6368	D	2353.0282	1177.0178	2336.0017	1168.5045	2335.0177	1168.0125	21
6	673.3039	337.1556			655.2933	328.1503	D	2238.0013	1119.5043	2220.9747	1110.9910	2219.9907	1110.4990	20
7	802.3465	401.6769			784.3359	392.6716	E	2122.9743	1061.9908	2105.9478	1053.4775	2104.9638	1052.9855	19
8	873.3836	437.1954			855.3731	428.1902	A	1993.9318	997.4695	1976.9052	988.9562	1975.9212	988.4642	18
9	974.4313	487.7193			956.4207	478.7140	T	1922.8946	961.9510	1905.8681	953.4377	1904.8841	952.9457	17
10	1075.4790	538.2431			1057.4684	529.2378	T	1821.8470	911.4271	1804.8204	902.9138	1803.8364	902.4218	16
11	1172.5317	586.7695			1154.5212	577.7642	P	1720.7993	860.9033	1703.7727	852.3900	1702.7887	851.8980	15
12	1285.6158	643.3115			1267.6052	634.3063	L	1623.7465	812.3769	1606.7200	803.8636	1605.7360	803.3716	14
13	1399.6587	700.3330	1382.6322	691.8197	1381.6482	691.3277	N	1510.6625	755.8349	1493.6359	747.3216	1492.6519	746.8296	13
14	1500.7064	750.8568	1483.6799	742.3436	1482.6958	741.8516	T	1396.6195	698.8134	1379.5930	690.3001	1378.6090	689.8081	12
15	1613.7905	807.3989	1596.7639	798.8856	1595.7799	798.3936	I	1295.5718	648.2896	1278.5453	639.7763	1277.5613	639.2843	11
16	1700.8225	850.9149	1683.7960	842.4016	1682.8119	841.9096	S	**1182.4878**	591.7475	1165.4612	583.2343	1164.4772	582.7422	10
17	1771.8596	***886.4334***	1754.8331	877.9202	1753.8491	877.4282	A	**1095.4558**	548.2315	1078.4292	539.7182	1077.4452	539.2262	9
18	1900.9022	950.9547	1883.8757	942.4415	1882.8916	941.9495	E	1024.4186	512.7130	1007.3921	504.1997	1006.4081	503.7077	8
19	2060.9329	1030.9701	2043.9063	1022.4568	2042.9223	1021.9648	C	895.3760	448.1917	878.3495	439.6784	877.3655	439.1864	7
20	2188.9914	***1094.9994***	2171.9649	1086.4861	2170.9809	1085.9941	Q	735.3454	368.1763	718.3189	359.6631	717.3348	359.1711	6
21	2303.0344	1152.0208	2286.0078	1143.5075	2285.0238	1143.0155	N	607.2868	304.1470	590.2603	295.6338	589.2763	295.1418	5
22	2390.0664	1195.5368	2373.0398	1187.0236	2372.0558	1186.5316	S	493.2439	247.1256	476.2173	238.6123	475.2333	238.1203	4
23	2550.0970	***1275.5522***	2533.0705	1267.0389	2532.0865	1266.5469	C	406.2119	203.6096	389.1853	195.0963			3
24	2649.1655	1325.0864	2632.1389	1316.5731	2631.1549	1316.0811	V	246.1812	123.5942	229.1547	115.0810			2

25							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SLELDDEATTPLNTISAECQNSCVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.5	2794.2637	-0.0054	SLELDDEATTPLNTISAECQNSCVK
4.3	2794.2637	-0.0053	MDEYALMIGTSSSESTSKNISLDGAR

Mascot: http://www.matrixscience.com/

AT5G10360.1

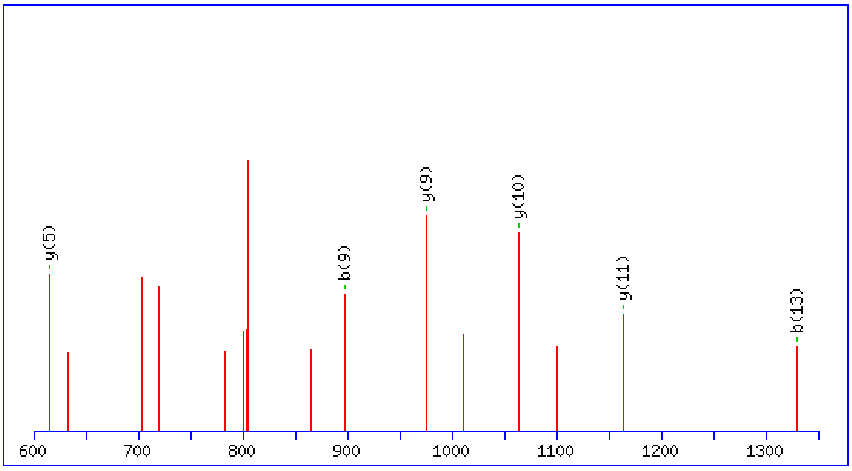
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSQEVSGDALGEEFK**
Found in **AT5G10360.1** in **TAIR_Arabidopsis**, Symbols: EMB3010 | EMB3010 (EMBRYO DEFECTIVE 3010); structural constituent of ribosome | chr5:3258735-3260143 REVERSE

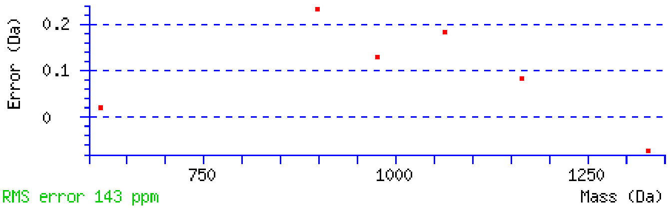
Match to Query 7052: 1624.715148 from(813.364850,2+) index(5027)
Title: Elution from: 44.991 to 44.991 scan no 6408 cid35.00 polarity:+
Data file D12h-3_3.mgf

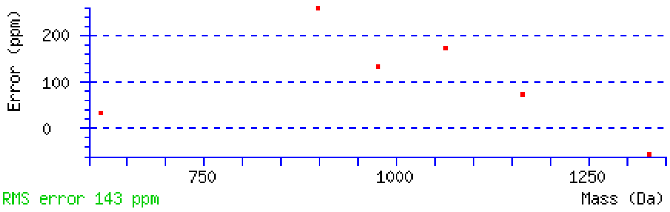
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1624.7175
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0014
Matches : 6/158 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							15
2	203.1174	102.0624			185.1069	93.0571	S	1511.6437	756.3255	1493.6201	747.3137	1493.6331	747.3202	14
3	333.1701	167.0887	315.1465	158.0769	315.1595	158.0834	Q	1423.6146	712.3109	1405.5910	703.2991	1405.6040	703.3057	13
4	463.2097	232.1085	445.1861	223.0967	445.1991	223.1032	E	1293.5619	647.2846	1275.5384	638.2728	1275.5514	638.2793	12
5	563.2752	282.1412	545.2516	273.1294	545.2646	273.1359	V	*1163.5223*	582.2648	1145.4987	573.2530	1145.5117	573.2595	11
6	651.3042	326.1558	633.2806	317.1440	633.2937	317.1505	S	*1063.4569*	532.2321	1045.4333	523.2203	1045.4463	523.2268	10
7	709.3227	355.1650	691.2991	346.1532	691.3122	346.1597	G	*975.4278*	488.2175	957.4042	479.2057	957.4172	479.2123	9
8	825.3467	413.1770	807.3231	404.1652	807.3361	404.1717	D	917.4093	459.2083	899.3857	450.1965	899.3987	450.2030	8
9	*897.3809*	449.1941	879.3573	440.1823	879.3703	440.1888	A	801.3853	401.1963	783.3617	392.1845	783.3748	392.1910	7
10	1011.4620	506.2346	993.4384	497.2228	993.4514	497.2293	L	729.3512	365.1792	711.3276	356.1674	711.3406	356.1739	6
11	1069.4804	535.2439	1051.4569	526.2321	1051.4699	526.2386	G	*615.2701*	308.1387	597.2465	299.1269	597.2595	299.1334	5
12	1199.5201	600.2637	1181.4965	591.2519	1181.5095	591.2584	E	557.2516	279.1294	539.2280	270.1176	539.2410	270.1241	4
13	*1329.5597*	665.2835	1311.5361	656.2717	1311.5491	656.2782	E	427.2120	214.1096	409.1884	205.0978	409.2014	205.1043	3
14	1477.6252	739.3162	1459.6016	730.3044	1459.6146	730.3109	F	297.1723	149.0898	279.1487	140.0780			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT5G10360.1

NCBI **BLAST** search of LSQEVSGDALGEEFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.2	1624.7175	-0.0023	ISQEVSGDALGEEFK
37.2	1624.7175	-0.0023	LSQEVSGDALGEEFK
2.0	1624.7154	-0.0003	GCSSRVSLTFHEPK
0.5	1624.7161	-0.0009	EAVEKMEDLMKER

AT5G10440.1

Mascot Search Results

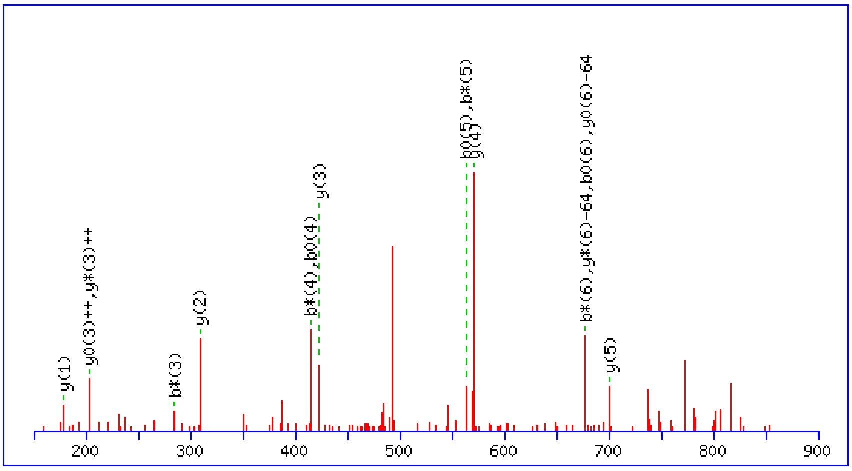
Peptide View

MS/MS Fragmentation of **KIGEMIER**
Found in **AT5G10440.1** in **TAIR_Arabidopsis**, Symbols: CYCD4;2 | CYCD4;2 (CYCLIN D4;2); cyclin-dependent protein kinase | chr5:3280612-3282343 REVERSE

Match to Query 2633: 1002.483064 from(502.248808,2+) index(3145)
Title: Elution from: 31.472 to 31.472 scan no 3915 cid35.00 polarity:+
Data file C7-3_1.mgf

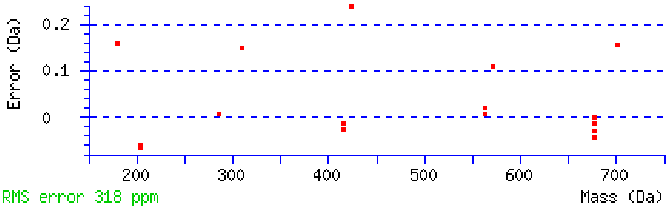
Click mouse within plot area to zoom in by factor of two about that point

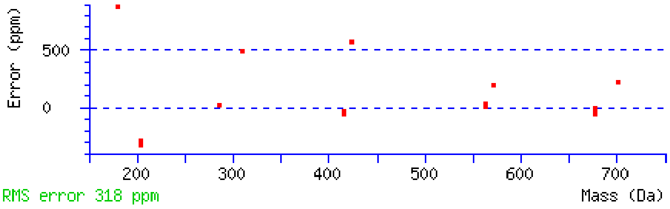
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1002.4812
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 32 **Expect:** 0.0068
Matches : 16/118 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							8
2	245.1774	123.0923	227.1538	114.0805			I	873.3995	437.2034	855.3759	428.1916	855.3889	428.1981	7
3	303.1959	152.1016	285.1723	143.0898			G	759.3184	380.1628	741.2948	371.1510	741.3078	371.1575	6
4	433.2355	217.1214	415.2120	208.1096	415.2250	208.1161	E	***701.2999***	351.1536	683.2763	342.1418	683.2893	342.1483	5
5	581.2680	291.1376	563.2444	282.1258	563.2574	282.1323	M	***571.2603***	286.1338	553.2367	277.1220	553.2497	277.1285	4
6	695.3491	348.1782	677.3255	339.1664	677.3385	339.1729	I	***423.2278***	212.1175	405.2042	203.1058	405.2173	203.1123	3
7	825.3887	413.1980	807.3651	404.1862	807.3781	404.1927	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of KIGEMIER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G10440.1

32.1	1002.4812	0.0018	KIGEMIER
11.3	1002.4812	0.0018	LSDMKLER
10.9	1002.4812	0.0018	SLEDLMKR
8.9	1002.4812	0.0018	MEDALIKR
5.1	1002.4839	-0.0008	EAVMAGVRR
4.5	1002.4812	0.0018	LKVMEAER
4.3	1002.4812	0.0018	MAEIKVER
1.6	1002.4835	-0.0004	WLKEMAAK
1.4	1002.4839	-0.0008	GAVEMAVRR
0.4	1002.4839	-0.0008	VDPSRMKR

AT5G10450.1

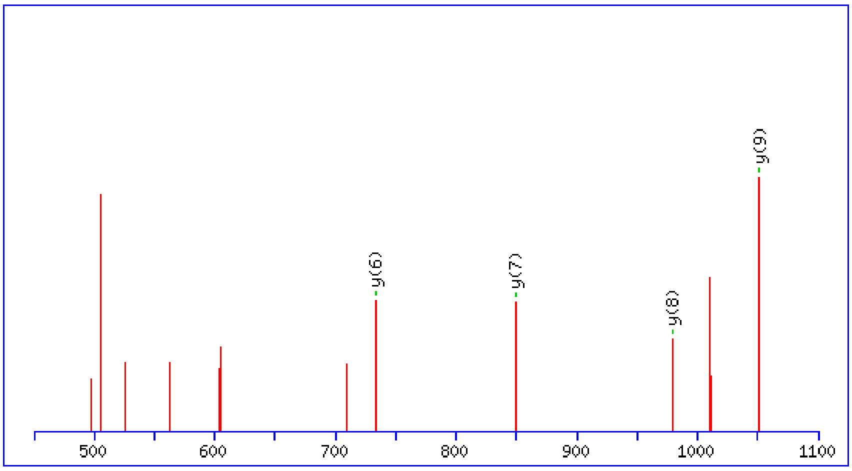
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAAEDTMLAYK**
Found in **AT5G10450.1** in **TAIR_Arabidopsis**, Symbols: AFT1, GRF6 | GRF6 (G-BOX REGULATING FACTOR 6); protein phosphorylated amino acid binding | chr5:3284453-3286262 REVERSE

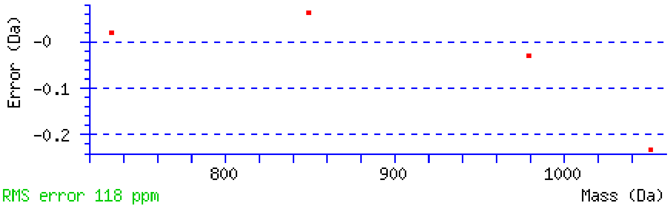
Match to Query 4056: 1224.536952 from(613.275752,2+) index(3306)
Title: Elution from: 32.725 to 32.725 scan no 4119 cid35.00 polarity:+
Data file C7-1_3.mgf

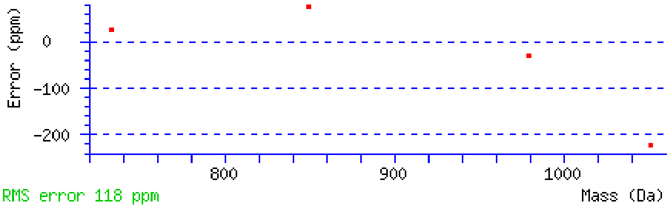
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1224.5340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0062
Matches : 4/90 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							11
2	175.0861	88.0467	157.0756	79.0414	A	1123.4966	562.2519	1105.4730	553.2402	1105.4861	553.2467	10
3	247.1203	124.0638	229.1097	115.0585	A	***1051.4625***	526.2349	1033.4389	517.2231	1033.4519	517.2296	9
4	377.1599	189.0836	359.1494	180.0783	E	***979.4283***	490.2178	961.4047	481.2060	961.4178	481.2125	8
5	493.1839	247.0956	475.1733	238.0903	D	***849.3887***	425.1980	831.3651	416.1862	831.3781	416.1927	7
6	595.2286	298.1179	577.2180	289.1127	T	***733.3647***	367.1860	715.3411	358.1742	715.3542	358.1807	6
7	727.2661	364.1367	709.2556	355.1314	M	631.3200	316.1636	613.2964	307.1518			5
8	841.3472	421.1773	823.3367	412.1720	L	499.2825	250.1449	481.2589	241.1331			4
9	913.3814	457.1943	895.3708	448.1890	A	385.2014	193.1043	367.1778	184.0925			3
10	1077.4417	539.2245	1059.4312	530.2192	Y	313.1672	157.0873	295.1437	148.0755			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TAAEDTMLAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G10450.1

Score	Mr(calc)	Delta	Sequence
30.7	1224.5340	0.0029	TAAEDTMIAYK
30.7	1224.5340	0.0029	TAAEDTMLAYK
1.3	1224.5394	-0.0024	AGNMPVQYRR
0.5	1224.5390	-0.0020	GCAKSYGPFPK

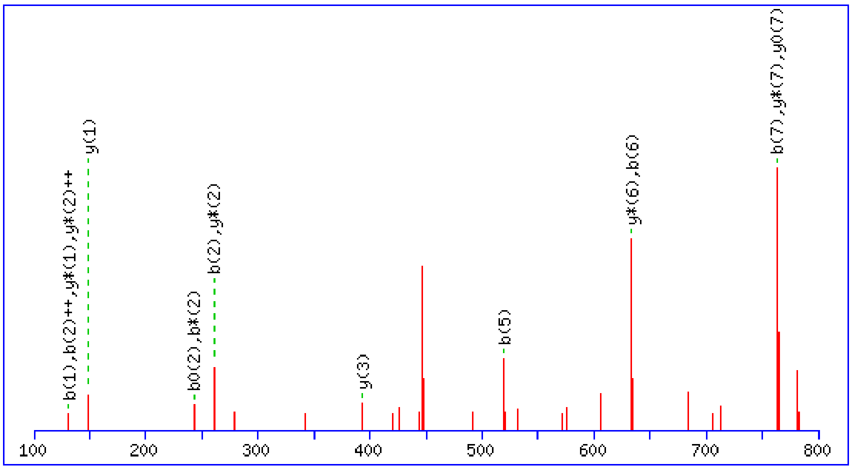
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEVVGLKK**
Found in **AT5G10470.1** in **TAIR_Arabidopsis**, Symbols: | kinesin motor protein-related | chr5:3290122-3297249 REVERSE

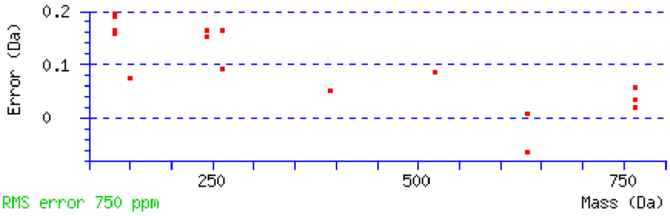
Match to Query 1369: 910.510504 from(456.262528,2+) index(1218)
Title: Elution from: 20.698 to 20.698 scan no 1785 cid35.00 polarity:+
Data file D12h-2_2.mgf

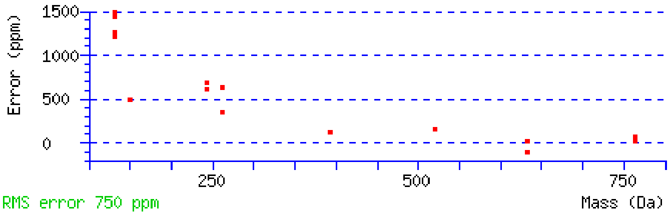
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 910.5114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0018
Matches : 16/70 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***131.0599***	66.0336	113.0363	57.0218			Q							8
2	***261.0996***	131.0534	243.0760	122.0416	243.0890	122.0481	E	781.4660	391.2367	763.4424	382.2249	763.4555	382.2314	7
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	V	651.4264	326.2168	633.4028	317.2050			6
4	461.2304	231.1189	443.2069	222.1071	443.2199	222.1136	V	551.3610	276.1841	533.3374	267.1723			5
5	***519.2489***	260.1281	501.2254	251.1163	501.2384	251.1228	G	451.2955	226.1514	433.2719	217.1396			4
6	***633.3300***	317.1687	615.3065	308.1569	615.3195	308.1634	L	**393.2770**	197.1421	375.2534	188.1303			3
7	***763.4191***	382.2132	745.3955	373.2014	745.4085	373.2079	K	279.1959	140.1016	261.1723	131.0898			2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QEVVGLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.0	910.5114	-0.0009	QEVVGLKK
23.8	910.5114	-0.0009	ELRLIEK

17.5	910.5114	-0.0009	ILERLEK
17.5	910.5114	-0.0009	IRELIEK
17.5	910.5114	-0.0009	LLERIEK
17.5	910.5114	-0.0009	RELLLEK
14.8	910.5114	-0.0009	AAADLLAKK
14.8	910.5114	-0.0009	AIQELAKK
12.6	910.5114	-0.0009	EKAKSIPK
12.4	910.5114	-0.0009	LILREEK

AT5G10540.1

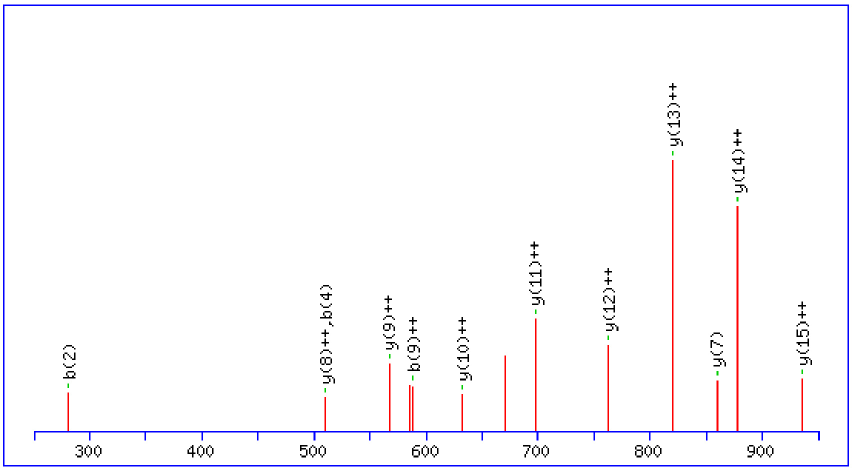
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDINEEELRPYFSLPK**
Found in **AT5G10540.1** in **TAIR_Arabidopsis**, Symbols: | peptidase M3 family protein / thimet oligopeptidase family protein | chr5:3328120-3332463 FORWARD

Match to Query 9039: 2032.923141 from(678.648323,3+) index(8298)
Title: Elution from: 74.474 to 74.474 scan no 11058 cid35.00 polarity:+
Data file D12h-2_3.mgf

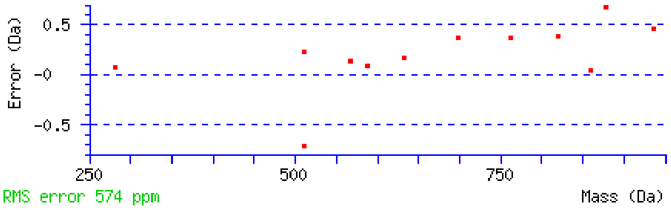
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

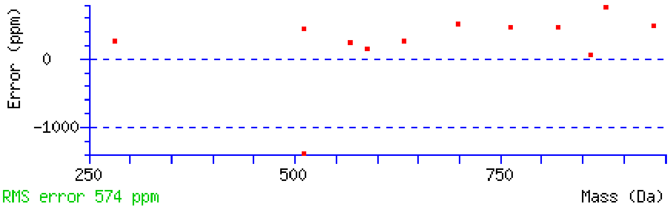


Monoisotopic mass of neutral peptide Mr(calc): 2032.9268
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 6.5e-006
Matches : 12/166 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							16
2	**281.0916**	141.0494			263.0811	132.0442	D	1869.8738	935.4405	1851.8502	926.4287	1851.8632	926.4352	15
3	395.1727	198.0900			377.1622	189.0847	I	1753.8498	877.4285	1735.8262	868.4167	1735.8392	868.4232	14
4	**511.2097**	256.1085	493.1861	247.0967	493.1991	247.1032	N	1639.7687	820.3880	1621.7451	811.3762	1621.7581	811.3827	13
5	641.2493	321.1283	623.2258	312.1165	623.2388	312.1230	E	1523.7317	762.3695	1505.7081	753.3577	1505.7211	753.3642	12
6	771.2890	386.1481	753.2654	377.1363	753.2784	377.1428	E	1393.6921	697.3497	1375.6685	688.3379	1375.6815	688.3444	11
7	901.3286	451.1679	883.3050	442.1561	883.3180	442.1627	E	1263.6524	632.3299	1245.6288	623.3181	1245.6419	623.3246	10
8	1015.4097	508.2085	997.3861	499.1967	997.3991	499.2032	L	1133.6128	567.3100	1115.5892	558.2982	1115.6022	558.3048	9
9	1175.4989	588.2531	1157.4754	579.2413	1157.4884	579.2478	R	1019.5317	510.2695	1001.5081	501.2577	1001.5211	501.2642	8
10	1273.5487	637.2780	1255.5252	628.2662	1255.5382	628.2727	P	859.4424	430.2249	841.4189	421.2131	841.4319	421.2196	7
11	1437.6091	719.3082	1419.5855	710.2964	1419.5985	710.3029	Y	761.3926	381.2000	743.3691	372.1882	743.3821	372.1947	6
12	1585.6746	793.3409	1567.6510	784.3291	1567.6640	784.3356	F	597.3323	299.1698	579.3087	290.1580	579.3217	290.1645	5
13	1673.7036	837.3554	1655.6800	828.3437	1655.6931	828.3502	S	449.2668	225.1371	431.2433	216.1253	431.2563	216.1318	4
14	1787.7847	894.3960	1769.7611	885.3842	1769.7742	885.3907	L	361.2378	181.1225	343.2142	172.1107			3
15	1885.8345	943.4209	1867.8109	934.4091	1867.8240	934.4156	P	247.1567	124.0820	229.1331	115.0702			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT5G10540.1





NCBI **BLAST** search of YDINEEELRPYFSLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.8	2032.9268	-0.0037	YDINEEELRPYFSLPK
13.3	2032.9277	-0.0046	YLKPMVAWEPEVTFMR
10.9	2032.9176	0.0055	VTADQSDRFNDAVLSLMK
7.7	2032.9176	0.0055	AKTQVAASFASEGAGMNELK
6.4	2032.9198	0.0033	MHKDTKYVLFLDDDVR
6.4	2032.9203	0.0029	LHDGGLAHGDLTTSNMLVR
4.4	2032.9277	-0.0046	YLKPMVAWEPEVTFMR
4.2	2032.9203	0.0028	NCISQRVPEPPSVSTHAK
3.4	2032.9198	0.0033	VHDLPSVDMFVPTADPVR
2.9	2032.9280	-0.0048	MKKGVEESINVDGSDFIK

Mascot: http://www.matrixscience.com/

AT5G10790.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNMSPYLSSSIIGK**
Found in **AT5G10790.1** in **TAIR_Arabidopsis**, Symbols: UBP22 | UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); ubiquitin-specific protease | chr5:3410639-3412560 FORWARD

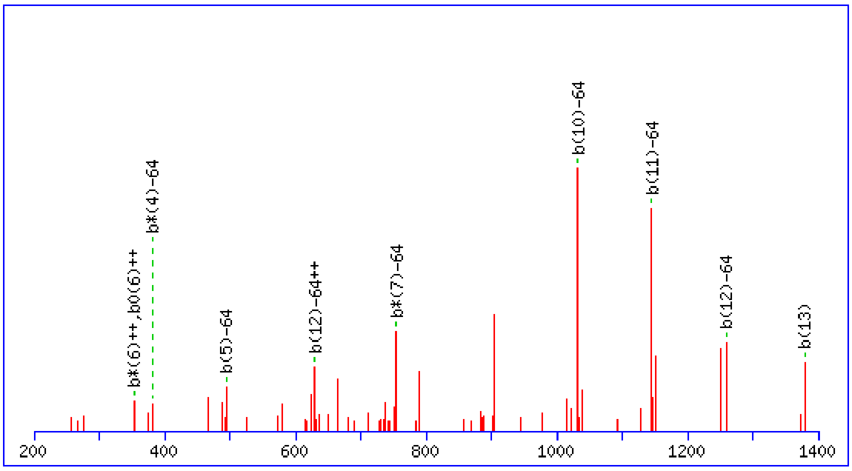
Match to Query 6723: 1524.782106 from(763.398329,2+) index(7199)
Title: Elution from: 63.909 to 63.909 scan no 9320 cid35.00 polarity:+
Data file D12h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

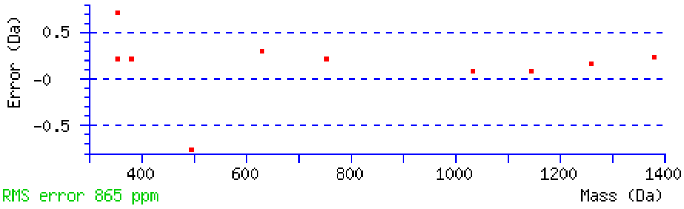
Label all possible matches ○ Label matches used for scoring ●

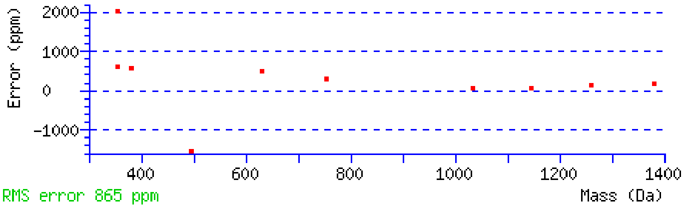
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1524.7858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.044
Matches : 10/216 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	228.1343	114.5708	211.1077	106.0575			N	1348.7107	674.8590	1331.6842	666.3457	1330.7001	665.8537	13
3	311.1714	156.0893	294.1448	147.5761			M	1234.6678	617.8375	1217.6412	609.3243	1216.6572	608.8322	12
4	398.2034	199.6053	381.1769	191.0921	380.1928	190.6001	S	1151.6307	576.3190	1134.6041	567.8057	1133.6201	567.3137	11
5	***495.2562***	248.1317	478.2296	239.6185	477.2456	239.1264	P	1064.5986	532.8030	1047.5721	524.2897	1046.5881	523.7977	10
6	658.3195	329.6634	641.2930	321.1501	640.3089	320.6581	Y	967.5459	484.2766	950.5193	475.7633	949.5353	475.2713	9
7	771.4036	386.2054	754.3770	377.6921	753.3930	377.2001	L	804.4825	402.7449	787.4560	394.2316	786.4720	393.7396	8
8	858.4356	429.7214	841.4090	421.2082	840.4250	420.7162	S	691.3985	346.2029	674.3719	337.6896	673.3879	337.1976	7
9	945.4676	473.2374	928.4411	464.7242	927.4571	464.2322	S	604.3665	302.6869	587.3399	294.1736	586.3559	293.6816	6
10	***1032.4997***	516.7535	1015.4731	508.2402	1014.4891	507.7482	S	517.3344	259.1708	500.3079	250.6576	499.3239	250.1656	5
11	***1145.5837***	573.2955	1128.5572	564.7822	1127.5731	564.2902	I	430.3024	215.6548	413.2758	207.1416			4
12	***1258.6678***	629.8375	1241.6412	621.3243	1240.6572	620.8322	I	317.2183	159.1128	300.1918	150.5995			3
13	1315.6892	658.3483	1298.6627	649.8350	1297.6787	649.3430	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1





AT5G10790.1

NCBI **BLAST** search of LNMSPYLSSSIIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.6	1524.7858	-0.0036	LNMSPYLSSSIIGK
3.3	1524.7792	0.0029	MEIFMDIAKRQK
2.3	1524.7831	-0.0010	ENNMKNGGVLKGHK

AT5G10860.1

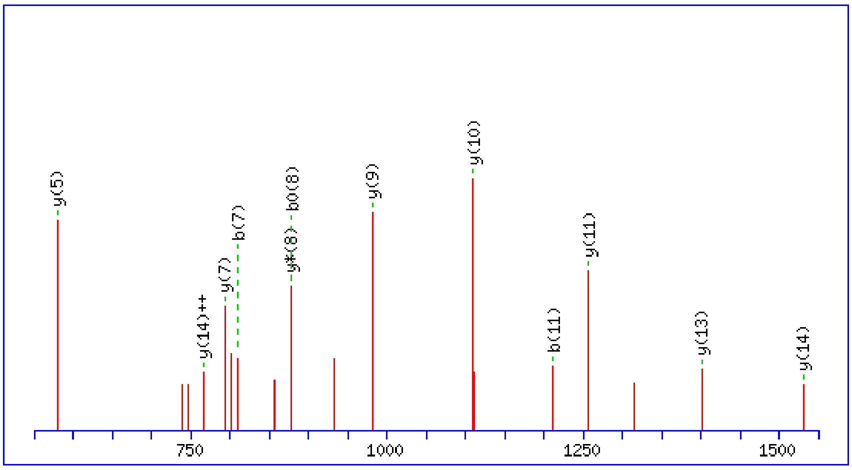
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEESGFESTTISDVMK**
Found in **AT5G10860.1** in **TAIR_Arabidopsis**, Symbols: | CBS domain-containing protein | chr5:3429174-3430143 REVERSE

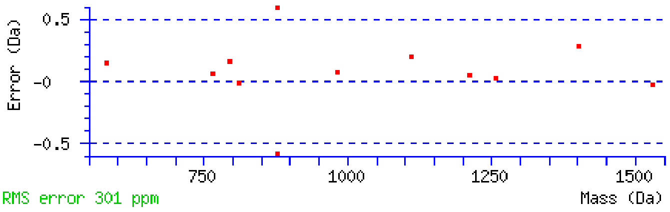
Match to Query 8437: 1789.775348 from(895.894950,2+) index(6954)
Title: Elution from: 64.537 to 64.537 scan no 9144 cid35.00 polarity:+
Data file D1d-1_1.mgf

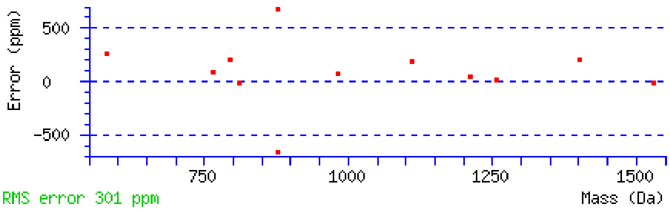
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1550 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1789.7750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 5.2e-005
Matches : 12/142 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.0478	66.5275			M							16
2	261.0904	131.0488	243.0798	122.0435	E	1659.7418	830.3745	1642.7153	821.8613	1641.7312	821.3693	15
3	390.1329	195.5701	372.1224	186.5648	E	***1530.6992***	765.8532	1513.6727	757.3400	1512.6887	756.8480	14
4	477.1650	239.0861	459.1544	230.0808	S	***1401.6566***	701.3319	1384.6301	692.8187	1383.6461	692.3267	13
5	534.1864	267.5969	516.1759	258.5916	G	1314.6246	657.8159	1297.5980	649.3027	1296.6140	648.8107	12
6	681.2549	341.1311	663.2443	332.1258	F	***1257.6031***	629.3052	1240.5766	620.7919	1239.5926	620.2999	11
7	**810.2974**	405.6524	792.2869	396.6471	E	***1110.5347***	555.7710	1093.5082	547.2577	1092.5242	546.7657	10
8	897.3295	449.1684	879.3189	440.1631	S	***981.4921***	491.2497	964.4656	482.7364	963.4816	482.2444	9
9	998.3772	499.6922	980.3666	490.6869	T	894.4601	447.7337	877.4335	439.2204	876.4495	438.7284	8
10	1099.4248	550.2161	1081.4143	541.2108	T	***793.4124***	397.2098	776.3859	388.6966	775.4019	388.2046	7
11	**1212.5089**	606.7581	1194.4983	597.7528	I	692.3647	346.6860	675.3382	338.1727	674.3542	337.6807	6
12	1299.5409	650.2741	1281.5304	641.2688	S	***579.2807***	290.1440	562.2541	281.6307	561.2701	281.1387	5
13	1414.5679	707.7876	1396.5573	698.7823	D	492.2486	246.6280	475.2221	238.1147	474.2381	237.6227	4
14	1513.6363	757.3218	1495.6257	748.3165	V	377.2217	189.1145	360.1952	180.6012			3
15	1644.6768	822.8420	1626.6662	813.8367	M	278.1533	139.5803	261.1267	131.0670			2
16					K	147.1128	74.0600	130.0863	65.5468			1





AT5G10860.1

NCBI **BLAST** search of MEESGFESTTISDVMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.8	1789.7750	0.0003	MEESGFESTTISDVMK

AT5G11170.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIVINYDMPDSADTYLHR**
Found in **AT5G11170.1** in **TAIR_Arabidopsis**, Symbols: | DEAD/DEAH box helicase, putative (RH15) | chr5:3553335-3556647 FORWARD

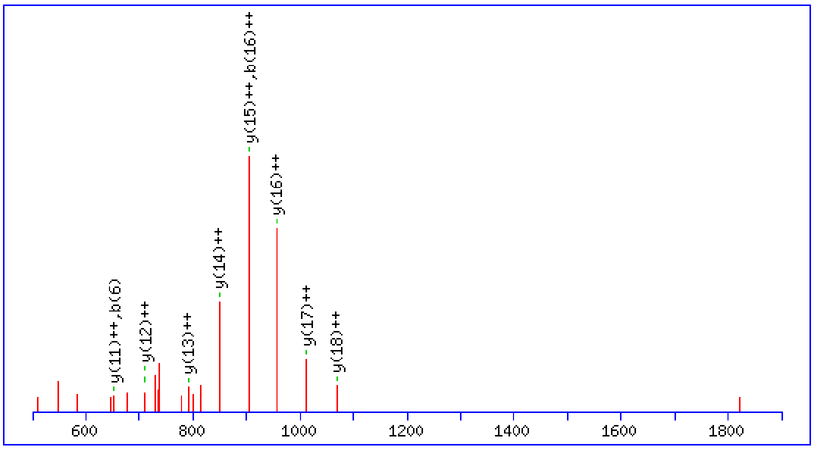
Match to Query 10053: 2235.063426 from(746.028418,3+) index(8122)
Title: Elution from: 71.558 to 71.558 scan no 10608 cid35.00 polarity:+
Data file C7-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

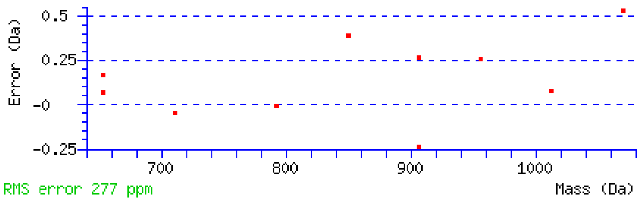
Show Y-axis ☐

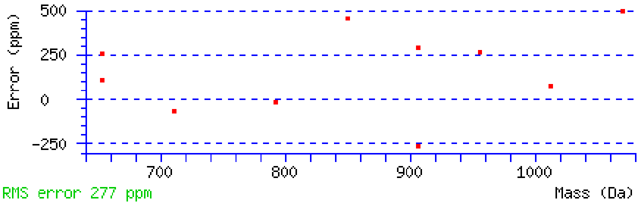


Monoisotopic mass of neutral peptide Mr(calc): 2235.0630
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00014
Matches : 10/192 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							19
2	214.1186	107.5629	197.0921	99.0497			N	2137.0019	1069.0046	2119.9753	1060.4913	2118.9913	1059.9993	18
3	327.2027	164.1050	310.1761	155.5917			I	2022.9590	1011.9831	2005.9324	1003.4698	2004.9484	1002.9778	17
4	426.2711	213.6392	409.2445	205.1259			V	1909.8749	955.4411	1892.8483	946.9278	1891.8643	946.4358	16
5	539.3552	270.1812	522.3286	261.6679			I	1810.8065	905.9069	1793.7799	897.3936	1792.7959	896.9016	15
6	653.3981	327.2027	636.3715	318.6894			N	1697.7224	849.3648	1680.6959	840.8516	1679.7118	840.3596	14
7	816.4614	408.7343	799.4349	400.2211			Y	1583.6795	792.3434	1566.6529	783.8301	1565.6689	783.3381	13
8	931.4884	466.2478	914.4618	457.7345	913.4778	457.2425	D	1420.6162	710.8117	1403.5896	702.2984	1402.6056	701.8064	12
9	1062.5288	531.7681	1045.5023	523.2548	1044.5183	522.7628	M	1305.5892	653.2982	1288.5627	644.7850	1287.5786	644.2930	11
10	1159.5816	580.2944	1142.5551	571.7812	1141.5710	571.2892	P	1174.5487	587.7780	1157.5222	579.2647	1156.5382	578.7727	10
11	1274.6085	637.8079	1257.5820	629.2946	1256.5980	628.8026	D	1077.4960	539.2516	1060.4694	530.7383	1059.4854	530.2463	9
12	1361.6406	681.3239	1344.6140	672.8107	1343.6300	672.3186	S	962.4690	481.7381	945.4425	473.2249	944.4585	472.7329	8
13	1432.6777	716.8425	1415.6511	708.3292	1414.6671	707.8372	A	875.4370	438.2221	858.4104	429.7089	857.4264	429.2169	7
14	1547.7046	774.3560	1530.6781	765.8427	1529.6941	765.3507	D	804.3999	402.7036	787.3733	394.1903	786.3893	393.6983	6
15	1648.7523	824.8798	1631.7258	816.3665	1630.7417	815.8745	T	689.3729	345.1901	672.3464	336.6768	671.3624	336.1848	5
16	1811.8156	906.4115	1794.7891	897.8982	1793.8051	897.4062	Y	588.3253	294.6663	571.2987	286.1530			4
17	1924.8997	962.9535	1907.8732	954.4402	1906.8891	953.9482	L	425.2619	213.1346	408.2354	204.6213			3
18	2061.9586	1031.4829	2044.9321	1022.9697	2043.9481	1022.4777	H	312.1779	156.5926	295.1513	148.0793			2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT5G11170.1





NCBI **BLAST** search of VNIVINYDMPDSADTYLHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.9	2235.0630	0.0004	VNIVINYDMPDSADTYLHR
3.0	2235.0689	-0.0055	ESEKIEMTSPVVTKEGGGEGR
0.6	2235.0570	0.0065	YGQVTPNPRFHGYQAGGSSGR

Mascot: http://www.matrixscience.com/

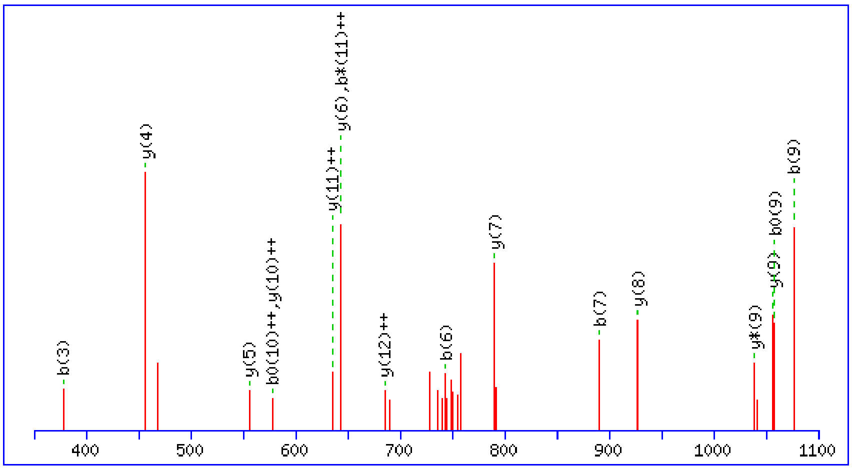
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVDVEHFSVPQGR**
Found in **AT5G11420.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25460.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Protein of unknown function DUF642 (InterPro:IPR006946); contains InterPro domain Gala

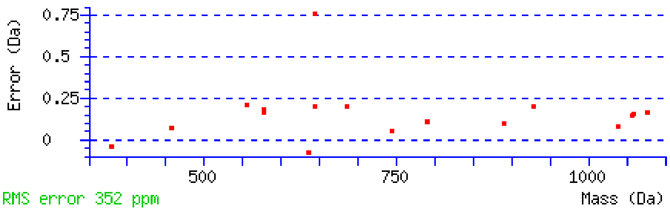
Match to Query 6018: 1531.743770 from(766.879161,2+) index(4328)
Title: Elution from: 42.183 to 42.183 scan no 5574 cid35.00 polarity:+
Data file D1d-1_3.mgf

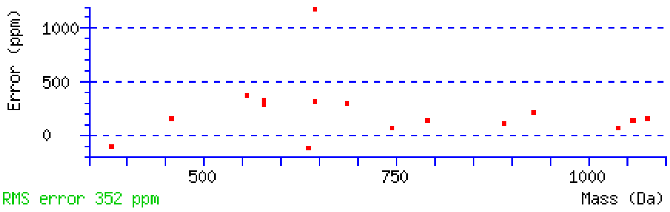
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1531.7420
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 3.2e-005
Matches : 17/110 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							13
2	263.1390	132.0731					V	1369.6859	685.3466	1352.6593	676.8333	1351.6753	676.3413	12
3	**378.1660**	189.5866			360.1554	180.5813	D	1270.6175	635.8124	1253.5909	627.2991	1252.6069	626.8071	11
4	477.2344	239.1208			459.2238	230.1155	V	1155.5905	578.2989	1138.5640	569.7856	1137.5800	569.2936	10
5	606.2770	303.6421			588.2664	294.6368	E	***1056.5221***	528.7647	1039.4956	520.2514	1038.5116	519.7594	9
6	**743.3359**	372.1716			725.3253	363.1663	H	***927.4795***	464.2434	910.4530	455.7301	909.4690	455.2381	8
7	**890.4043**	445.7058			872.3937	436.7005	F	***790.4206***	395.7139	773.3941	387.2007	772.4100	386.7087	7
8	977.4363	489.2218			959.4258	480.2165	S	***643.3522***	322.1797	626.3257	313.6665	625.3416	313.1745	6
9	**1076.5047**	538.7560			1058.4942	529.7507	V	***556.3202***	278.6637	539.2936	270.1504			5
10	1173.5575	587.2824			1155.5469	578.2771	P	***457.2518***	229.1295	440.2252	220.6162			4
11	1301.6161	651.3117	1284.5895	642.7984	1283.6055	642.3064	Q	360.1990	180.6031	343.1724	172.0899			3
12	1358.6375	679.8224	1341.6110	671.3091	1340.6270	670.8171	G	232.1404	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YVDVEHFSVPQGR

AT5G11420.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.6	1531.7420	0.0018	YVDVEHFSVPQGR
1.5	1531.7413	0.0025	IVNDGRMKEDEAR

AT5G11670.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIFGSGSPFDPVVYDGK**
Found in **AT5G11670.1** in **TAIR_Arabidopsis**, Symbols: ATNADP-ME2 | ATNADP-ME2 (NADP-MALIC ENZYME 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr5:3754457-3758041 FORWARD

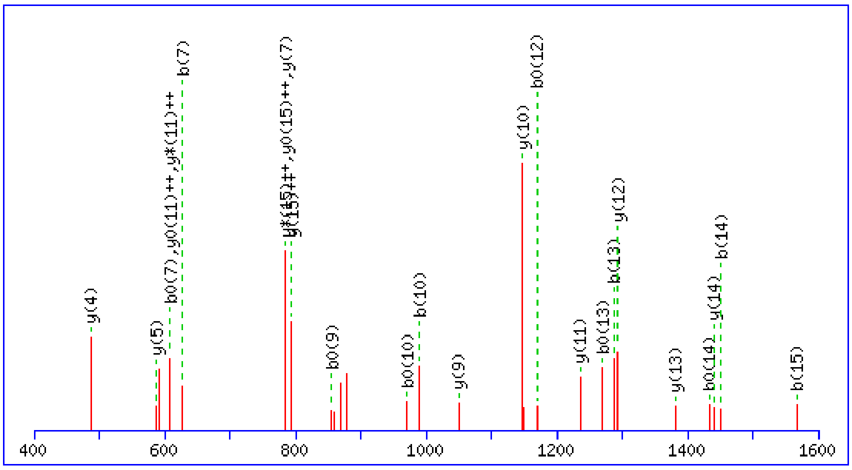
Match to Query 8054: 1772.798614 from(887.406583,2+) index(8674)
Title: Elution from: 80.495 to 80.495 scan no 11759 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

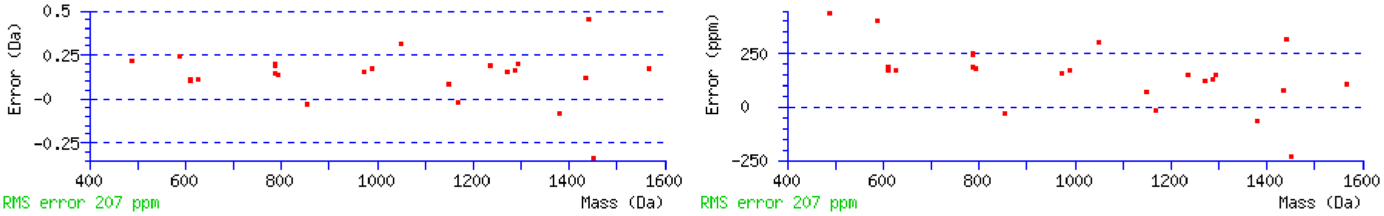
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1772.7982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 75 **Expect:** 2.9e-007
Matches : 25/148 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							17
2	187.1225	94.0649			I	1701.7713	851.3893	1683.7477	842.3775	1683.7607	842.3840	16
3	335.1880	168.0976			F	1587.6902	794.3487	1569.6666	785.3370	1569.6796	785.3435	15
4	393.2065	197.1069			G	***1439.6248***	720.3160	1421.6012	711.3042	1421.6142	711.3107	14
5	481.2355	241.1214	463.2250	232.1161	S	***1381.6063***	691.3068	1363.5827	682.2950	1363.5957	682.3015	13
6	539.2540	270.1307	521.2435	261.1254	G	***1293.5772***	647.2922	1275.5536	638.2804	1275.5666	638.2870	12
7	**627.2831**	314.1452	609.2725	305.1399	S	***1235.5587***	618.2830	1217.5351	609.2712	1217.5481	609.2777	11
8	725.3329	363.1701	707.3223	354.1648	P	***1147.5296***	574.2685	1129.5061	565.2567	1129.5191	565.2632	10
9	873.3983	437.2028	855.3878	428.1975	F	***1049.4798***	525.2436	1031.4563	516.2318	1031.4693	516.2383	9
10	**989.4223**	495.2148	971.4118	486.2095	D	901.4144	451.2108	883.3908	442.1990	883.4038	442.2056	8
11	1087.4721	544.2397	1069.4616	535.2344	P	***785.3904***	393.1988	767.3668	384.1871	767.3798	384.1936	7
12	1187.5376	594.2724	1169.5270	585.2671	V	687.3406	344.1739	669.3170	335.1622	669.3300	335.1687	6
13	**1287.6030**	644.3051	1269.5925	635.2999	V	***587.2752***	294.1412	569.2516	285.1294	569.2646	285.1359	5
14	**1451.6634**	726.3353	1433.6528	717.3300	Y	***487.2097***	244.1085	469.1861	235.0967	469.1991	235.1032	4
15	**1567.6874**	784.3473	1549.6768	775.3420	D	323.1494	162.0783	305.1258	153.0665	305.1388	153.0730	3
16	1625.7059	813.3566	1607.6953	804.3513	G	207.1254	104.0663	189.1018	95.0545			2
17					K	149.1069	75.0571	131.0833	66.0453			1

AT5G11670.1



NCBI **BLAST** search of AIFGSGSPFDPVVYDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.0	1772.7982	0.0005	AIFGSGSPFDPVVYDGK
4.7	1772.7971	0.0015	SSKSTKVGDIMTEENK

Mascot: http://www.matrixscience.com/

AT5G12110.1

Mascot Search Results

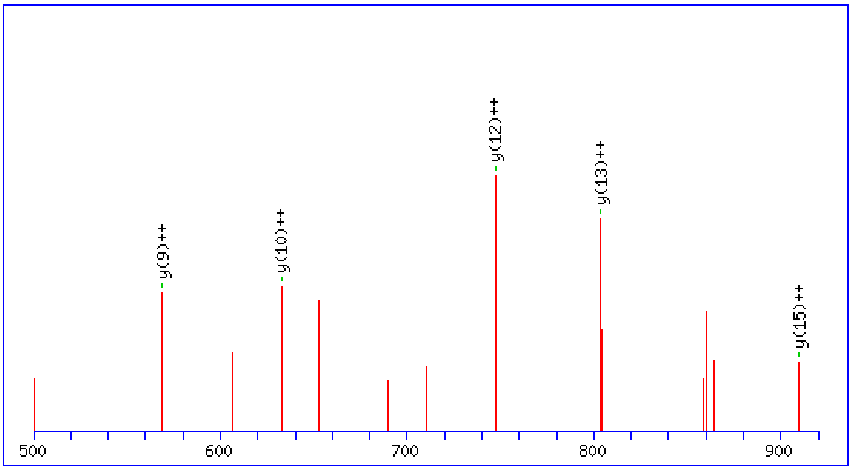
Peptide View

MS/MS Fragmentation of **SSVLLEVKPWDDETDMK**
Found in **AT5G12110.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1B alpha-subunit 1 (eEF1Balpha1) | chr5:3914484-3915733 FORWARD

Match to Query 9448: 1990.954470 from(664.658766,3+) index(8299)
Title: Elution from: 75.785 to 75.785 scan no 11019 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

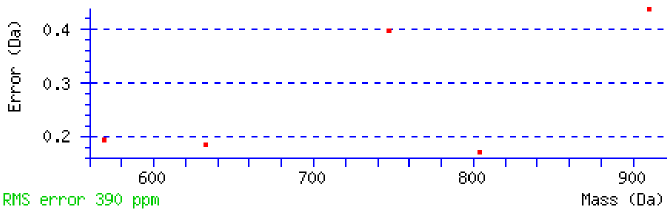
Or, Plot from 500 to 920 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

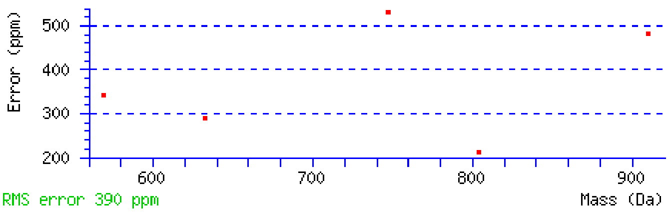


Monoisotopic mass of neutral peptide Mr(calc): 1990.9558
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00021
Matches : 5/174 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	175.0713	88.0393			157.0608	79.0340	S	1904.9310	952.9691	1887.9045	944.4559	1886.9204	943.9639	16
3	274.1397	137.5735			256.1292	128.5682	V	1817.8990	909.4531	1800.8724	900.9399	1799.8884	900.4478	15
4	387.2238	194.1155			369.2132	185.1103	L	1718.8306	859.9189	1701.8040	851.4056	1700.8200	850.9136	14
5	500.3079	250.6576			482.2973	241.6523	L	1605.7465	803.3769	1588.7200	794.8636	1587.7359	794.3716	13
6	629.3505	315.1789			611.3399	306.1736	E	1492.6624	746.8349	1475.6359	738.3216	1474.6519	737.8296	12
7	728.4189	364.7131			710.4083	355.7078	V	1363.6198	682.3136	1346.5933	673.8003	1345.6093	673.3083	11
8	856.5138	428.7606	839.4873	420.2473	838.5033	419.7553	K	1264.5514	632.7794	1247.5249	624.2661	1246.5409	623.7741	10
9	953.5666	477.2869	936.5401	468.7737	935.5560	468.2817	P	1136.4565	568.7319	1119.4299	560.2186	1118.4459	559.7266	9
10	1139.6459	570.3266	1122.6194	561.8133	1121.6354	561.3213	W	1039.4037	520.2055	1022.3772	511.6922	1021.3931	511.2002	8
11	1254.6729	627.8401	1237.6463	619.3268	1236.6623	618.8348	D	853.3244	427.1658	836.2978	418.6526	835.3138	418.1606	7
12	1369.6998	685.3535	1352.6733	676.8403	1351.6892	676.3483	D	738.2974	369.6524	721.2709	361.1391	720.2869	360.6471	6
13	1498.7424	749.8748	1481.7159	741.3616	1480.7318	740.8696	E	623.2705	312.1389	606.2440	303.6256	605.2599	303.1336	5
14	1599.7901	800.3987	1582.7635	791.8854	1581.7795	791.3934	T	494.2279	247.6176	477.2014	239.1043	476.2173	238.6123	4
15	1714.8170	857.9121	1697.7905	849.3989	1696.8065	848.9069	D	393.1802	197.0938	376.1537	188.5805	375.1697	188.0885	3
16	1845.8575	923.4324	1828.8310	914.9191	1827.8469	914.4271	M	278.1533	139.5803	261.1267	131.0670			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT5G12110.1





NCBI **BLAST** search of SSVLLEVKPWDDETDMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.3	1990.9558	-0.0013	SSVLIDIKPWDDETDMK
43.3	1990.9558	-0.0013	SSVLLEVKPWDDETDMK
14.8	1990.9497	0.0048	SWNSYIPDGENRVLGER
11.2	1990.9571	-0.0026	VFEEDHIKSQCSIFPR
4.8	1990.9571	-0.0026	MAAISPWLSSPQSFSNPR
3.5	1990.9531	0.0014	TAETLAMDYHRGAGVEVR
2.1	1990.9596	-0.0051	AAEEDVNSDPSFLGGSKLR
1.4	1990.9571	-0.0026	ADELQKHEPLVAYYCR
1.3	1990.9564	-0.0020	IQEQNTERGCVLEMLR
0.8	1990.9517	0.0028	INQIEEEEEDKCKSIK

Mascot: http://www.matrixscience.com/

AT5G12140.1

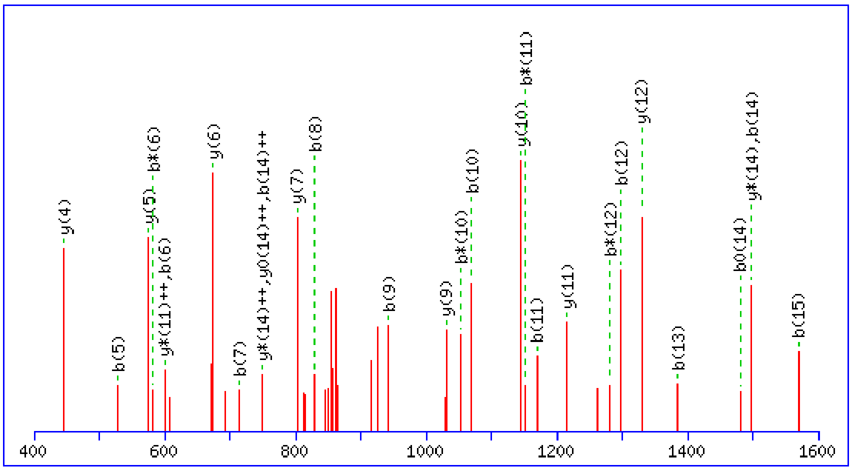
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIDANANDLQVESLAR**
Found in **AT5G12140.1** in **TAIR_Arabidopsis**, Symbols: ATCYS1 | ATCYS1 (A. THALIANA CYSTATIN-1); cysteine protease inhibitor | chr5:3923296-3923937 REVERSE

Match to Query 7907: 1742.843506 from(872.429029,2+) index(6218)
Title: Elution from: 54.367 to 54.367 scan no 7987 cid35.00 polarity:+
Data file D6h-3_3.mgf

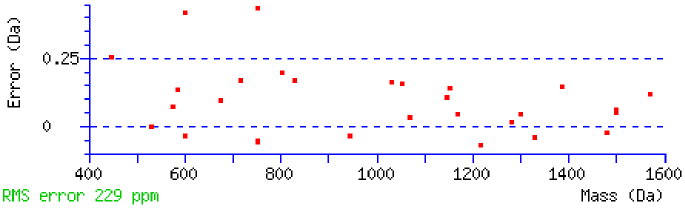
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

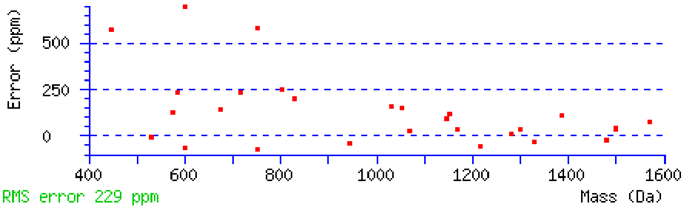


Monoisotopic mass of neutral peptide Mr(calc): 1742.8435
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 8.2e-012
Matches : 29/166 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							16
2	229.1183	115.0628			211.1077	106.0575	I	1628.8238	814.9156	1611.7973	806.4023	1610.8133	805.9103	15
3	344.1452	172.5763			326.1347	163.5710	D	1515.7398	758.3735	1498.7132	749.8603	1497.7292	749.3682	14
4	415.1823	208.0948			397.1718	199.0895	A	1400.7128	700.8601	1383.6863	692.3468	1382.7023	691.8548	13
5	***529.2253***	265.1163	512.1987	256.6030	511.2147	256.1110	N	**1329.6757**	665.3415	1312.6492	656.8282	1311.6652	656.3362	12
6	***600.2624***	300.6348	583.2358	292.1216	582.2518	291.6295	A	**1215.6328**	608.3200	1198.6062	599.8068	1197.6222	599.3148	11
7	***714.3053***	357.6563	697.2788	349.1430	696.2947	348.6510	N	**1144.5957**	572.8015	1127.5691	564.2882	1126.5851	563.7962	10
8	***829.3323***	415.1698	812.3057	406.6565	811.3217	406.1645	D	**1030.5527**	515.7800	1013.5262	507.2667	1012.5422	506.7747	9
9	***942.4163***	471.7118	925.3898	463.1985	924.4057	462.7065	L	915.5258	458.2665	898.4993	449.7533	897.5152	449.2613	8
10	***1070.4749***	535.7411	1053.4483	527.2278	1052.4643	526.7358	Q	**802.4417**	401.7245	785.4152	393.2112	784.4312	392.7192	7
11	***1169.5433***	585.2753	1152.5168	576.7620	1151.5327	576.2700	V	**674.3832**	337.6952	657.3566	329.1819	656.3726	328.6899	6
12	***1298.5859***	649.7966	1281.5594	641.2833	1280.5753	640.7913	E	**575.3148**	288.1610	558.2882	279.6477	557.3042	279.1557	5
13	***1385.6179***	693.3126	1368.5914	684.7993	1367.6074	684.3073	S	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	4
14	***1498.7020***	749.8546	1481.6754	741.3414	1480.6914	740.8494	L	359.2401	180.1237	342.2136	171.6104			3
15	***1569.7391***	785.3732	1552.7126	776.8599	1551.7285	776.3679	A	246.1561	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1

AT5G12140.1





NCBI **BLAST** search of DIDANANDLQVESLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
116.6	1742.8435	0.0000	DIDANANDLQVESLAR

Mascot: http://www.matrixscience.com/

AT5G12250.1

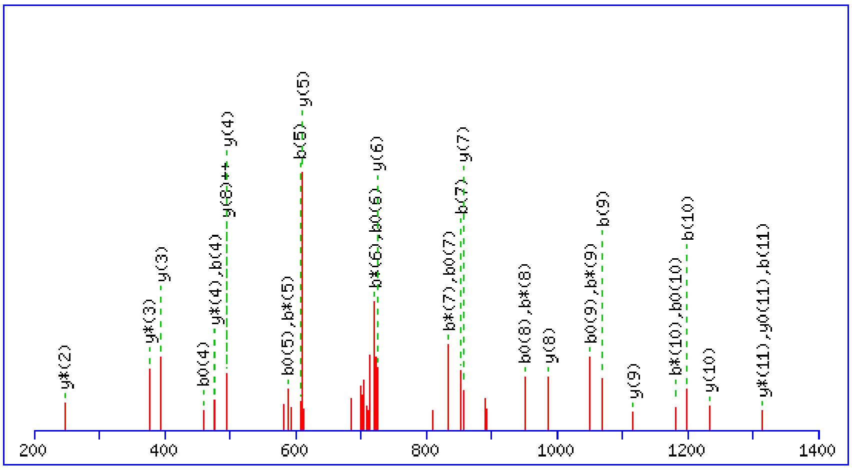
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVDEQMINVQNK**
Found in **AT5G12250.1** in **TAIR_Arabidopsis**, Symbols: TUB6 | TUB6 (BETA-6 TUBULIN) | chr5:3961318-3962972 REVERSE

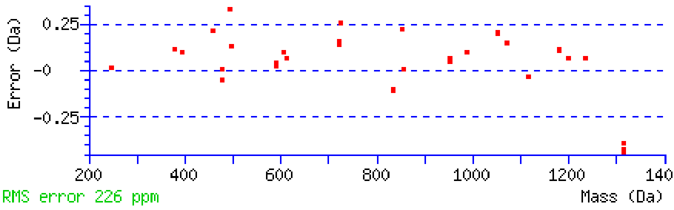
Match to Query 6410: 1462.630678 from(732.322615,2+) index(3658)
Title: Elution from: 35.250 to 35.250 scan no 4506 cid35.00 polarity:+
Data file 0-1_1.mgf

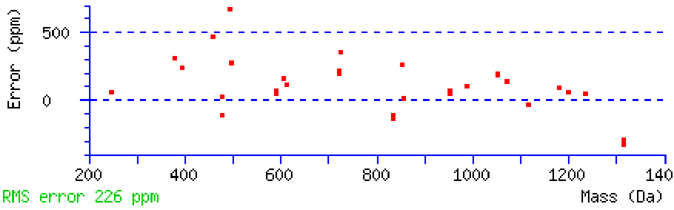
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1462.6316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.9e-007
Matches : 33/108 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							12
2	231.1124	116.0598			213.1018	107.0545	V	1333.5993	667.3033	1315.5757	658.2915	1315.5887	658.2980	11
3	347.1363	174.0718			329.1258	165.0665	D	***1233.5338***	617.2706	1215.5103	608.2588	1215.5233	608.2653	10
4	***477.1760***	239.0916			459.1654	230.0863	E	***1117.5099***	559.2586	1099.4863	550.2468	1099.4993	550.2533	9
5	***607.2286***	304.1179	589.2050	295.1061	589.2180	295.1127	Q	***987.4702***	494.2388	969.4466	485.2270			8
6	739.2661	370.1367	721.2425	361.1249	721.2556	361.1314	M	***857.4176***	429.2124	839.3940	420.2006			7
7	***853.3472***	427.1773	835.3236	418.1655	835.3367	418.1720	I	***725.3801***	363.1937	707.3565	354.1819			6
8	969.3842	485.1957	951.3606	476.1840	951.3737	476.1905	N	***611.2990***	306.1531	593.2754	297.1413			5
9	***1069.4497***	535.2285	1051.4261	526.2167	1051.4391	526.2232	V	***495.2620***	248.1346	477.2384	239.1228			4
10	***1199.5023***	600.2548	1181.4787	591.2430	1181.4918	591.2495	Q	***395.1965***	198.1019	377.1729	189.0901			3
11	***1315.5393***	658.2733	1297.5157	649.2615	1297.5287	649.2680	N	265.1439	133.0756	247.1203	124.0638			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EVDEQMINVQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G12250.1

Score	Mr(calc)	Delta	Sequence
74.1	1462.6316	-0.0009	EVDEQMINVQNK
74.1	1462.6316	-0.0009	EVDEQMLNVQNK
15.0	1462.6265	0.0042	FLGMFSKTMEDK
9.3	1462.6339	-0.0032	VYMDPNISVHEK
5.8	1462.6316	-0.0009	QLQAVVADDMDNK
5.3	1462.6289	0.0017	DVLEEVCDELTK
5.0	1462.6265	0.0042	FLGMFSKTMEDK
0.8	1462.6269	0.0038	NLHSAAVMGVDGMK

Mascot: http://www.matrixscience.com/

AT5G12420.1

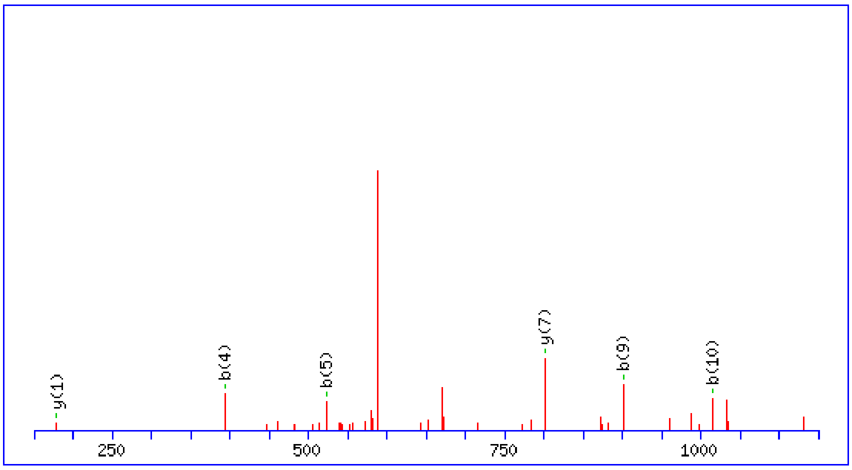
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSEAEAVGFIR**
Found in **AT5G12420.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16350.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48523.1); contains InterPro domain Protein of unknown function UPF0089 (InterPro:IPR004255); contains Inter

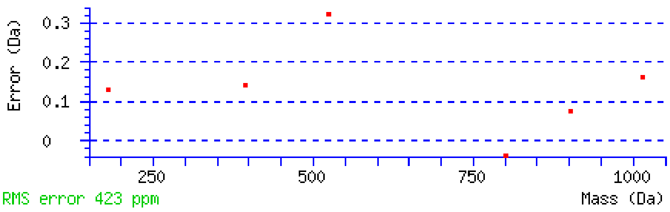
Match to Query 3875: 1192.548620 from(597.281586,2+) index(1752)
Title: Elution from: 21.470 to 21.470 scan no 2280 cid35.00 polarity:+
Data file D6h-2_3.mgf

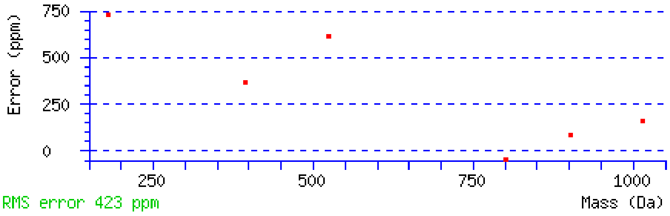
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1192.5516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.011
Matches : 6/88 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							11
2	191.0811	96.0442	173.0705	87.0389	S	1091.5142	546.2607	1073.4906	537.2489	1073.5036	537.2555	10
3	321.1207	161.0640	303.1101	152.0587	E	1003.4851	502.2462	985.4616	493.2344	985.4746	493.2409	9
4	***393.1548***	197.0811	375.1443	188.0758	A	873.4455	437.2264	855.4219	428.2146	855.4349	428.2211	8
5	***523.1945***	262.1009	505.1839	253.0956	E	**801.4114**	401.2093	783.3878	392.1975	783.4008	392.2040	7
6	595.2286	298.1179	577.2180	289.1127	A	671.3717	336.1895	653.3482	327.1777			6
7	695.2941	348.1507	677.2835	339.1454	V	599.3376	300.1724	581.3140	291.1606			5
8	753.3126	377.1599	735.3020	368.1546	G	499.2721	250.1397	481.2486	241.1279			4
9	***901.3780***	451.1926	883.3674	442.1874	F	441.2536	221.1305	423.2301	212.1187			3
10	***1015.4591***	508.2332	997.4485	499.2279	I	293.1882	147.0977	275.1646	138.0859			2
11					R	**179.1071**	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TSEAEAVGFIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G12420.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.5	1192.5516	-0.0030	TSEAEAVGFIR
17.3	1192.5469	0.0017	QAVCGFDLLR
10.7	1192.5469	0.0017	ELNCVQFLR
6.8	1192.5521	-0.0035	ASLSPNSRTSR
6.7	1192.5496	-0.0010	SWNRMPTKR
4.6	1192.5469	0.0017	NMAVSWSGAKK
3.8	1192.5521	-0.0035	KEQSSPTRSR
3.8	1192.5516	-0.0030	SVSDKSWDKK
3.1	1192.5516	-0.0030	GESYLDVIQR
3.1	1192.5516	-0.0030	LSDFSNVLER

AT5G13120.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVIGLYGDDVPQTVENFR**
Found in **AT5G13120.1** in **TAIR_Arabidopsis**, Symbols: | peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein | chr5:4162717-4164723 REVERSE

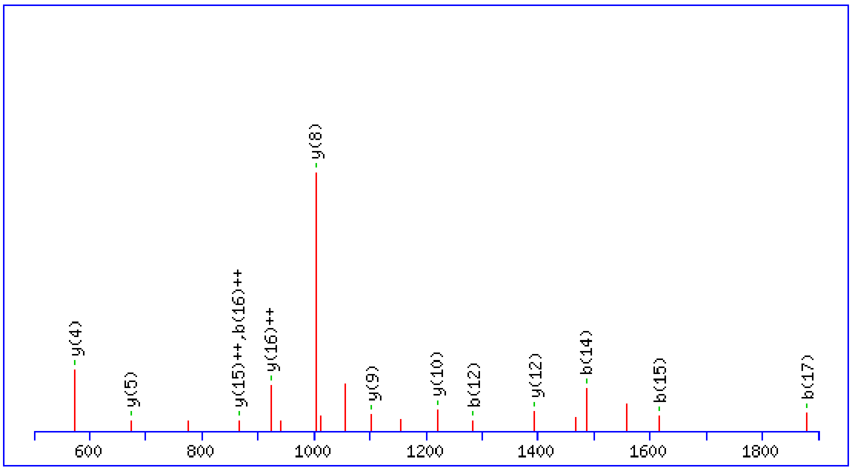
Match to Query 9464: 2056.973082 from(1029.493817,2+) index(9152)
Title: Elution from: 81.887 to 81.887 scan no 12336 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

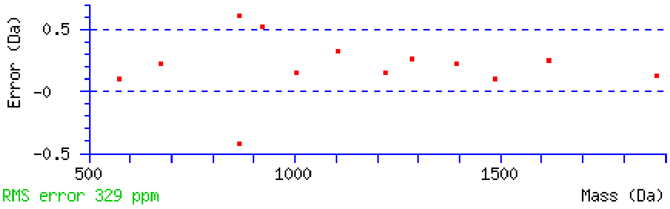
Show Y-axis ☐

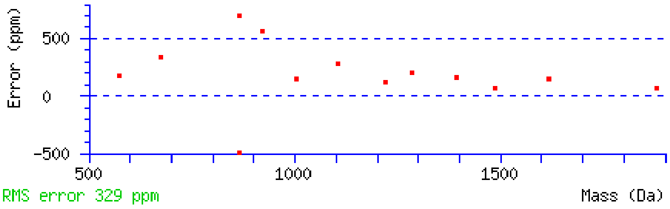


Monoisotopic mass of neutral peptide Mr(calc): 2056.9740
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 3.9e-006
Matches : 13/162 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							18
2	215.1538	108.0805					V	1943.9002	972.4537	1925.8766	963.4419	1925.8896	963.4484	17
3	329.2349	165.1211					I	1843.8347	922.4210	1825.8112	913.4092	1825.8242	913.4157	16
4	387.2534	194.1303					G	1729.7536	865.3805	1711.7301	856.3687	1711.7431	856.3752	15
5	501.3345	251.1709					L	1671.7351	836.3712	1653.7116	827.3594	1653.7246	827.3659	14
6	665.3949	333.2011					Y	1557.6540	779.3307	1539.6305	770.3189	1539.6435	770.3254	13
7	723.4134	362.2103					G	***1393.5937***	697.3005	1375.5701	688.2887	1375.5831	688.2952	12
8	839.4374	420.2223			821.4268	411.2170	D	1335.5752	668.2912	1317.5516	659.2794	1317.5646	659.2859	11
9	955.4613	478.2343			937.4508	469.2290	D	***1219.5512***	610.2792	1201.5276	601.2674	1201.5406	601.2740	10
10	1055.5268	528.2670			1037.5162	519.2618	V	***1103.5272***	552.2672	1085.5036	543.2555	1085.5167	543.2620	9
11	1153.5766	577.2919			1135.5660	568.2866	P	***1003.4618***	502.2345	985.4382	493.2227	985.4512	493.2292	8
12	***1283.6292***	642.3183	1265.6057	633.3065	1265.6187	633.3130	Q	905.4120	453.2096	887.3884	444.1978	887.4014	444.2043	7
13	1385.6739	693.3406	1367.6504	684.3288	1367.6634	684.3353	T	775.3593	388.1833	757.3357	379.1715	757.3488	379.1780	6
14	***1485.7394***	743.3733	1467.7158	734.3615	1467.7288	734.3681	V	***673.3146***	337.1609	655.2910	328.1492	655.3040	328.1557	5
15	***1615.7790***	808.3932	1597.7554	799.3814	1597.7685	799.3879	E	***573.2492***	287.1282	555.2256	278.1164	555.2386	278.1229	4
16	1731.8160	866.4116	1713.7924	857.3999	1713.8055	857.4064	N	443.2095	222.1084	425.1860	213.0966			3
17	***1879.8815***	940.4444	1861.8579	931.4326	1861.8709	931.4391	F	327.1725	164.0899	309.1490	155.0781			2
18							R	179.1071	90.0572	161.0835	81.0454			1

AT5G13120.1





NCBI **BLAST** search of IVIGLYGDDVPQTVENFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.7	2056.9740	-0.0009	IVIGLYGDDVPQTVENFR
3.0	2056.9760	-0.0029	AQMMEILNLMLQDLKSR
1.8	2056.9740	-0.0009	INNSFDQTAIDIAQIFPK
1.6	2056.9767	-0.0036	IGAVHSVVFAGFSADSLAQR
1.4	2056.9767	-0.0036	KLAALADVYVNDAFGTAHR
0.1	2056.9693	0.0038	YASYVAIQGMRIFKQDK

Mascot: http://www.matrixscience.com/

AT5G13230.1

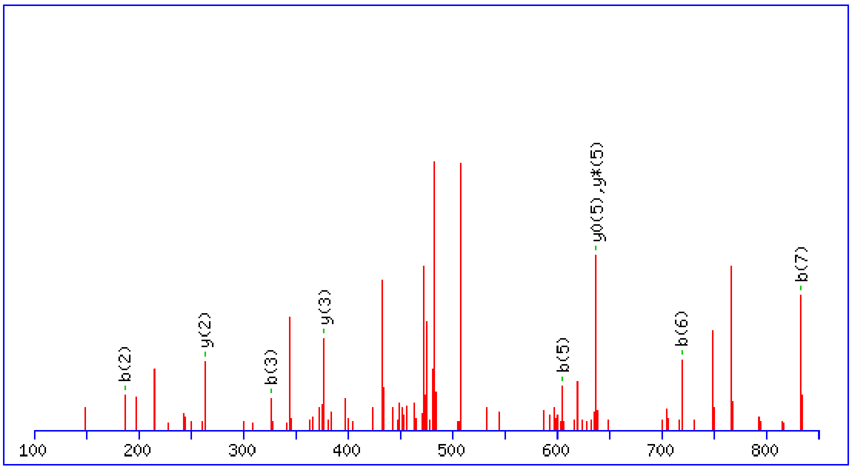
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIHCDILK**
Found in **AT5G13230.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:4222517-4224985 FORWARD

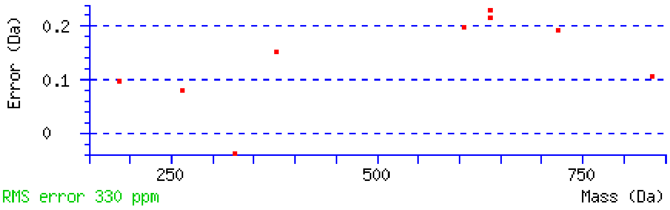
Match to Query 2354: 980.476796 from(491.245674,2+) index(1984)
Title: Elution from: 24.001 to 24.001 scan no 2575 cid35.00 polarity:+
Data file D12h-3_1.mgf

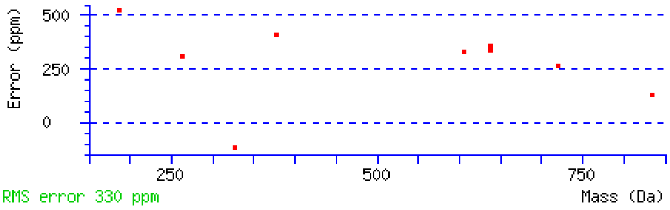
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 980.4758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.011
Matches : 9/56 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							8
2	***187.1225***	94.0649			I	909.4489	455.2281	891.4253	446.2163	891.4383	446.2228	7
3	***327.1725***	164.0899			H	795.3678	398.1875	777.3442	389.1757	777.3572	389.1822	6
4	489.1973	245.1023			C	655.3178	328.1625	637.2942	319.1507	637.3072	319.1572	5
5	***605.2212***	303.1143	587.2107	294.1090	D	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
6	***719.3023***	360.1548	701.2918	351.1495	I	**377.2691**	189.1382	359.2455	180.1264			3
7	***833.3834***	417.1954	815.3729	408.1901	L	**263.1880**	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AIHCDILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.3	980.4758	0.0010	AIHCDILK
21.4	980.4758	0.0010	MPPKQQPK

AT5G13230.1

6.9	980.4758	0.0010	MAIFSRTK
5.5	980.4758	0.0010	IIDPVCPR
4.8	980.4758	0.0010	MSTARFIK
4.5	980.4758	0.0010	NHPTLMIK
0.3	980.4758	0.0010	DMYKKLR

AT5G13420.1

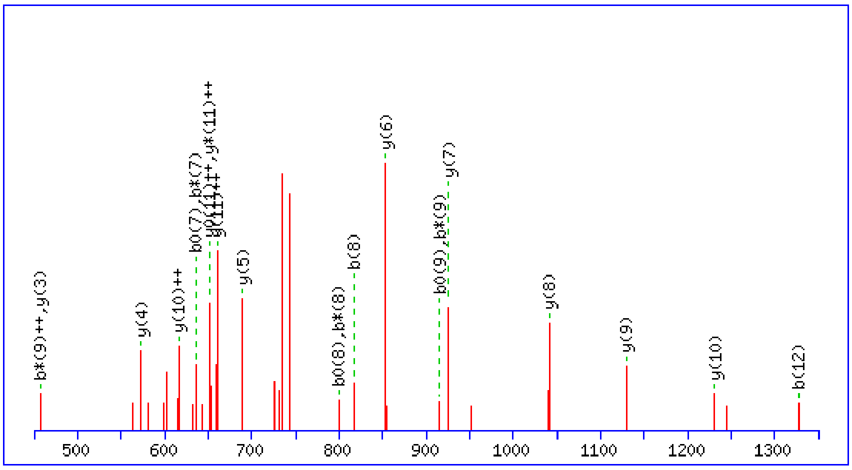
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AISTSNAYNDQFR**
Found in **AT5G13420.1** in **TAIR_Arabidopsis**, Symbols: | transaldolase, putative | chr5:4302083-4304215 REVERSE

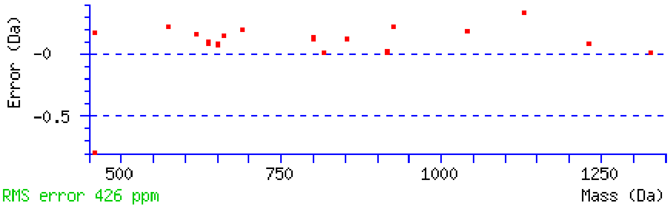
Match to Query 6586: 1504.627350 from(753.320951,2+) index(2942)
Title: Elution from: 30.110 to 30.110 scan no 3681 cid35.00 polarity:+
Data file C7-3_1.mgf

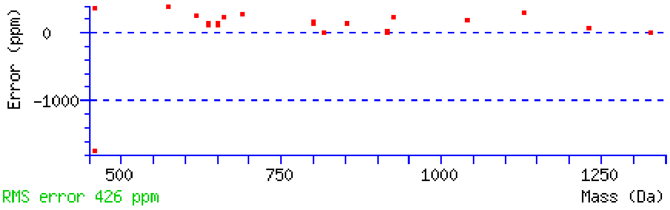
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1504.6285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 2.6e-007
Matches : 21/124 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					**A**							13
2	187.1225	94.0649					**I**	1433.6016	717.3044	1415.5780	708.2927	1415.5910	708.2992	12
3	275.1516	138.0794			257.1410	129.0741	**S**	1319.5205	660.2639	1301.4969	651.2521	1301.5099	651.2586	11
4	377.1963	189.1018			359.1857	180.0965	**T**	***1231.4914***	616.2494	1213.4679	607.2376	1213.4809	607.2441	10
5	465.2254	233.1163			447.2148	224.1110	**S**	***1129.4467***	565.2270	1111.4232	556.2152	1111.4362	556.2217	9
6	581.2624	291.1348	563.2388	282.1230	563.2518	282.1295	**N**	***1041.4177***	521.2125	1023.3941	512.2007	1023.4071	512.2072	8
7	653.2965	327.1519	635.2729	318.1401	635.2859	318.1466	**A**	***925.3807***	463.1940	907.3571	454.1822	907.3701	454.1887	7
8	**817.3569**	409.1821	799.3333	400.1703	799.3463	400.1768	**Y**	***853.3465***	427.1769	835.3229	418.1651	835.3360	418.1716	6
9	933.3939	467.2006	915.3703	458.1888	915.3833	458.1953	**N**	***689.2862***	345.1467	671.2626	336.1349	671.2756	336.1414	5
10	1049.4178	525.2126	1031.3943	516.2008	1031.4073	516.2073	**D**	***573.2492***	287.1282	555.2256	278.1164	555.2386	278.1229	4
11	1179.4705	590.2389	1161.4469	581.2271	1161.4599	581.2336	**Q**	***457.2252***	229.1162	439.2016	220.1044			3
12	**1327.5359**	664.2716	1309.5124	655.2598	1309.5254	655.2663	**F**	327.1725	164.0899	309.1490	155.0781			2
13							**R**	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AISTSNAYNDQFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G13420.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.0	1504.6285	-0.0011	AISTSNAYNDQFR

Mascot: http://www.matrixscience.com/

AT5G13430.1

Mascot Search Results

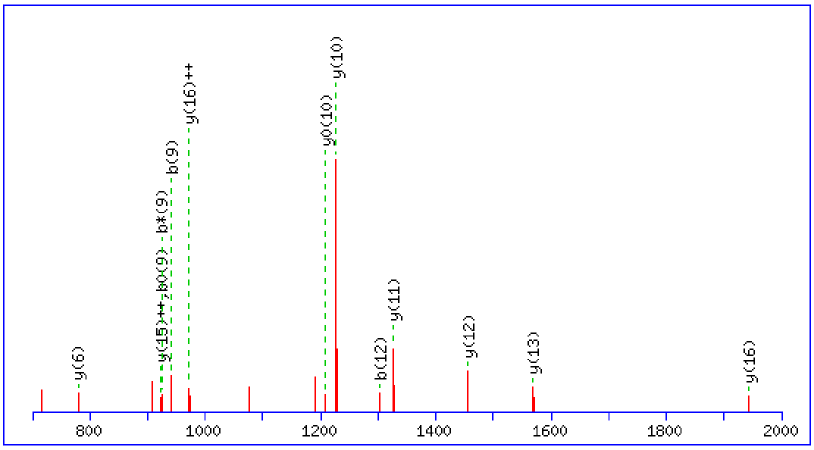
Peptide View

MS/MS Fragmentation of **GPAPYNLEVPTYSFLEENK**
Found in **AT5G13430.1** in **TAIR_Arabidopsis**, Symbols: | ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative | chr5:4305417-4307402 REVERSE

Match to Query 9713: 2167.043838 from(1084.529195,2+) index(9274)
Title: Elution from: 83.567 to 83.567 scan no 12592 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

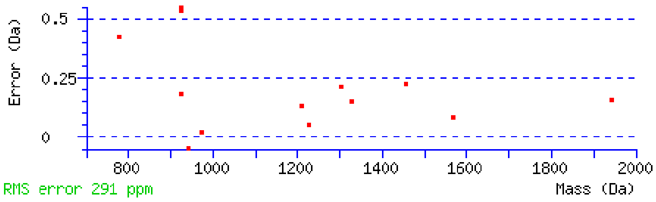
Or, Plot from 700 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

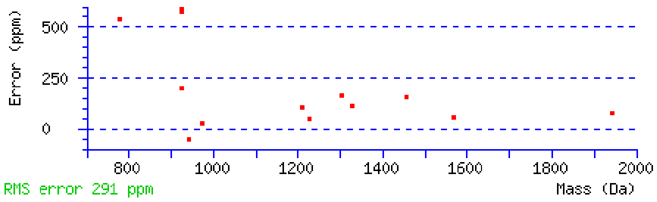


Monoisotopic mass of neutral peptide Mr(calc): 2167.0473
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0018
Matches : 13/188 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							19
2	155.0815	78.0444					P	2111.0332	1056.0202	2094.0066	1047.5069	2093.0226	1047.0149	18
3	226.1186	113.5629					A	2013.9804	1007.4938	1996.9539	998.9806	1995.9698	998.4886	17
4	323.1714	162.0893					P	***1942.9433***	971.9753	1925.9167	963.4620	1924.9327	962.9700	16
5	486.2347	243.6210					Y	1845.8905	923.4489	1828.8640	914.9356	1827.8800	914.4436	15
6	600.2776	300.6425	583.2511	292.1292			N	1682.8272	841.9172	1665.8006	833.4040	1664.8166	832.9120	14
7	713.3617	357.1845	696.3352	348.6712			L	***1568.7843***	784.8958	1551.7577	776.3825	1550.7737	775.8905	13
8	842.4043	421.7058	825.3777	413.1925	824.3937	412.7005	E	***1455.7002***	728.3537	1438.6737	719.8405	1437.6896	719.3485	12
9	**941.4727**	471.2400	924.4462	462.7267	923.4621	462.2347	V	***1326.6576***	663.8324	1309.6311	655.3192	1308.6470	654.8272	11
10	1038.5255	519.7664	1021.4989	511.2531	1020.5149	510.7611	P	***1227.5892***	614.2982	1210.5626	605.7850	1209.5786	605.2930	10
11	1139.5732	570.2902	1122.5466	561.7769	1121.5626	561.2849	T	1130.5364	565.7719	1113.5099	557.2586	1112.5259	556.7666	9
12	**1302.6365**	651.8219	1285.6099	643.3086	1284.6259	642.8166	Y	1029.4888	515.2480	1012.4622	506.7347	1011.4782	506.2427	8
13	1389.6685	695.3379	1372.6420	686.8246	1371.6579	686.3326	S	866.4254	433.7163	849.3989	425.2031	848.4149	424.7111	7
14	1536.7369	768.8721	1519.7104	760.3588	1518.7264	759.8668	F	***779.3934***	390.2003	762.3668	381.6871	761.3828	381.1951	6
15	1649.8210	825.4141	1632.7944	816.9009	1631.8104	816.4088	L	632.3250	316.6661	615.2984	308.1529	614.3144	307.6608	5
16	1778.8636	889.9354	1761.8370	881.4222	1760.8530	880.9301	E	519.2409	260.1241	502.2144	251.6108	501.2304	251.1188	4
17	1907.9062	954.4567	1890.8796	945.9435	1889.8956	945.4514	E	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
18	2021.9491	1011.4782	2004.9226	1002.9649	2003.9385	1002.4729	N	261.1557	131.0815	244.1292	122.5682			2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT5G13430.1





NCBI **BLAST** search of GPAPYNLEVPTYSFLEENK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.8	2167.0473	-0.0035	GPAPYNLEVPTYSFLEENK
6.9	2167.0480	-0.0042	SSIPTNLAWQEMFRSASSR

Mascot: http://www.matrixscience.com/

AT5G13440.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LANSVDVGSLRDPQEDSVR**
Found in **AT5G13440.1** in **TAIR_Arabidopsis**, Symbols: | ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative | chr5:4308434-4310025 REVERSE

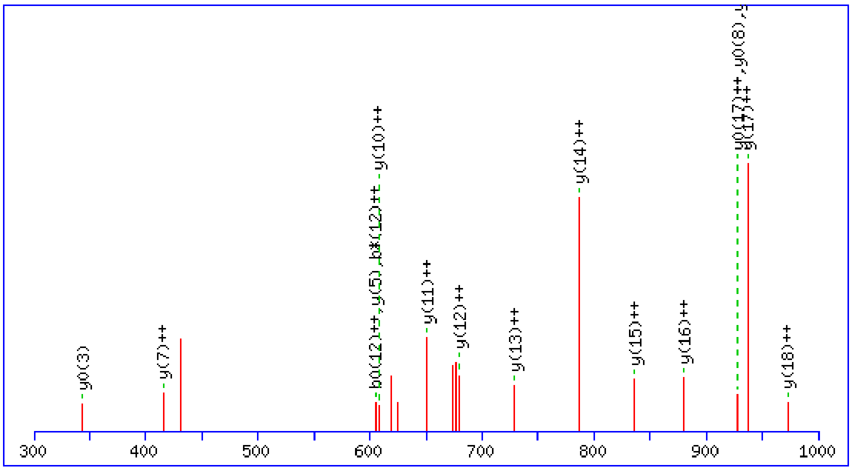
Match to Query 9046: 2056.015035 from(686.345621,3+) index(3898)
Title: Elution from: 37.882 to 37.882 scan no 5003 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

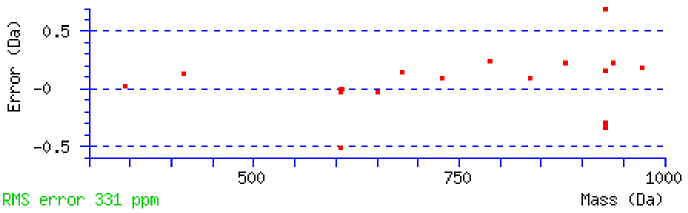
Show Y-axis ☐

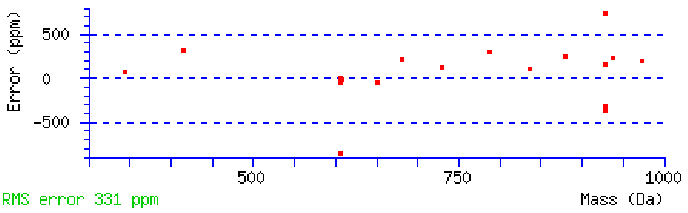


Monoisotopic mass of neutral peptide Mr(calc): 2056.0185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 5.2e-007
Matches : 18/202 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							19
2	185.1285	93.0679					A	1943.9417	972.4745	1926.9152	963.9612	1925.9312	963.4692	18
3	299.1714	150.0893	282.1448	141.5761			N	1872.9046	936.9559	1855.8781	928.4427	1854.8940	927.9507	17
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	S	1758.8617	879.9345	1741.8351	871.4212	1740.8511	870.9292	16
5	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	V	1671.8297	836.4185	1654.8031	827.9052	1653.8191	827.4132	15
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	D	1572.7612	786.8843	1555.7347	778.3710	1554.7507	777.8790	14
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	V	1457.7343	729.3708	1440.7077	720.8575	1439.7237	720.3655	13
8	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	G	1358.6659	679.8366	1341.6393	671.3233	1340.6553	670.8313	12
9	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	S	1301.6444	651.3258	1284.6179	642.8126	1283.6339	642.3206	11
10	956.5047	478.7560	939.4782	470.2427	938.4942	469.7507	L	1214.6124	607.8098	1197.5858	599.2966	1196.6018	598.8046	10
11	1112.6058	556.8066	1095.5793	548.2933	1094.5953	547.8013	R	1101.5283	551.2678	1084.5018	542.7545	1083.5178	542.2625	9
12	1227.6328	614.3200	1210.6062	605.8068	1209.6222	605.3148	D	945.4272	473.2172	928.4007	464.7040	927.4167	464.2120	8
13	1324.6856	662.8464	1307.6590	654.3331	1306.6750	653.8411	P	830.4003	415.7038	813.3737	407.1905	812.3897	406.6985	7
14	1452.7441	726.8757	1435.7176	718.3624	1434.7336	717.8704	Q	733.3475	367.1774	716.3210	358.6641	715.3369	358.1721	6
15	1581.7867	791.3970	1564.7602	782.8837	1563.7762	782.3917	E	605.2889	303.1481	588.2624	294.6348	587.2784	294.1428	5
16	1696.8137	848.9105	1679.7871	840.3972	1678.8031	839.9052	D	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
17	1783.8457	892.4265	1766.8191	883.9132	1765.8351	883.4212	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
18	1882.9141	941.9607	1865.8876	933.4474	1864.9035	932.9554	V	274.1874	137.5973	257.1608	129.0840			2
19							R	175.1190	88.0631	158.0924	79.5498			1

AT5G13440.1





NCBI **BLAST** search of LANSVDVGSLRDPQEDSVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.0	2056.0185	-0.0035	LANSVDVGSLRDPQEDSVR
1.2	2056.0185	-0.0035	QTRVPSETEQKSTEPSPR

Mascot: http://www.matrixscience.com/

AT5G13450.1

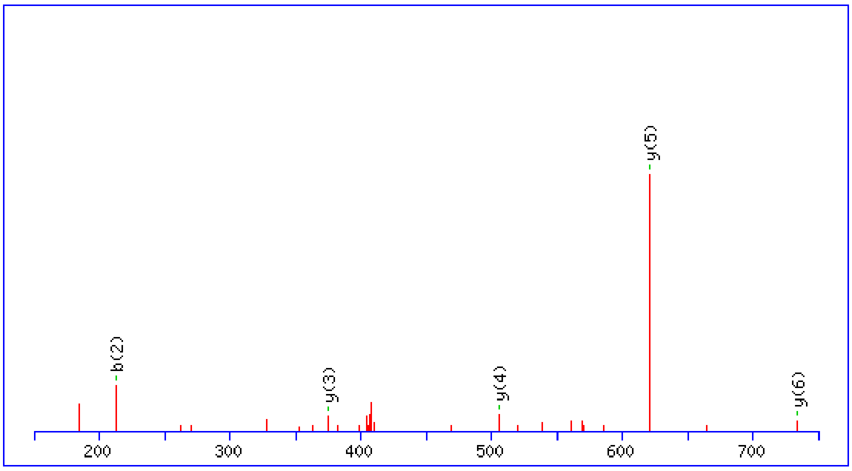
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLDMSIR**
Found in **AT5G13450.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative | chr5:4310561-4311944 REVERSE

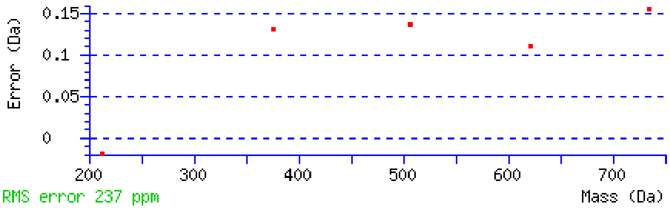
Match to Query 1159: 832.446494 from(417.230523,2+) index(3587)
Title: Elution from: 35.339 to 35.339 scan no 4537 cid35.00 polarity:+
Data file 0-1_2.mgf

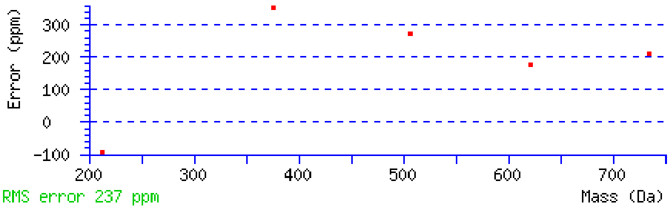
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 832.4477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0021
Matches : 5/52 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							7
2	213.1598	107.0835			L	***734.3865***	367.6969	717.3600	359.1836	716.3760	358.6916	6
3	328.1867	164.5970	310.1761	155.5917	D	***621.3025***	311.1549	604.2759	302.6416	603.2919	302.1496	5
4	459.2272	230.1172	441.2166	221.1119	M	***506.2755***	253.6414	489.2490	245.1281	488.2650	244.6361	4
5	546.2592	273.6332	528.2486	264.6280	S	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
6	659.3433	330.1753	641.3327	321.1700	I	288.2030	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VLDMSIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.1	832.4477	-0.0012	VLDMSIR
10.4	832.4443	0.0022	IVDPAYR

AT5G13450.1

10.4	832.4477	-0.0012	IVDSLMR
10.2	832.4477	-0.0012	VISDIMR
10.2	832.4477	-0.0012	VLMEAVR
6.9	832.4477	-0.0012	IVVNGGMK
2.3	832.4477	-0.0012	VVEMLAR

AT5G13450.2

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELTETLQEIIGAGK**
Found in **AT5G13450.2** in **TAIR_Arabidopsis**, Symbols: | ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative | chr5:4310561-4311944 REVERSE

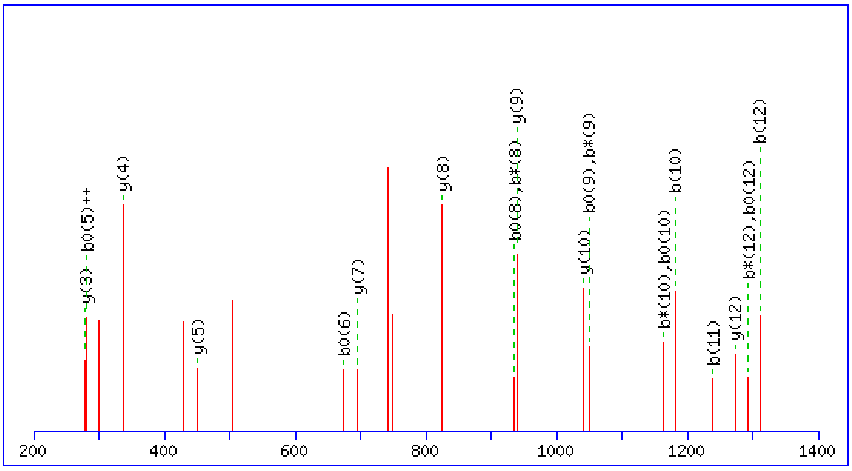
Match to Query 6037: 1516.753260 from(759.383906,2+) index(9085)
Title: Elution from: 85.464 to 85.464 scan no 12524 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

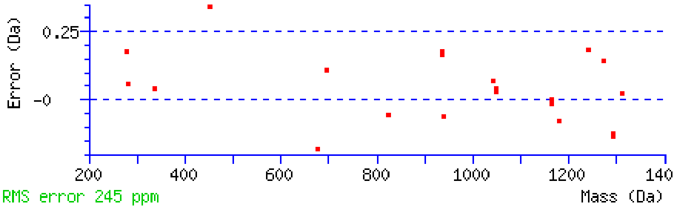
Label all possible matches ○ Label matches used for scoring ●

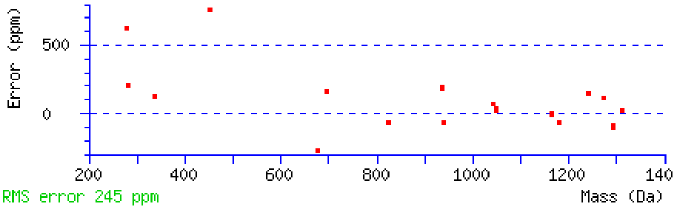
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1516.7561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 7e-007
Matches : 21/132 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							14
2	245.1280	123.0676			227.1174	114.0624	L	1387.7237	694.3655	1369.7002	685.3537	1369.7132	685.3602	13
3	347.1727	174.0900			329.1622	165.0847	T	***1273.6426***	637.3250	1255.6191	628.3132	1255.6321	628.3197	12
4	477.2123	239.1098			459.2018	230.1045	E	1171.5979	586.3026	1153.5744	577.2908	1153.5874	577.2973	11
5	579.2571	290.1322			561.2465	281.1269	T	***1041.5583***	521.2828	1023.5347	512.2710	1023.5477	512.2775	10
6	693.3382	347.1727			675.3276	338.1674	L	***939.5136***	470.2604	921.4900	461.2486	921.5030	461.2552	9
7	823.3908	412.1990	805.3672	403.1872	805.3802	403.1938	Q	***825.4325***	413.2199	807.4089	404.2081	807.4219	404.2146	8
8	953.4304	477.2189	935.4068	468.2071	935.4199	468.2136	E	***695.3798***	348.1936	677.3563	339.1818	677.3693	339.1883	7
9	1067.5115	534.2594	1049.4879	525.2476	1049.5010	525.2541	I	565.3402	283.1737	547.3166	274.1620			6
10	**1181.5926**	591.3000	1163.5690	582.2882	1163.5821	582.2947	I	***451.2591***	226.1332	433.2355	217.1214			5
11	**1239.6111**	620.3092	1221.5875	611.2974	1221.6006	611.3039	G	***337.1780***	169.0926	319.1544	160.0809			4
12	**1311.6453**	656.3263	1293.6217	647.3145	1293.6347	647.3210	A	***279.1595***	140.0834	261.1359	131.0716			3
13	1369.6638	685.3355	1351.6402	676.3237	1351.6532	676.3302	G	207.1254	104.0663	189.1018	95.0545			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ELTETLQEIIGAGK

AT5G13450.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.1	1516.7561	-0.0028	ELTETLQEIIGAGK
1.9	1516.7529	0.0004	VLLYKLHHYQNA
0.7	1516.7502	0.0030	FTIALYEAFNGKK

AT5G13510.1

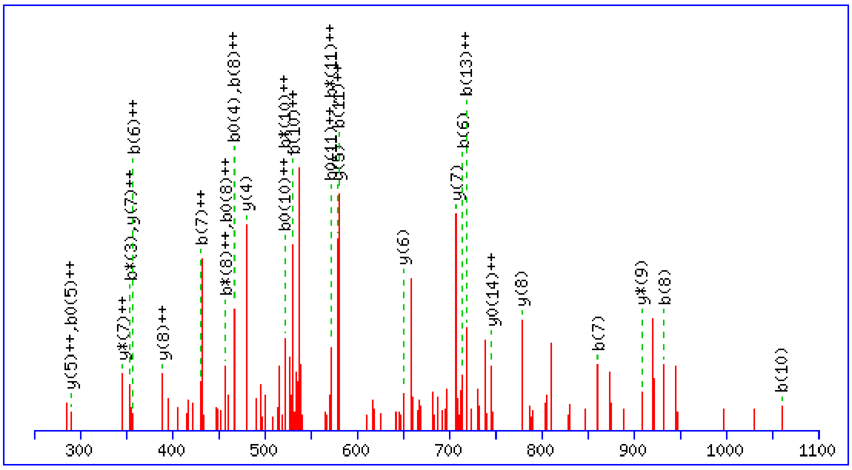
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLENNDFAGAVFEGK**
Found in **AT5G13510.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L10 family protein | chr5:4341297-4341959 FORWARD

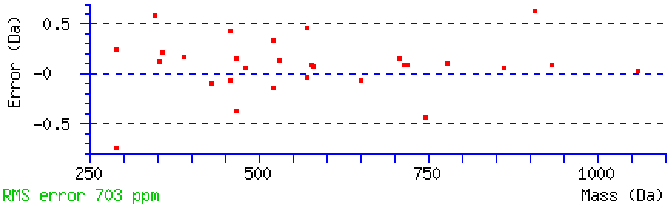
Match to Query 7025: 1637.803197 from(546.941675,3+) index(4764)
Title: Elution from: 46.869 to 46.869 scan no 6132 cid35.00 polarity:+
Data file D1d-1-2.mgf

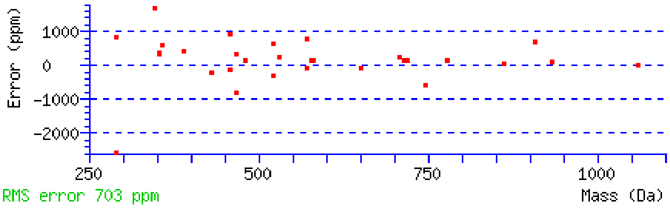
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1637.8049
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0017
Matches : 31/160 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							15
2	242.1863	121.5968	225.1598	113.0835			L	1510.7172	755.8623	1493.6907	747.3490	1492.7067	746.8570	14
3	371.2289	186.1181	354.2023	177.6048	353.2183	177.1128	E	1397.6332	699.3202	1380.6066	690.8070	1379.6226	690.3149	13
4	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	N	1268.5906	634.7989	1251.5640	626.2857	1250.5800	625.7937	12
5	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	N	1154.5477	577.7775	1137.5211	569.2642	1136.5371	568.7722	11
6	**714.3417**	***357.6745***	697.3151	349.1612	696.3311	348.6692	D	1040.5047	520.7560	1023.4782	512.2427	1022.4942	511.7507	10
7	**861.4101**	***431.2087***	844.3836	422.6954	843.3995	422.2034	F	925.4778	463.2425	908.4512	454.7293	907.4672	454.2373	9
8	**932.4472**	***466.7272***	915.4207	458.2140	914.4367	457.7220	A	**778.4094**	389.7083	761.3828	381.1951	760.3988	380.7030	8
9	989.4687	495.2380	972.4421	486.7247	971.4581	486.2327	G	**707.3723**	354.1898	690.3457	345.6765	689.3617	345.1845	7
10	**1060.5058**	***530.7565***	1043.4793	522.2433	1042.4952	521.7513	A	**650.3508**	325.6790	633.3243	317.1658	632.3402	316.6738	6
11	1159.5742	***580.2907***	1142.5477	571.7775	1141.5636	571.2855	V	**579.3137**	290.1605	562.2871	281.6472	561.3031	281.1552	5
12	1306.6426	653.8250	1289.6161	645.3117	1288.6321	644.8197	F	**480.2453**	240.6263	463.2187	232.1130	462.2347	231.6210	4
13	1435.6852	***718.3462***	1418.6587	709.8330	1417.6747	709.3410	E	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
14	1492.7067	***746.8570***	1475.6801	738.3437	1474.6961	737.8517	G	204.1343	102.5708	187.1077	94.0575			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KLENNDFAGAVFEGK

AT5G13510.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.3	1637.8049	-0.0017	KLENNDFAGAVFEGK
11.5	1637.8058	-0.0026	MGTMVLPWQGFISR
7.7	1637.8058	-0.0026	MGTMVLPWQGFISR

AT5G13630.1

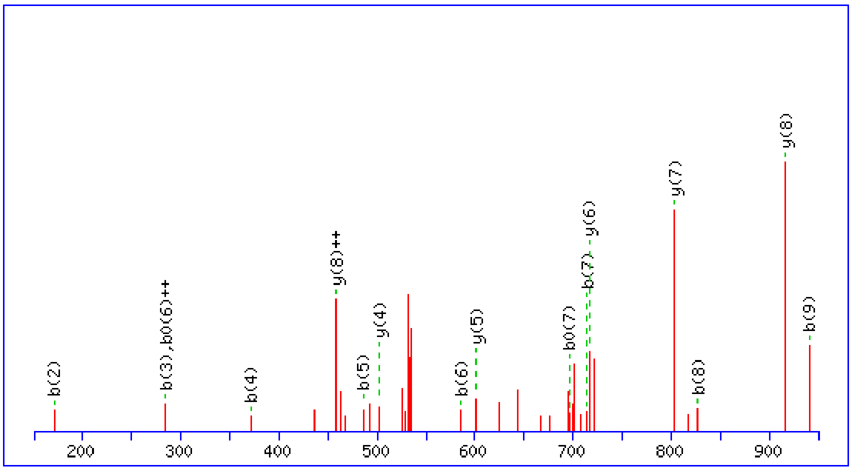
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GILSDVELLK**
Found in **AT5G13630.1** in **TAIR_Arabidopsis**, Symbols: CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5) | chr5:4387570-4392085 REVERSE

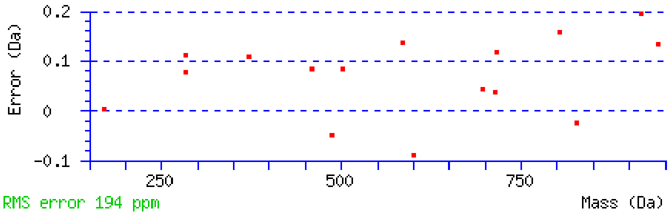
Match to Query 3435: 1085.634384 from(543.824468,2+) index(8727)
Title: Elution from: 77.065 to 77.065 scan no 11495 cid35.00 polarity:+
Data file C7-2_1.mgf

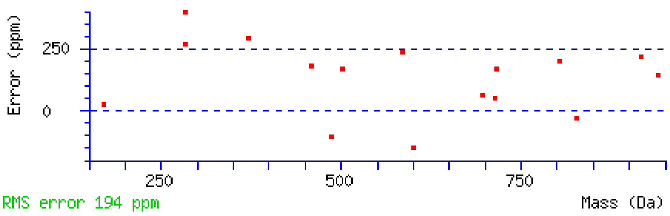
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1085.6332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 7.4e-006
Matches : 16/78 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180			**G**							**10**
2	***171.1128***	86.0600			**I**	1029.6190	515.3132	1012.5925	506.7999	1011.6085	506.3079	**9**
3	***284.1969***	142.6021			**L**	**916.5350**	458.7711	899.5084	450.2579	898.5244	449.7658	**8**
4	***371.2289***	186.1181	353.2183	177.1128	**S**	**803.4509**	402.2291	786.4244	393.7158	785.4403	393.2238	**7**
5	***486.2558***	243.6316	468.2453	234.6263	**D**	**716.4189**	358.7131	699.3923	350.1998	698.4083	349.7078	**6**
6	***585.3243***	293.1658	567.3137	284.1605	**V**	**601.3919**	301.1996	584.3654	292.6863	583.3814	292.1943	**5**
7	***714.3668***	357.6871	696.3563	348.6818	**E**	**502.3235**	251.6654	485.2970	243.1521	484.3130	242.6601	**4**
8	***827.4509***	414.2291	809.4403	405.2238	**L**	373.2809	187.1441	356.2544	178.6308			**3**
9	***940.5350***	470.7711	922.5244	461.7658	**L**	260.1969	130.6021	243.1703	122.0888			**2**
10					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GILSDVELLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G13630.1

Score	Mr(calc)	Delta	Sequence
56.7	1085.6332	0.0012	GILSDVELLK
14.8	1085.6332	0.0012	IGVTLDVEIK
10.5	1085.6332	0.0012	IEKDVLLEK
10.0	1085.6346	-0.0002	GLLHKVTYR
5.5	1085.6346	-0.0002	AVLPFERVR
5.1	1085.6332	0.0012	IDDVLSALLK
4.5	1085.6332	0.0012	VLGESLDLIK

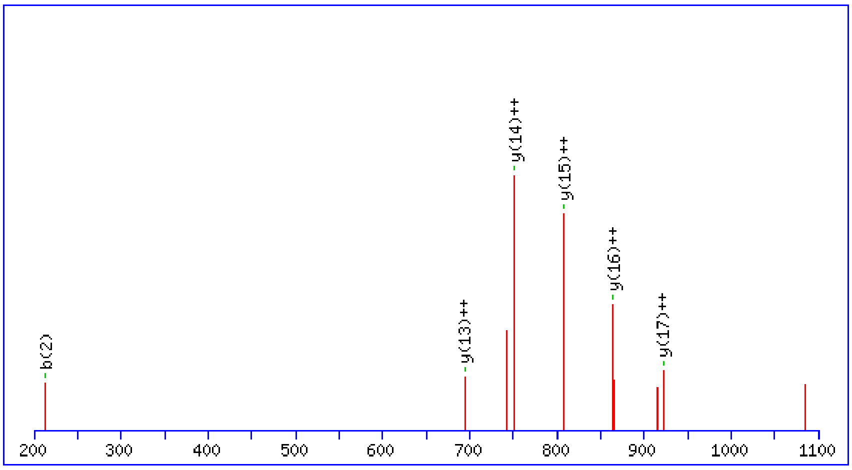
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIIDTPGHSDFGGEVER**
Found in **AT5G13650.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor family protein | chr5:4397824-4402367 FORWARD

Match to Query 8774: 1940.922774 from(647.981534,3+) index(4857)
Title: Elution from: 43.348 to 43.348 scan no 6094 cid35.00 polarity:+
Data file 0-3_3.mgf

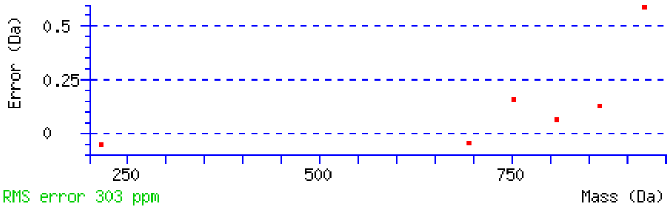
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

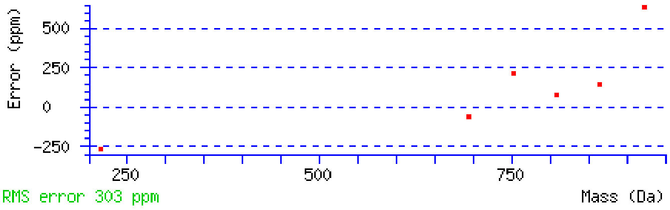


Monoisotopic mass of neutral peptide Mr(calc): 1940.9228
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0013
Matches : 6/192 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							18
2	214.1186	107.5629	197.0921	99.0497			N	1842.8617	921.9345	1825.8351	913.4212	1824.8511	912.9292	17
3	327.2027	164.1050	310.1761	155.5917			I	1728.8188	864.9130	1711.7922	856.3997	1710.8082	855.9077	16
4	440.2867	220.6470	423.2602	212.1337			I	1615.7347	808.3710	1598.7081	799.8577	1597.7241	799.3657	15
5	555.3137	278.1605	538.2871	269.6472	537.3031	269.1552	D	1502.6506	751.8290	1485.6241	743.3157	1484.6401	742.8237	14
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	T	1387.6237	694.3155	1370.5971	685.8022	1369.6131	685.3102	13
7	753.4141	377.2107	736.3876	368.6974	735.4036	368.2054	P	1286.5760	643.7916	1269.5495	635.2784	1268.5654	634.7864	12
8	810.4356	405.7214	793.4090	397.2082	792.4250	396.7162	G	1189.5232	595.2653	1172.4967	586.7520	1171.5127	586.2600	11
9	947.4945	474.2509	930.4680	465.7376	929.4839	465.2456	H	1132.5018	566.7545	1115.4752	558.2413	1114.4912	557.7492	10
10	1034.5265	517.7669	1017.5000	509.2536	1016.5160	508.7616	S	995.4429	498.2251	978.4163	489.7118	977.4323	489.2198	9
11	1149.5535	575.2804	1132.5269	566.7671	1131.5429	566.2751	D	908.4108	454.7091	891.3843	446.1958	890.4003	445.7038	8
12	1296.6219	648.8146	1279.5953	640.3013	1278.6113	639.8093	F	793.3839	397.1956	776.3573	388.6823	775.3733	388.1903	7
13	1353.6434	677.3253	1336.6168	668.8120	1335.6328	668.3200	G	646.3155	323.6614	629.2889	315.1481	628.3049	314.6561	6
14	1410.6648	705.8360	1393.6383	697.3228	1392.6543	696.8308	G	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
15	1539.7074	770.3573	1522.6809	761.8441	1521.6968	761.3521	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
16	1638.7758	819.8916	1621.7493	811.3783	1620.7653	810.8863	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
17	1767.8184	884.4128	1750.7919	875.8996	1749.8079	875.4076	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
18							R	175.1190	88.0631	158.0924	79.5498			1

AT5G13650.1





NCBI **BLAST** search of VNIIDTPGHSDFGGEVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.1	1940.9228	-0.0001	VNIIDTPGHSDFGGEVER
2.2	1940.9224	0.0004	DMGLLNTCGVEVVYEVK
0.1	1940.9257	-0.0029	MDGEEMVMVVKLKSSDK
0.1	1940.9257	-0.0029	MDGEEMVMVVKLKSSDK
0.1	1940.9257	-0.0029	MDGEEMVMVVKLKSSDK

Mascot: http://www.matrixscience.com/

AT5G13870.1

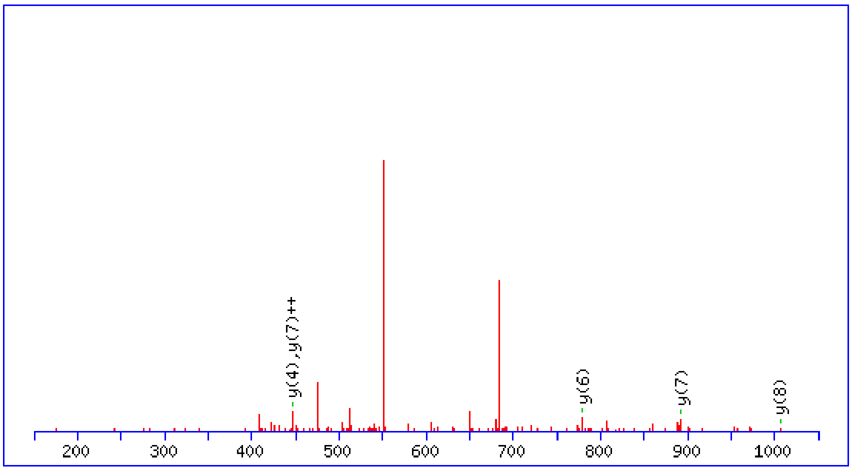
Mascot Search Results

Peptide View

MS/MS Fragmentation of **INLWFDPSK**
Found in **AT5G13870.1** in **TAIR_Arabidopsis**, Symbols: EXGT-A4 | EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds | chr5:4475091-4476219 REVERSE

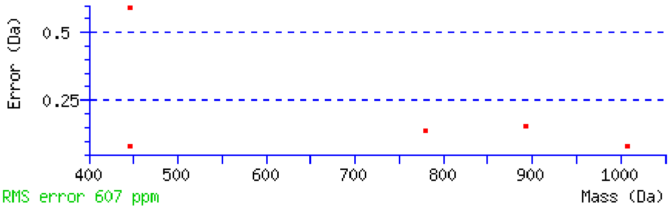
Match to Query 2956: 1118.574642 from(560.294597,2+) index(5204)
Title: Elution from: 49.150 to 49.150 scan no 6748 cid35.00 polarity:+
Data file D1d-1_3.mgf

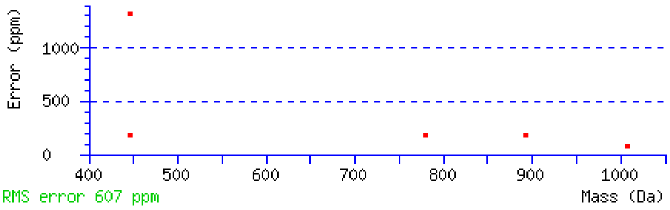
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1118.5760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.042
Matches : 5/82 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							9
2	228.1343	114.5708	211.1077	106.0575			N	*1006.4993*	503.7533	989.4727	495.2400	988.4887	494.7480	8
3	341.2183	171.1128	324.1918	162.5995			L	*892.4563*	446.7318	875.4298	438.2185	874.4458	437.7265	7
4	527.2976	264.1525	510.2711	255.6392			W	*779.3723*	390.1898	762.3457	381.6765	761.3617	381.1845	6
5	674.3661	337.6867	657.3395	329.1734			F	593.2930	297.1501	576.2664	288.6368	575.2824	288.1448	5
6	789.3930	395.2001	772.3665	386.6869	771.3824	386.1949	D	*446.2245*	223.6159	429.1980	215.1026	428.2140	214.6106	4
7	886.4458	443.7265	869.4192	435.2132	868.4352	434.7212	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
8	973.4778	487.2425	956.4512	478.7293	955.4672	478.2373	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of INLWFDPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G13870.1

22.3	1118.5760	-0.0014	INLWFDPSK
14.0	1118.5754	-0.0007	INLANSCSLK
12.0	1118.5754	-0.0007	ILCKAEETR
6.4	1118.5720	0.0026	LVETNTWTR
5.4	1118.5754	-0.0007	LLLSEGMSNR
3.3	1118.5720	0.0026	LGEPNSLFSR
2.9	1118.5754	-0.0007	LLENDKTMR
2.8	1118.5754	-0.0007	LLNSMQELR
2.5	1118.5760	-0.0014	YYLLYQTR
2.4	1118.5720	0.0026	IWEQSSLTR

AT5G13930.1

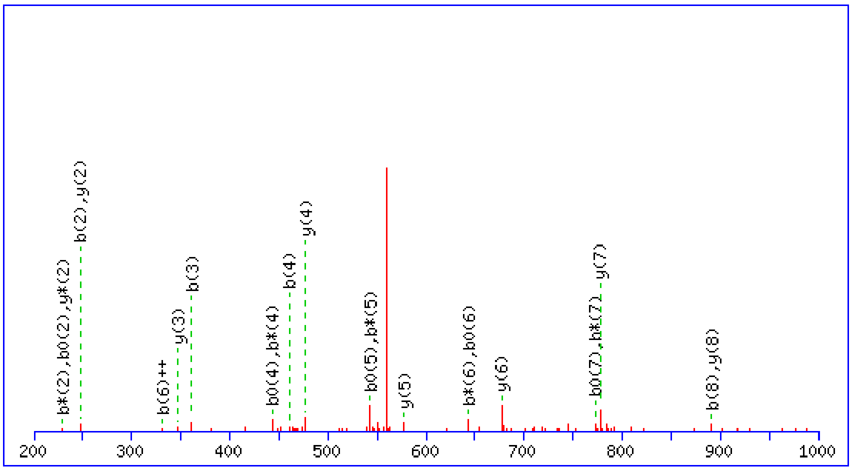
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDIVVVEVPK**
Found in **AT5G13930.1** in **TAIR_Arabidopsis**, Symbols: CHS, TT4, ATCHS | ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase | chr5:4488764-4490037 FORWARD

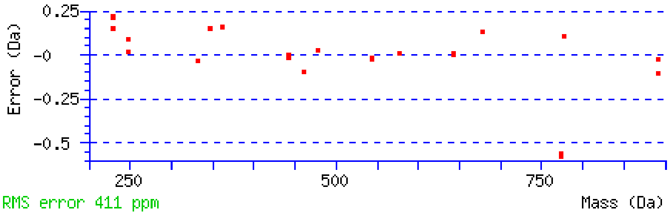
Match to Query 3884: 1136.606222 from(569.310387,2+) index(5136)
Title: Elution from: 46.095 to 46.095 scan no 6407 cid35.00 polarity:+
Data file C7-3_1.mgf

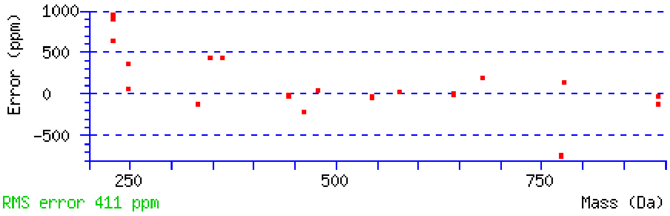
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1136.6085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 4e-005
Matches : 23/100 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							10
2	**247.0839**	124.0456	229.0603	115.0338	229.0733	115.0403	D	1007.5632	504.2852	989.5396	495.2734	989.5526	495.2799	9
3	**361.1650**	181.0861	343.1414	172.0743	343.1544	172.0809	I	***891.5392***	446.2732	873.5156	437.2614	873.5286	437.2680	8
4	**461.2304**	231.1189	443.2069	222.1071	443.2199	222.1136	V	***777.4581***	389.2327	759.4345	380.2209	759.4475	380.2274	7
5	561.2959	281.1516	543.2723	272.1398	543.2853	272.1463	V	***677.3926***	339.2000	659.3691	330.1882	659.3821	330.1947	6
6	661.3613	331.1843	643.3378	322.1725	643.3508	322.1790	V	***577.3272***	289.1672	559.3036	280.1554	559.3166	280.1620	5
7	791.4010	396.2041	773.3774	387.1923	773.3904	387.1988	E	***477.2618***	239.1345	459.2382	230.1227	459.2512	230.1292	4
8	**891.4664**	446.2369	873.4428	437.2251	873.4559	437.2316	V	***347.2221***	174.1147	329.1985	165.1029			3
9	989.5162	495.2617	971.4926	486.2500	971.5057	486.2565	P	***247.1567***	124.0820	229.1331	115.0702			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QDIVVVEVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G13930.1

Score	Mr(calc)	Delta	Sequence
45.4	1136.6085	-0.0023	QDIVVVEVPK
3.8	1136.6085	-0.0023	GELGLAEPVIK
1.2	1136.6038	0.0024	MLTKFLSIR

AT5G14040.1

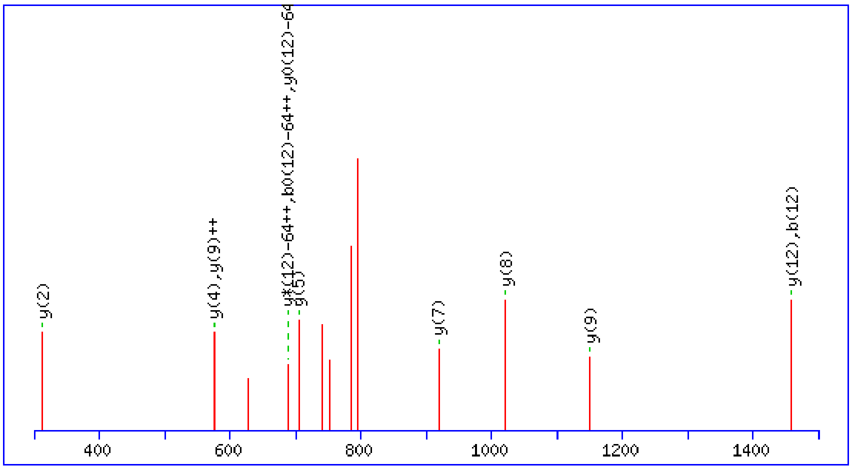
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FASFETIVEMIYK**
Found in **AT5G14040.1** in **TAIR_Arabidopsis**, Symbols: | mitochondrial phosphate transporter | chr5:4531061-4532967 REVERSE

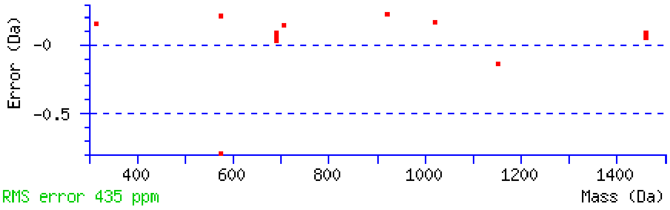
Match to Query 7289: 1606.736704 from(804.375628,2+) index(10652)
Title: Elution from: 101.783 to 101.783 scan no 15282 cid35.00 polarity:+
Data file C7-1_2.mgf

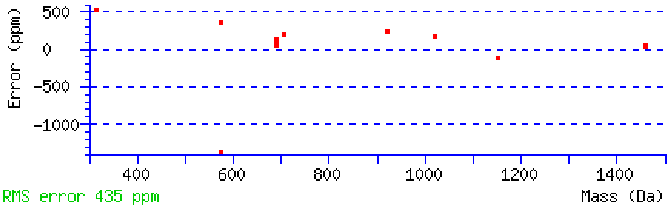
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1606.7381
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 71 **Expect:** 6.5e-007
Matches : 13/172 fragment ions using 11 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	149.0727	75.0400			F							13
2	221.1069	111.0571			A	***1459.6800***	730.3436	1441.6564	721.3318	1441.6694	721.3383	12
3	309.1359	155.0716	291.1254	146.0663	S	1387.6458	694.3265	1369.6222	685.3147	1369.6352	685.3213	11
4	457.2014	229.1043	439.1908	220.0990	F	1299.6167	650.3120	1281.5932	641.3002	1281.6062	641.3067	10
5	587.2410	294.1241	569.2304	285.1189	E	***1151.5513***	576.2793	1133.5277	567.2675	1133.5407	567.2740	9
6	**689.2857**	345.1465	671.2752	336.1412	T	***1021.5117***	511.2595	1003.4881	502.2477	1003.5011	502.2542	8
7	803.3668	402.1871	785.3563	393.1818	I	***919.4669***	460.2371	901.4434	451.2253	901.4564	451.2318	7
8	903.4323	452.2198	885.4217	443.2145	V	805.3858	403.1966	787.3623	394.1848	787.3753	394.1913	6
9	1033.4719	517.2396	1015.4613	508.2343	E	***705.3204***	353.1638	687.2968	344.1520	687.3098	344.1586	5
10	1181.5043	591.2558	1163.4938	582.2505	M	***575.2808***	288.1440	557.2572	279.1322			4
11	1295.5854	648.2964	1277.5749	639.2911	I	427.2483	214.1278	409.2248	205.1160			3
12	**1459.6458**	730.3265	1441.6352	721.3213	Y	***313.1672***	157.0873	295.1437	148.0755			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FASFETIVEMIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G14040.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.8	1606.7381	-0.0014	FASFETIVEMIYK
11.7	1606.7390	-0.0023	HDSLNLNEMTRKK
9.2	1606.7378	-0.0011	GYTQRDWIHSVPK
8.9	1606.7390	-0.0023	MGSLHLNSNNNKLK
4.4	1606.7359	0.0008	LLAELDPMLFDDGK
4.1	1606.7330	0.0037	NLVPVNENEEYLR
3.4	1606.7390	-0.0023	AKEALDAVPNCRNK
3.2	1606.7412	-0.0045	AMAARVEFQYRTK
2.7	1606.7363	0.0004	VDLSDAPMKGTVNNK
2.0	1606.7352	0.0016	KTQGFSLFNGFDTK

Mascot: http://www.matrixscience.com/

AT5G14200.1

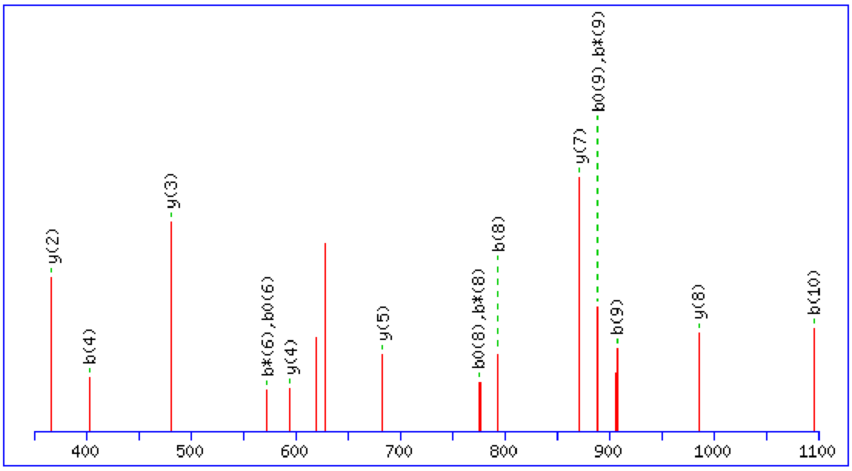
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANVLDASILWR**
Found in **AT5G14200.1** in **TAIR_Arabidopsis**, Symbols: | 3-isopropylmalate dehydrogenase, chloroplast, putative | chr5:4576222-4578113 FORWARD

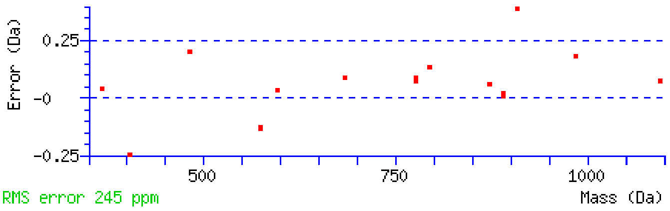
Match to Query 4544: 1272.637418 from(637.325985,2+) index(9027)
Title: Elution from: 80.183 to 80.183 scan no 12081 cid35.00 polarity:+
Data file C7-1_2.mgf

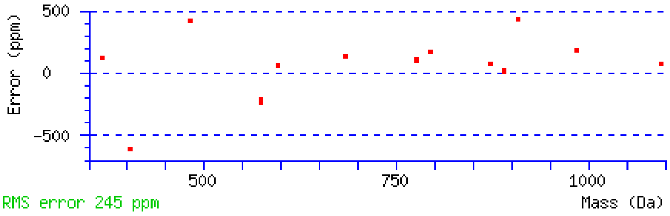
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1272.6403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.5e-005
Matches : 16/102 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							11
2	189.0784	95.0428	171.0548	86.0311			N	1201.6134	601.3103	1183.5898	592.2985	1183.6028	592.3051	10
3	289.1439	145.0756	271.1203	136.0638			V	1085.5764	543.2918	1067.5528	534.2801	1067.5658	534.2866	9
4	**403.2250**	202.1161	385.2014	193.1043			L	***985.5110***	493.2591	967.4874	484.2473	967.5004	484.2538	8
5	519.2489	260.1281	501.2254	251.1163	501.2384	251.1228	D	***871.4299***	436.2186	853.4063	427.2068	853.4193	427.2133	7
6	591.2831	296.1452	573.2595	287.1334	573.2725	287.1399	A	755.4059	378.2066	737.3823	369.1948	737.3953	369.2013	6
7	679.3122	340.1597	661.2886	331.1479	661.3016	331.1544	S	***683.3717***	342.1895	665.3482	333.1777	665.3612	333.1842	5
8	**793.3933**	397.2003	775.3697	388.1885	775.3827	388.1950	I	***595.3427***	298.1750	577.3191	289.1632			4
9	**907.4744**	454.2408	889.4508	445.2290	889.4638	445.2355	L	***481.2616***	241.1344	463.2380	232.1226			3
10	**1095.5477**	548.2775	1077.5242	539.2657	1077.5372	539.2722	W	***367.1805***	184.0939	349.1569	175.0821			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of ANVLDASILWR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G14200.1

Score	Mr(calc)	Delta	Sequence
57.9	1272.6403	-0.0029	ANVLDASILWR
14.2	1272.6380	-0.0006	SIKDQPNISVR
12.7	1272.6410	-0.0036	LDAKMLPVETK
10.9	1272.6381	-0.0006	ATISISPNALNR
10.5	1272.6403	-0.0029	FHLVKESELR
7.0	1272.6380	-0.0006	ENSVGALLNLAR
5.3	1272.6354	0.0021	EIADVQEISKK
3.7	1272.6407	-0.0033	HVTRNVGKSQK
1.9	1272.6354	0.0021	IGDKLKEEEAK
1.7	1272.6362	0.0012	ITAICPMNVLK

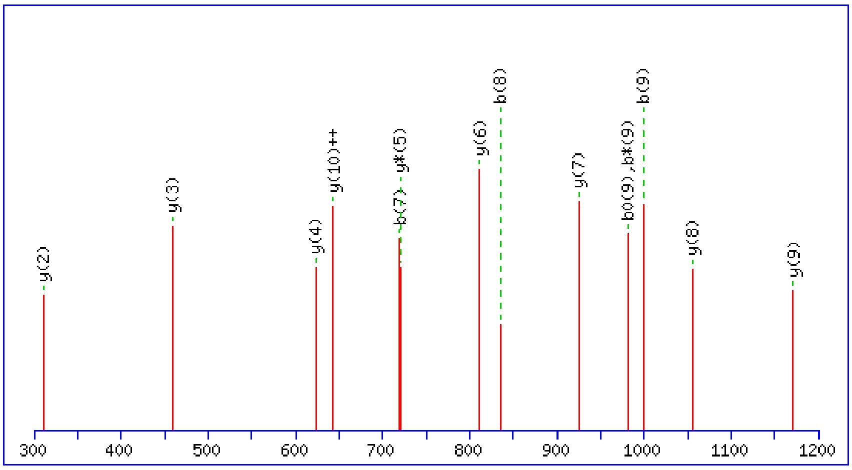
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVLDQLANYFMR**
Found in **AT5G14260.1** in **TAIR_Arabidopsis**, Symbols: | SET domain-containing protein | chr5:4601142-4603876 FORWARD

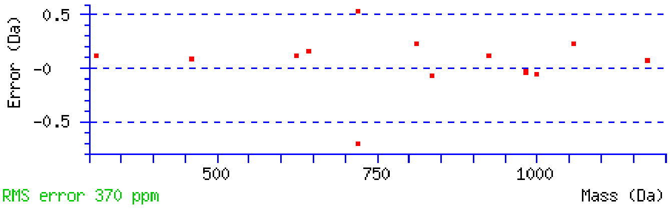
Match to Query 5337: 1456.670084 from(729.342318,2+) index(10150)
Title: Elution from: 101.317 to 101.317 scan no 14902 cid35.00 polarity:+
Data file D1d-1_3.mgf

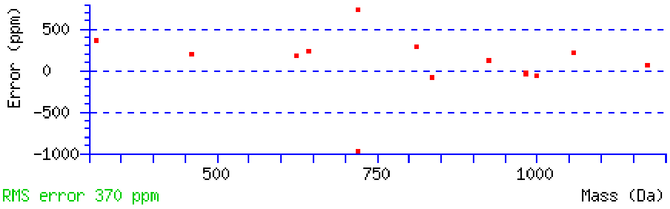
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1456.6727
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 1.1e-006
Matches : 14/102 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							12
2	173.1069	87.0571					V	1385.6458	693.3266	1367.6223	684.3148	1367.6353	684.3213	11
3	287.1880	144.0976					L	1285.5804	643.2938	1267.5568	634.2820	1267.5698	634.2886	10
4	403.2120	202.1096			385.2014	193.1043	D	***1171.4993***	586.2533	1153.4757	577.2415	1153.4887	577.2480	9
5	533.2646	267.1359	515.2410	258.1241	515.2540	258.1307	Q	***1055.4753***	528.2413	1037.4517	519.2295			8
6	647.3457	324.1765	629.3221	315.1647	629.3351	315.1712	L	***925.4227***	463.2150	907.3991	454.2032			7
7	**719.3798**	360.1936	701.3563	351.1818	701.3693	351.1883	A	***811.3416***	406.1744	793.3180	397.1626			6
8	**835.4168**	418.2121	817.3933	409.2003	817.4063	409.2068	N	739.3074	370.1573	721.2838	361.1456			5
9	**999.4772**	500.2422	981.4536	491.2304	981.4666	491.2370	Y	***623.2704***	312.1389	605.2468	303.1271			4
10	1147.5427	574.2750	1129.5191	565.2632	1129.5321	565.2697	F	***459.2101***	230.1087	441.1865	221.0969			3
11	1279.5802	640.2937	1261.5566	631.2819	1261.5696	631.2884	M	***311.1446***	156.0759	293.1210	147.0642			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AVLDQLANYFMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G14260.1

Score	Mr(calc)	Delta	Sequence
67.5	1456.6727	-0.0026	AVLDQLANYFMR
11.2	1456.6671	0.0030	NPNSKIGIYYDR
4.8	1456.6700	0.0001	YGNVDFLVEMIK
2.5	1456.6705	-0.0004	EDIDRTYKIMR
1.2	1456.6725	-0.0024	DLDVTPEGDLELK
0.4	1456.6657	0.0043	NALVNMYLKCGR

AT5G14320.1

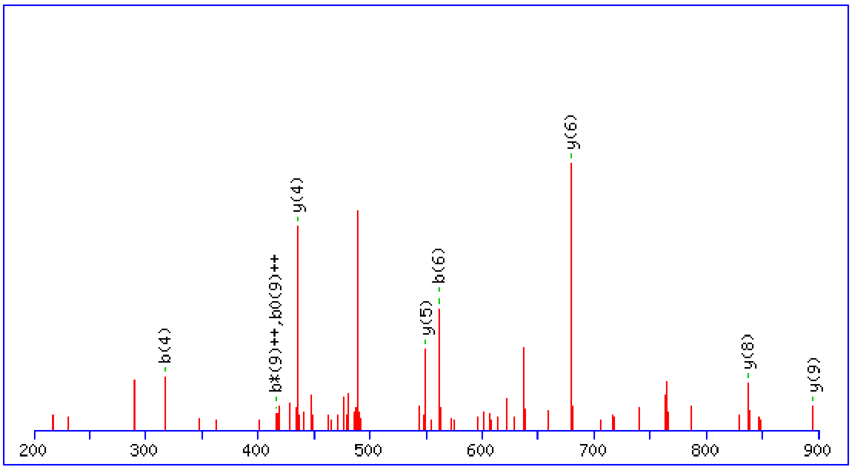
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGGVEIPANK**
Found in **AT5G14320.1** in **TAIR_Arabidopsis**, Symbols: | 30S ribosomal protein S13, chloroplast (CS13) | chr5:4617842-4618775 REVERSE

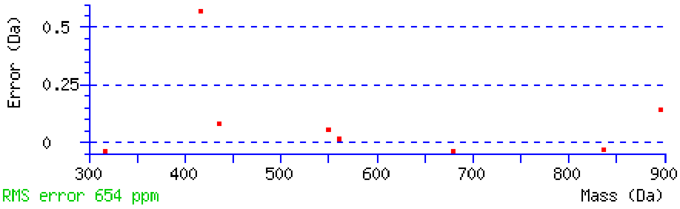
Match to Query 2370: 994.509984 from(498.262268,2+) index(2003)
Title: Elution from: 24.020 to 24.020 scan no 2607 cid35.00 polarity:+
Data file D6h-1_2.mgf

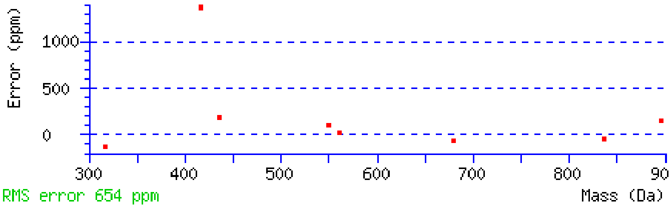
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.5092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0022
Matches : 9/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							10
2	159.0912	80.0492					G	***895.4510***	448.2291	877.4274	439.2173	877.4404	439.2239	9
3	217.1097	109.0585					G	***837.4325***	419.2199	819.4089	410.2081	819.4219	410.2146	8
4	**317.1752**	159.0912					V	779.4140	390.2106	761.3904	381.1988	761.4034	381.2054	7
5	447.2148	224.1110			429.2042	215.1058	E	***679.3485***	340.1779	661.3250	331.1661	661.3380	331.1726	6
6	**561.2959**	281.1516			543.2853	272.1463	I	***549.3089***	275.1581	531.2853	266.1463			5
7	659.3457	330.1765			641.3351	321.1712	P	***435.2278***	218.1175	417.2042	209.1058			4
8	731.3798	366.1936			713.3693	357.1883	A	337.1780	169.0926	319.1544	160.0809			3
9	847.4168	424.2121	829.3933	415.2003	829.4063	415.2068	N	265.1439	133.0756	247.1203	124.0638			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VGGVEIPANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G14320.1

34.1	994.5092	0.0008	VGGVEIPANK
11.8	994.5118	-0.0018	KALELGGHR
1.4	994.5092	0.0008	ELAPSTIPR
0.2	994.5118	-0.0018	ADHARALVK

AT5G14580.1

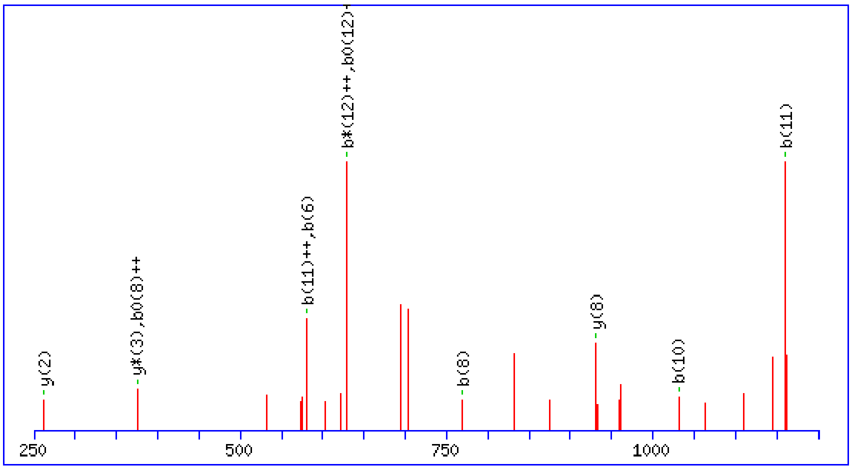
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEESASVSTRKLK**
Found in **AT5G14580.1** in **TAIR_Arabidopsis**, Symbols: | polyribonucleotide nucleotidyltransferase, putative | chr5:4697615-4703016 REVERSE

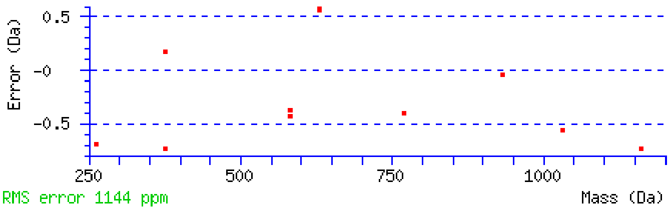
Match to Query 5889: 1422.702556 from(712.358554,2+) index(5576)
Title: Elution from: 48.832 to 48.832 scan no 6970 cid35.00 polarity:+
Data file C7-1_1.mgf

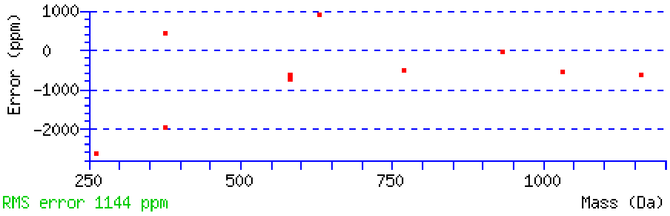
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1422.7039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.032
Matches : 11/116 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							13
2	203.0811	102.0442			185.0705	93.0389	E	1351.6770	676.3421	1333.6534	667.3304	1333.6664	667.3369	12
3	333.1207	167.0640			315.1101	158.0587	E	1221.6374	611.3223	1203.6138	602.3105	1203.6268	602.3170	11
4	421.1497	211.0785			403.1392	202.0732	S	1091.5978	546.3025	1073.5742	537.2907	1073.5872	537.2972	10
5	493.1839	247.0956			475.1733	238.0903	A	1003.5687	502.2880	985.5451	493.2762	985.5581	493.2827	9
6	***581.2130***	291.1101			563.2024	282.1048	S	**931.5345**	466.2709	913.5110	457.2591	913.5240	457.2656	8
7	681.2784	341.1428			663.2678	332.1376	V	843.5055	422.2564	825.4819	413.2446	825.4949	413.2511	7
8	***769.3075***	385.1574			751.2969	376.1521	S	743.4400	372.2237	725.4164	363.2119	725.4295	363.2184	6
9	871.3522	436.1797			853.3416	427.1744	T	655.4110	328.2091	637.3874	319.1973	637.4004	319.2038	5
10	***1031.4414***	516.2244	1013.4178	507.2126	1013.4309	507.2191	R	553.3663	277.1868	535.3427	268.1750			4
11	***1161.5305***	581.2689	1143.5069	572.2571	1143.5199	572.2636	K	393.2770	197.1421	375.2534	188.1303			3
12	1275.6116	638.3094	1257.5880	629.2976	1257.6010	629.3041	L	**263.1880**	132.0976	245.1644	123.0858			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AEESASVSTRKLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G14580.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	1422.7039	-0.0013	AEESASVSTRKLK
14.6	1422.6987	0.0038	MEKILEFLGSNK
9.2	1422.7047	-0.0022	MLKMAARDTGALK
8.1	1422.7021	0.0005	SKMEVMLQSVIK
3.5	1422.6987	0.0038	AMSGKYVAEVPLK
2.8	1422.7034	-0.0009	DSVDTILATSFLK
2.5	1422.6991	0.0034	RDIISSMGRELK
2.5	1422.6991	0.0034	SLMERVRQELK
1.7	1422.6987	0.0039	QFVAEVVTMGSLK
1.5	1422.7039	-0.0013	NKNGIGSTSSVTIK

AT5G14660.1

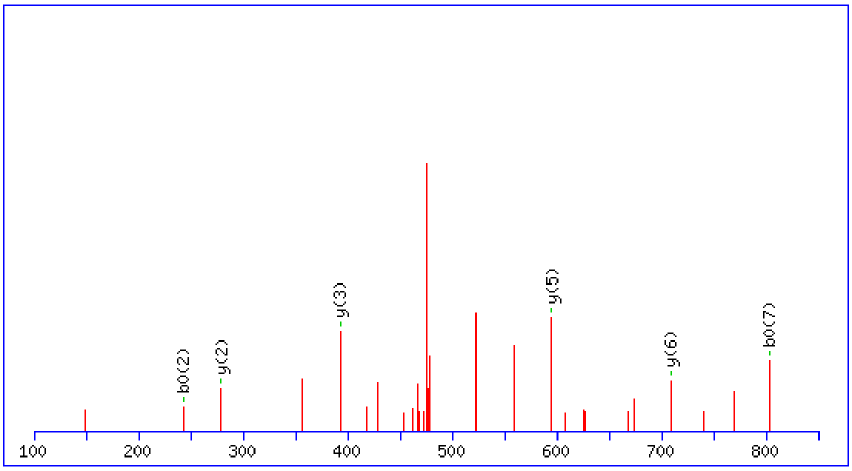
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EELEALEK**
Found in **AT5G14660.1** in **TAIR_Arabidopsis**, Symbols: DEF2, PDF1B | PDF1B (PEPTIDE DEFORMYLASE 1B); peptide deformylase | chr5:4727132-4728674 REVERSE

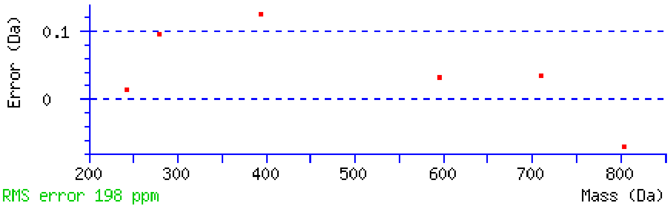
Match to Query 1835: 968.455118 from(485.234835,2+) index(1147)
Title: Elution from: 18.265 to 18.265 scan no 1641 cid35.00 polarity:+
Data file D12h-2_3.mgf

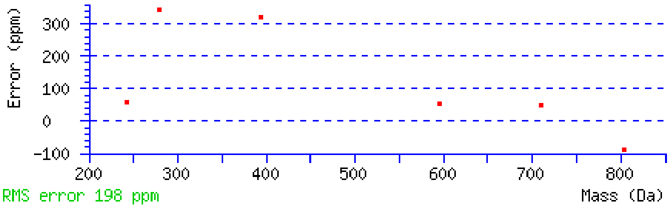
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 968.4545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0063
Matches : 6/68 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							8
2	261.0865	131.0469	243.0760	122.0416	E	839.4221	420.2147	821.3985	411.2029	821.4115	411.2094	7
3	375.1676	188.0875	357.1571	179.0822	L	***709.3825***	355.1949	691.3589	346.1831	691.3719	346.1896	6
4	505.2073	253.1073	487.1967	244.1020	E	***595.3014***	298.1543	577.2778	289.1425	577.2908	289.1490	5
5	577.2414	289.1243	559.2308	280.1191	A	465.2617	233.1345	447.2382	224.1227	447.2512	224.1292	4
6	691.3225	346.1649	673.3119	337.1596	L	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	821.3621	411.1847	803.3516	402.1794	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EELEALEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.1	968.4545	0.0007	EELEALEK

AT5G14660.1

18.1	968.4571	-0.0020	SEGPAEIVR
17.4	968.4545	0.0007	LEAEEIEK
7.9	968.4545	0.0007	EAIELEEK
7.2	968.4571	-0.0020	QKQPAEEK
4.0	968.4544	0.0007	LIDDEVEK
4.0	968.4544	0.0007	LLDDEVEK
0.2	968.4524	0.0027	MNHLGQIK
0.2	968.4571	-0.0020	QLLSEDPR

AT5G14740.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAGVGAAIEYAVLHLK**
Found in **AT5G14740.1** in **TAIR_Arabidopsis**, Symbols: CA18, BETA CA2, CA2 | CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758260-4762385 FORWARD

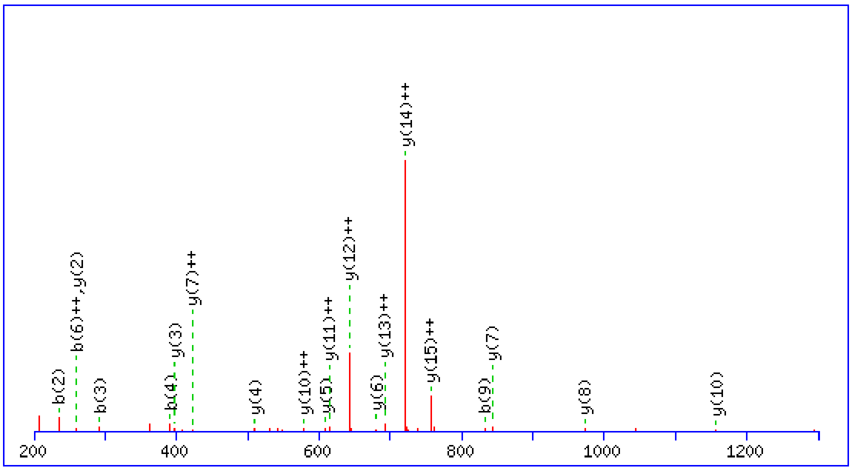
Match to Query 7900: 1673.914911 from(558.978913,3+) index(10298)
Title: Elution from: 97.836 to 97.836 scan no 14615 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

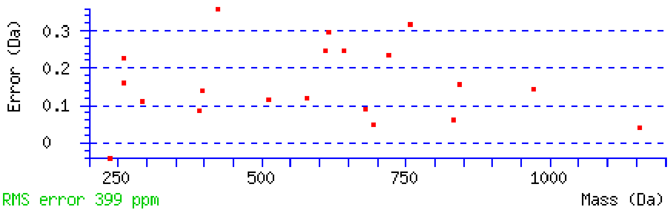
Show Y-axis ☐

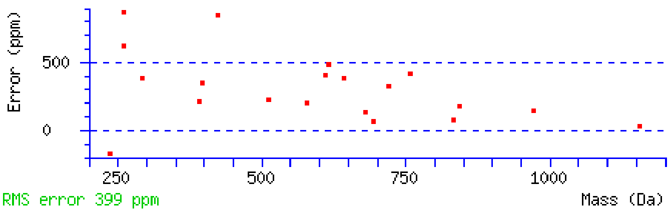


Monoisotopic mass of neutral peptide Mr(calc): 1673.9141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 2.1e-006
Matches : 20/120 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			**Y**							**16**
2	**235.1077**	118.0575			**A**	1511.8580	756.4327	1494.8315	747.9194	1493.8475	747.4274	**15**
3	**292.1292**	146.5682			**G**	1440.8209	720.9141	1423.7944	712.4008	1422.8104	711.9088	**14**
4	**391.1976**	196.1024			**V**	1383.7995	692.4034	1366.7729	683.8901	1365.7889	683.3981	**13**
5	448.2191	224.6132			**G**	1284.7310	642.8692	1267.7045	634.3559	1266.7205	633.8639	**12**
6	519.2562	260.1317			**A**	1227.7096	614.3584	1210.6830	605.8452	1209.6990	605.3531	**11**
7	590.2933	295.6503			**A**	***1156.6725***	578.8399	1139.6459	570.3266	1138.6619	569.8346	**10**
8	703.3774	352.1923			**I**	1085.6354	543.3213	1068.6088	534.8080	1067.6248	534.3160	**9**
9	**832.4199**	416.7136	814.4094	407.7083	**E**	***972.5513***	486.7793	955.5247	478.2660	954.5407	477.7740	**8**
10	995.4833	498.2453	977.4727	489.2400	**Y**	***843.5087***	422.2580	826.4822	413.7447			**7**
11	1066.5204	533.7638	1048.5098	524.7586	**A**	***680.4454***	340.7263	663.4188	332.2130			**6**
12	1165.5888	583.2980	1147.5782	574.2928	**V**	***609.4083***	305.2078	592.3817	296.6945			**5**
13	1278.6729	639.8401	1260.6623	630.8348	**L**	***510.3398***	255.6736	493.3133	247.1603			**4**
14	1415.7318	708.3695	1397.7212	699.3642	**H**	***397.2558***	199.1315	380.2292	190.6183			**3**
15	1528.8158	764.9116	1510.8053	755.9063	**L**	***260.1969***	130.6021	243.1703	122.0888			**2**
16					**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT5G14740.1





NCBI **BLAST** search of YAGVGAAIEYAVLHLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.5	1673.9141	0.0008	YAGVGAAIEYAVLHLK
2.7	1673.9100	0.0049	VPGGRNSLESFLIASK

Mascot: http://www.matrixscience.com/

AT5G14740.2

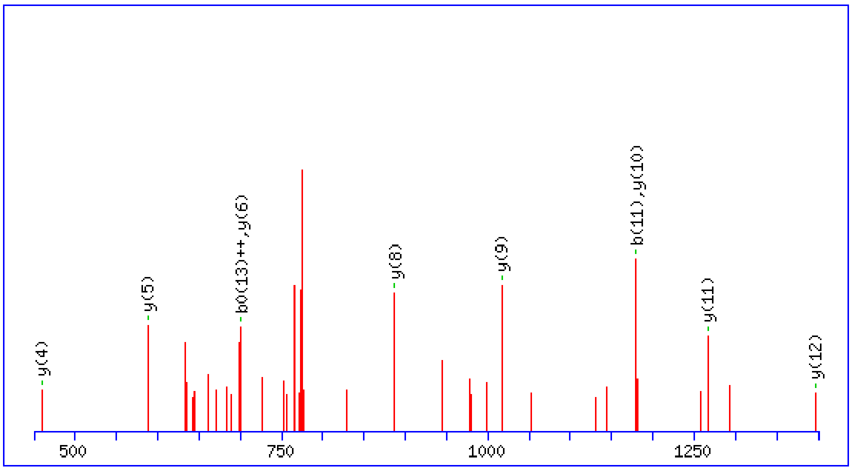
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNESYEDAIEALKK**
Found in **AT5G14740.2** in **TAIR_Arabidopsis**, Symbols: CA18, BETA CA2, CA2 | CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4760539-4762385 FORWARD

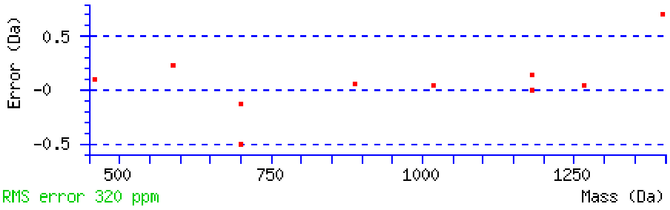
Match to Query 7001: 1565.754322 from(783.884437,2+) index(5544)
Title: Elution from: 50.169 to 50.169 scan no 6992 cid35.00 polarity:+
Data file 0-3_1.mgf

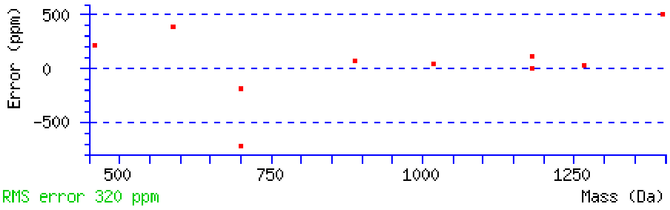
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



`Monoisotopic mass of neutral peptide Mr(calc):` 1565.7573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 1.7e-007
Matches : 10/142 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							14
2	172.0717	86.5395	155.0451	78.0262			N	1509.7431	755.3752	1492.7166	746.8619	1491.7326	746.3699	13
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	E	***1395.7002***	698.3537	1378.6737	689.8405	1377.6896	689.3485	12
4	388.1463	194.5768	371.1197	186.0635	370.1357	185.5715	S	***1266.6576***	633.8324	1249.6311	625.3192	1248.6470	624.8272	11
5	551.2096	276.1084	534.1831	267.5952	533.1991	267.1032	Y	***1179.6256***	590.3164	1162.5990	581.8032	1161.6150	581.3111	10
6	680.2522	340.6297	663.2257	332.1165	662.2416	331.6245	E	***1016.5623***	508.7848	999.5357	500.2715	998.5517	499.7795	9
7	795.2792	398.1432	778.2526	389.6299	777.2686	389.1379	D	***887.5197***	444.2635	870.4931	435.7502	869.5091	435.2582	8
8	866.3163	433.6618	849.2897	425.1485	848.3057	424.6565	A	772.4927	386.7500	755.4662	378.2367	754.4822	377.7447	7
9	979.4003	490.2038	962.3738	481.6905	961.3898	481.1985	I	***701.4556***	351.2314	684.4291	342.7182	683.4450	342.2262	6
10	1108.4429	554.7251	1091.4164	546.2118	1090.4324	545.7198	E	***588.3715***	294.6894	571.3450	286.1761	570.3610	285.6841	5
11	1179.4800	590.2437	1162.4535	581.7304	1161.4695	581.2384	A	***459.3289***	230.1681	442.3024	221.6548			4
12	1292.5641	646.7857	1275.5376	638.2724	1274.5535	637.7804	L	388.2918	194.6496	371.2653	186.1363			3
13	1420.6591	710.8332	1403.6325	702.3199	1402.6485	701.8279	K	275.2078	138.1075	258.1812	129.5942			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GNESYEDAIEALKK

AT5G14740.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.1	1565.7573	-0.0029	GNESYEDAIEALKK
1.4	1565.7546	-0.0003	EILENHGGEERQR
0.6	1565.7508	0.0036	EVTEEYTKHMKR
0.3	1565.7573	-0.0030	KEYDETDLANIQK

AT5G14780.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVEDLNEMLPK**
Found in **AT5G14780.1** in **TAIR_Arabidopsis**, Symbols: FDH | FDH (FORMATE DEHYDROGENASE); NAD binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr5:4777046-4779193 FORWARD

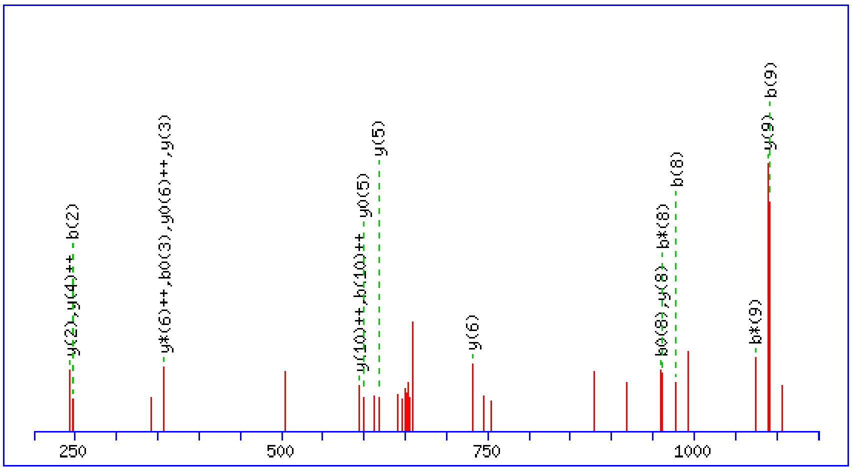
Match to Query 4729: 1333.657450 from(667.836001,2+) index(7533)
Title: Elution from: 66.400 to 66.400 scan no 9924 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1150 Da Full range

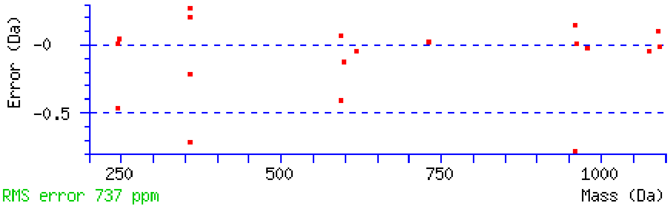
Label all possible matches ○ Label matches used for scoring ●

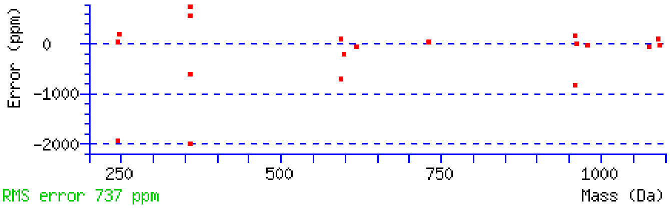
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1333.6588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00099
Matches : 19/98 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							11
2	**247.1441**	124.0757					V	1187.5977	594.3025	1170.5711	585.7892	1169.5871	585.2972	10
3	376.1867	188.5970			358.1761	179.5917	E	***1088.5292***	544.7683	1071.5027	536.2550	1070.5187	535.7630	9
4	491.2136	246.1105			473.2031	237.1052	D	***959.4866***	480.2470	942.4601	471.7337	941.4761	471.2417	8
5	604.2977	302.6525			586.2871	293.6472	L	844.4597	422.7335	827.4332	414.2202	826.4491	413.7282	7
6	718.3406	359.6740	701.3141	351.1607	700.3301	350.6687	N	***731.3756***	366.1915	714.3491	357.6782	713.3651	357.1862	6
7	847.3832	424.1953	830.3567	415.6820	829.3727	415.1900	E	***617.3327***	309.1700	600.3062	300.6567	599.3221	300.1647	5
8	**978.4237**	489.7155	961.3972	481.2022	960.4131	480.7102	M	488.2901	244.6487	471.2636	236.1354			4
9	**1091.5078**	546.2575	1074.4812	537.7443	1073.4972	537.2522	L	***357.2496***	179.1285	340.2231	170.6152			3
10	1188.5605	594.7839	1171.5340	586.2706	1170.5500	585.7786	P	***244.1656***	122.5864	227.1390	114.0731			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FVEDLNEMLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G14780.1

Score	Mr(calc)	Delta	Sequence
35.7	1333.6588	-0.0013	FVEDLNEMLPK
10.7	1333.6561	0.0014	SRYCRGVPDPK
9.3	1333.6568	0.0007	RWNDFWSVPK
6.3	1333.6586	-0.0011	RSISLGDSTENR

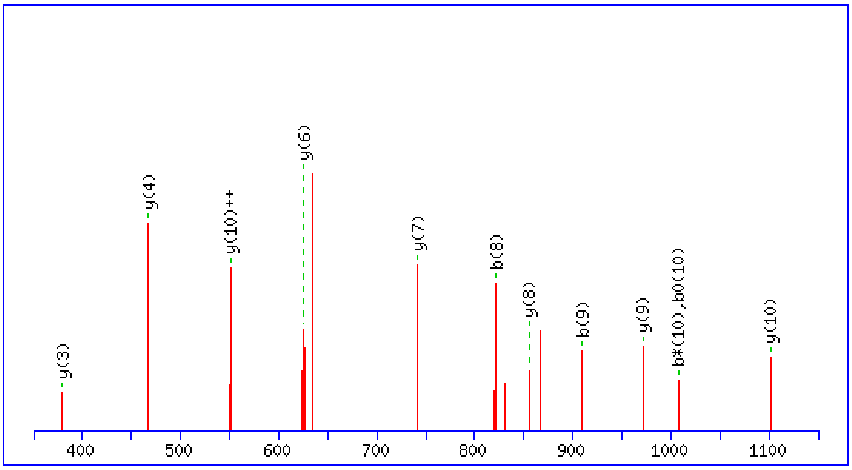
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALQDIDGVSNLK**
Found in **AT5G14910.1** in **TAIR_Arabidopsis**, Symbols: | heavy-metal-associated domain-containing protein | chr5:4823818-4825199 FORWARD

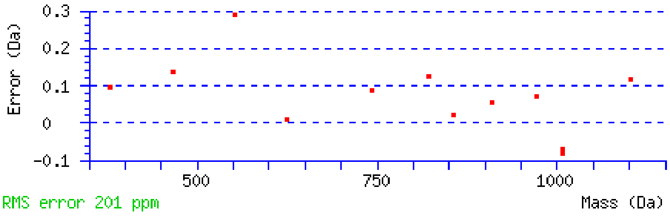
Match to Query 4563: 1286.626718 from(644.320635,2+) index(4609)
Title: Elution from: 42.019 to 42.019 scan no 5782 cid35.00 polarity:+
Data file 0-3_2.mgf

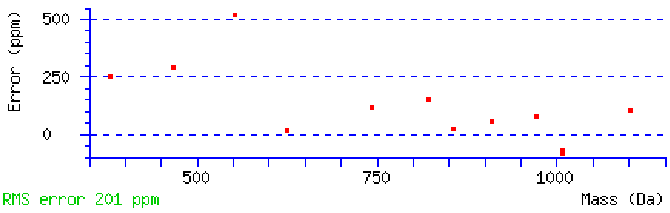
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1286.6276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 4.6e-006
Matches : 12/116 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							12
2	187.1225	94.0649					L	1215.6008	608.3040	1197.5772	599.2922	1197.5902	599.2987	11
3	317.1752	159.0912	299.1516	150.0794			Q	***1101.5197***	551.2635	1083.4961	542.2517	1083.5091	542.2582	10
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	D	***971.4670***	486.2372	953.4435	477.2254	953.4565	477.2319	9
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	I	***855.4431***	428.2252	837.4195	419.2134	837.4325	419.2199	8
6	663.3042	332.1558	645.2806	323.1440	645.2937	323.1505	D	***741.3620***	371.1846	723.3384	362.1728	723.3514	362.1793	7
7	721.3227	361.1650	703.2991	352.1532	703.3122	352.1597	G	***625.3380***	313.1726	607.3144	304.1608	607.3274	304.1673	6
8	**821.3882**	411.1977	803.3646	402.1859	803.3776	402.1924	V	567.3195	284.1634	549.2959	275.1516	549.3089	275.1581	5
9	**909.4172**	455.2123	891.3937	446.2005	891.4067	446.2070	S	***467.2540***	234.1307	449.2304	225.1189	449.2435	225.1254	4
10	1025.4542	513.2308	1007.4306	504.2190	1007.4437	504.2255	N	***379.2250***	190.1161	361.2014	181.1043			3
11	1139.5353	570.2713	1121.5117	561.2595	1121.5248	561.2660	L	263.1880	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ALQDIDGVSNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G14910.1

Score	Mr(calc)	Delta	Sequence
62.0	1286.6276	-0.0009	ALQDIDGVSNLK
14.3	1286.6277	-0.0010	SPKGSPKELSDK
13.1	1286.6276	-0.0009	KLANLDDGDIAK
5.6	1286.6276	-0.0009	RLPVDETSLDK
4.8	1286.6303	-0.0036	IAPRESNQAGVK
2.9	1286.6229	0.0038	SLLINLHSCSK
1.3	1286.6276	-0.0009	EIAEVANGVDKK
1.2	1286.6229	0.0038	LADCVGLTLGPR
0.9	1286.6303	-0.0036	VDPARLGREEK
0.6	1286.6276	-0.0009	QEVEKNGIKLD

Mascot: http://www.matrixscience.com/

AT5G15090.1

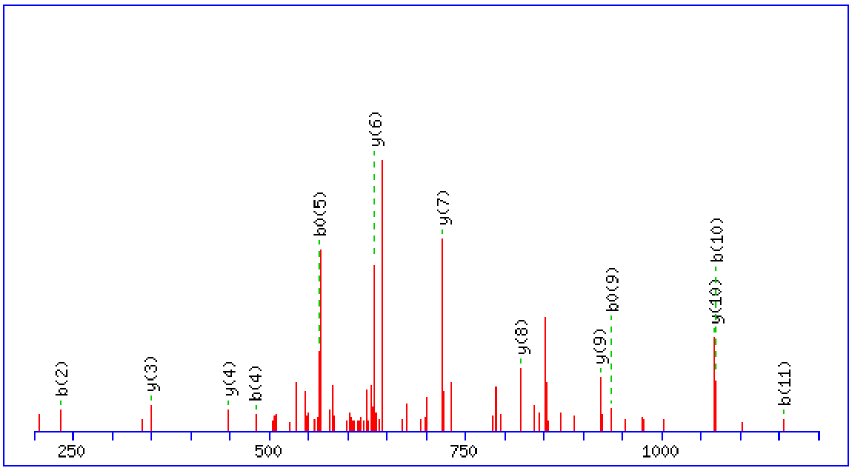
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFFTVSGEVDSK**
Found in **AT5G15090.1** in **TAIR_Arabidopsis**, Symbols: | porin, putative / voltage-dependent anion-selective channel protein, putative | chr5:4889644-4891392 REVERSE

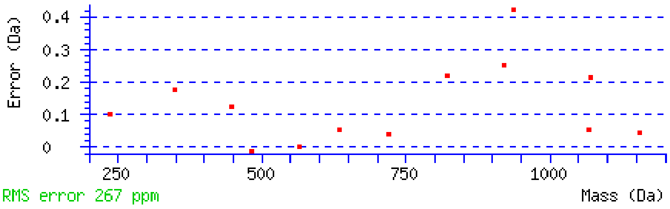
Match to Query 4904: 1301.614348 from(651.814450,2+) index(5620)
Title: Elution from: 50.368 to 50.368 scan no 7067 cid35.00 polarity:+
Data file D12h-3_1.mgf

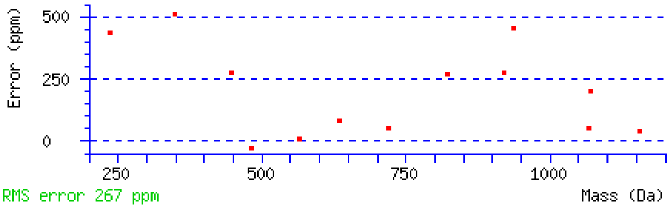
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1301.6140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 7.5e-006
Matches : 13/108 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							12
2	***235.1077***	118.0575	217.0972	109.0522	F	1215.5892	608.2982	1198.5626	599.7850	1197.5786	599.2930	11
3	382.1761	191.5917	364.1656	182.5864	F	***1068.5208***	534.7640	1051.4942	526.2508	1050.5102	525.7587	10
4	***483.2238***	242.1155	465.2132	233.1103	T	***921.4524***	461.2298	904.4258	452.7165	903.4418	452.2245	9
5	582.2922	291.6498	564.2817	282.6445	V	***820.4047***	410.7060	803.3781	402.1927	802.3941	401.7007	8
6	669.3243	335.1658	651.3137	326.1605	S	***721.3363***	361.1718	704.3097	352.6585	703.3257	352.1665	7
7	726.3457	363.6765	708.3352	354.6712	G	***634.3042***	317.6558	617.2777	309.1425	616.2937	308.6505	6
8	855.3883	428.1978	837.3777	419.1925	E	577.2828	289.1450	560.2562	280.6318	559.2722	280.1397	5
9	954.4567	477.7320	936.4462	468.7267	V	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6185	4
10	***1069.4837***	535.2455	1051.4731	526.2402	D	***349.1718***	175.0895	332.1452	166.5763	331.1612	166.0842	3
11	***1156.5157***	578.7615	1138.5051	569.7562	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SFFTVSGEVDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G15090.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.0	1301.6140	0.0004	SFFTVSGEVDSK
4.8	1301.6139	0.0004	KDYLYDGVDSK
0.2	1301.6108	0.0036	CVETRIYMSK

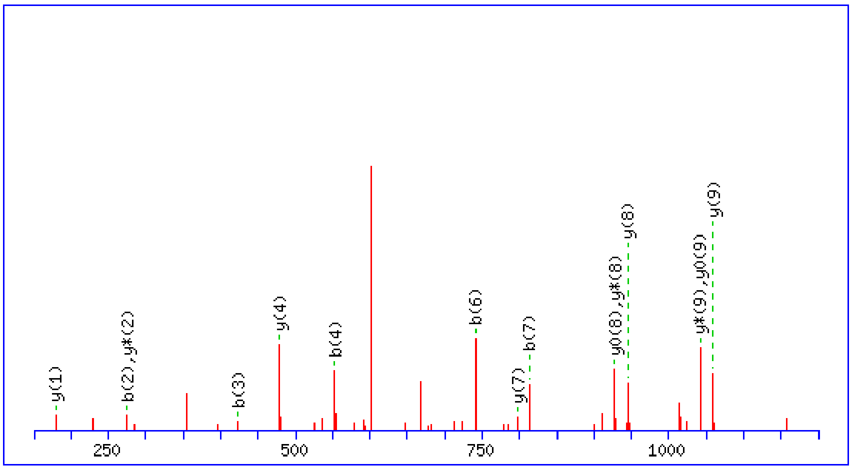
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RIFEGEALLR**
Found in **AT5G15200.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S9 (RPS9B) | chr5:4935127-4936337 REVERSE

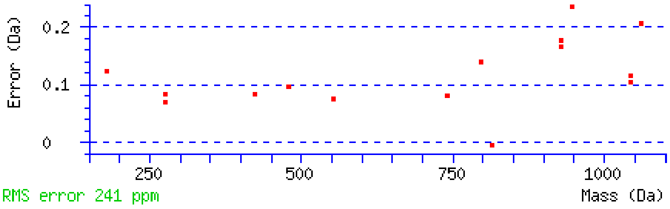
Match to Query 3938: 1218.628574 from(610.321563,2+) index(4609)
Title: Elution from: 44.339 to 44.339 scan no 5872 cid35.00 polarity:+
Data file D1d-2_1.mgf

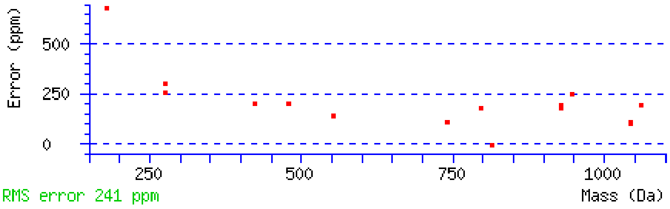
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1218.6297
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.7e-005
Matches : 17/94 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							10
2	***275.1776***	138.0925	257.1540	129.0807			I	**1059.5477**	530.2775	1041.5242	521.2657	1041.5372	521.2722	9
3	***423.2431***	212.1252	405.2195	203.1134			F	**945.4666**	473.2370	927.4431	464.2252	927.4561	464.2317	8
4	***553.2827***	277.1450	535.2591	268.1332	535.2721	268.1397	E	**797.4012**	399.2042	779.3776	390.1924	779.3906	390.1990	7
5	611.3012	306.1542	593.2776	297.1424	593.2906	297.1490	G	667.3616	334.1844	649.3380	325.1726	649.3510	325.1791	6
6	***741.3408***	371.1741	723.3172	362.1623	723.3303	362.1688	E	609.3431	305.1752	591.3195	296.1634	591.3325	296.1699	5
7	***813.3750***	407.1911	795.3514	398.1793	795.3644	398.1858	A	**479.3034**	240.1554	461.2799	231.1436			4
8	***927.4561***	464.2317	909.4325	455.2199	909.4455	455.2264	L	407.2693	204.1383	389.2457	195.1265			3
9	***1041.5372***	521.2722	1023.5136	512.2604	1023.5266	512.2669	L	293.1882	147.0977	275.1646	138.0859			2
10							R	**179.1071**	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RIFEGEALLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G15200.1

57.6	1218.6297	-0.0011	RIFEGEALLR
22.9	1218.6297	-0.0011	LRVDFTPSLR
21.4	1218.6275	0.0011	QTKDGSLGKLR
18.2	1218.6250	0.0036	RLGLWGMLTR
17.2	1218.6297	-0.0011	RFEIIEGIAR
16.8	1218.6301	-0.0016	RNLVGRSELR
16.2	1218.6270	0.0015	ASLFGEALAISK
13.1	1218.6275	0.0011	RLETQLSSLR
9.7	1218.6301	-0.0016	IRVTVARNDR
9.2	1218.6297	-0.0011	RLVDSTLPFR

AT5G15200.2

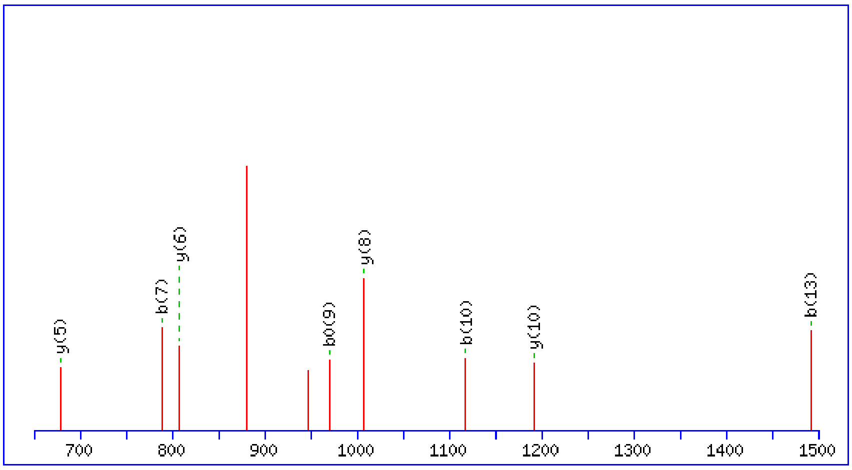
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDYVLALTVENFLER**
Found in **AT5G15200.2** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S9 (RPS9B) | chr5:4935605-4936337 REVERSE

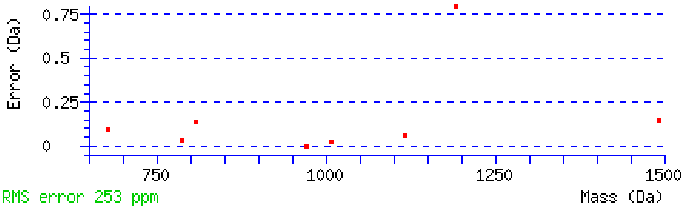
Match to Query 8579: 1793.954782 from(897.984667,2+) index(11282)
Title: Elution from: 124.559 to 124.559 scan no 17107 cid35.00 polarity:+
Data file D1d-2_1.mgf

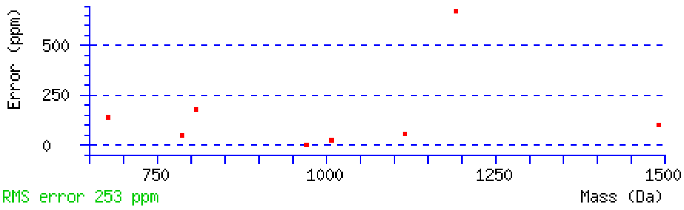
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1793.9563
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00058
Matches : 8/144 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**15**
2	229.1183	115.0628			211.1077	106.0575	**D**	1681.8796	841.4434	1664.8530	832.9301	1663.8690	832.4381	**14**
3	392.1816	196.5944			374.1710	187.5892	**Y**	1566.8526	783.9299	1549.8261	775.4167	1548.8421	774.9247	**13**
4	491.2500	246.1287			473.2395	237.1234	**V**	1403.7893	702.3983	1386.7627	693.8850	1385.7787	693.3930	**12**
5	604.3341	302.6707			586.3235	293.6654	**L**	1304.7209	652.8641	1287.6943	644.3508	1286.7103	643.8588	**11**
6	675.3712	338.1892			657.3606	329.1840	**A**	***1191.6368***	596.3220	1174.6103	587.8088	1173.6262	587.3168	**10**
7	***788.4553***	394.7313			770.4447	385.7260	**L**	1120.5997	560.8035	1103.5732	552.2902	1102.5891	551.7982	**9**
8	889.5029	445.2551			871.4924	436.2498	**T**	***1007.5156***	504.2615	990.4891	495.7482	989.5051	495.2562	**8**
9	988.5714	494.7893			970.5608	485.7840	**V**	906.4680	453.7376	889.4414	445.2243	888.4574	444.7323	**7**
10	***1117.6140***	559.3106			1099.6034	550.3053	**E**	***807.3995***	404.2034	790.3730	395.6901	789.3890	395.1981	**6**
11	1231.6569	616.3321	1214.6303	607.8188	1213.6463	607.3268	**N**	***678.3570***	339.6821	661.3304	331.1688	660.3464	330.6768	**5**
12	1378.7253	689.8663	1361.6987	681.3530	1360.7147	680.8610	**F**	564.3140	282.6606	547.2875	274.1474	546.3035	273.6554	**4**
13	***1491.8094***	746.4083	1474.7828	737.8950	1473.7988	737.4030	**L**	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	**3**
14	1620.8520	810.9296	1603.8254	802.4163	1602.8414	801.9243	**E**	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LDYVLALTVENFLER

AT5G15200.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.4	1793.9563	-0.0015	LDYVLALTVENFLER
0.4	1793.9557	-0.0009	ESSGVMSLSSKKAGLVSK

AT5G15450.1

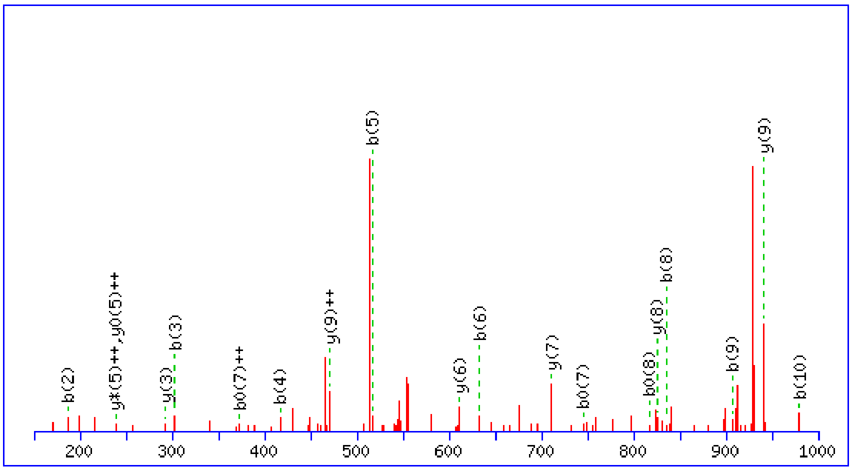
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIDLVDEAAAK**
Found in **AT5G15450.1** in **TAIR_Arabidopsis**, Symbols: APG6, CLPB3, CLPB-P | APG6/CLPB-P/CLPB3 (ALBINO AND PALE GREEN 6); ATP binding / ATPase | chr5:5014402-5018258 REVERSE

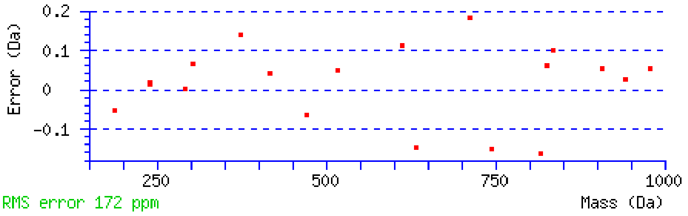
Match to Query 3082: 1126.552566 from(564.283559,2+) index(3794)
Title: Elution from: 38.627 to 38.627 scan no 4839 cid35.00 polarity:+
Data file D12h-2_2.mgf

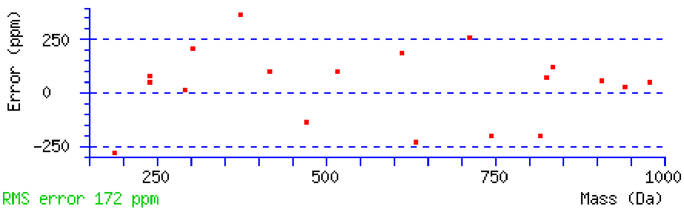
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1126.5514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0056
Matches : 19/88 fragment ions using 65 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244			**A**							**11**
2	***187.1225***	94.0649			**I**	1055.5246	528.2659	1037.5010	519.2541	1037.5140	519.2606	**10**
3	***303.1465***	152.0769	285.1359	143.0716	**D**	**941.4435**	471.2254	923.4199	462.2136	923.4329	462.2201	**9**
4	***417.2276***	209.1174	399.2170	200.1122	**L**	**825.4195**	413.2134	807.3959	404.2016	807.4089	404.2081	**8**
5	***517.2930***	259.1502	499.2825	250.1449	**V**	**711.3384**	356.1728	693.3148	347.1610	693.3278	347.1675	**7**
6	***633.3170***	317.1622	615.3065	308.1569	**D**	**611.2729**	306.1401	593.2493	297.1283	593.2624	297.1348	**6**
7	763.3567	382.1820	745.3461	373.1767	**E**	495.2489	248.1281	477.2254	239.1163	477.2384	239.1228	**5**
8	***835.3908***	418.1990	817.3802	409.1938	**A**	365.2093	183.1083	347.1857	174.0965			**4**
9	***907.4250***	454.2161	889.4144	445.2108	**A**	**293.1752**	147.0912	275.1516	138.0794			**3**
10	***979.4591***	490.2332	961.4485	481.2279	**A**	221.1410	111.0741	203.1174	102.0624			**2**
11					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of AIDLVDEAAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G15450.1

Score	Mr(calc)	Delta	Sequence
29.2	1126.5514	0.0012	AIDLVDEAAAK
7.8	1126.5514	0.0012	VSPEVSVVDGK
7.3	1126.5523	0.0003	ICPGLPLAMK
6.6	1126.5514	0.0012	LEGLEDALQK

AT5G15530.1

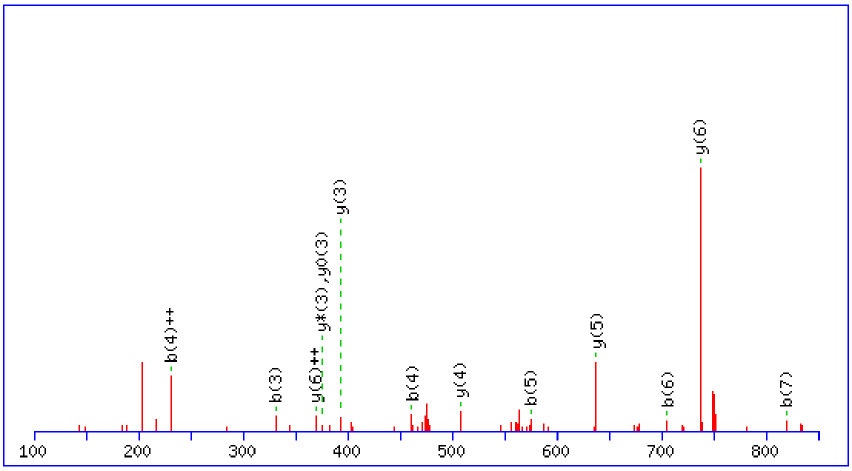
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIVELELK**
Found in **AT5G15530.1** in **TAIR_Arabidopsis**, Symbols: BCCP2, CAC1-B | BCCP2 (biotin carboxyl carrier protein 2); biotin binding | chr5:5038958-5040440 FORWARD

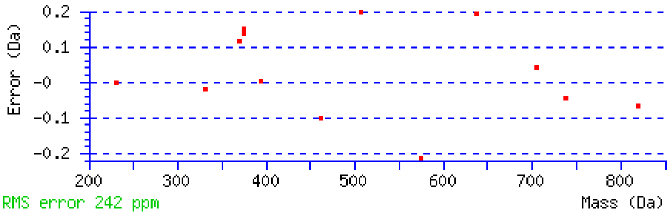
Match to Query 2123: 966.512464 from(484.263508,2+) index(5811)
Title: Elution from: 51.519 to 51.519 scan no 7379 cid35.00 polarity:+
Data file 0-3_2.mgf

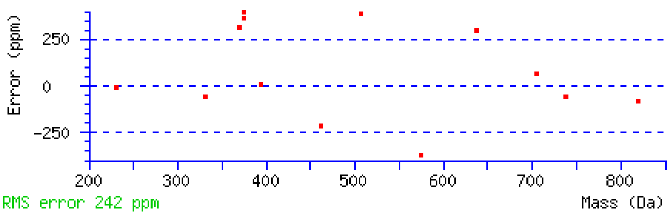
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 966.5116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00045
Matches : 14/66 fragment ions using 26 most intense peaks (help)

#	b	b⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	117.0313	59.0193	99.0207	50.0140	D							8
2	***231.1124***	116.0598	213.1018	107.0545	I	851.4949	426.2511	833.4713	417.2393	833.4843	417.2458	7
3	***331.1778***	166.0925	313.1672	157.0873	V	**737.4138**	369.2105	719.3902	360.1987	719.4032	360.2052	6
4	***461.2174***	231.1124	443.2069	222.1071	E	**637.3483**	319.1778	619.3247	310.1660	619.3378	310.1725	5
5	***575.2985***	288.1529	557.2880	279.1476	L	**507.3087**	254.1580	489.2851	245.1462	489.2981	245.1527	4
6	***705.3382***	353.1727	687.3276	344.1674	E	**393.2276**	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	***819.4193***	410.2133	801.4087	401.2080	L	263.1880	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DIVELELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.1	966.5116	0.0009	DIVELELK

AT5G15530.1

22.5	966.5116	0.0009	DVLELIEK
7.0	966.5116	0.0009	LEVEVEIK
2.8	966.5116	0.0009	DDLLLLEK
1.8	966.5143	-0.0018	ITLSKHEK
1.4	966.5116	0.0009	ELEVVLEK

AT5G15650.1

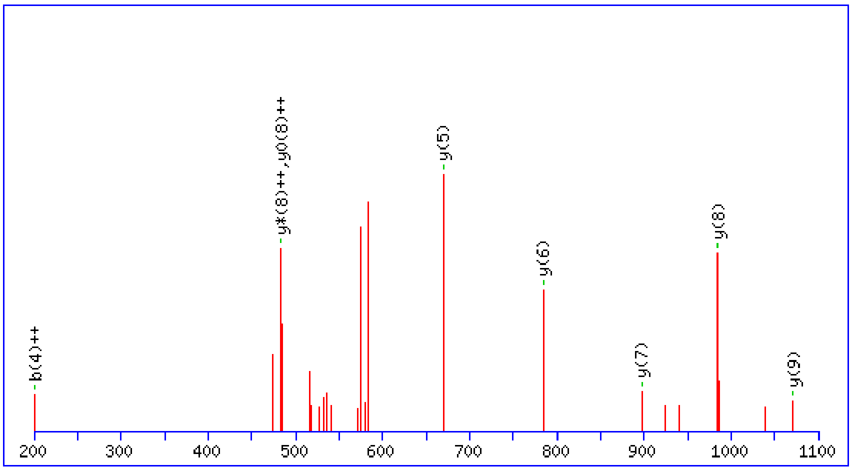
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSLDPYFDK**
Found in **AT5G15650.1** in **TAIR_Arabidopsis**, Symbols: RGP2 | RGP2 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 2); alpha-1,4-glucan-protein synthase (UDP-forming) | chr5:5092206-5094096 FORWARD

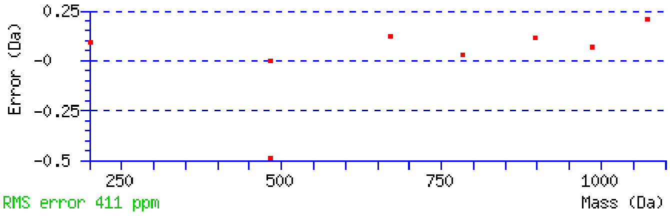
Match to Query 3815: 1183.573978 from(592.794265,2+) index(5600)
Title: Elution from: 49.301 to 49.301 scan no 7140 cid35.00 polarity:+
Data file D6h-3_3.mgf

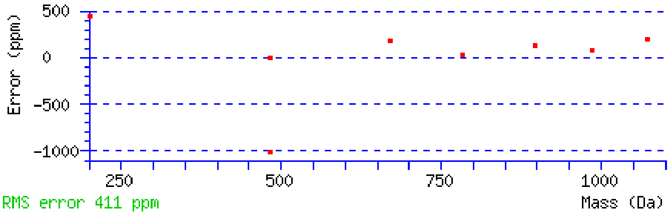
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1183.5761
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00012
Matches : 9/86 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							10
2	201.1234	101.0653	183.1128	92.0600	S	***1071.4993***	536.2533	1054.4728	527.7400	1053.4888	527.2480	9
3	288.1554	144.5813	270.1448	135.5761	S	***984.4673***	492.7373	967.4407	484.2240	966.4567	483.7320	8
4	401.2395	201.1234	383.2289	192.1181	L	***897.4353***	449.2213	880.4087	440.7080	879.4247	440.2160	7
5	516.2664	258.6368	498.2558	249.6316	D	***784.3512***	392.6792	767.3246	384.1660	766.3406	383.6740	6
6	613.3192	307.1632	595.3086	298.1579	P	***669.3243***	335.1658	652.2977	326.6525	651.3137	326.1605	5
7	776.3825	388.6949	758.3719	379.6896	Y	572.2715	286.6394	555.2449	278.1261	554.2609	277.6341	4
8	923.4509	462.2291	905.4403	453.2238	F	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
9	1038.4779	519.7426	1020.4673	510.7373	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LSSLDPYFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G15650.1

Score	Mr(calc)	Delta	Sequence
43.7	1183.5761	-0.0021	LSSLDPYFDK
2.4	1183.5768	-0.0028	VAELAGHCTAR
2.2	1183.5736	0.0004	DWVMYFPVK
0.3	1183.5729	0.0010	CILEMIFSR

AT5G15890.1

Mascot Search Results

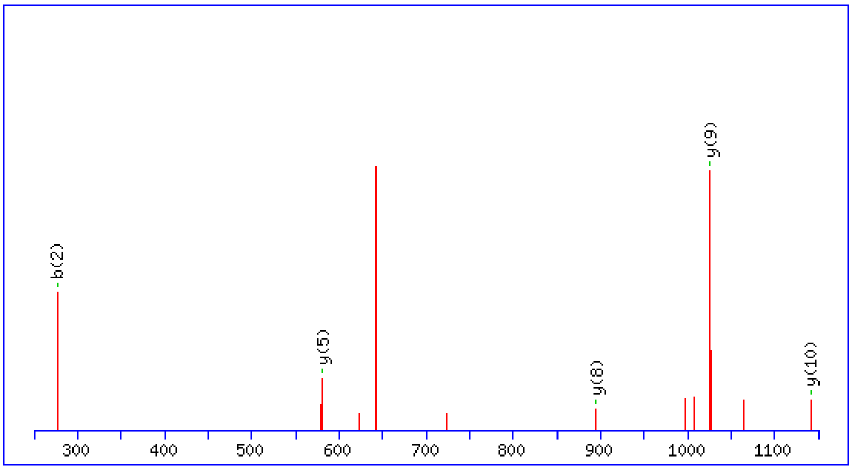
Peptide View

MS/MS Fragmentation of **RNETIPEADLK**
Found in **AT5G15890.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G15900.1); similar to hypothetical protein [Cleome spinosa] (GB:ABD96865.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253) | chr5:51876

Match to Query 5134: 1300.621070 from(651.317811,2+) index(5396)
Title: Elution from: 47.697 to 47.697 scan no 6749 cid35.00 polarity:+
Data file D6h-1_1.mgf

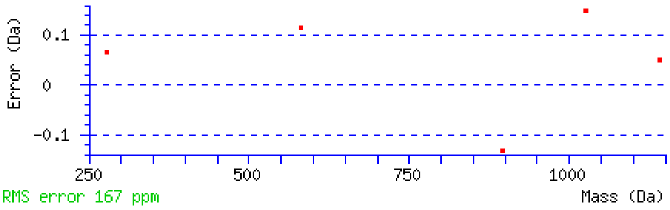
Click mouse within plot area to zoom in by factor of two about that point

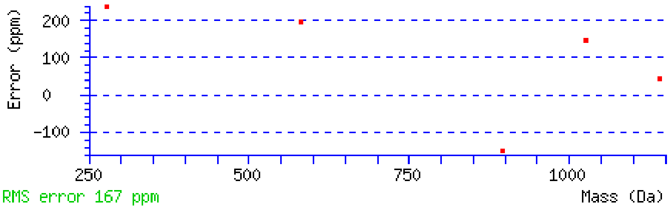
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1300.6199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.012
Matches : 5/112 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							11
2	277.1335	139.0704	259.1099	130.0586			N	***1141.5380***	571.2726	1123.5144	562.2608	1123.5274	562.2673	10
3	407.1732	204.0902	389.1496	195.0784	389.1626	195.0849	E	***1025.5010***	513.2541	1007.4774	504.2423	1007.4904	504.2488	9
4	509.2179	255.1126	491.1943	246.1008	491.2073	246.1073	T	***895.4613***	448.2343	877.4378	439.2225	877.4508	439.2290	8
5	623.2990	312.1531	605.2754	303.1413	605.2884	303.1478	I	793.4166	397.2120	775.3930	388.2002	775.4061	388.2067	7
6	721.3488	361.1780	703.3252	352.1662	703.3382	352.1727	P	679.3355	340.1714	661.3119	331.1596	661.3250	331.1661	6
7	851.3884	426.1978	833.3648	417.1860	833.3778	417.1926	E	***581.2857***	291.1465	563.2621	282.1347	563.2752	282.1412	5
8	923.4225	462.2149	905.3990	453.2031	905.4120	453.2096	A	451.2461	226.1267	433.2225	217.1149	433.2355	217.1214	4
9	1039.4465	520.2269	1021.4229	511.2151	1021.4360	511.2216	D	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
10	1153.5276	577.2674	1135.5040	568.2557	1135.5171	568.2622	L	263.1880	132.0976	245.1644	123.0858			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RNETIPEADLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G15890.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.7	1300.6199	0.0011	RNETIPEADLK
18.6	1300.6226	-0.0015	RDDTLLHSAVR
5.7	1300.6222	-0.0011	VSSYQTGYIIR
4.2	1300.6248	-0.0038	QYHVNSLAVPR
0.8	1300.6226	-0.0015	SNTRLPPEVNR

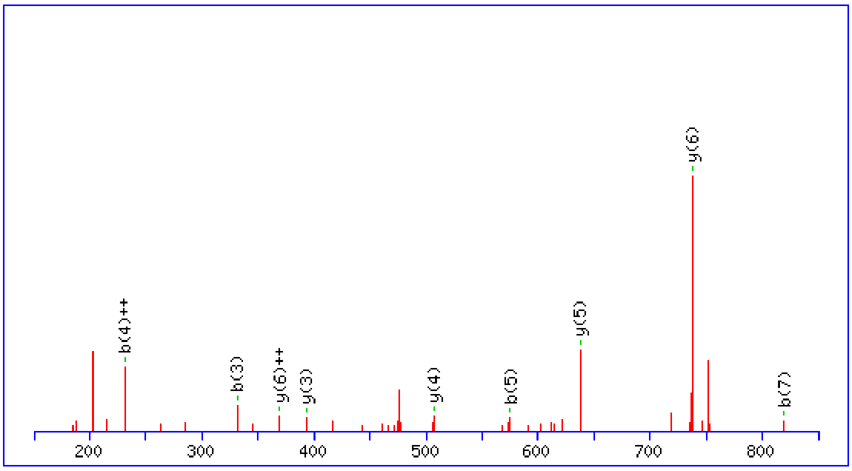
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIVEIIQK**
Found in **AT5G15920.1** in **TAIR_Arabidopsis**, Symbols: | structural maintenance of chromosomes (SMC) family protein (MSS2) | chr5:5196213-5199562 FORWARD

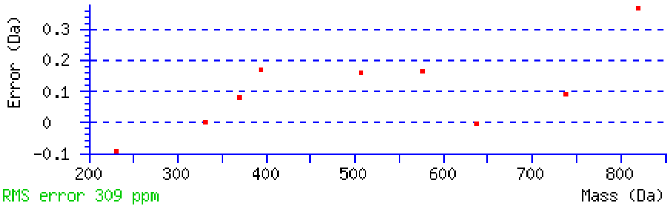
Match to Query 2326: 966.525172 from(484.269862,2+) index(6162)
Title: Elution from: 54.340 to 54.340 scan no 7771 cid35.00 polarity:+
Data file C7-2_1.mgf

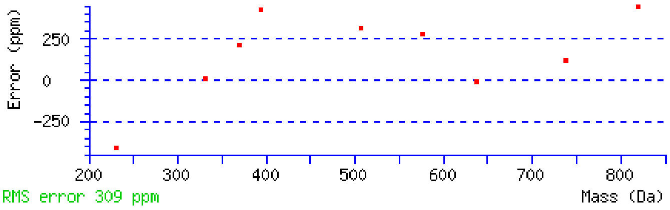
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 966.5246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0022
Matches : 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							8
2	***231.1124***	116.0598			213.1018	107.0545	I	851.5079	426.2576	833.4843	417.2458	833.4973	417.2523	7
3	***331.1778***	166.0925			313.1672	157.0873	V	***737.4268***	369.2170	719.4032	360.2052	719.4162	360.2118	6
4	461.2174	231.1124			443.2069	222.1071	E	***637.3613***	319.1843	619.3378	310.1725	619.3508	310.1790	5
5	***575.2985***	288.1529			557.2880	279.1476	I	***507.3217***	254.1645	489.2981	245.1527			4
6	689.3796	345.1935			671.3691	336.1882	I	***393.2406***	197.1239	375.2170	188.1122			3
7	***819.4323***	410.2198	801.4087	401.2080	801.4217	401.2145	Q	279.1595	140.0834	261.1359	131.0716			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DIVEIIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.4	966.5246	0.0006	DIVEIIQK

AT5G15920.1

32.4	966.5246	0.0006	DIVELQLK
25.3	966.5246	0.0006	NLVLEELK
21.3	966.5246	0.0006	NLIDELIK
14.4	966.5273	-0.0021	LNVLKDPR
13.4	966.5246	0.0006	EVIIDQIK
12.9	966.5273	-0.0021	NLLQGGPKK
11.2	966.5246	0.0006	AEALAILEK
9.3	966.5246	0.0006	INIELVEK
6.2	966.5246	0.0006	NLEDLIIK

AT5G15970.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SISDAAVGGVNFVK**
Found in **AT5G15970.1** in **TAIR_Arabidopsis**, Symbols: COR6.6, KIN2 | KIN2 (COLD-RESPONSIVE 6.6) | chr5:5211969-5212444 FORWARD

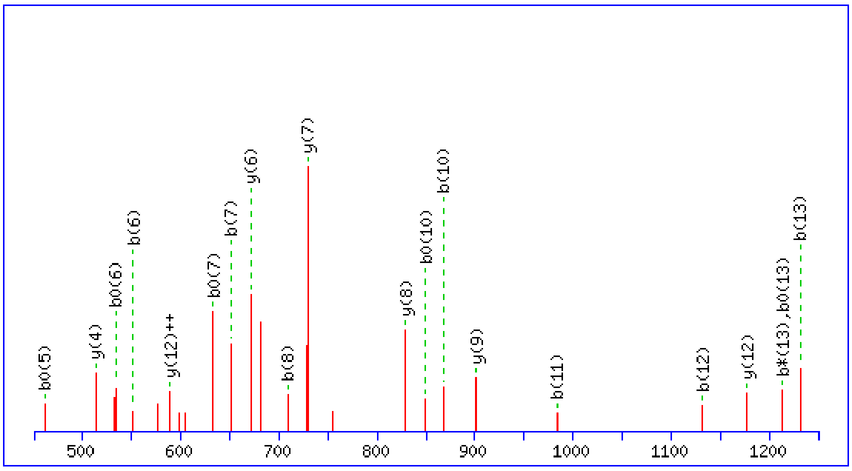
Match to Query 5207: 1378.667362 from(690.340957,2+) index(5676)
Title: Elution from: 51.586 to 51.586 scan no 7184 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1250 Da Full range

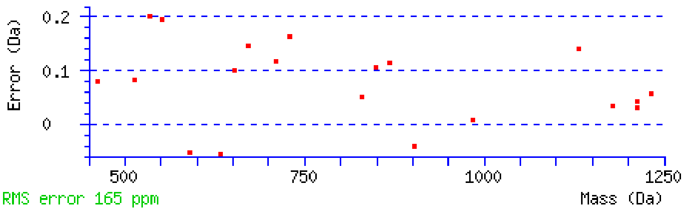
Label all possible matches ○ Label matches used for scoring ●

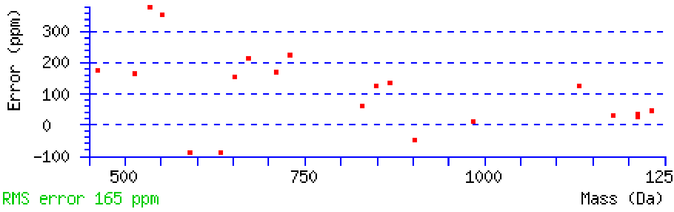
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1378.6669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 1.3e-006
Matches : 20/116 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							14
2	203.1174	102.0624			185.1069	93.0571	I	1291.6451	646.3262	1273.6215	637.3144	1273.6345	637.3209	13
3	291.1465	146.0769			273.1359	137.0716	S	***1177.5640***	589.2856	1159.5404	580.2738	1159.5534	580.2804	12
4	407.1705	204.0889			389.1599	195.0836	D	1089.5349	545.2711	1071.5114	536.2593	1071.5244	536.2658	11
5	479.2046	240.1060			461.1941	231.1007	A	973.5110	487.2591	955.4874	478.2473			10
6	***551.2388***	276.1230			533.2282	267.1177	A	***901.4768***	451.2420	883.4532	442.2303			9
7	***651.3042***	326.1558			633.2937	317.1505	V	***829.4427***	415.2250	811.4191	406.2132			8
8	***709.3227***	355.1650			691.3122	346.1597	G	***729.3772***	365.1922	711.3536	356.1805			7
9	767.3412	384.1743			749.3307	375.1690	G	***671.3587***	336.1830	653.3351	327.1712			6
10	***867.4067***	434.2070			849.3961	425.2017	V	613.3402	307.1737	595.3166	298.1620			5
11	***983.4437***	492.2255	965.4201	483.2137	965.4331	483.2202	N	***513.2748***	257.1410	495.2512	248.1292			4
12	***1131.5091***	566.2582	1113.4855	557.2464	1113.4986	557.2529	F	397.2378	199.1225	379.2142	190.1107			3
13	***1231.5746***	616.2909	1213.5510	607.2791	1213.5640	607.2856	V	249.1723	125.0898	231.1487	116.0780			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SISDAAVGGVNFVK

AT5G15970.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.7	1378.6669	0.0005	SISDAAVGGVNFVK
13.4	1378.6669	0.0005	ATDLNQGVVYGVK
4.3	1378.6647	0.0027	AENGSKSKSIDVK
3.0	1378.6678	-0.0004	LRICFVEAMPK
2.6	1378.6669	0.0005	QAADQVDKFLTK
1.5	1378.6669	0.0005	GLPPESSAEHIVK
0.1	1378.6673	0.0000	NIRGTSGNKDAVK

AT5G16050.1

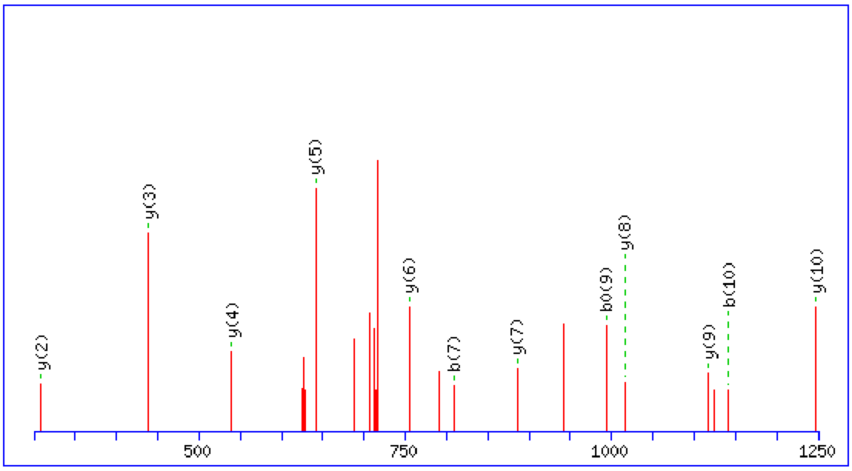
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVETEELTVEER**
Found in **AT5G16050.1** in **TAIR_Arabidopsis**, Symbols: GF14 UPSILON, GRF5 | GRF5 (GENERAL REGULATORY FACTOR 5); protein phosphorylated amino acid binding | chr5:5244011-5245405 REVERSE

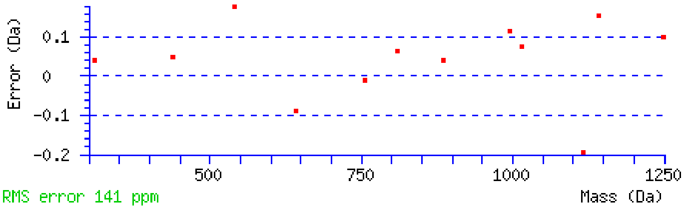
Match to Query 5758: 1448.641330 from(725.327941,2+) index(3131)
Title: Elution from: 30.907 to 30.907 scan no 3890 cid35.00 polarity:+
Data file 0-1_3.mgf

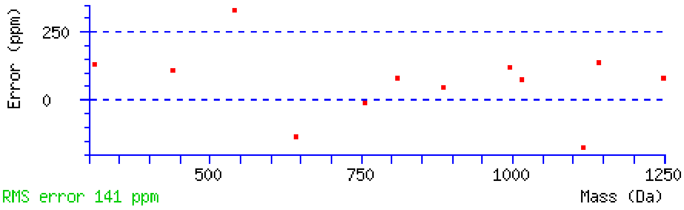
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1448.6441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 4.4e-009
Matches : 12/108 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							12
2	203.1174	102.0624	185.1069	93.0571	V	1347.6067	674.3070	1329.5831	665.2952	1329.5961	665.3017	11
3	333.1571	167.0822	315.1465	158.0769	E	***1247.5412***	624.2742	1229.5176	615.2624	1229.5306	615.2690	10
4	435.2018	218.1045	417.1912	209.0992	T	***1117.5016***	559.2544	1099.4780	550.2426	1099.4910	550.2491	9
5	565.2414	283.1243	547.2308	274.1191	E	***1015.4569***	508.2321	997.4333	499.2203	997.4463	499.2268	8
6	695.2810	348.1442	677.2705	339.1389	E	***885.4172***	443.2123	867.3937	434.2005	867.4067	434.2070	7
7	**809.3621**	405.1847	791.3516	396.1794	L	***755.3776***	378.1924	737.3540	369.1807	737.3670	369.1872	6
8	911.4068	456.2071	893.3963	447.2018	T	***641.2965***	321.1519	623.2729	312.1401	623.2859	312.1466	5
9	1011.4723	506.2398	993.4617	497.2345	V	***539.2518***	270.1295	521.2282	261.1177	521.2412	261.1243	4
10	**1141.5119**	571.2596	1123.5014	562.2543	E	***439.1863***	220.0968	421.1628	211.0850	421.1758	211.0915	3
11	1271.5516	636.2794	1253.5410	627.2741	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
12					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TVETEELTVEER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G16050.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.8	1448.6441	-0.0027	TVETEELTVEER
8.2	1448.6447	-0.0034	THRCAQIKEER
6.4	1448.6386	0.0027	VLHSEREEFER
3.7	1448.6416	-0.0003	ELVVYPADEPMR
0.6	1448.6386	0.0027	STIQHFVNEAER
0.4	1448.6386	0.0027	EADAIWDAIDRR

AT5G16070.1

MATRIX SCIENCE Mascot Search Results

Peptide View

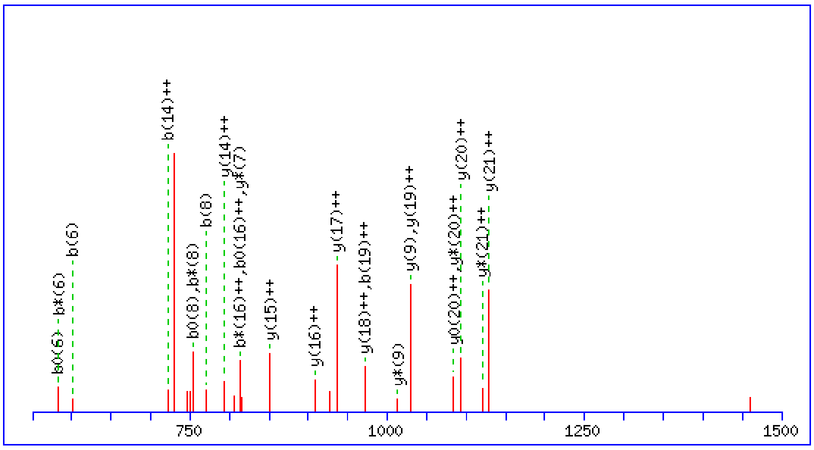
MS/MS Fragmentation of **TLAENAGLDTQDVIISLTSEHDK**
Found in **AT5G16070.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr5:5247552-5251053 REVERSE

Match to Query 10344: 2469.222789 from(824.081539,3+) index(9321)
Title: Elution from: 84.104 to 84.104 scan no 12674 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1500 Da Full range

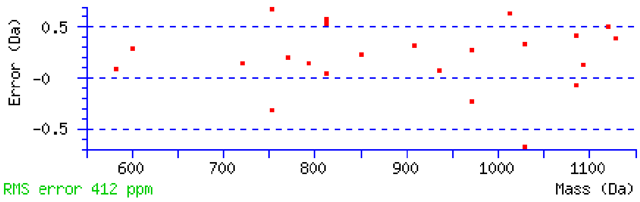
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

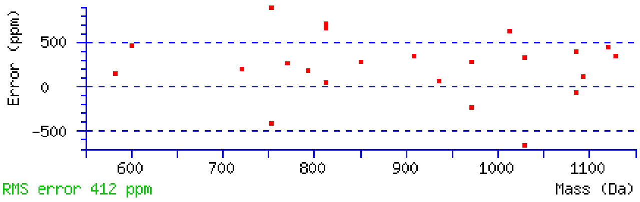


Monoisotopic mass of neutral peptide Mr(calc): 2469.2235
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 1.8e-005
Matches : 24/254 fragment ions using 22 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311			84.0444	42.5258	T							23
2	215.1390	108.0731			197.1285	99.0679	L	2369.1831	1185.0952	2352.1565	1176.5819	2351.1725	1176.0899	22
3	286.1761	143.5917			268.1656	134.5864	A	2256.0990	1128.5531	2239.0725	1120.0399	2238.0884	1119.5479	21
4	415.2187	208.1130			397.2082	199.1077	E	2185.0619	1093.0346	2168.0353	1084.5213	2167.0513	1084.0293	20
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	N	2056.0193	1028.5133	2038.9928	1020.0000	2038.0087	1019.5080	19
6	**600.2988**	300.6530	583.2722	292.1397	582.2882	291.6477	A	1941.9764	971.4918	1924.9498	962.9786	1923.9658	962.4865	18
7	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	G	1870.9393	935.9733	1853.9127	927.4600	1852.9287	926.9680	17
8	**770.4043**	385.7058	753.3777	377.1925	752.3937	376.7005	L	1813.9178	907.4625	1796.8913	898.9493	1795.9072	898.4573	16
9	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	D	1700.8337	850.9205	1683.8072	842.4072	1682.8232	841.9152	15
10	986.4789	493.7431	969.4524	485.2298	968.4684	484.7378	T	1585.8068	793.4070	1568.7802	784.8938	1567.7962	784.4018	14
11	1114.5375	557.7724	1097.5109	549.2591	1096.5269	548.7671	Q	1484.7591	742.8832	1467.7326	734.3699	1466.7485	733.8779	13
12	1229.5644	615.2859	1212.5379	606.7726	1211.5539	606.2806	D	1356.7005	678.8539	1339.6740	670.3406	1338.6900	669.8486	12
13	1328.6329	664.8201	1311.6063	656.3068	1310.6223	655.8148	V	1241.6736	621.3404	1224.6470	612.8272	1223.6630	612.3352	11
14	1441.7169	**721.3621**	1424.6904	712.8488	1423.7064	712.3568	I	1142.6052	571.8062	1125.5786	563.2930	1124.5946	562.8009	10
15	1554.8010	777.9041	1537.7744	769.3909	1536.7904	768.8988	I	1029.5211	515.2642	1012.4946	506.7509	1011.5105	506.2589	9
16	1641.8330	821.4201	1624.8065	812.9069	1623.8224	812.4149	S	916.4371	458.7222	899.4105	450.2089	898.4265	449.7169	8
17	1754.9171	877.9622	1737.8905	869.4489	1736.9065	868.9569	L	829.4050	415.2061	812.3785	406.6929	811.3945	406.2009	7
18	1855.9648	928.4860	1838.9382	919.9727	1837.9542	919.4807	T	716.3210	358.6641	699.2944	350.1508	698.3104	349.6588	6
19	1942.9968	**972.0020**	1925.9702	963.4888	1924.9862	962.9967	S	615.2733	308.1403	598.2467	299.6270	597.2627	299.1350	5
20	2072.0394	1036.5233	2055.0128	1028.0100	2054.0288	1027.5180	E	528.2413	264.6243	511.2147	256.1110	510.2307	255.6190	4
21	2209.0983	1105.0528	2192.0717	1096.5395	2191.0877	1096.0475	H	399.1987	200.1030	382.1721	191.5897	381.1881	191.0977	3
22	2324.1252	1162.5663	2307.0987	1154.0530	2306.1147	1153.5610	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
23							K	147.1128	74.0600	130.0863	65.5468			1

AT5G16070.1





NCBI **BLAST** search of TLAENAGLDTQDVIISLTSEHDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.8	2469.2235	-0.0007	TLAENAGLDTQDVIISLTSEHDK
7.2	2469.2284	-0.0056	IVSLLEDTKPKTHMDFGYTMK
5.5	2469.2284	-0.0056	IVSLLEDTKPKTHMDFGYTMK
0.0	2469.2288	-0.0060	DQVYWIPPPDNAGSSKDAGIAIR

Mascot: http://www.matrixscience.com/

AT5G16130.1

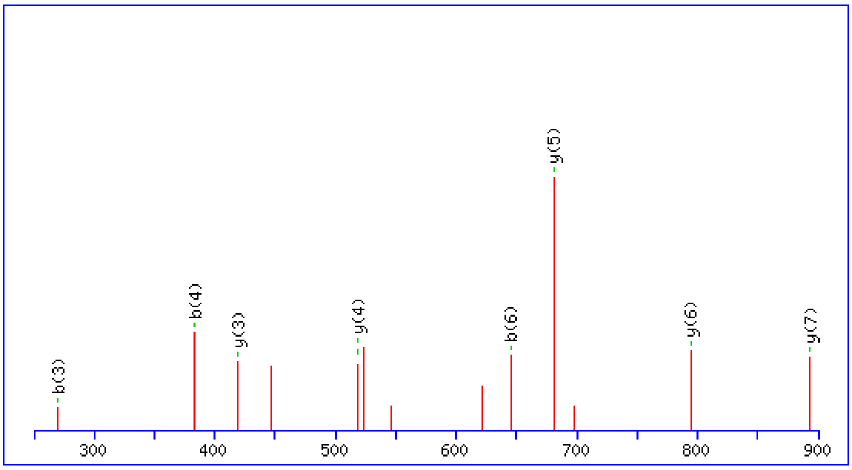
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVVIYVPFR**
Found in **AT5G16130.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S7 (RPS7C) | chr5:5268987-5269915 FORWARD

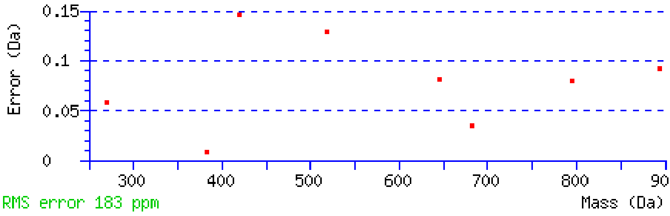
Match to Query 2942: 1062.623554 from(532.319053,2+) index(7269)
Title: Elution from: 64.786 to 64.786 scan no 9498 cid35.00 polarity:+
Data file C7-1_3.mgf

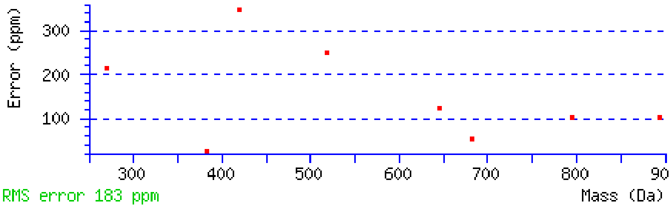
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1062.6226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 4.4e-005
Matches : 8/48 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	72.0444	36.5258	A					9
2	171.1128	86.0600	V	992.5928	496.8000	975.5662	488.2867	8
3	**270.1812**	135.5942	V	***893.5244***	447.2658	876.4978	438.7525	7
4	**383.2653**	192.1363	I	***794.4559***	397.7316	777.4294	389.2183	6
5	546.3286	273.6679	Y	***681.3719***	341.1896	664.3453	332.6763	5
6	**645.3970**	323.2022	V	***518.3085***	259.6579	501.2820	251.1446	4
7	742.4498	371.7285	P	***419.2401***	210.1237	402.2136	201.6104	3
8	889.5182	445.2627	F	322.1874	161.5973	305.1608	153.0840	2
9			R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of AVVIYVPFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.6	1062.6226	0.0010	AVVIYVPFR

AT5G16130.1

0.3	1062.6219	0.0016	VISMVRKSK

Mascot: http://www.matrixscience.com/

AT5G16400.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQDMVFLK**
Found in **AT5G16400.1** in **TAIR_Arabidopsis**, Symbols: TRXF2, ATF2 | ATF2/TRXF2 (THIOREDOXIN F2); thiol-disulfide exchange intermediate | chr5:5363908-5365252 REVERSE

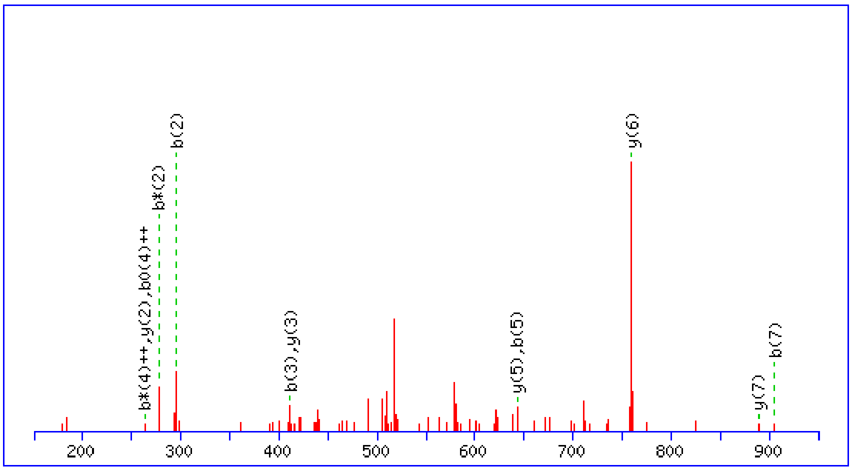
Match to Query 3124: 1052.488208 from(527.251380,2+) index(6069)
Title: Elution from: 53.022 to 53.022 scan no 7655 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

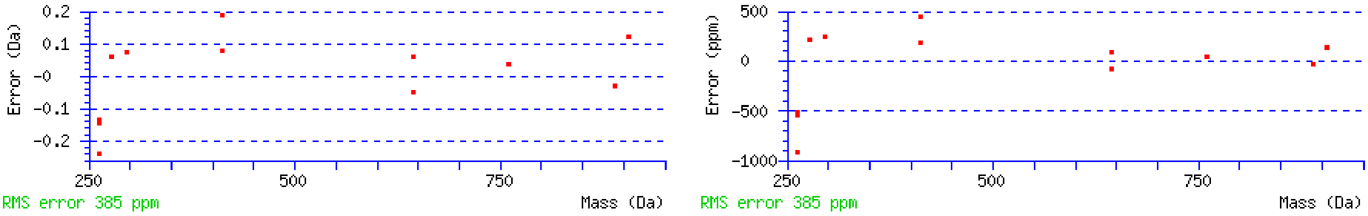
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1052.4861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27  Expect: 0.013
Matches : 12/68 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	165.0676	83.0375					Y							8
2	***295.1203***	148.0638	277.0967	139.0520			Q	***889.4330***	445.2201	871.4094	436.2084	871.4225	436.2149	7
3	***411.1443***	206.0758	393.1207	197.0640	393.1337	197.0705	D	***759.3804***	380.1938	741.3568	371.1820	741.3698	371.1885	6
4	543.1818	272.0945	525.1582	263.0827	525.1712	263.0892	M	***643.3564***	322.1818	625.3328	313.1700			5
5	***643.2472***	322.1273	625.2237	313.1155	625.2367	313.1220	V	511.3189	256.1631	493.2953	247.1513			4
6	791.3127	396.1600	773.2891	387.1482	773.3021	387.1547	F	***411.2534***	206.1303	393.2298	197.1186			3
7	***905.3938***	453.2005	887.3702	444.1887	887.3832	444.1952	L	***263.1880***	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of YQDMVFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.3	1052.4861	0.0021	YQDMVFLK

AT5G16400.1

6.9	1052.4908	-0.0026	YEYTVLEK
6.6	1052.4899	-0.0017	SKAMMARTK
5.0	1052.4861	0.0021	IFMFNDLK
4.2	1052.4899	-0.0017	SKAMMARTK
4.1	1052.4861	0.0021	FMKDFDIK
3.1	1052.4913	-0.0030	YTTKEKDR
2.1	1052.4865	0.0017	SFNKMQLR
0.5	1052.4881	0.0001	MVMMKKMK
0.3	1052.4861	0.0021	MLYPSFGTK

AT5G16570.1

Mascot Search Results

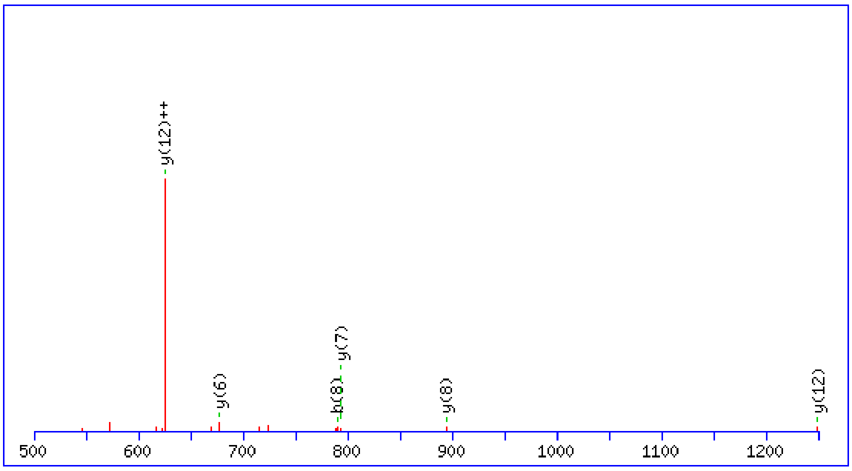
Peptide View

MS/MS Fragmentation of **TLPGPVTDPSQLPK**
Found in **AT5G16570.1** in **TAIR_Arabidopsis**, Symbols: GLN1;4 | GLN1;4 (Glutamine synthetase 1;4); glutamate-ammonia ligase | chr5:5421901-5424526 REVERSE

Match to Query 6331: 1464.741400 from(733.377976,2+) index(5378)
Title: Elution from: 47.074 to 47.074 scan no 6680 cid35.00 polarity:+
Data file D1d-3_1.mgf

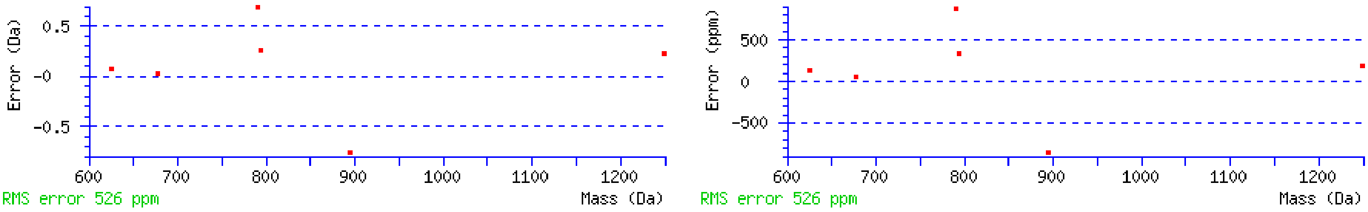
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1464.7401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.018
Matches : 6/128 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							14
2	217.1331	109.0702			199.1225	100.0649	L	1363.7026	682.3549	1345.6790	673.3432	1345.6921	673.3497	13
3	315.1829	158.0951			297.1723	149.0898	P	***1249.6215***	625.3144	1231.5979	616.3026	1231.6110	616.3091	12
4	373.2014	187.1043			355.1908	178.0990	G	1151.5717	576.2895	1133.5481	567.2777	1133.5612	567.2842	11
5	471.2512	236.1292			453.2406	227.1239	P	1093.5532	547.2802	1075.5296	538.2685	1075.5427	538.2750	10
6	571.3166	286.1620			553.3061	277.1567	V	995.5034	498.2553	977.4798	489.2436	977.4929	489.2501	9
7	673.3613	337.1843			655.3508	328.1790	T	***895.4380***	448.2226	877.4144	439.2108	877.4274	439.2173	8
8	789.3853	395.1963			771.3748	386.1910	D	***793.3933***	397.2003	775.3697	388.1885	775.3827	388.1950	7
9	887.4351	444.2212			869.4246	435.2159	P	***677.3693***	339.1883	659.3457	330.1765	659.3587	330.1830	6
10	975.4642	488.2357			957.4536	479.2304	S	579.3195	290.1634	561.2959	281.1516	561.3089	281.1581	5
11	1105.5168	553.2621	1087.4933	544.2503	1087.5063	544.2568	Q	491.2904	246.1488	473.2668	237.1371			4
12	1219.5979	610.3026	1201.5743	601.2908	1201.5874	601.2973	L	361.2378	181.1225	343.2142	172.1107			3
13	1317.6477	659.3275	1299.6241	650.3157	1299.6372	650.3222	P	247.1567	124.0820	229.1331	115.0702			2
14							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of TLPGPVTDPSQLPK

AT5G16570.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.3	1464.7401	0.0013	TLPGPVTDPSQLPK
4.3	1464.7431	-0.0017	VGGSVRPSKRNTGK

AT5G16620.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NYAFEDISPEETTK**
Found in **AT5G16620.1** in **TAIR_Arabidopsis**, Symbols: TIC40, ATTIC40, PDE120 | PDE120 (PIGMENT DEFECTIVE EMBRYO) | chr5:5450811-5454259 FORWARD

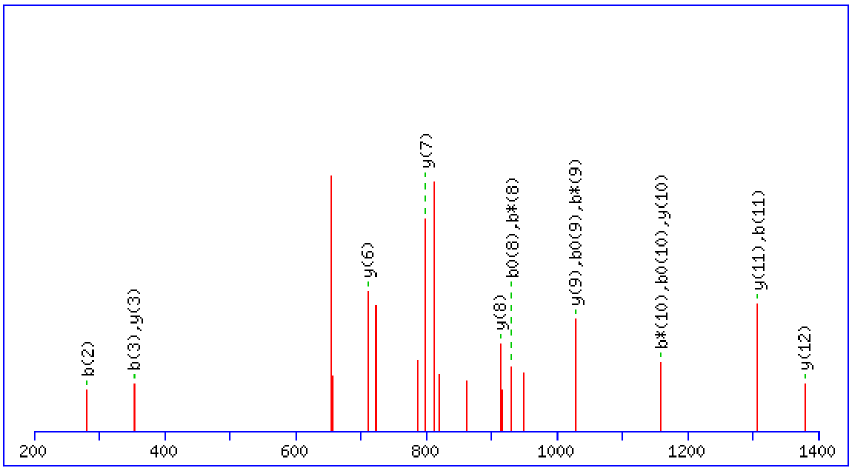
Match to Query 7528: 1658.691246 from(830.352899,2+) index(5449)
Title: Elution from: 48.453 to 48.453 scan no 6899 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1400 Da Full range

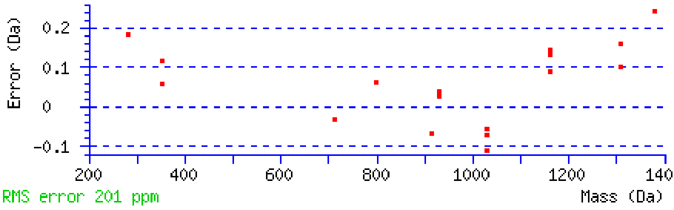
Label all possible matches ○ Label matches used for scoring ●

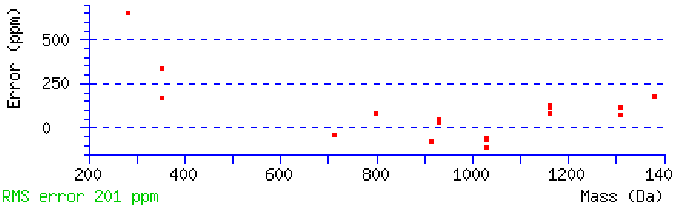
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1658.6888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1e-006
Matches : 17/146 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							14
2	**281.1046**	141.0560	263.0811	132.0442			Y	1543.6591	772.3332	1525.6355	763.3214	1525.6485	763.3279	13
3	**353.1388**	177.0730	335.1152	168.0612			A	***1379.5987***	690.3030	1361.5751	681.2912	1361.5882	681.2977	12
4	501.2042	251.1058	483.1807	242.0940			F	***1307.5646***	654.2859	1289.5410	645.2741	1289.5540	645.2806	11
5	631.2439	316.1256	613.2203	307.1138	613.2333	307.1203	E	***1159.4991***	580.2532	1141.4755	571.2414	1141.4886	571.2479	10
6	747.2678	374.1376	729.2443	365.1258	729.2573	365.1323	D	***1029.4595***	515.2334	1011.4359	506.2216	1011.4489	506.2281	9
7	861.3489	431.1781	843.3254	422.1663	843.3384	422.1728	I	***913.4355***	457.2214	895.4119	448.2096	895.4250	448.2161	8
8	949.3780	475.1926	931.3544	466.1808	931.3674	466.1874	S	***799.3544***	400.1808	781.3308	391.1691	781.3439	391.1756	7
9	1047.4278	524.2175	1029.4042	515.2057	1029.4172	515.2123	P	***711.3254***	356.1663	693.3018	347.1545	693.3148	347.1610	6
10	1177.4674	589.2374	1159.4438	580.2256	1159.4569	580.2321	E	613.2756	307.1414	595.2520	298.1296	595.2650	298.1361	5
11	**1307.5071**	654.2572	1289.4835	645.2454	1289.4965	645.2519	E	483.2359	242.1216	465.2123	233.1098	465.2254	233.1163	4
12	1409.5518	705.2795	1391.5282	696.2677	1391.5412	696.2742	T	***353.1963***	177.1018	335.1727	168.0900	335.1857	168.0965	3
13	1511.5965	756.3019	1493.5729	747.2901	1493.5859	747.2966	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NYAFEDISPEETTK

AT5G16620.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.3	1658.6888	0.0024	NYAFEDISPEETTK
13.3	1658.6888	0.0024	FDFELSDSEKPDSK
3.9	1658.6878	0.0034	MEEDRATMTGAVATR
0.3	1658.6953	-0.0040	ITGSNNDEARGSCKK

AT5G16660.1

Mascot Search Results

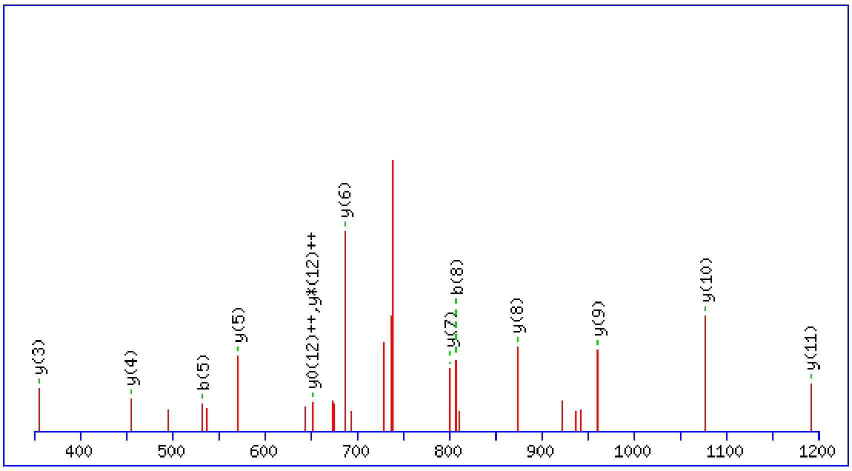
Peptide View

MS/MS Fragmentation of **IGQLNSAIDNVSSR**
Found in **AT5G16660.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62132.1) | chr5:5465702-5467009 REVERSE

Match to Query 6480: 1492.699764 from(747.357158,2+) index(4180)
Title: Elution from: 38.991 to 38.991 scan no 5205 cid35.00 polarity:+
Data file C7-3_1.mgf

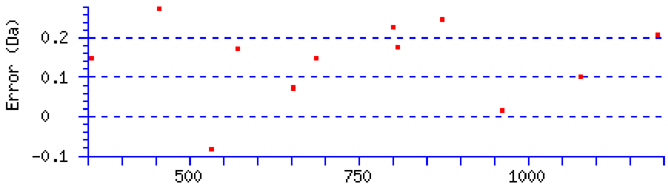
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

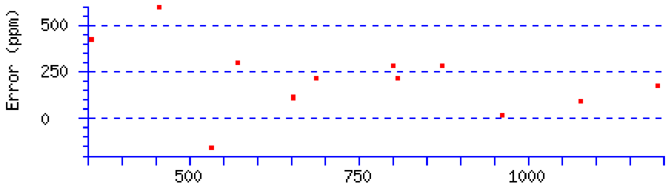


Monoisotopic mass of neutral peptide Mr(calc): 1492.6990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 6.2e-009
Matches : 13/140 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							14
2	173.1069	87.0571					G	1379.6252	690.3162	1361.6016	681.3044	1361.6146	681.3110	13
3	303.1595	152.0834	285.1359	143.0716			Q	1321.6067	661.3070	1303.5831	652.2952	1303.5961	652.3017	12
4	417.2406	209.1239	399.2170	200.1122			L	***1191.5540***	596.2807	1173.5305	587.2689	1173.5435	587.2754	11
5	**533.2776**	267.1424	515.2540	258.1307			N	***1077.4729***	539.2401	1059.4494	530.2283	1059.4624	530.2348	10
6	621.3067	311.1570	603.2831	302.1452	603.2961	302.1517	S	***961.4360***	481.2216	943.4124	472.2098	943.4254	472.2163	9
7	693.3408	347.1741	675.3172	338.1623	675.3303	338.1688	A	***873.4069***	437.2071	855.3833	428.1953	855.3963	428.2018	8
8	**807.4219**	404.2146	789.3983	395.2028	789.4114	395.2093	I	***801.3727***	401.1900	783.3492	392.1782	783.3622	392.1847	7
9	923.4459	462.2266	905.4223	453.2148	905.4353	453.2213	D	***687.2916***	344.1495	669.2681	335.1377	669.2811	335.1442	6
10	1039.4829	520.2451	1021.4593	511.2333	1021.4723	511.2398	N	***571.2677***	286.1375	553.2441	277.1257	553.2571	277.1322	5
11	1139.5484	570.2778	1121.5248	561.2660	1121.5378	561.2725	V	***455.2307***	228.1190	437.2071	219.1072	437.2201	219.1137	4
12	1227.5774	614.2923	1209.5538	605.2806	1209.5668	605.2871	S	***355.1652***	178.0862	337.1416	169.0745	337.1547	169.0810	3
13	1315.6065	658.3069	1297.5829	649.2951	1297.5959	649.3016	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
14							R	179.1071	90.0572	161.0835	81.0454			1



RMS error 273 ppm



RMS error 273 ppm

NCBI **BLAST** search of IGQLNSAIDNVSSR

AT5G16660.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
92.0	1492.6990	0.0007	IGQLNSAIDNVSSR
13.1	1492.6963	0.0034	SLLKDELDNTNSK
9.1	1492.7019	-0.0022	VAEIEGAEKEKMK
3.7	1492.7016	-0.0019	GNGRVLVVDGGGSQR
3.5	1492.6965	0.0033	MGYVTYKRNSVR
1.9	1492.7019	-0.0022	EQIMVLIGETGSGK
0.6	1492.6987	0.0010	HCLWEVPLVGHK
0.5	1492.7017	-0.0019	GSVPNGTNPSTRRK
0.1	1492.7012	-0.0015	DTVANIWDIRSGK

AT5G16710.1

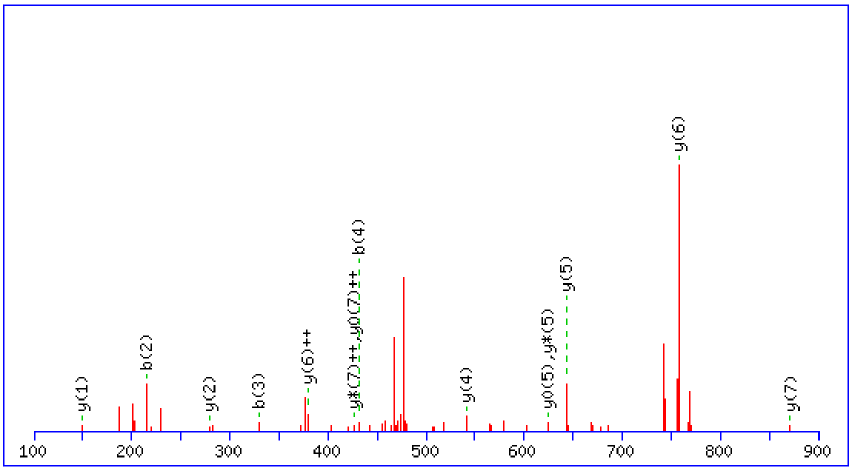
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLTMEEK**
Found in **AT5G16710.1** in **TAIR_Arabidopsis**, Symbols: DHAR3 | DHAR3 (DEHYDROASCORBATE REDUCTASE 1); glutathione dehydrogenase (ascorbate) | chr5:5483315-5484929 FORWARD

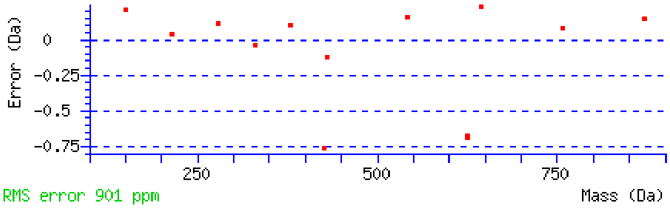
Match to Query 2202: 970.491236 from(486.252894,2+) index(3030)
Title: Elution from: 30.559 to 30.559 scan no 3783 cid35.00 polarity:+
Data file D6h-1_3.mgf

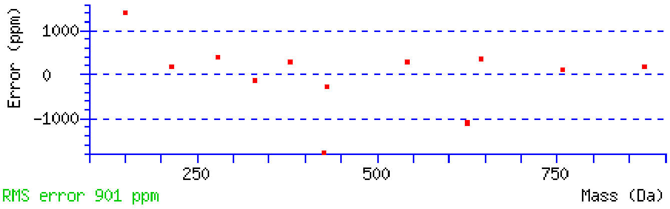
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 970.4887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0083
Matches : 14/62 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400			V							8
2	**215.1538**	108.0805			L	***871.4306***	436.2189	853.4070	427.2071	853.4200	427.2136	7
3	**329.2349**	165.1211			L	***757.3495***	379.1784	739.3259	370.1666	739.3389	370.1731	6
4	**431.2796**	216.1435	413.2691	207.1382	T	***643.2684***	322.1378	625.2448	313.1260	625.2578	313.1325	5
5	563.3172	282.1622	545.3066	273.1569	M	***541.2237***	271.1155	523.2001	262.1037	523.2131	262.1102	4
6	693.3568	347.1820	675.3462	338.1767	E	409.1861	205.0967	391.1625	196.0849	391.1756	196.0914	3
7	823.3964	412.2018	805.3858	403.1966	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
8					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VLLTMEEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.3	970.4887	0.0025	VLLTMEEK

AT5G16710.1

1.7	970.4914	-0.0002	VALQCLQK

Mascot: http://www.matrixscience.com/

AT5G16750.1

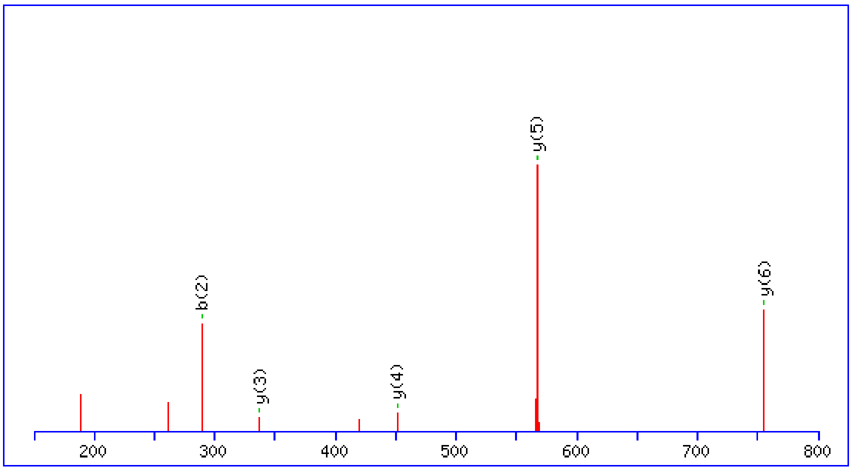
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VWDLNAK**
Found in **AT5G16750.1** in **TAIR_Arabidopsis**, Symbols: TOZ | TOZ (TORMOZEMBRYO DEFECTIVE); nucleotide binding | chr5:5504544-5509269 REVERSE

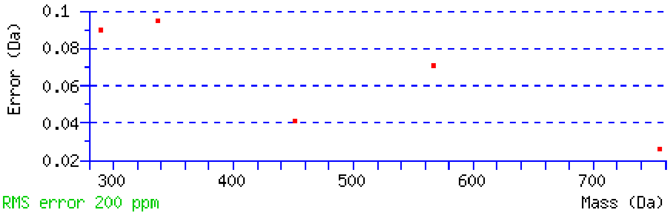
Match to Query 1323: 854.416964 from(428.215758,2+) index(7092)
Title: Elution from: 61.864 to 61.864 scan no 9231 cid35.00 polarity:+
Data file C7-2_3.mgf

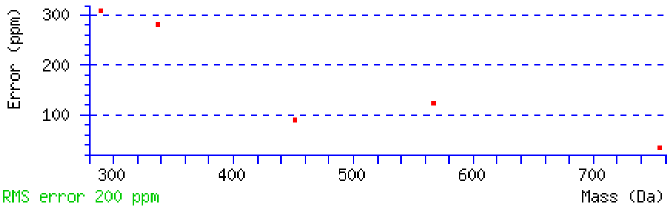
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 854.4146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0093
Matches : 5/52 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							7
2	289.1461	145.0767					W	*755.3565*	378.1819	737.3329	369.1701	737.3459	369.1766	6
3	405.1701	203.0887			387.1595	194.0834	D	*567.2831*	284.1452	549.2595	275.1334	549.2725	275.1399	5
4	519.2512	260.1292			501.2406	251.1239	L	*451.2591*	226.1332	433.2355	217.1214			4
5	635.2882	318.1477	617.2646	309.1359	617.2776	309.1424	N	*337.1780*	169.0926	319.1544	160.0809			3
6	707.3223	354.1648	689.2987	345.1530	689.3118	345.1595	A	221.1410	111.0741	203.1174	102.0624			2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VWDLNAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.3	854.4146	0.0023	VWDLNAK
28.3	854.4169	0.0001	VWDLWK

AT5G16750.1

13.3	854.4146	0.0023	GEVINWK
6.0	854.4146	0.0023	FHDSVLK
3.6	854.4151	0.0019	RSEGKHK
1.6	854.4180	-0.0011	EMITPVR

AT5G16810.1

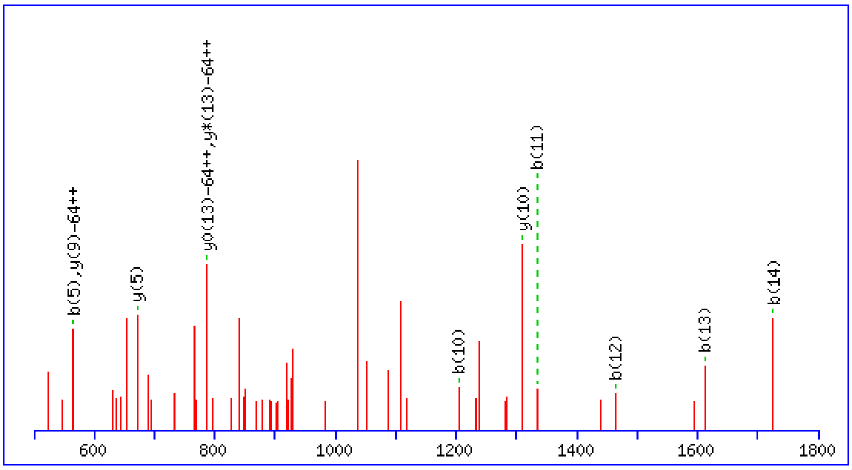
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQGVWNPYEKEQMIK**
Found in **AT5G16810.1** in **TAIR_Arabidopsis**, Symbols: | ATP binding / protein kinase | chr5:5526863-5529881 REVERSE

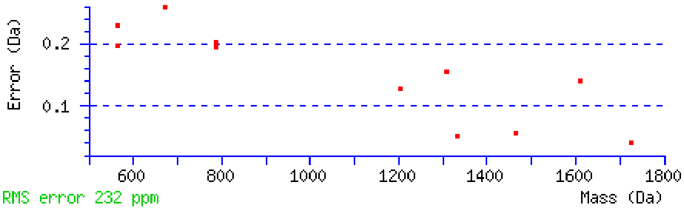
Match to Query 8849: 1872.824396 from(937.419474,2+) index(9730)
Title: Elution from: 91.811 to 91.811 scan no 13541 cid35.00 polarity:+
Data file D1d-1_1.mgf

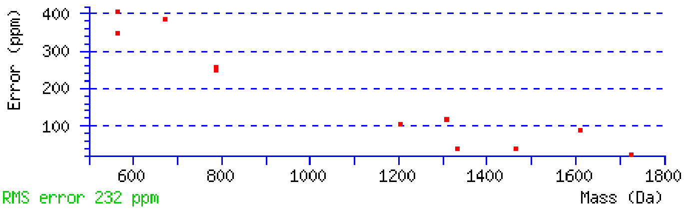
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1872.8203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 **Expect:** 0.00092
Matches : 11/238 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							15
2	219.0890	110.0481	201.0654	101.0363	201.0784	101.0428	Q	1785.7985	893.4029	1767.7749	884.3911	1767.7879	884.3976	14
3	277.1075	139.0574	259.0839	130.0456	259.0969	130.0521	G	1655.7458	828.3766	1637.7223	819.3648	1637.7353	819.3713	13
4	377.1729	189.0901	359.1494	180.0783	359.1624	180.0848	V	1597.7273	799.3673	1579.7038	790.3555	1579.7168	790.3620	12
5	***565.2463***	283.1268	547.2227	274.1150	547.2358	274.1215	W	1497.6619	749.3346	1479.6383	740.3228	1479.6513	740.3293	11
6	681.2833	341.1453	663.2597	332.1335	663.2727	332.1400	N	**1309.5885**	655.2979	1291.5649	646.2861	1291.5779	646.2926	10
7	779.3331	390.1702	761.3095	381.1584	761.3225	381.1649	P	1193.5515	597.2794	1175.5279	588.2676	1175.5409	588.2741	9
8	943.3935	472.2004	925.3699	463.1886	925.3829	463.1951	Y	1095.5017	548.2545	1077.4781	539.2427	1077.4911	539.2492	8
9	1073.4331	537.2202	1055.4095	528.2084	1055.4225	528.2149	E	931.4413	466.2243	913.4178	457.2125	913.4308	457.2190	7
10	***1203.5221***	602.2647	1185.4986	593.2529	1185.5116	593.2594	K	801.4017	401.2045	783.3781	392.1927	783.3912	392.1992	6
11	***1333.5618***	667.2845	1315.5382	658.2727	1315.5512	658.2792	E	**671.3127**	336.1600	653.2891	327.1482	653.3021	327.1547	5
12	***1463.6144***	732.3108	1445.5908	723.2991	1445.6038	723.3056	Q	541.2731	271.1402	523.2495	262.1284			4
13	***1611.6468***	806.3271	1593.6233	797.3153	1593.6363	797.3218	M	411.2204	206.1138	393.1968	197.1020			3
14	***1725.7279***	863.3676	1707.7044	854.3558	1707.7174	854.3623	I	263.1880	132.0976	245.1644	123.0858			2
15							K	149.1069	75.0571	131.0833	66.0453			1





AT5G16810.1

NCBI **BLAST** search of SQGVWNPYEKEQMIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.4	1872.8203	0.0041	SQGVWNPYEKEQMIK
17.7	1872.8228	0.0016	TKREDDESNIEEFIK
10.0	1872.8189	0.0055	NVLLSQVCCNSMWIK
5.6	1872.8210	0.0034	NMVGIVEMTEEAFLEK
1.8	1872.8270	-0.0026	MLCEDGKLSLAMQVNK
0.2	1872.8270	-0.0026	MMEEAEAKMSAEVIRK
0.1	1872.8281	-0.0037	SSENAVSRVSFGADHKR

AT5G16850.1

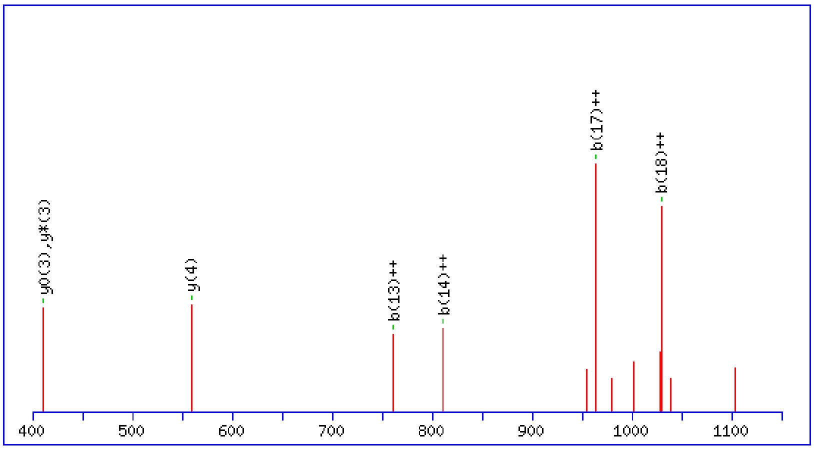
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLIYPFLEEASKDVSSKECSR**
Found in **AT5G16850.1** in **TAIR_Arabidopsis**, Symbols: ATTERT | ATTERT (TELOMERASE REVERSE TRANSCRIPTASE); telomeric template RNA reverse transcriptase | chr5:5538326-5543447 REVERSE

Match to Query 10398: 2485.121574 from(829.381134,3+) index(10778)
Title: Elution from: 108.614 to 108.614 scan no 15693 cid35.00 polarity:+
Data file D12h-1_2.mgf

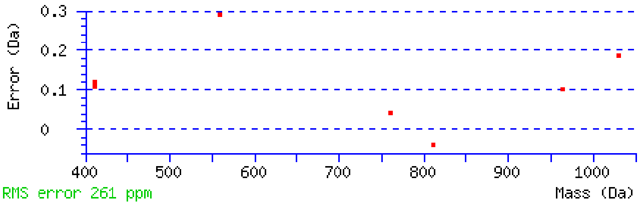
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

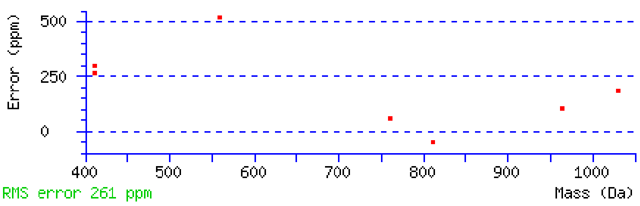


Monoisotopic mass of neutral peptide Mr(calc): 2485.1249
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.032
Matches : 7/216 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							21
2	217.1331	109.0702			199.1225	100.0649	L	2384.0875	1192.5474	2366.0639	1183.5356	2366.0769	1183.5421	20
3	331.2142	166.1107			313.2036	157.1054	I	2270.0064	1135.5068	2251.9828	1126.4950	2251.9958	1126.5016	19
4	495.2746	248.1409			477.2640	239.1356	Y	2155.9253	1078.4663	2137.9017	1069.4545	2137.9147	1069.4610	18
5	593.3243	297.1658			575.3138	288.1605	P	1991.8649	996.4361	1973.8414	987.4243	1973.8544	987.4308	17
6	741.3898	371.1985			723.3792	362.1933	F	1893.8151	947.4112	1875.7916	938.3994	1875.8046	938.4059	16
7	855.4709	428.2391			837.4603	419.2338	L	1745.7497	873.3785	1727.7261	864.3667	1727.7391	864.3732	15
8	985.5105	493.2589			967.5000	484.2536	E	1631.6686	816.3379	1613.6450	807.3261	1613.6580	807.3326	14
9	1115.5502	558.2787			1097.5396	549.2734	E	1501.6290	751.3181	1483.6054	742.3063	1483.6184	742.3128	13
10	1187.5843	594.2958			1169.5737	585.2905	A	1371.5893	686.2983	1353.5657	677.2865	1353.5788	677.2930	12
11	1275.6134	638.3103			1257.6028	629.3050	S	1299.5552	650.2812	1281.5316	641.2694	1281.5446	641.2759	11
12	1405.7024	703.3548	1387.6788	694.3430	1387.6918	694.3496	K	1211.5261	606.2667	1193.5025	597.2549	1193.5156	597.2614	10
13	1521.7264	***761.3668***	1503.7028	752.3550	1503.7158	752.3615	D	1081.4371	541.2222	1063.4135	532.2104	1063.4265	532.2169	9
14	1621.7918	***811.3996***	1603.7682	802.3878	1603.7813	802.3943	V	965.4131	483.2102	947.3895	474.1984	947.4025	474.2049	8
15	1709.8209	855.4141	1691.7973	846.4023	1691.8103	846.4088	S	865.3477	433.1775	847.3241	424.1657	847.3371	424.1722	7
16	1797.8500	899.4286	1779.8264	890.4168	1779.8394	890.4233	S	777.3186	389.1629	759.2950	380.1511	759.3080	380.1577	6
17	1927.9390	***964.4731***	1909.9154	955.4613	1909.9284	955.4678	K	689.2895	345.1484	671.2660	336.1366	671.2790	336.1431	5
18	2057.9786	***1029.4929***	2039.9550	1020.4812	2039.9680	1020.4877	E	559.2005	280.1039	541.1769	271.0921	541.1899	271.0986	4
19	2220.0033	1110.5053	2201.9797	1101.4935	2201.9928	1101.5000	C	429.1609	215.0841	411.1373	206.0723	411.1503	206.0788	3
20	2308.0324	1154.5198	2290.0088	1145.5080	2290.0218	1145.5146	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
21							R	179.1071	90.0572	161.0835	81.0454			1

AT5G16850.1





NCBI **BLAST** search of TLIYPFLEEASKDVSSKECSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.0	2485.1249	-0.0034	TLIYPFLEEASKDVSSKECSR
21.9	2485.1245	-0.0029	MLVYQDILTGDELLSDSFPYK
21.9	2485.1245	-0.0029	MLVYQDLLTGDELLSDSFPYK
10.2	2485.1278	-0.0062	IHGNQLAEMPFIGTRYMYRR
8.4	2485.1229	-0.0013	DRSNRSAVMLPYSFLPNMAAAK
8.4	2485.1229	-0.0013	DRSNRSAVMLPYSFLPNMAAAK
3.9	2485.1262	-0.0047	RGELHLAVRFTCTSVSSMLMK
3.0	2485.1190	0.0026	IDLPDFLICFDFTTERFGPR
2.3	2485.1224	-0.0008	RTVSDVGAARSDVVGDGPELGHTR
1.4	2485.1258	-0.0042	MLPGEVFGVFCKVKCQDSLTK

AT5G16970.1

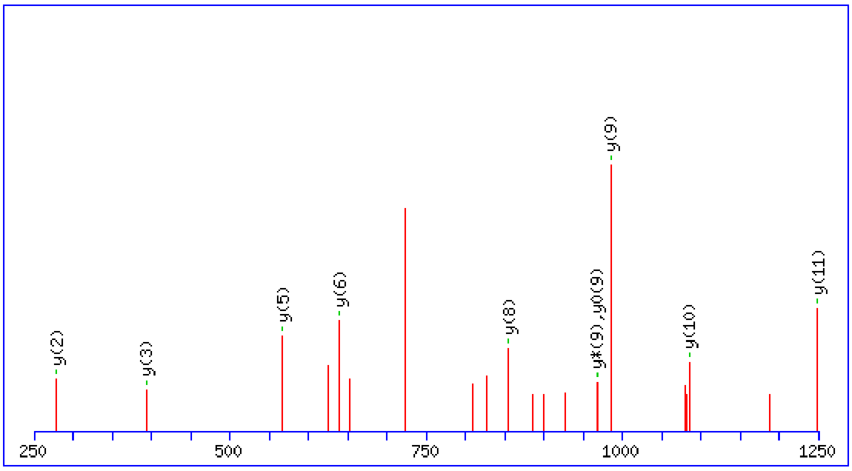
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITYVEDVADGLEK**
Found in **AT5G16970.1** in **TAIR_Arabidopsis**, Symbols: AT-AER | AT-AER (ALKENAL REDUCTASE); 2-alkenal reductase | chr5:5576294-5578004 REVERSE

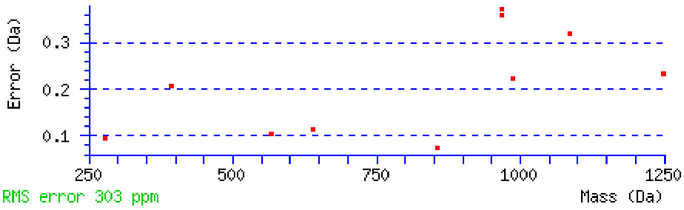
Match to Query 6166: 1464.681134 from(733.347843,2+) index(6929)
Title: Elution from: 61.389 to 61.389 scan no 8906 cid35.00 polarity:+
Data file D12h-3_1.mgf

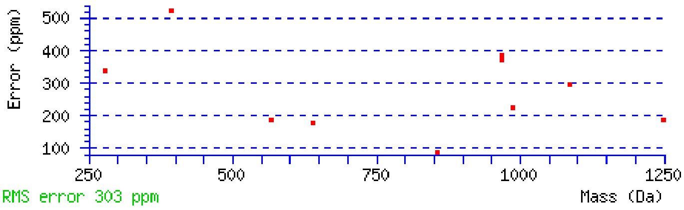
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1464.6776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 3.1e-008
Matches : 10/116 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			**I**							**13**
2	217.1331	109.0702	199.1225	100.0649	**T**	1351.6038	676.3055	1333.5802	667.2938	1333.5932	667.3003	**12**
3	381.1935	191.1004	363.1829	182.0951	**Y**	***1249.5591***	625.2832	1231.5355	616.2714	1231.5485	616.2779	**11**
4	481.2589	241.1331	463.2483	232.1278	**V**	***1085.4987***	543.2530	1067.4751	534.2412	1067.4882	534.2477	**10**
5	611.2985	306.1529	593.2880	297.1476	**E**	***985.4333***	493.2203	967.4097	484.2085	967.4227	484.2150	**9**
6	727.3225	364.1649	709.3119	355.1596	**D**	***855.3937***	428.2005	837.3701	419.1887	837.3831	419.1952	**8**
7	827.3880	414.1976	809.3774	405.1923	**V**	739.3697	370.1885	721.3461	361.1767	721.3591	361.1832	**7**
8	899.4221	450.2147	881.4115	441.2094	**A**	***639.3042***	320.1558	621.2806	311.1440	621.2937	311.1505	**6**
9	1015.4461	508.2267	997.4355	499.2214	**D**	***567.2701***	284.1387	549.2465	275.1269	549.2595	275.1334	**5**
10	1073.4646	537.2359	1055.4540	528.2306	**G**	451.2461	226.1267	433.2225	217.1149	433.2355	217.1214	**4**
11	1187.5457	594.2765	1169.5351	585.2712	**L**	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	**3**
12	1317.5853	659.2963	1299.5747	650.2910	**E**	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	**2**
13					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of ITYVEDVADGLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G16970.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.4	1464.6776	0.0035	ITYVEDVADGLEK
20.9	1464.6832	-0.0021	EFLSEEVEMVLK
11.1	1464.6829	-0.0018	QSGDGGGGFVIPAKR
10.0	1464.6837	-0.0025	CDLLVTANGKTEK
8.1	1464.6789	0.0022	ENMMVLRQGLEK
8.0	1464.6803	0.0009	FQGVEEQITELR
5.7	1464.6837	-0.0025	EAEMISLQKQQK
3.8	1464.6830	-0.0018	GTPFAAQTAAGNAIR
3.5	1464.6803	0.0009	VGLELNEYGAQQK
3.4	1464.6778	0.0034	WGMEGLKNTVWK

AT5G17050.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFVWSLK**
Found in **AT5G17050.1** in **TAIR_Arabidopsis**, Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr5:5607831-5609395 REVERSE

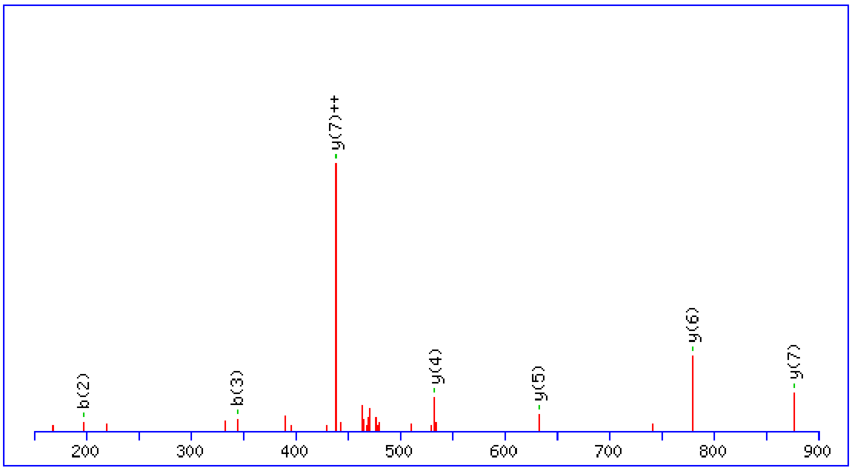
Match to Query 2244: 974.559868 from(488.287210,2+) index(7593)
Title: Elution from: 67.698 to 67.698 scan no 10003 cid35.00 polarity:+
Data file D6h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

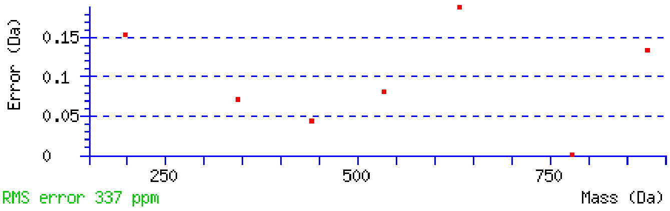
Label all possible matches ○ Label matches used for scoring ●

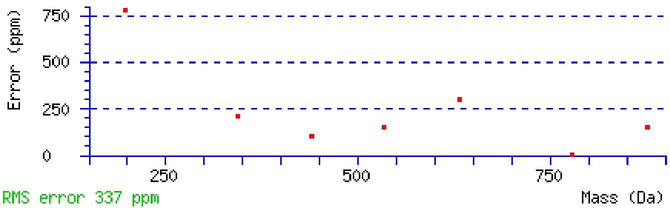
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 974.5589
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.003
Matches : 7/56 fragment ions using 8 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415			V							8
2	**197.1285**	99.0679			P	**876.4978**	438.7525	859.4713	430.2393	858.4872	429.7473	7
3	**344.1969**	172.6021			F	**779.4450**	390.2262	762.4185	381.7129	761.4345	381.2209	6
4	443.2653	222.1363			V	**632.3766**	316.6919	615.3501	308.1787	614.3661	307.6867	5
5	629.3446	315.1759			W	**533.3082**	267.1577	516.2817	258.6445	515.2976	258.1525	4
6	716.3766	358.6919	698.3661	349.6867	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
7	829.4607	415.2340	811.4501	406.2287	L	260.1969	130.6021	243.1703	122.0888			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VPFVWSLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	974.5589	0.0009	VPFVWSLK

AT5G17050.1

Mascot: http://www.matrixscience.com/

AT5G17240.1

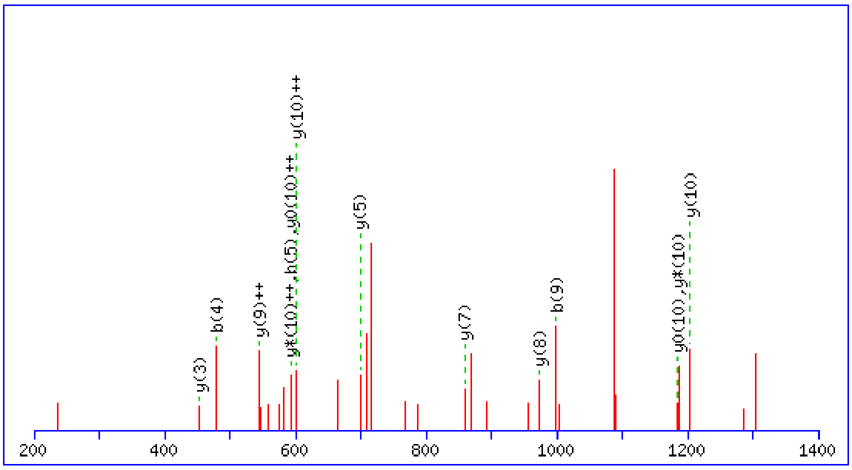
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MNNLLGTQDRLR**
Found in **AT5G17240.1** in **TAIR_Arabidopsis**, Symbols: SDG40 | SDG40 (SET DOMAIN GROUP 40) | chr5:5666856-5668851 FORWARD

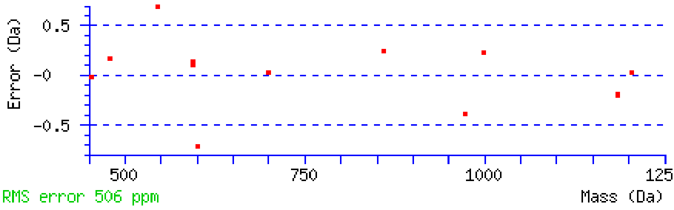
Match to Query 5641: 1450.687506 from(726.351029,2+) index(6900)
Title: Elution from: 60.625 to 60.625 scan no 9027 cid35.00 polarity:+
Data file 0-2_3.mgf

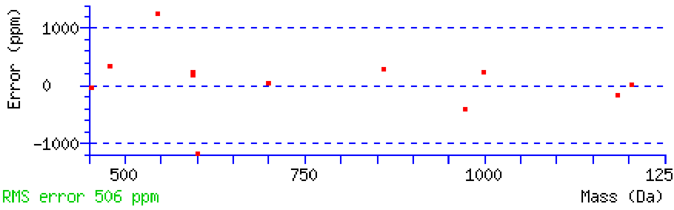
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1450.6837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.028
Matches : 14/112 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	133.0448	67.0260					M							12
2	249.0818	125.0445	231.0582	116.0327			N	1319.6535	660.3304	1301.6299	651.3186	1301.6429	651.3251	11
3	365.1188	183.0630	347.0952	174.0512			N	***1203.6165***	602.3119	1185.5929	593.3001	1185.6059	593.3066	10
4	**479.1999**	240.1036	461.1763	231.0918			L	1087.5795	544.2934	1069.5559	535.2816	1069.5689	535.2881	9
5	**593.2810**	297.1441	575.2574	288.1323			L	***973.4984***	487.2528	955.4748	478.2410	955.4878	478.2475	8
6	651.2995	326.1534	633.2759	317.1416			G	***859.4173***	430.2123	841.3937	421.2005	841.4067	421.2070	7
7	753.3442	377.1757	735.3206	368.1639	735.3336	368.1705	T	801.3988	401.2030	783.3752	392.1912	783.3882	392.1977	6
8	883.3968	442.2021	865.3733	433.1903	865.3863	433.1968	Q	***699.3541***	350.1807	681.3305	341.1689	681.3435	341.1754	5
9	**999.4208**	500.2141	981.3972	491.2023	981.4103	491.2088	D	569.3014	285.1543	551.2778	276.1426	551.2909	276.1491	4
10	1159.5101	580.2587	1141.4865	571.2469	1141.4995	571.2534	R	***453.2774***	227.1424	435.2539	218.1306			3
11	1273.5912	637.2992	1255.5676	628.2874	1255.5806	628.2939	L	293.1882	147.0977	275.1646	138.0859			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MNNLLGTQDRLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G17240.1

Score	Mr(calc)	Delta	Sequence
26.1	1450.6837	0.0038	MNNLLGTQDRLR
15.9	1450.6902	-0.0027	ATKTDDFAPFPVK
11.5	1450.6833	0.0042	LKCAIDLDFPSR
11.4	1450.6911	-0.0036	GSNNVLGGVGDRRK
9.8	1450.6884	-0.0009	RSSDSTGSVLLPGR
8.4	1450.6907	-0.0032	LSYSRHTDLNVK
7.8	1450.6907	-0.0032	YGNLNQALLNQGK
7.0	1450.6907	-0.0032	DAWNSKRDTLVK
5.5	1450.6855	0.0020	FGTWPVAMLAQSK
3.4	1450.6880	-0.0005	ISKFEAALENGEK

AT5G17310.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQTPTDEIVVPYDK**
Found in **AT5G17310.2** in **TAIR_Arabidopsis**, Symbols: | UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative | chr5:5696957-5700847 REVERSE

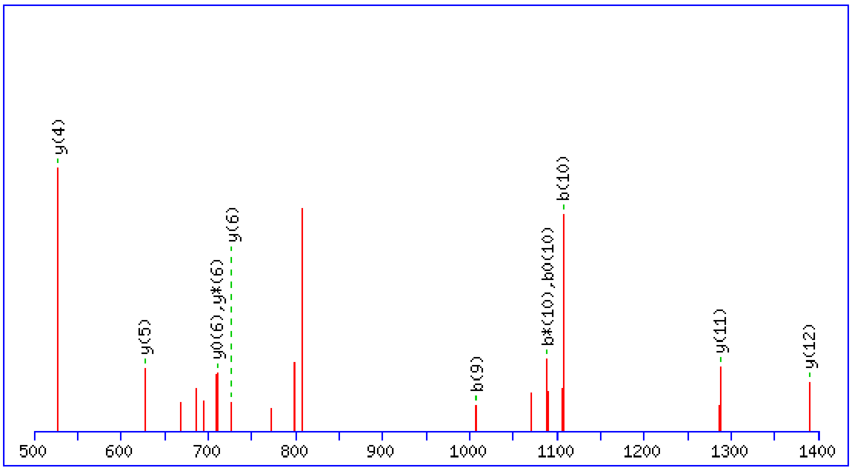
Match to Query 7405: 1632.785752 from(817.400152,2+) index(5958)
Title: Elution from: 53.942 to 53.942 scan no 7581 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1400 Da Full range

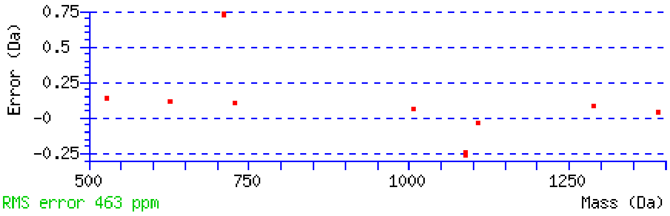
Label all possible matches ○ Label matches used for scoring ●

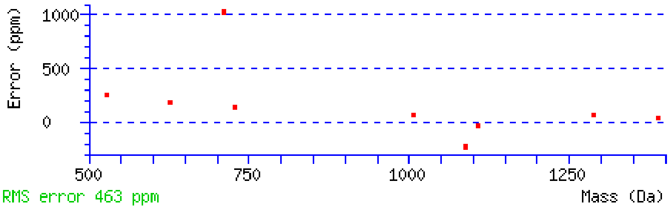
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1632.7823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00038
Matches : 11/148 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							14
2	245.1410	123.0741	227.1174	114.0624			Q	1519.7085	760.3579	1501.6849	751.3461	1501.6979	751.3526	13
3	347.1857	174.0965	329.1622	165.0847	329.1752	165.0912	T	***1389.6558***	695.3316	1371.6323	686.3198	1371.6453	686.3263	12
4	445.2355	223.1214	427.2120	214.1096	427.2250	214.1161	P	***1287.6111***	644.3092	1269.5875	635.2974	1269.6006	635.3039	11
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	T	1189.5613	595.2843	1171.5377	586.2725	1171.5508	586.2790	10
6	663.3042	332.1558	645.2806	323.1440	645.2937	323.1505	D	1087.5166	544.2619	1069.4930	535.2502	1069.5061	535.2567	9
7	793.3439	397.1756	775.3203	388.1638	775.3333	388.1703	E	971.4926	486.2500	953.4691	477.2382	953.4821	477.2447	8
8	907.4250	454.2161	889.4014	445.2043	889.4144	445.2108	I	841.4530	421.2301	823.4294	412.2184	823.4424	412.2249	7
9	**1007.4904**	504.2488	989.4668	495.2370	989.4798	495.2436	V	***727.3719***	364.1896	709.3483	355.1778	709.3613	355.1843	6
10	**1107.5559**	554.2816	1089.5323	545.2698	1089.5453	545.2763	V	***627.3065***	314.1569	609.2829	305.1451	609.2959	305.1516	5
11	1205.6056	603.3065	1187.5821	594.2947	1187.5951	594.3012	P	***527.2410***	264.1241	509.2174	255.1124	509.2304	255.1189	4
12	1369.6660	685.3366	1351.6424	676.3249	1351.6554	676.3314	Y	429.1912	215.0992	411.1676	206.0875	411.1807	206.0940	3
13	1485.6900	743.3486	1467.6664	734.3368	1467.6794	734.3434	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IQTPTDEIVVPYDK

AT5G17310.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.8	1632.7823	0.0035	IQTPTDEIVVPYDK
2.5	1632.7883	-0.0026	QLAEMEDPIGRVLK

Mascot: http://www.matrixscience.com/

AT5G17710.1

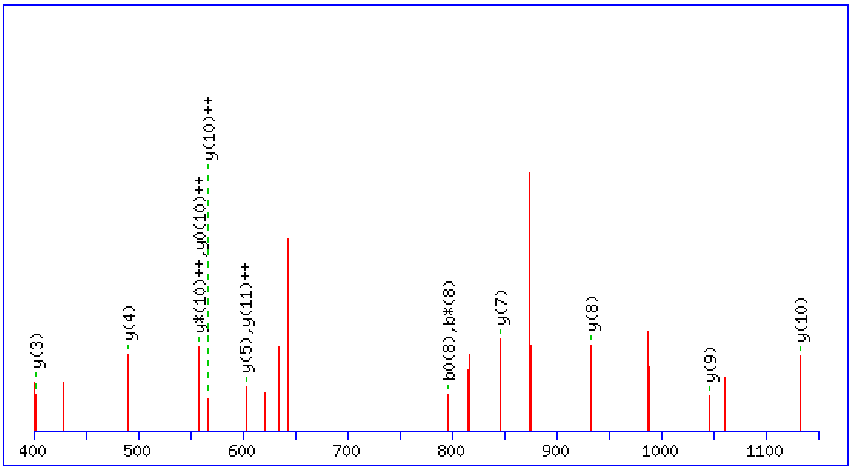
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VASLSNELSVER**
Found in **AT5G17710.1** in **TAIR_Arabidopsis**, Symbols: EMB1241 | EMB1241 (EMBRYO DEFECTIVE 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization | chr5:5839562-5841641 REVERSE

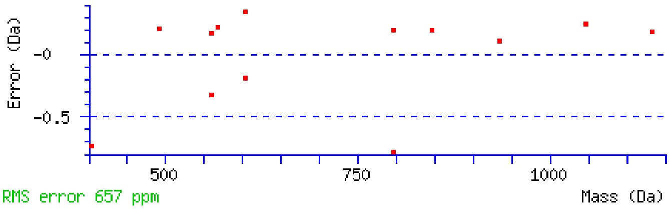
Match to Query 5100: 1302.676194 from(652.345373,2+) index(4465)
Title: Elution from: 41.343 to 41.343 scan no 5551 cid35.00 polarity:+
Data file 0-1_1.mgf

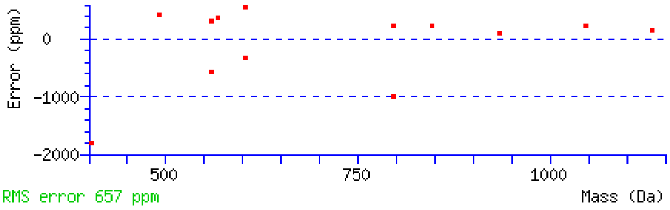
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1302.6779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00052
Matches : 13/116 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							12
2	171.1128	86.0600					A	1204.6168	602.8120	1187.5903	594.2988	1186.6062	593.8068	11
3	258.1448	129.5761			240.1343	120.5708	S	***1133.5797***	567.2935	1116.5531	558.7802	1115.5691	558.2882	10
4	371.2289	186.1181			353.2183	177.1128	L	***1046.5477***	523.7775	1029.5211	515.2642	1028.5371	514.7722	9
5	458.2609	229.6341			440.2504	220.6288	S	***933.4636***	467.2354	916.4370	458.7222	915.4530	458.2302	8
6	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	N	***846.4316***	423.7194	829.4050	415.2061	828.4210	414.7141	7
7	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	E	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	6
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	L	***603.3461***	302.1767	586.3195	293.6634	585.3355	293.1714	5
9	901.4625	451.2349	884.4360	442.7216	883.4520	442.2296	S	***490.2620***	245.6346	473.2354	237.1214	472.2514	236.6293	4
10	1000.5310	500.7691	983.5044	492.2558	982.5204	491.7638	V	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
11	1129.5735	565.2904	1112.5470	556.7771	1111.5630	556.2851	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VASLSNELSVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G17710.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.0	1302.6779	-0.0017	VASLSNELSVER
0.7	1302.6754	0.0008	LLEGWMRASPK

AT5G17920.1

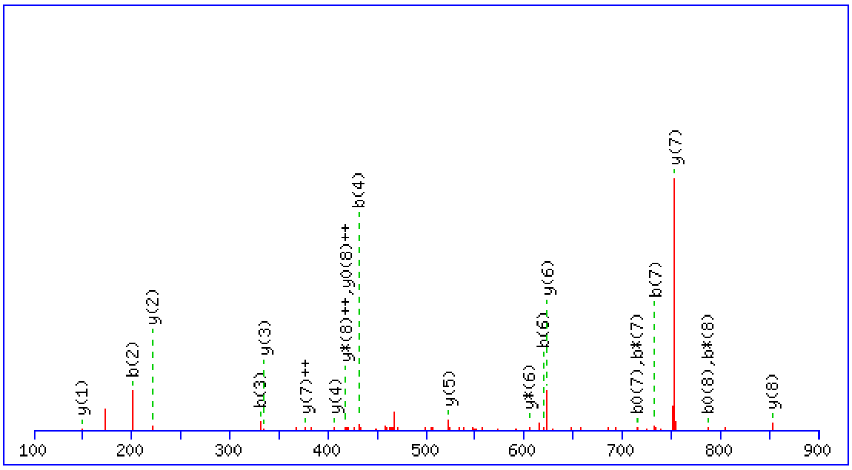
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEVNALAK**
Found in **AT5G17920.1** in **TAIR_Arabidopsis**, Symbols: ATMETS, ATMS1, ATCIMS | ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase | chr5:5935773-5939197 FORWARD

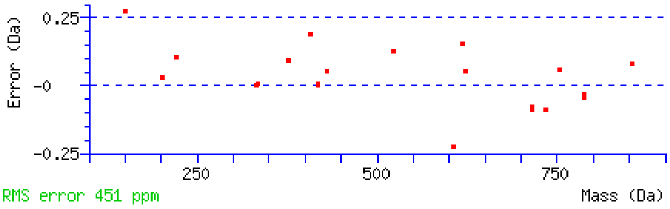
Match to Query 2069: 952.522566 from(477.268559,2+) index(2213)
Title: Elution from: 24.613 to 24.613 scan no 2804 cid35.00 polarity:+
Data file 0-1_3.mgf

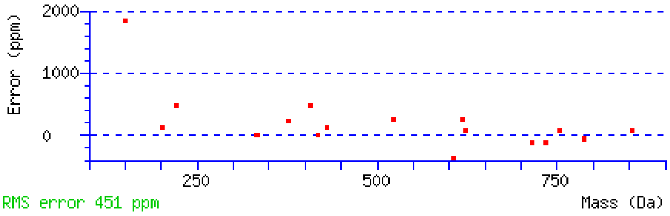
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 952.5220
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 4.7e-007
Matches : 21/72 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							9
2	**201.1382**	101.0727					V	***853.4638***	427.2355	835.4402	418.2237	835.4532	418.2303	8
3	**331.1778**	166.0925			313.1672	157.0873	E	***753.3983***	377.2028	735.3748	368.1910	735.3878	368.1975	7
4	**431.2433**	216.1253			413.2327	207.1200	V	***623.3587***	312.1830	605.3351	303.1712			6
5	547.2802	274.1438	529.2567	265.1320	529.2697	265.1385	N	***523.2933***	262.1503	505.2697	253.1385			5
6	**619.3144**	310.1608	601.2908	301.1490	601.3038	301.1556	A	***407.2563***	204.1318	389.2327	195.1200			4
7	**733.3955**	367.2014	715.3719	358.1896	715.3849	358.1961	L	***335.2221***	168.1147	317.1985	159.1029			3
8	805.4296	403.2185	787.4061	394.2067	787.4191	394.2132	A	***221.1410***	111.0741	203.1174	102.0624			2
9							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VVEVNALAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G17920.1

Score	Mr(calc)	Delta	Sequence
71.3	952.5220	0.0006	VVEVNALAK
15.5	952.5220	0.0006	VLNLEGVAK
9.0	952.5220	0.0006	VLLQSAPSK
8.7	952.5220	0.0006	LVNTLGTPK
6.4	952.5220	0.0006	SKTPLPTAK
4.5	952.5242	-0.0016	VVLEGIWK
4.2	952.5220	0.0006	TILGNLSPK
3.2	952.5220	0.0006	VTSGGIIAPK
2.0	952.5220	0.0006	LQEQLLAK
0.8	952.5246	-0.0021	QGRAPLVAK

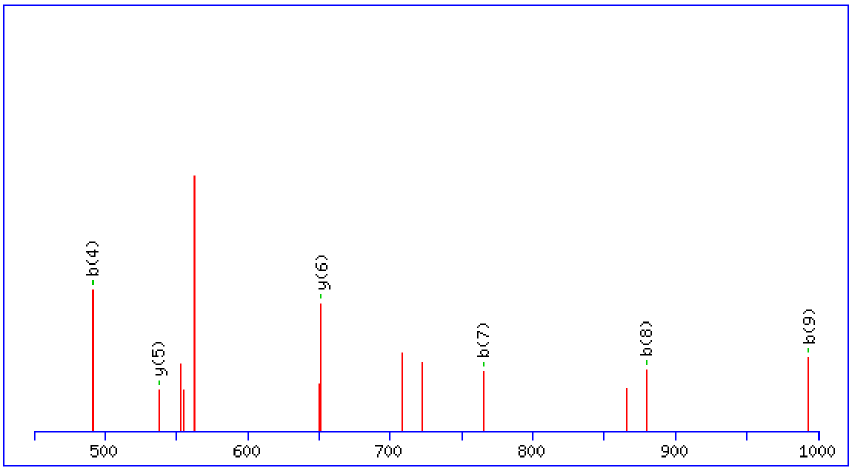
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEIQIASILK**
Found in **AT5G18070.1** in **TAIR_Arabidopsis**, Symbols: | DRT101 (DNA-DAMAGE-REPAIR/TOLERATION 101); intramolecular transferase, phosphotransferases | chr5:5981119-5982789 FORWARD

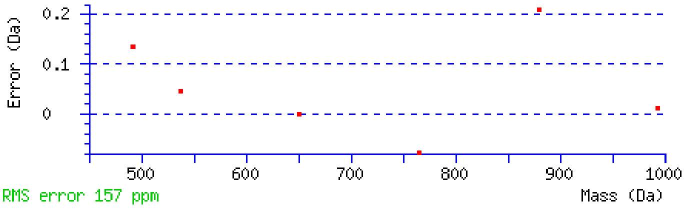
Match to Query 3962: 1140.601586 from(571.308069,2+) index(9388)
Title: Elution from: 83.665 to 83.665 scan no 12553 cid35.00 polarity:+
Data file C7-2_1.mgf

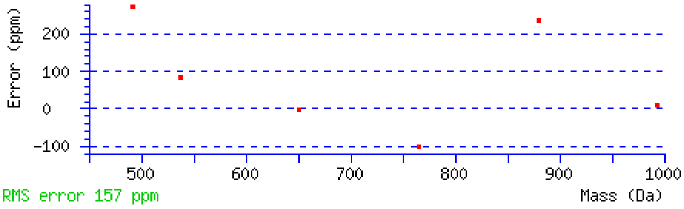
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1140.6035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.012
Matches : 6/96 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							10
2	247.0709	124.0391			229.0603	115.0338	E	1025.5868	513.2970	1007.5632	504.2852	1007.5762	504.2917	9
3	361.1520	181.0796			343.1414	172.0743	I	895.5471	448.2772	877.5235	439.2654	877.5366	439.2719	8
4	***491.2046***	246.1060	473.1810	237.0942	473.1941	237.1007	Q	781.4660	391.2367	763.4424	382.2249	763.4555	382.2314	7
5	605.2857	303.1465	587.2621	294.1347	587.2752	294.1412	I	**651.4134**	326.2103	633.3898	317.1985	633.4028	317.2050	6
6	677.3199	339.1636	659.2963	330.1518	659.3093	330.1583	A	**537.3323**	269.1698	519.3087	260.1580	519.3217	260.1645	5
7	***765.3489***	383.1781	747.3254	374.1663	747.3384	374.1728	S	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
8	***879.4300***	440.2187	861.4065	431.2069	861.4195	431.2134	I	377.2691	189.1382	359.2455	180.1264			3
9	***993.5111***	497.2592	975.4876	488.2474	975.5006	488.2539	L	263.1880	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DEIQIASILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G18070.1

Score	Mr(calc)	Delta	Sequence
24.7	1140.6035	-0.0019	DEIQIASILK
24.0	1140.6034	-0.0018	TVGAGVIGTILE
11.8	1140.5987	0.0029	AVCVITGLPAK
10.6	1140.6035	-0.0019	LDSEAIQILK
10.6	1140.6035	-0.0019	SLPDSEKIIK
9.6	1140.6035	-0.0019	VVSAEPISLSK
8.3	1140.5998	0.0018	FLFWKVYK
3.7	1140.5987	0.0029	AQLVSLPCLK
3.7	1140.6035	-0.0019	AVIGAELESLK
3.7	1140.6035	-0.0019	DLAEAKLEIK

AT5G18380.1

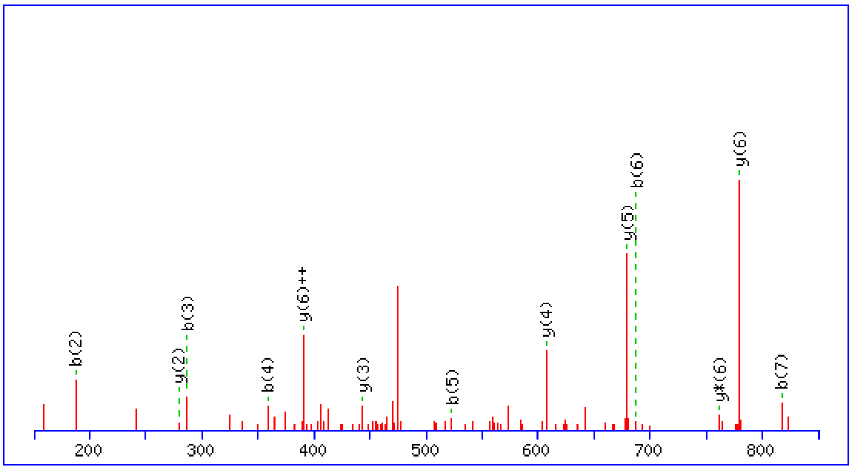
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVAYYQK**
Found in **AT5G18380.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S16 (RPS16C) | chr5:6090255-6090695 REVERSE

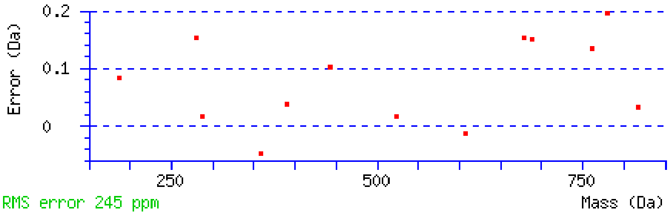
Match to Query 2128: 964.486062 from(483.250307,2+) index(2470)
Title: Elution from: 26.570 to 26.570 scan no 3120 cid35.00 polarity:+
Data file C7-1_2.mgf

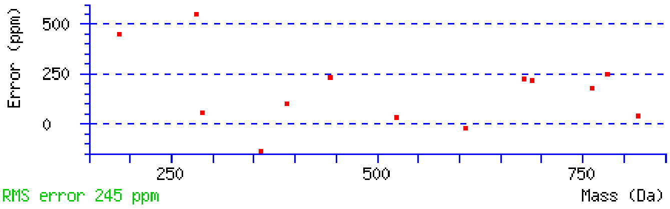
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 964.4878
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0021
Matches : 13/44 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	73.0414	37.0244			A					8
2	***187.1225***	94.0649			L	893.4609	447.2341	875.4374	438.2223	7
3	***287.1880***	144.0976			V	**779.3798**	390.1936	761.3563	381.1818	6
4	***359.2221***	180.1147			A	**679.3144**	340.1608	661.2908	331.1490	5
5	***523.2825***	262.1449			Y	**607.2802**	304.1438	589.2567	295.1320	4
6	***687.3429***	344.1751			Y	**443.2199**	222.1136	425.1963	213.1018	3
7	***817.3955***	409.2014	799.3719	400.1896	Q	**279.1595**	140.0834	261.1359	131.0716	2
8					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of ALVAYYQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.4	964.4878	-0.0017	ALVAYYQK
13.0	964.4882	-0.0022	LAAVDVAHR

AT5G18380.1

7.4	964.4856	0.0005	SSTLPPPQK
6.3	964.4878	-0.0017	FQYEKLK

Mascot: http://www.matrixscience.com/

AT5G18590.1

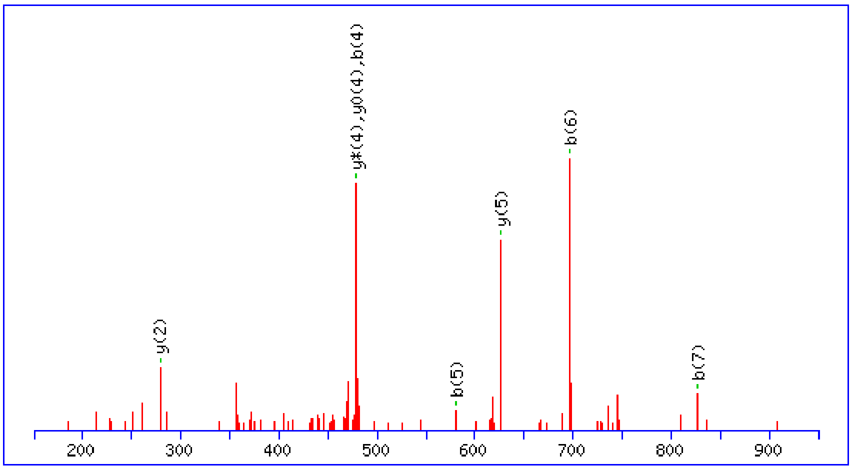
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SKQETDKK**
Found in **AT5G18590.1** in **TAIR_Arabidopsis**, Symbols: | kelch repeat-containing protein | chr5:6178518-6182188 REVERSE

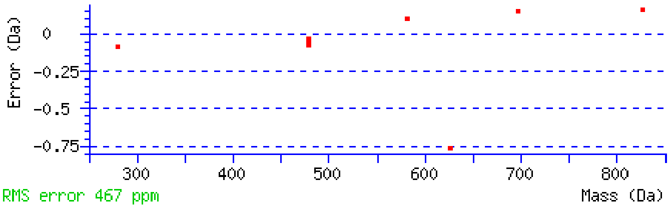
Match to Query 2280: 974.467942 from(488.241247,2+) index(2631)
Title: Elution from: 27.330 to 27.330 scan no 3287 cid35.00 polarity:+
Data file C7-1_1.mgf

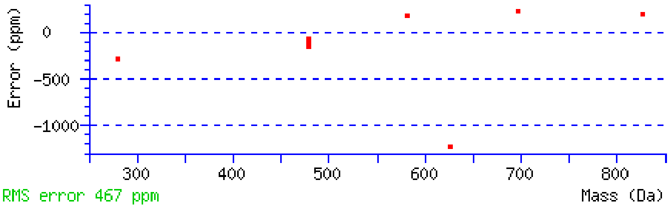
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 974.4677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.011
Matches : 8/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	**S**							**8**
2	219.1254	110.0663	201.1018	101.0545	201.1148	101.0610	**K**	887.4459	444.2266	869.4223	435.2148	869.4353	435.2213	**7**
3	349.1780	175.0926	331.1544	166.0809	331.1675	166.0874	**Q**	757.3569	379.1821	739.3333	370.1703	739.3463	370.1768	**6**
4	***479.2176***	240.1125	461.1941	231.1007	461.2071	231.1072	**E**	**627.3042**	314.1558	609.2806	305.1440	609.2937	305.1505	**5**
5	***581.2624***	291.1348	563.2388	282.1230	563.2518	282.1295	**T**	497.2646	249.1359	479.2410	240.1241	479.2540	240.1307	**4**
6	***697.2863***	349.1468	679.2628	340.1350	679.2758	340.1415	**D**	395.2199	198.1136	377.1963	189.1018	377.2093	189.1083	**3**
7	***827.3754***	414.1913	809.3518	405.1795	809.3648	405.1860	**K**	**279.1959**	140.1016	261.1723	131.0898			**2**
8							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of SKQETDKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.4	974.4677	0.0003	SKQETDKK
12.1	974.4699	-0.0020	GIFEENKK

AT5G18590.1

12.0	974.4704	-0.0024	NKGGNKSQK
8.1	974.4656	0.0023	MQRQPRK
7.9	974.4699	-0.0020	EQTFPSKK
6.2	974.4699	-0.0020	NLAEDFKK
2.7	974.4699	-0.0020	YVEAEVVR
2.0	974.4699	-0.0020	EAFDNLKK
2.0	974.4699	-0.0020	EFVQSQVK
2.0	974.4699	-0.0020	GKVQEFEK

AT5G18980.1

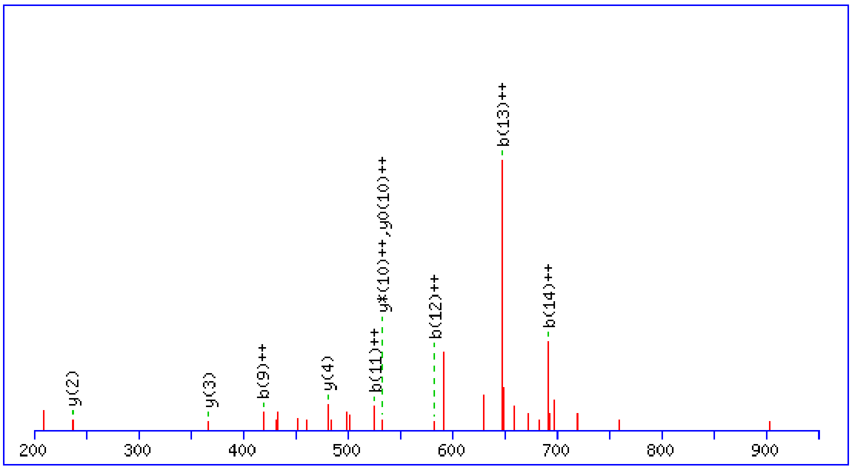
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAAGEAIAMLVLESK**
Found in **AT5G18980.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr5:6334946-6337945 REVERSE

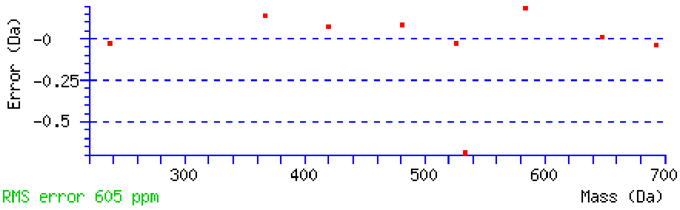
Match to Query 6454: 1530.791208 from(511.271012,3+) index(9182)
Title: Elution from: 82.586 to 82.586 scan no 12545 cid35.00 polarity:+
Data file C7-2_3.mgf

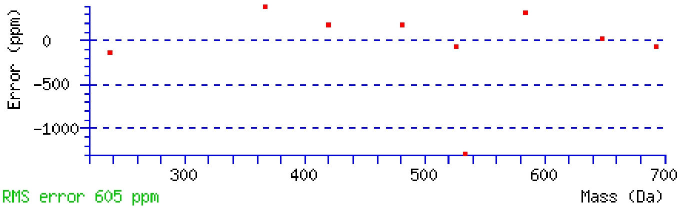
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1530.7904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.03
Matches : 10/130 fragment ions using 21 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478			I							15
2	187.1225	94.0649			A	1417.7166	709.3619	1399.6930	700.3501	1399.7060	700.3566	14
3	259.1567	130.0820			A	1345.6824	673.3448	1327.6588	664.3330	1327.6718	664.3396	13
4	317.1752	159.0912			G	1273.6483	637.3278	1255.6247	628.3160	1255.6377	628.3225	12
5	447.2148	224.1110	429.2042	215.1058	E	1215.6298	608.3185	1197.6062	599.3067	1197.6192	599.3132	11
6	519.2489	260.1281	501.2384	251.1228	A	1085.5901	543.2987	1067.5665	534.2869	1067.5796	534.2934	10
7	633.3300	317.1687	615.3195	308.1634	I	1013.5560	507.2816	995.5324	498.2698	995.5454	498.2763	9
8	705.3642	353.1857	687.3536	344.1805	A	899.4749	450.2411	881.4513	441.2293	881.4643	441.2358	8
9	837.4017	***419.2045***	819.3912	410.1992	M	827.4407	414.2240	809.4171	405.2122	809.4302	405.2187	7
10	951.4828	476.2450	933.4723	467.2398	L	695.4032	348.2052	677.3796	339.1935	677.3926	339.2000	6
11	1051.5483	***526.2778***	1033.5377	517.2725	V	581.3221	291.1647	563.2985	282.1529	563.3115	282.1594	5
12	1165.6294	***583.3183***	1147.6188	574.3130	L	**481.2567**	241.1320	463.2331	232.1202	463.2461	232.1267	4
13	1295.6690	***648.3381***	1277.6584	639.3329	E	**367.1756**	184.0914	349.1520	175.0796	349.1650	175.0861	3
14	1383.6981	***692.3527***	1365.6875	683.3474	S	**237.1359**	119.0716	219.1124	110.0598	219.1254	110.0663	2
15					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IAAGEAIAMLVLESK

AT5G18980.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.8	1530.7904	0.0008	IAAGEAIAMLVLESK
2.9	1530.7897	0.0015	LGALGVEWRPSSIK

Mascot: http://www.matrixscience.com/

AT5G19220.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EILLNLLR**
Found in **AT5G19220.1** in **TAIR_Arabidopsis**, Symbols: APL1, ADG2 | ADG2 (ADPG PYROPHOSPHORYLASE 2); glucose-1-phosphate adenylyltransferase | chr5:6463933-6466777 REVERSE

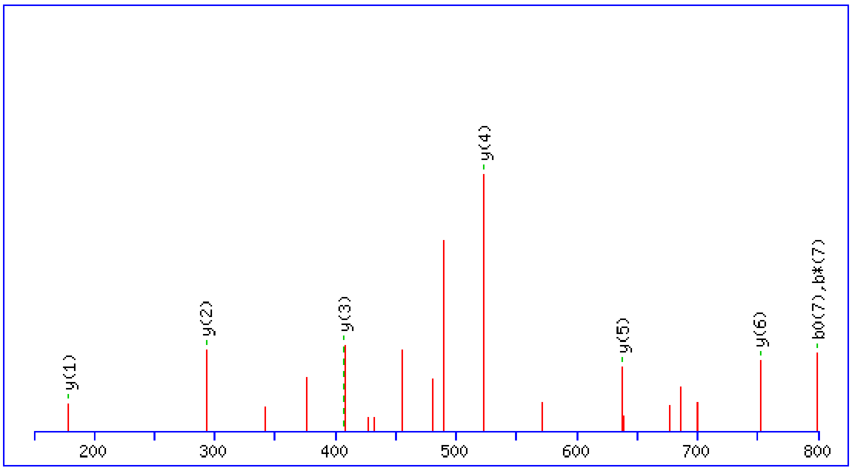
Match to Query 2619: 994.583076 from(498.298814,2+) index(9155)
Title: Elution from: 80.799 to 80.799 scan no 12125 cid35.00 polarity:+
Data file D12h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 800 Da Full range

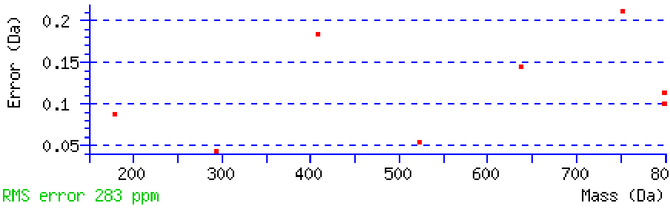
Label all possible matches ○ Label matches used for scoring ●

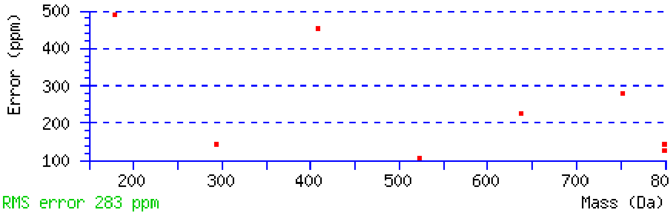
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 994.5819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.8e-006
Matches : 8/62 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	131.0469	66.0271			113.0363	57.0218	**E**					**8**
2	245.1280	123.0676			227.1174	114.0624	**I**	865.5496	433.2784	847.5260	424.2666	**7**
3	359.2091	180.1082			341.1985	171.1029	**L**	***751.4685***	376.2379	733.4449	367.2261	**6**
4	473.2902	237.1487			455.2796	228.1435	**L**	***637.3874***	319.1973	619.3638	310.1855	**5**
5	589.3272	295.1672	571.3036	286.1554	571.3166	286.1620	**N**	***523.3063***	262.1568	505.2827	253.1450	**4**
6	703.4083	352.2078	685.3847	343.1960	685.3977	343.2025	**L**	***407.2693***	204.1383	389.2457	195.1265	**3**
7	817.4894	409.2483	799.4658	400.2365	799.4788	400.2431	**L**	***293.1882***	147.0977	275.1646	138.0859	**2**
8							**R**	***179.1071***	90.0572	161.0835	81.0454	**1**





NCBI **BLAST** search of EILLNLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.5	994.5819	0.0011	EILLNLLR

AT5G19220.1

25.0	994.5819	0.0011	EILILLNR
25.0	994.5819	0.0012	ELLLLVQR
23.0	994.5819	0.0012	ELVQILLR
22.9	994.5846	-0.0015	VPRQVLLR
9.8	994.5819	0.0012	IPVTATLIR
9.8	994.5846	-0.0015	LNVRPLLR
1.1	994.5846	-0.0015	PLVRLQVR
0.3	994.5819	0.0011	IKDPLKAAK

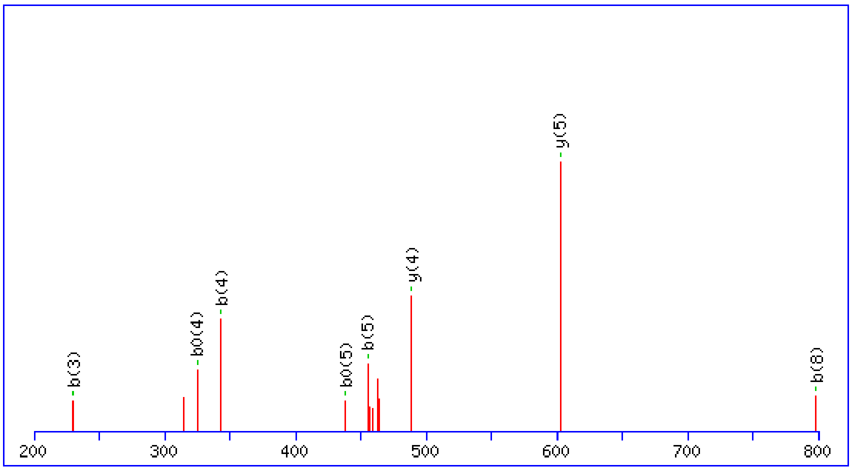
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGGILGWVK**
Found in **AT5G19370.1** in **TAIR_Arabidopsis**, Symbols: | rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein | chr5:6524249-6526631 REVERSE

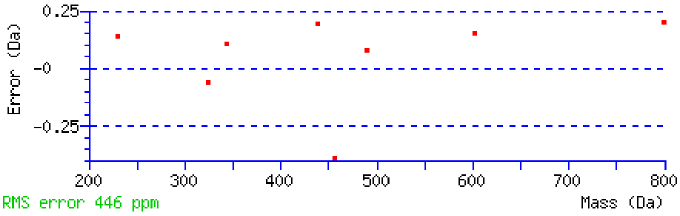
Match to Query 1904: 943.512816 from(472.763684,2+) index(7741)
Title: Elution from: 68.928 to 68.928 scan no 10265 cid35.00 polarity:+
Data file D6h-2_3.mgf

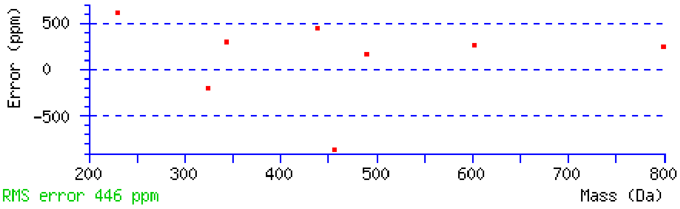
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 943.5127
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0003
Matches : 8/64 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	116.0342	58.5207	98.0237	49.5155	D					9
2	173.0557	87.0315	155.0451	78.0262	G	829.4931	415.2502	812.4665	406.7369	8
3	*230.0771*	115.5422	212.0666	106.5369	G	772.4716	386.7394	755.4450	378.2262	7
4	*343.1612*	172.0842	325.1506	163.0790	I	715.4501	358.2287	698.4236	349.7154	6
5	*456.2453*	228.6263	438.2347	219.6210	L	**602.3661**	301.6867	585.3395	293.1734	5
6	513.2667	257.1370	495.2562	248.1317	G	**489.2820**	245.1446	472.2554	236.6314	4
7	699.3461	350.1767	681.3355	341.1714	W	432.2605	216.6339	415.2340	208.1206	3
8	*798.4145*	399.7109	780.4039	390.7056	V	246.1812	123.5942	229.1547	115.0810	2
9					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of DGGILGWVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G19370.1

37.0	943.5127	0.0001	DGGILGWVK
3.5	943.5100	0.0028	WRNGKQR

AT5G19440.1

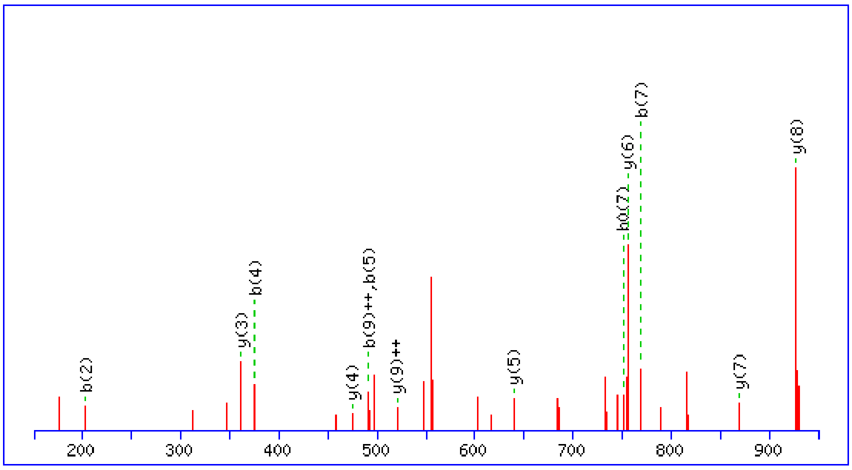
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLGIDYIPLK**
Found in **AT5G19440.1** in **TAIR_Arabidopsis**, Symbols: | cinnamyl-alcohol dehydrogenase, putative (CAD) | chr5:6556495-6558125 FORWARD

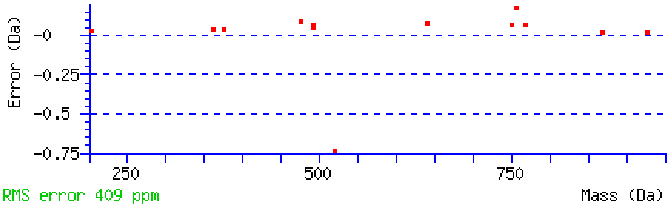
Match to Query 3733: 1128.606846 from(565.310699,2+) index(7559)
Title: Elution from: 66.047 to 66.047 scan no 9783 cid35.00 polarity:+
Data file C7-2_2.mgf

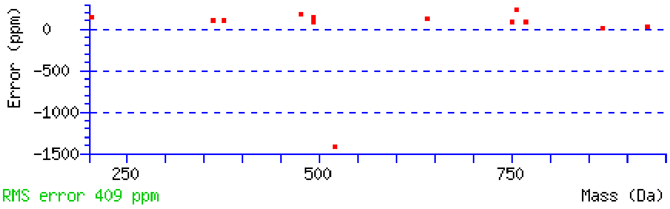
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 950 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1128.6057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.013
Matches : 13/80 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	S							10
2	**203.1174**	102.0624	185.1069	93.0571	L	1041.5839	521.2956	1023.5603	512.2838	1023.5733	512.2903	9
3	261.1359	131.0716	243.1254	122.0663	G	***927.5028***	464.2550	909.4792	455.2433	909.4922	455.2498	8
4	**375.2170**	188.1122	357.2065	179.1069	I	***869.4843***	435.2458	851.4607	426.2340	851.4737	426.2405	7
5	**491.2410**	246.1241	473.2304	237.1189	D	***755.4032***	378.2052	737.3796	369.1935	737.3926	369.2000	6
6	655.3014	328.1543	637.2908	319.1490	Y	***639.3792***	320.1933	621.3557	311.1815			5
7	**769.3825**	385.1949	751.3719	376.1896	I	***475.3189***	238.1631	457.2953	229.1513			4
8	867.4323	434.2198	849.4217	425.2145	P	***361.2378***	181.1225	343.2142	172.1107			3
9	981.5134	491.2603	963.5028	482.2550	L	263.1880	132.0976	245.1644	123.0858			2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SLGIDYIPLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G19440.1

27.5	1128.6057	0.0011	SLGIDYIPLK

AT5G19510.1

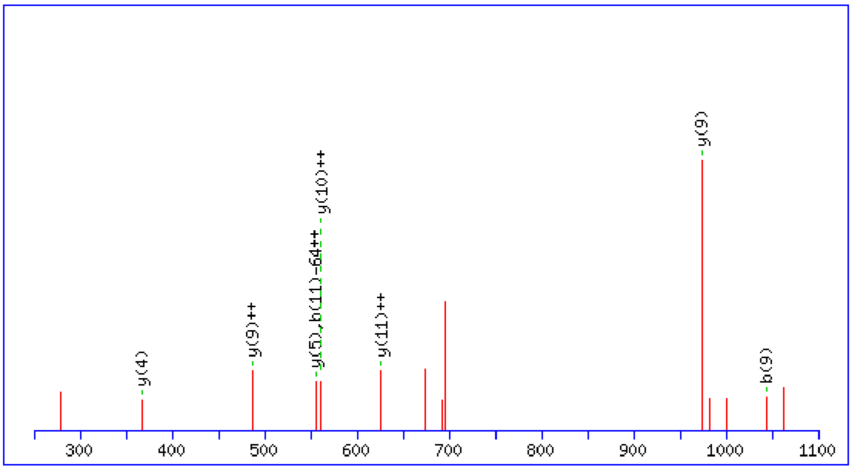
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVEMPGLFWGASK**
Found in **AT5G19510.1** in **TAIR_Arabidopsis**, Symbols: | elongation factor 1B alpha-subunit 2 (eEF1Balpha2) | chr5:6581856-6583139 REVERSE

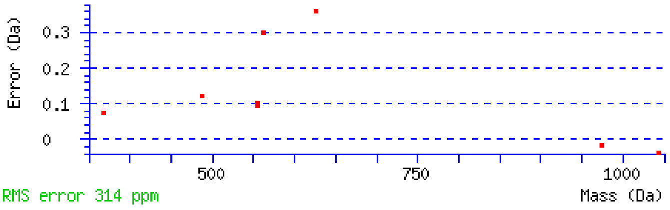
Match to Query 5803: 1408.625384 from(705.319968,2+) index(7065)
Title: Elution from: 61.084 to 61.084 scan no 9020 cid35.00 polarity:+
Data file D1d-3_1.mgf

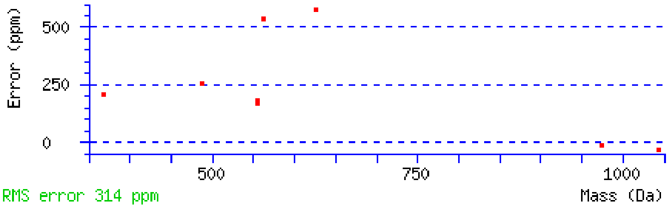
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1408.6255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.042
Matches : 8/168 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165			**G**							**13**
2	159.0912	80.0492			**V**	1351.6143	676.3108	1333.5907	667.2990	1333.6038	667.3055	**12**
3	289.1309	145.0691	271.1203	136.0638	**E**	1251.5489	626.2781	1233.5253	617.2663	1233.5383	617.2728	**11**
4	437.1633	219.0853	419.1527	210.0800	**M**	1121.5092	561.2583	1103.4857	552.2465	1103.4987	552.2530	**10**
5	535.2131	268.1102	517.2025	259.1049	**P**	***973.4768***	487.2420	955.4532	478.2303	955.4662	478.2368	**9**
6	593.2316	297.1194	575.2210	288.1141	**G**	875.4270	438.2171	857.4034	429.2054	857.4164	429.2119	**8**
7	707.3127	354.1600	689.3021	345.1547	**L**	817.4085	409.2079	799.3849	400.1961	799.3980	400.2026	**7**
8	855.3781	428.1927	837.3676	419.1874	**F**	703.3274	352.1673	685.3038	343.1556	685.3169	343.1621	**6**
9	1043.4515	522.2294	1025.4410	513.2241	**W**	***555.2620***	278.1346	537.2384	269.1228	537.2514	269.1293	**5**
10	1101.4700	551.2386	1083.4594	542.2334	**G**	***367.1886***	184.0979	349.1650	175.0861	349.1780	175.0926	**4**
11	1173.5042	587.2557	1155.4936	578.2504	**A**	309.1701	155.0887	291.1465	146.0769	291.1595	146.0834	**3**
12	1261.5332	631.2703	1243.5227	622.2650	**S**	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	**2**
13					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of GVEMPGLFWGASK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G19510.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.4	1408.6255	-0.0001	GVEMPGLFWGASK
12.9	1408.6233	0.0021	DDLYNMLPASVR
6.2	1408.6280	-0.0027	ELQLATDNFSEK
3.9	1408.6294	-0.0040	RSPEDRPMMKK
3.9	1408.6294	-0.0040	RSPEDRPMMKK
0.1	1408.6260	-0.0006	NGVAYPKNQPMR

AT5G19680.1

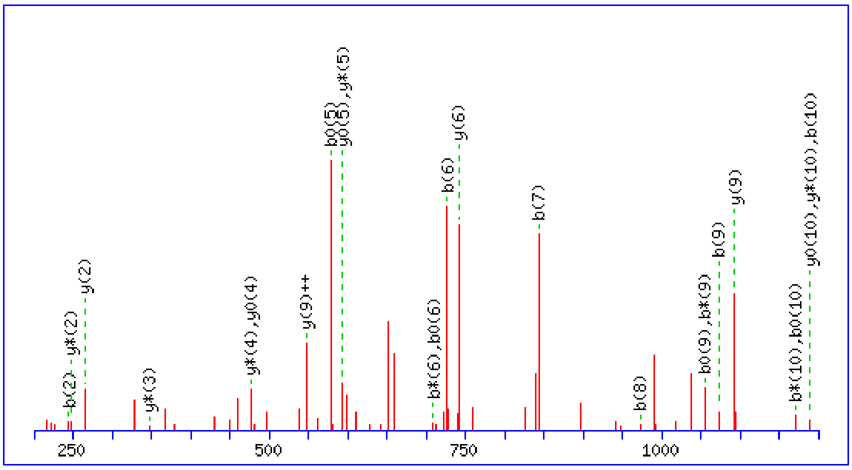
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELYVSKNEVNK**
Found in **AT5G19680.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat family protein | chr5:6649665-6651566 FORWARD

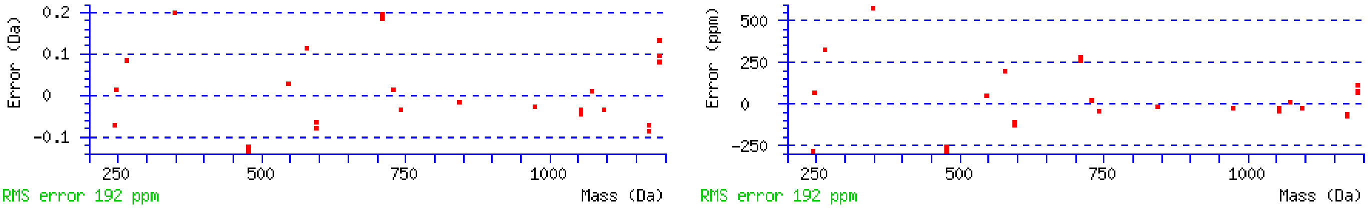
Match to Query 4595: 1336.643868 from(669.329210,2+) index(7987)
Title: Elution from: 71.719 to 71.719 scan no 10622 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1336.6433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.014
Matches : 25/104 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							11
2	***245.1280***	123.0676			227.1174	114.0624	L	1207.6110	604.3091	1189.5874	595.2973	1189.6004	595.3038	10
3	409.1884	205.0978			391.1778	196.0925	Y	**1093.5299**	547.2686	1075.5063	538.2568	1075.5193	538.2633	9
4	509.2538	255.1305			491.2433	246.1253	V	929.4695	465.2384	911.4459	456.2266	911.4589	456.2331	8
5	597.2829	299.1451			579.2723	290.1398	S	829.4040	415.2057	811.3805	406.1939	811.3935	406.2004	7
6	***727.3719***	364.1896	709.3483	355.1778	709.3613	355.1843	K	**741.3750**	371.1911	723.3514	362.1793	723.3644	362.1858	6
7	***843.4089***	422.2081	825.3853	413.1963	825.3983	413.2028	N	611.2859	306.1466	593.2624	297.1348	593.2754	297.1413	5
8	***973.4485***	487.2279	955.4250	478.2161	955.4380	478.2226	E	495.2489	248.1281	477.2254	239.1163	477.2384	239.1228	4
9	***1073.5140***	537.2606	1055.4904	528.2488	1055.5034	528.2553	V	365.2093	183.1083	347.1857	174.0965			3
10	***1189.5510***	595.2791	1171.5274	586.2673	1171.5404	586.2738	N	**265.1439**	133.0756	247.1203	124.0638			2
11							K	149.1069	75.0571	131.0833	66.0453			1



NCBI **BLAST** search of ELYVSKNEVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G19680.1

Score	Mr(calc)	Delta	Sequence
27.8	1336.6433	0.0006	ELYVSKNEVNK
8.6	1336.6408	0.0031	RFVGEPMFVPK
5.1	1336.6467	-0.0028	MLDVTGSKNLTK
2.8	1336.6460	-0.0021	VNKYNGNVVANK

AT5G19760.1

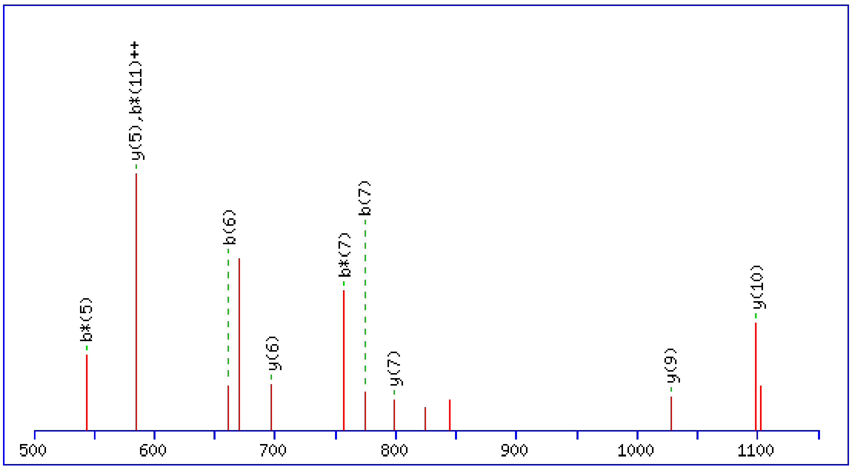
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MQADNTLPLAQR**
Found in **AT5G19760.1** in **TAIR_Arabidopsis**, Symbols: | dicarboxylate/tricarboxylate carrier (DTC) | chr5:6679593-6681847 REVERSE

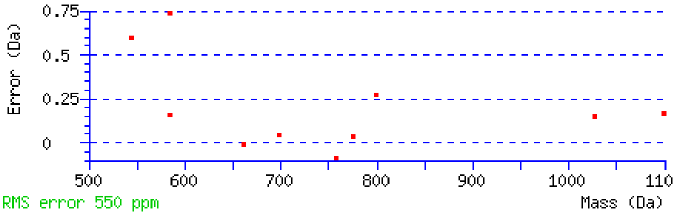
Match to Query 5116: 1356.678010 from(679.346281,2+) index(3465)
Title: Elution from: 33.505 to 33.505 scan no 4313 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

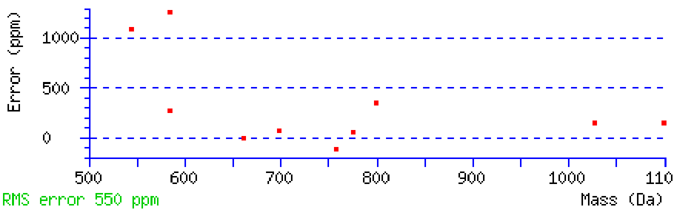


Monoisotopic mass of neutral peptide Mr(calc): 1356.6820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00029
Matches : 10/112 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					**M**							**12**
2	260.1063	130.5568	243.0798	122.0435			**Q**	1226.6488	613.8280	1209.6222	605.3148	1208.6382	604.8227	**11**
3	331.1435	166.0754	314.1169	157.5621			**A**	***1098.5902***	549.7987	1081.5637	541.2855	1080.5796	540.7935	**10**
4	446.1704	223.5888	429.1438	215.0756	428.1598	214.5836	**D**	***1027.5531***	514.2802	1010.5265	505.7669	1009.5425	505.2749	**9**
5	560.2133	280.6103	543.1868	272.0970	542.2028	271.6050	**N**	912.5261	456.7667	895.4996	448.2534	894.5156	447.7614	**8**
6	**661.2610**	331.1341	644.2345	322.6209	643.2504	322.1289	**T**	***798.4832***	399.7452	781.4567	391.2320	780.4727	390.7400	**7**
7	**774.3451**	387.6762	757.3185	379.1629	756.3345	378.6709	**L**	***697.4355***	349.2214	680.4090	340.7081			**6**
8	871.3978	436.2026	854.3713	427.6893	853.3873	427.1973	**P**	***584.3515***	292.6794	567.3249	284.1661			**5**
9	984.4819	492.7446	967.4553	484.2313	966.4713	483.7393	**L**	487.2987	244.1530	470.2722	235.6397			**4**
10	1055.5190	528.2631	1038.4925	519.7499	1037.5084	519.2579	**A**	374.2146	187.6110	357.1881	179.0977			**3**
11	1183.5776	592.2924	1166.5510	583.7792	1165.5670	583.2871	**Q**	303.1775	152.0924	286.1510	143.5791			**2**
12							**R**	175.1190	88.0631	158.0924	79.5498			**1**



RMS error 550 ppm



RMS error 550 ppm

NCBI **BLAST** search of MQADNTLPLAQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G19760.1

Score	Mr(calc)	Delta	Sequence
41.0	1356.6820	-0.0040	MQADNTLPLAQR

Mascot: http://www.matrixscience.com/

AT5G19770.1

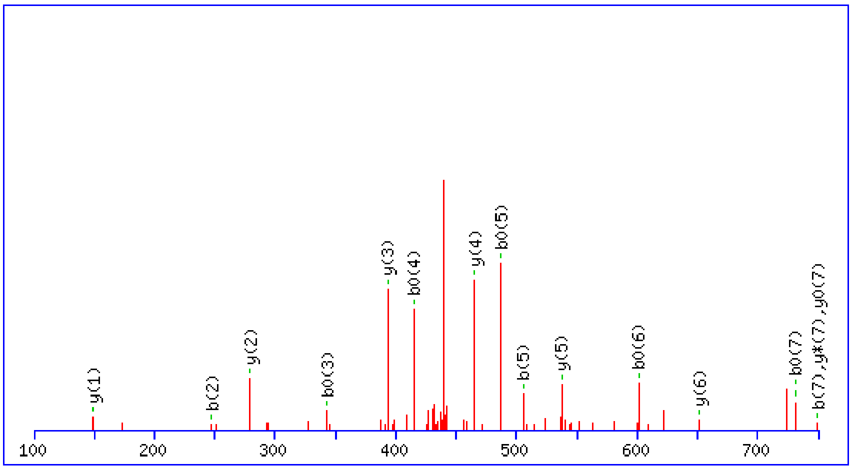
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDLAALEK**
Found in **AT5G19770.1** in **TAIR_Arabidopsis**, Symbols: TUA3 | TUA3 (tubulin alpha-3) | chr5:6682763-6684476 REVERSE

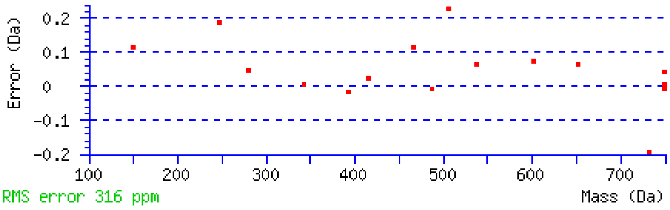
Match to Query 1535: 896.431178 from(449.222865,2+) index(2619)
Title: Elution from: 27.341 to 27.341 scan no 3261 cid35.00 polarity:+
Data file 0-3_2.mgf

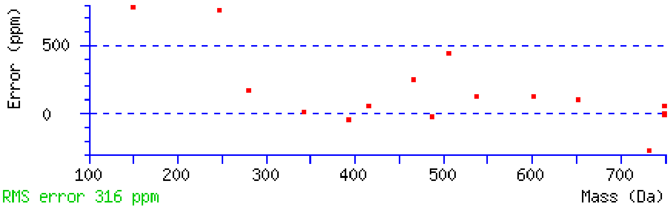
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 896.4333
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00017
Matches : 16/68 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							8
2	**247.0709**	124.0391	229.0603	115.0338	D	767.4010	384.2041	749.3774	375.1923	749.3904	375.1988	7
3	361.1520	181.0796	343.1414	172.0743	L	***651.3770***	326.1921	633.3534	317.1803	633.3664	317.1869	6
4	433.1861	217.0967	415.1756	208.0914	A	***537.2959***	269.1516	519.2723	260.1398	519.2853	260.1463	5
5	**505.2203**	253.1138	487.2097	244.1085	A	***465.2618***	233.1345	447.2382	224.1227	447.2512	224.1292	4
6	619.3014	310.1543	601.2908	301.1490	L	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
7	**749.3410**	375.1741	731.3304	366.1689	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
8					K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EDLAALEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.0	896.4333	-0.0021	EDLAALEK
19.6	896.4333	-0.0021	GEIEALEK

AT5G19770.1

19.6	896.4313	-0.0001	RHMALEK
13.0	896.4330	-0.0019	MFFGLFK
11.2	896.4333	-0.0021	EELELQK
11.2	896.4333	-0.0021	EIEELQK
9.8	896.4333	-0.0022	EDPSSLIK
9.8	896.4333	-0.0021	IEEELQK
9.8	896.4333	-0.0021	IEEQLEK
9.8	896.4333	-0.0021	IEQELEK

AT5G19940.1

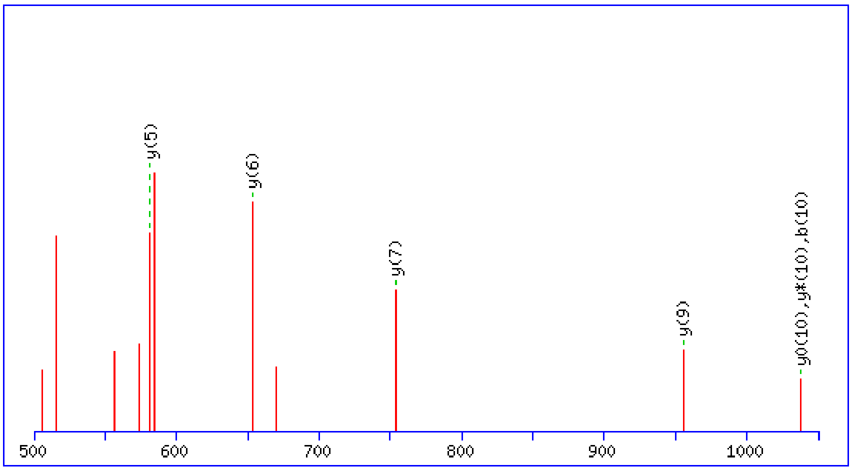
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVAQVAGELQK**
Found in **AT5G19940.1** in **TAIR_Arabidopsis**, Symbols: | plastid-lipid associated protein PAP-related / fibrillin-related | chr5:6739695-6740663 FORWARD

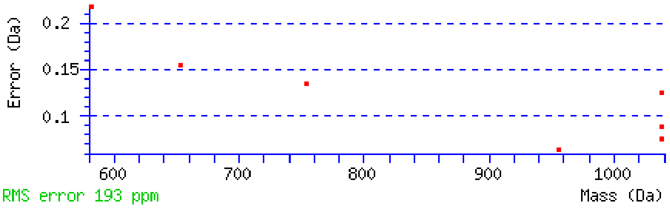
Match to Query 4204: 1184.581414 from(593.297983,2+) index(2431)
Title: Elution from: 26.744 to 26.744 scan no 3075 cid35.00 polarity:+
Data file 0-2_1.mgf

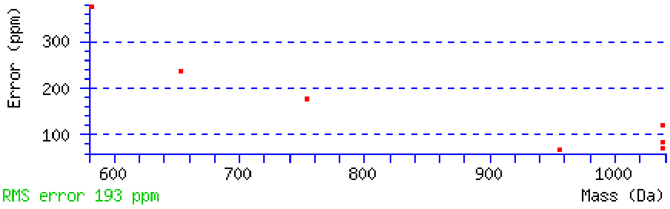
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1184.5829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0019
Matches : 7/108 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							11
2	231.1124	116.0598			213.1018	107.0545	V	1055.5506	528.2789	1037.5270	519.2671	1037.5400	519.2737	10
3	303.1465	152.0769			285.1359	143.0716	A	***955.4851***	478.2462	937.4616	469.2344	937.4746	469.2409	9
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	Q	883.4510	442.2291	865.4274	433.2173	865.4404	433.2239	8
5	533.2646	267.1359	515.2410	258.1241	515.2540	258.1307	V	***753.3983***	377.2028	735.3748	368.1910	735.3878	368.1975	7
6	605.2987	303.1530	587.2752	294.1412	587.2882	294.1477	A	***653.3329***	327.1701	635.3093	318.1583	635.3223	318.1648	6
7	663.3172	332.1623	645.2937	323.1505	645.3067	323.1570	G	***581.2987***	291.1530	563.2752	282.1412	563.2882	282.1477	5
8	793.3569	397.1821	775.3333	388.1703	775.3463	388.1768	E	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	4
9	907.4380	454.2226	889.4144	445.2108	889.4274	445.2173	L	393.2406	197.1239	375.2170	188.1122			3
10	1037.4906	519.2489	1019.4670	510.2372	1019.4801	510.2437	Q	279.1595	140.0834	261.1359	131.0716			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EVAQVAGELQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G19940.1

Score	Mr(calc)	Delta	Sequence
33.2	1184.5829	-0.0015	EVAQVAGELQK
11.4	1184.5829	-0.0015	EVDALLQEVR
1.7	1184.5782	0.0032	HKKIIDECK
0.9	1184.5782	0.0032	MEQKQHILK

AT5G19990.1

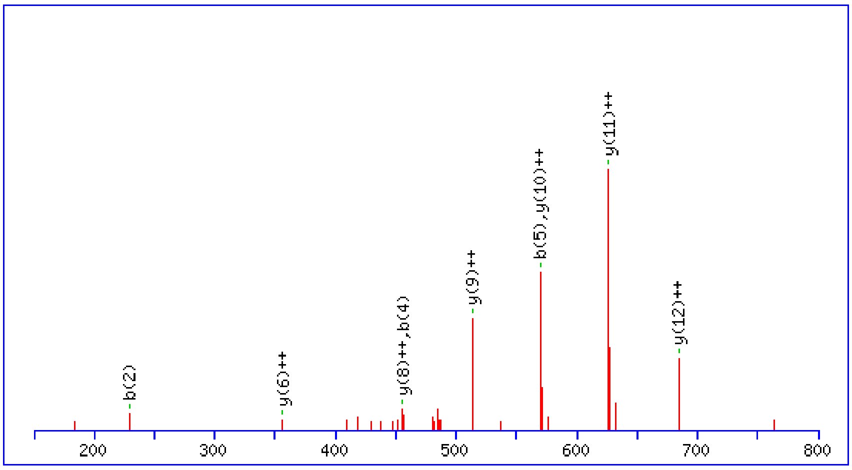
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDILDQALLRPGR**
Found in **AT5G19990.1** in **TAIR_Arabidopsis**, Symbols: ATSUG1, RPT6A | RPT6A; ATPase | chr5:6752146-6754920 FORWARD

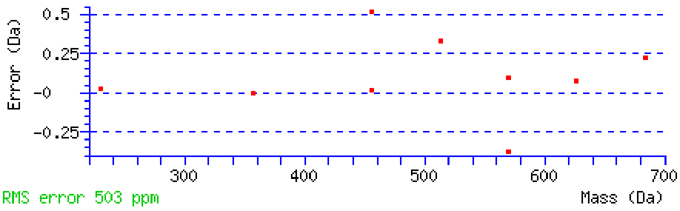
Match to Query 6207: 1478.858340 from(493.960056,3+) index(7929)
Title: Elution from: 69.279 to 69.279 scan no 10378 cid35.00 polarity:+
Data file C7-3_2.mgf

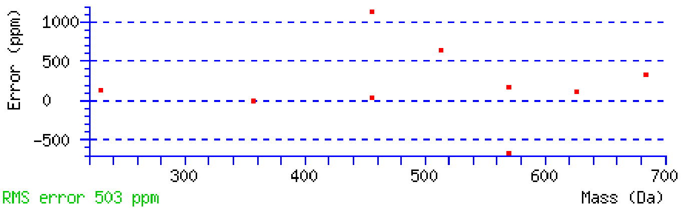
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1478.8569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 3.1e-005
Matches : 9/116 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	229.1183	115.0628			211.1077	106.0575	D	1366.7801	683.8937	1349.7536	675.3804	1348.7696	674.8884	12
3	342.2023	171.6048			324.1918	162.5995	I	1251.7532	626.3802	1234.7266	617.8670	1233.7426	617.3749	11
4	455.2864	228.1468			437.2758	219.1416	L	1138.6691	569.8382	1121.6426	561.3249	1120.6586	560.8329	10
5	570.3134	285.6603			552.3028	276.6550	D	1025.5851	513.2962	1008.5585	504.7829	1007.5745	504.2909	9
6	698.3719	349.6896	681.3454	341.1763	680.3614	340.6843	Q	910.5581	455.7827	893.5316	447.2694			8
7	769.4090	385.2082	752.3825	376.6949	751.3985	376.2029	A	782.4995	391.7534	765.4730	383.2401			7
8	882.4931	441.7502	865.4666	433.2369	864.4825	432.7449	L	711.4624	356.2348	694.4359	347.7216			6
9	995.5772	498.2922	978.5506	489.7790	977.5666	489.2869	L	598.3784	299.6928	581.3518	291.1795			5
10	1151.6783	576.3428	1134.6517	567.8295	1133.6677	567.3375	R	485.2943	243.1508	468.2677	234.6375			4
11	1248.7310	624.8692	1231.7045	616.3559	1230.7205	615.8639	P	329.1932	165.1002	312.1666	156.5870			3
12	1305.7525	653.3799	1288.7260	644.8666	1287.7419	644.3746	G	232.1404	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IDILDQALLRPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G19990.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.3	1478.8569	0.0015	IDILDQALLRPGR
5.6	1478.8569	0.0015	LQKEKASQLLHGK
2.8	1478.8569	0.0015	LNVLRPQLEELR
0.6	1478.8609	-0.0026	DVKLWQVHTLLK
0.4	1478.8569	0.0014	QDLVIHLGLKSTR

AT5G20000.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVIELPIK**
Found in **AT5G20000.1** in **TAIR_Arabidopsis**, Symbols: | (REGULATORY PARTICLE TRIPLE-A 6A); ATPase | chr5:6756917-6759552 FORWARD

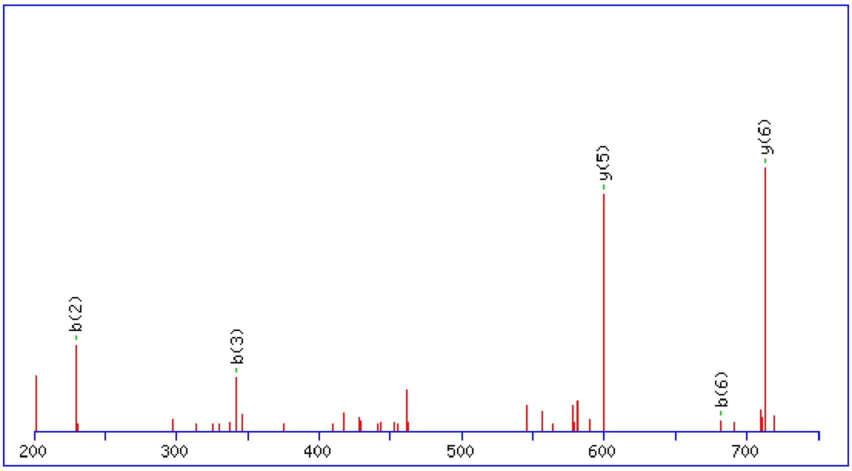
Match to Query 1594: 939.564480 from(470.789516,2+) index(6788)
Title: Elution from: 62.764 to 62.764 scan no 8880 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 750 Da Full range

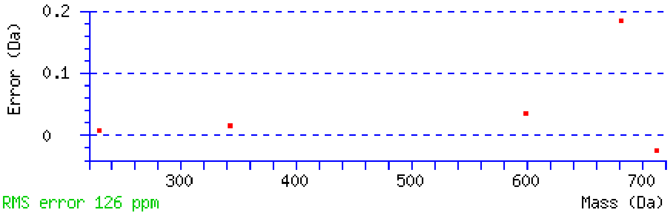
Label all possible matches ○ Label matches used for scoring ●

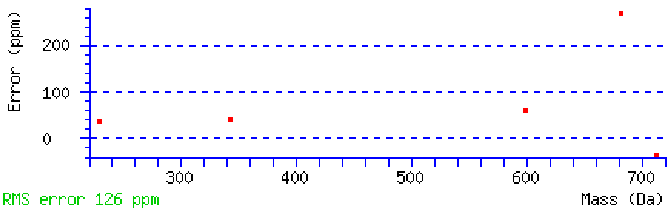
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 939.5641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0017
Matches : 5/62 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							8
2	*229.1183*	115.0628	211.1077	106.0575	V	811.5288	406.2680	794.5022	397.7547	793.5182	397.2627	7
3	*342.2023*	171.6048	324.1918	162.5995	I	**712.4604**	356.7338	695.4338	348.2205	694.4498	347.7285	6
4	471.2449	236.1261	453.2344	227.1208	E	**599.3763**	300.1918	582.3497	291.6785	581.3657	291.1865	5
5	584.3290	292.6681	566.3184	283.6629	L	470.3337	235.6705	453.3071	227.1572			4
6	*681.3818*	341.1945	663.3712	332.1892	P	357.2496	179.1285	340.2231	170.6152			3
7	794.4658	397.7366	776.4553	388.7313	I	260.1969	130.6021	243.1703	122.0888			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EVIELPIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.6	939.5641	0.0004	EVIELPIK

AT5G20000.1

15.6	939.5641	0.0004	DIIPILEK

Mascot: http://www.matrixscience.com/

AT5G20010.1

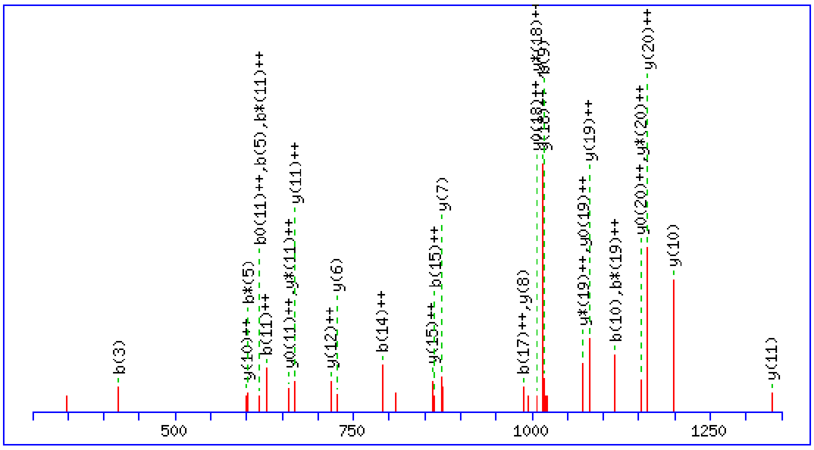
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KYEPTIGVEVHPLDFFTNCGK**
Found in **AT5G20010.1** in **TAIR_Arabidopsis**, Symbols: RAN1, ATRAN1, RAN-1 | RAN-1 (RAS RELATED NUCLEAR PROTEIN); GTP binding | chr5:6760366-6761749 FORWARD

Match to Query 10180: 2450.195874 from(817.739234,3+) index(8543)
Title: Elution from: 76.320 to 76.320 scan no 11487 cid35.00 polarity:+
Data file D12h-1_3.mgf

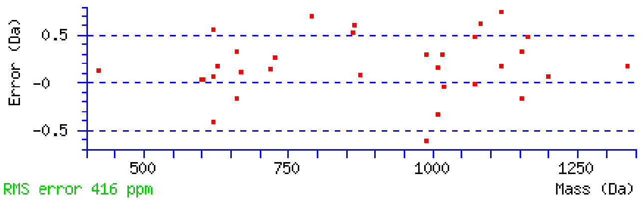
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

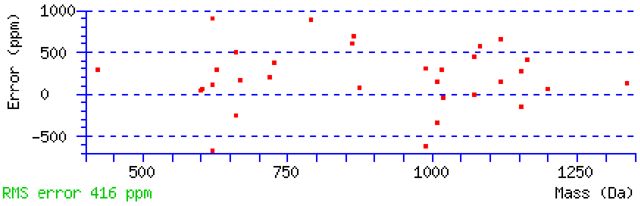


Monoisotopic mass of neutral peptide Mr(calc): 2450.1940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.1e-006
Matches : 33/228 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							21
2	292.1656	146.5864	275.1390	138.0731			Y	2323.1063	1162.0568	2306.0798	1153.5435	2305.0958	1153.0515	20
3	**421.2082**	211.1077	404.1816	202.5944	403.1976	202.1024	E	2160.0430	1080.5251	2143.0165	1072.0119	2142.0325	1071.5199	19
4	518.2609	259.6341	501.2344	251.1208	500.2504	250.6288	P	2031.0004	1016.0039	2013.9739	1007.4906	2012.9899	1006.9986	18
5	**619.3086**	310.1579	602.2821	301.6447	601.2980	301.1527	T	1933.9477	967.4775	1916.9211	958.9642	1915.9371	958.4722	17
6	732.3927	366.7000	715.3661	358.1867	714.3821	357.6947	I	1832.9000	916.9536	1815.8734	908.4404	1814.8894	907.9483	16
7	789.4141	395.2107	772.3876	386.6974	771.4036	386.2054	G	1719.8159	860.4116	1702.7894	851.8983	1701.8054	851.4063	15
8	888.4825	444.7449	871.4560	436.2316	870.4720	435.7396	V	1662.7945	831.9009	1645.7679	823.3876	1644.7839	822.8956	14
9	**1017.5251**	509.2662	1000.4986	500.7529	999.5146	500.2609	E	1563.7260	782.3667	1546.6995	773.8534	1545.7155	773.3614	13
10	**1116.5936**	558.8004	1099.5670	550.2871	1098.5830	549.7951	V	1434.6834	717.8454	1417.6569	709.3321	1416.6729	708.8401	12
11	1253.6525	***627.3299***	1236.6259	618.8166	1235.6419	618.3246	H	**1335.6150**	668.3112	1318.5885	659.7979	1317.6045	659.3059	11
12	1350.7052	675.8563	1333.6787	667.3430	1332.6947	666.8510	P	**1198.5561**	599.7817	1181.5296	591.2684	1180.5456	590.7764	10
13	1463.7893	732.3983	1446.7627	723.8850	1445.7787	723.3930	L	1101.5034	551.2553	1084.4768	542.7420	1083.4928	542.2500	9
14	1578.8162	***789.9118***	1561.7897	781.3985	1560.8057	780.9065	D	**988.4193**	494.7133	971.3927	486.2000	970.4087	485.7080	8
15	1725.8847	***863.4460***	1708.8581	854.9327	1707.8741	854.4407	F	**873.3924**	437.1998	856.3658	428.6865	855.3818	428.1945	7
16	1872.9531	936.9802	1855.9265	928.4669	1854.9425	927.9749	F	**726.3239**	363.6656	709.2974	355.1523	708.3134	354.6603	6
17	1974.0007	***987.5040***	1956.9742	978.9907	1955.9902	978.4987	T	579.2555	290.1314	562.2290	281.6181	561.2450	281.1261	5
18	2088.0437	1044.5255	2071.0171	1036.0122	2070.0331	1035.5202	N	478.2078	239.6076	461.1813	231.0943			4
19	2248.0743	1124.5408	2231.0478	1116.0275	2230.0638	1115.5355	C	364.1649	182.5861	347.1384	174.0728			3
20	2305.0958	***1153.0515***	2288.0692	1144.5383	2287.0852	1144.0462	G	204.1343	102.5708	187.1077	94.0575			2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT5G20010.1





NCBI **BLAST** search of KYEPTIGVEVHPLDFFTNCGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.4	2450.1940	0.0018	KYEPTIGVEVHPLDFFTNCGK

Mascot: http://www.matrixscience.com/

AT5G20290.1

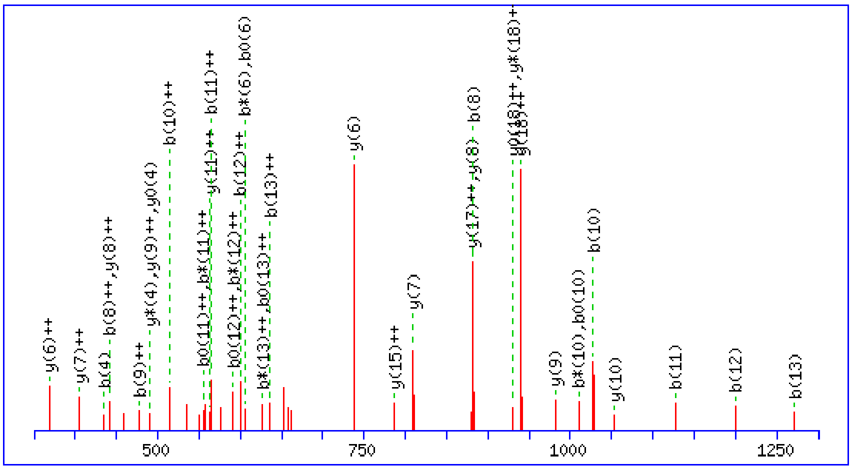
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDGEEGEEAAVAAPEEVKK**
Found in **AT5G20290.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S8 (RPS8A) | chr5:6851697-6853014 REVERSE

Match to Query 8965: 2006.892510 from(669.971446,3+) index(1174)
Title: Elution from: 18.553 to 18.553 scan no 1676 cid35.00 polarity:+
Data file D12h-2_3.mgf

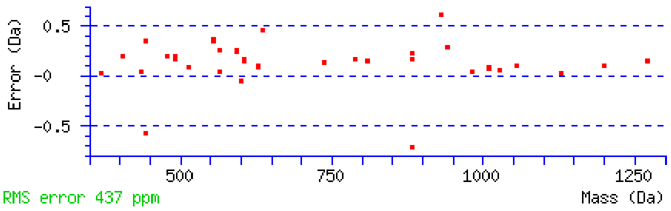
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

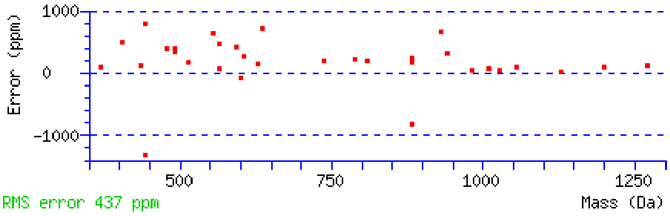


Monoisotopic mass of neutral peptide Mr(calc): 2006.8937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 2.2e-005
Matches : 40/208 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							19
2	247.1203	124.0638	229.0967	115.0520	229.1097	115.0585	D	1877.8119	939.4096	1859.7884	930.3978	1859.8014	930.4043	18
3	305.1388	153.0730	287.1152	144.0612	287.1282	144.0677	G	1761.7880	881.3976	1743.7644	872.3858	1743.7774	872.3923	17
4	**435.1784**	218.0928	417.1548	209.0811	417.1678	209.0876	E	1703.7695	852.3884	1685.7459	843.3766	1685.7589	843.3831	16
5	565.2180	283.1127	547.1945	274.1009	547.2075	274.1074	E	1573.7298	787.3686	1555.7063	778.3568	1555.7193	778.3633	15
6	623.2365	312.1219	605.2130	303.1101	605.2260	303.1166	G	1443.6902	722.3487	1425.6666	713.3370	1425.6796	713.3435	14
7	753.2762	377.1417	735.2526	368.1299	735.2656	368.1364	E	1385.6717	693.3395	1367.6481	684.3277	1367.6611	684.3342	13
8	**883.3158**	***442.1615***	865.2922	433.1497	865.3052	433.1563	E	1255.6321	628.3197	1237.6085	619.3079	1237.6215	619.3144	12
9	955.3499	***478.1786***	937.3264	469.1668	937.3394	469.1733	A	1125.5925	563.2999	1107.5689	554.2881	1107.5819	554.2946	11
10	**1027.3841**	***514.1957***	1009.3605	505.1839	1009.3735	505.1904	A	**1053.5583**	527.2828	1035.5347	518.2710	1035.5477	518.2775	10
11	**1127.4495**	***564.2284***	1109.4260	555.2166	1109.4390	555.2231	V	**981.5242**	491.2657	963.5006	482.2539	963.5136	482.2604	9
12	**1199.4837**	***600.2455***	1181.4601	591.2337	1181.4731	591.2402	A	**881.4587**	441.2330	863.4351	432.2212	863.4481	432.2277	8
13	**1271.5178**	***636.2626***	1253.4943	627.2508	1253.5073	627.2573	A	**809.4246**	405.2159	791.4010	396.2041	791.4140	396.2106	7
14	1369.5676	685.2875	1351.5441	676.2757	1351.5571	676.2822	P	**737.3904**	369.1988	719.3668	360.1871	719.3798	360.1936	6
15	1499.6073	750.3073	1481.5837	741.2955	1481.5967	741.3020	E	639.3406	320.1739	621.3170	311.1622	621.3300	311.1687	5
16	1629.6469	815.3271	1611.6233	806.3153	1611.6363	806.3218	E	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	4
17	1729.7123	865.3598	1711.6888	856.3480	1711.7018	856.3545	V	379.2614	190.1343	361.2378	181.1225			3
18	1859.8014	***930.4043***	1841.7778	921.3925	1841.7908	921.3990	K	279.1959	140.1016	261.1723	131.0898			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT5G20290.1





NCBI **BLAST** search of KDGEEGEEAAVAAPEEVKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.2	2006.8937	-0.0012	KDGEEGEEAAVAAPEEVKK
0.1	2006.8937	-0.0012	EKQPDNEIKTSEEDKPV

Mascot: http://www.matrixscience.com/

AT5G20600.1

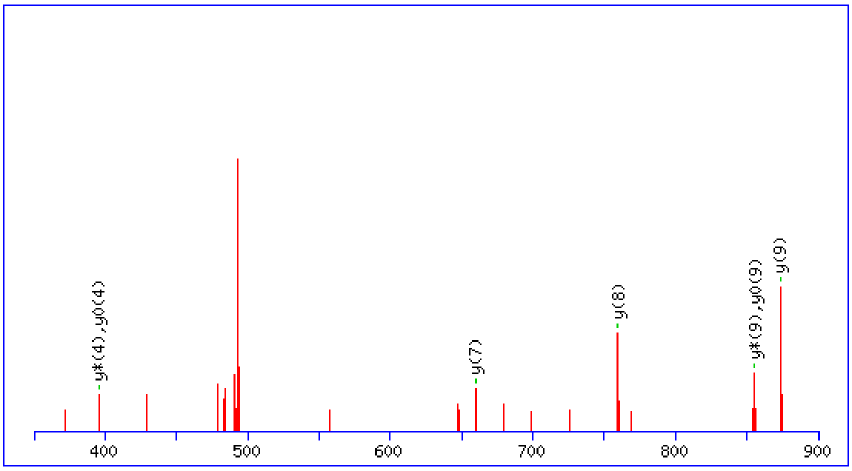
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KIVANGSSSK**
Found in **AT5G20600.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO43199.1); contains InterPro domain Nucleolar, Nop52; (InterPro:IPR010301) | chr5:6966347-6967945 REVERSE

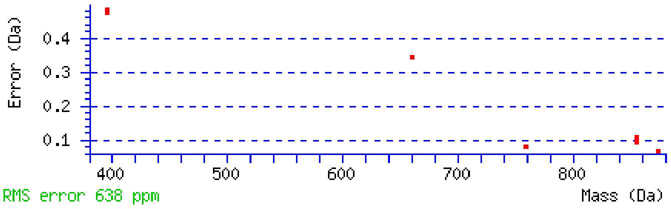
Match to Query 2470: 1002.513326 from(502.263939,2+) index(496)
Title: Elution from: 10.516 to 10.516 scan no 763 cid35.00 polarity:+
Data file D6h-3_1.mgf

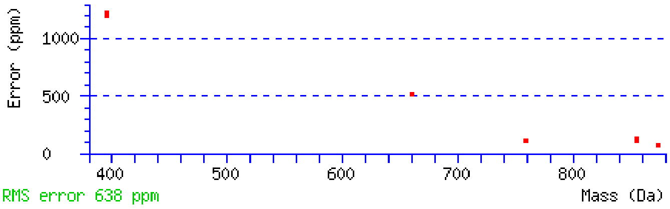
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1002.5120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.022
Matches : 8/94 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							10
2	245.1774	123.0923	227.1538	114.0805			I	***873.4303***	437.2188	855.4067	428.2070	855.4197	428.2135	9
3	345.2429	173.1251	327.2193	164.1133			V	***759.3492***	380.1782	741.3256	371.1664	741.3386	371.1729	8
4	417.2770	209.1421	399.2534	200.1303			A	***659.2837***	330.1455	641.2601	321.1337	641.2731	321.1402	7
5	533.3140	267.1606	515.2904	258.1488			N	587.2496	294.1284	569.2260	285.1166	569.2390	285.1231	6
6	591.3325	296.1699	573.3089	287.1581			G	471.2126	236.1099	453.1890	227.0981	453.2020	227.1046	5
7	679.3616	340.1844	661.3380	331.1726	661.3510	331.1791	S	413.1941	207.1007	395.1705	198.0889	395.1835	198.0954	4
8	767.3906	384.1990	749.3670	375.1872	749.3801	375.1937	S	325.1650	163.0861	307.1414	154.0743	307.1544	154.0809	3
9	855.4197	428.2135	837.3961	419.2017	837.4091	419.2082	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KIVANGSSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G20600.1

Score	Mr(calc)	Delta	Sequence
26.1	1002.5120	0.0013	KIVANGSSSK
22.0	1002.5142	-0.0009	EIVKEAFR
22.0	1002.5142	-0.0009	ELVLSFAGR
11.6	1002.5142	-0.0009	KLAEQFQK
10.0	1002.5116	0.0018	EIYVTELK
10.0	1002.5142	-0.0009	ELQAYLVR
10.0	1002.5147	-0.0014	KLAQRSER
10.0	1002.5142	-0.0009	KLLFAEDR
9.6	1002.5120	0.0013	KSNSALDKK
9.6	1002.5143	-0.0009	KYTPLAGNK

AT5G20640.1

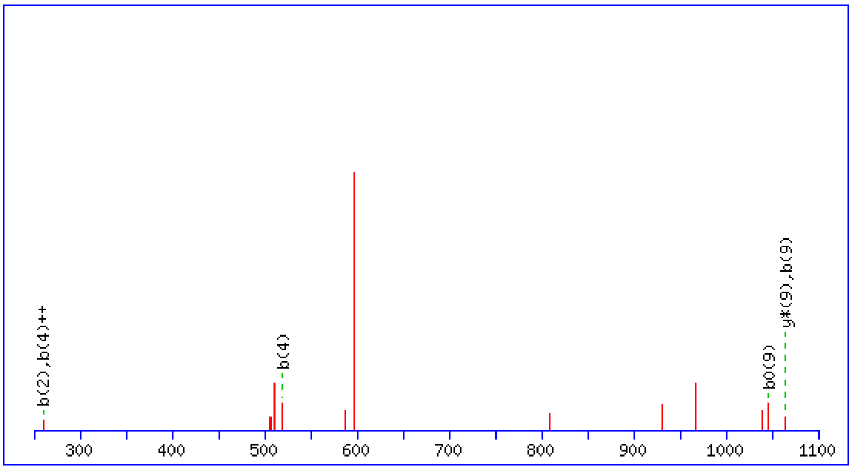
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EMEEMVGNKK**
Found in **AT5G20640.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G05910.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN71378.1); contains InterPro domain Protein of unknown function DUF567 (InterPro:IPR007612) | chr5:6984381-6985

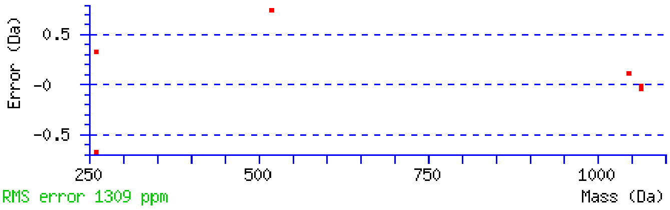
Match to Query 4077: 1209.534256 from(605.774404,2+) index(1100)
Title: Elution from: 18.642 to 18.642 scan no 1606 cid35.00 polarity:+
Data file D6h-2_2.mgf

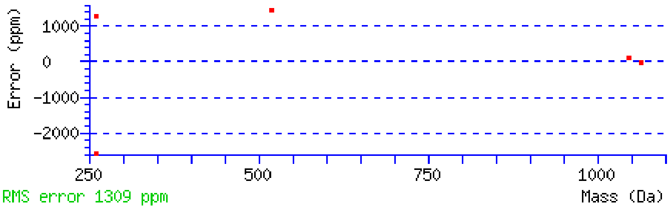
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1209.5369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 15 **Expect:** 0.045
Matches : 6/128 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	***261.0904***	131.0488			243.0798	122.0435	M	1081.5016	541.2545	1064.4751	532.7412	1063.4911	532.2492	9
3	390.1329	195.5701			372.1224	186.5648	E	950.4612	475.7342	933.4346	467.2209	932.4506	466.7289	8
4	***519.1755***	260.0914			501.1650	251.0861	E	821.4186	411.2129	804.3920	402.6996	803.4080	402.2076	7
5	666.2109	333.6091			648.2004	324.6038	M	692.3760	346.6916	675.3494	338.1783			6
6	765.2794	383.1433			747.2688	374.1380	V	545.3406	273.1739	528.3140	264.6606			5
7	822.3008	411.6540			804.2903	402.6488	G	446.2722	223.6397	429.2456	215.1264			4
8	936.3437	468.6755	919.3172	460.1622	918.3332	459.6702	N	389.2507	195.1290	372.2241	186.6157			3
9	***1064.4387***	532.7230	1047.4122	524.2097	1046.4281	523.7177	K	275.2078	138.1075	258.1812	129.5942			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EMEEMVGNKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G20640.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.7	1209.5369	-0.0027	EMEEMVGNKK
10.9	1209.5369	-0.0027	EMDMVGSSNLK

AT5G20720.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITPLPVSTGSTVLYSK**
Found in **AT5G20720.1** in **TAIR_Arabidopsis**, Symbols: CPN10, CHCPN10, ATCPN21, CPN21, CPN20 | CPN20 (CHAPERONIN 20); calmodulin binding | chr5:7015017-7016356 FORWARD

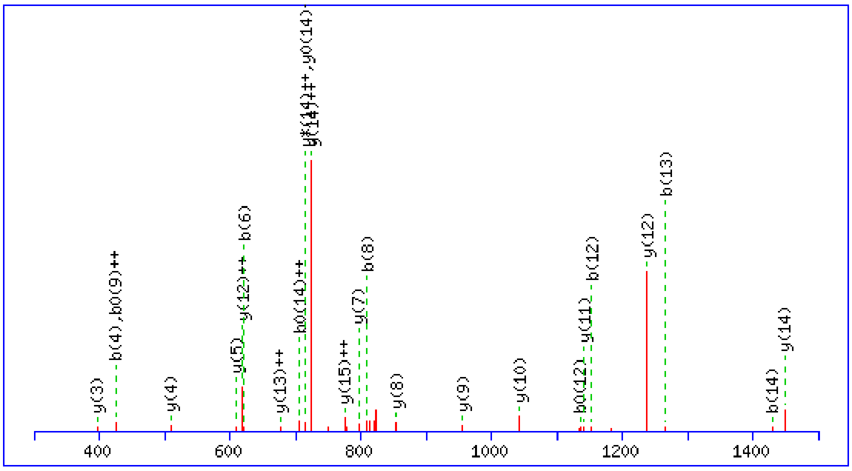
Match to Query 7588: 1661.919058 from(831.966805,2+) index(6289)
Title: Elution from: 55.760 to 55.760 scan no 8072 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

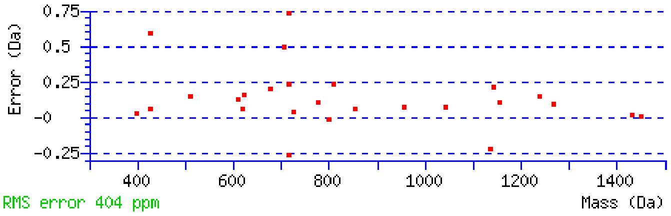
Show Y-axis ☐

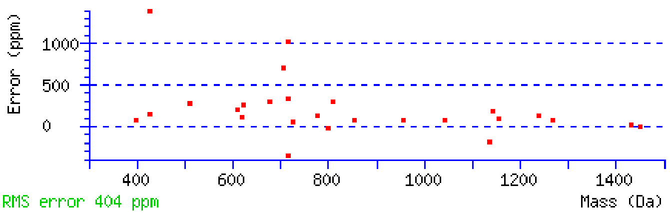


Monoisotopic mass of neutral peptide Mr(calc): 1661.9240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 1.5e-009
Matches : 26/146 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							16
2	215.1390	108.0731	197.1285	99.0679	T	1549.8472	775.4272	1532.8207	766.9140	1531.8366	766.4220	15
3	312.1918	156.5995	294.1812	147.5942	P	***1448.7995***	724.9034	1431.7730	716.3901	1430.7890	715.8981	14
4	**425.2758**	213.1416	407.2653	204.1363	L	1351.7468	676.3770	1334.7202	667.8637	1333.7362	667.3717	13
5	522.3286	261.6679	504.3180	252.6627	P	***1238.6627***	619.8350	1221.6361	611.3217	1220.6521	610.8297	12
6	**621.3970**	311.2022	603.3865	302.1969	V	***1141.6099***	571.3086	1124.5834	562.7953	1123.5994	562.3033	11
7	708.4291	354.7182	690.4185	345.7129	S	***1042.5415***	521.7744	1025.5150	513.2611	1024.5310	512.7691	10
8	**809.4767**	405.2420	791.4662	396.2367	T	***955.5095***	478.2584	938.4829	469.7451	937.4989	469.2531	9
9	866.4982	433.7527	848.4876	424.7475	G	***854.4618***	427.7345	837.4353	419.2213	836.4512	418.7293	8
10	953.5302	477.2688	935.5197	468.2635	S	***797.4403***	399.2238	780.4138	390.7105	779.4298	390.2185	7
11	1054.5779	527.7926	1036.5673	518.7873	T	710.4083	355.7078	693.3818	347.1945	692.3978	346.7025	6
12	**1153.6463**	577.3268	1135.6358	568.3215	V	***609.3606***	305.1840	592.3341	296.6707	591.3501	296.1787	5
13	**1266.7304**	633.8688	1248.7198	624.8635	L	***510.2922***	255.6498	493.2657	247.1365	492.2817	246.6445	4
14	**1429.7937**	715.4005	1411.7831	706.3952	Y	***397.2082***	199.1077	380.1816	190.5944	379.1976	190.1024	3
15	1516.8257	758.9165	1498.8152	749.9112	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
16					K	147.1128	74.0600	130.0863	65.5468			1

AT5G20720.1





NCBI **BLAST** search of ITPLPVSTGSTVLYSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.9	1661.9240	-0.0049	ITPLPVSTGSTVLYSK
7.7	1661.9141	0.0050	IPTLKSISFFSTHGK
0.6	1661.9174	0.0016	NTYPLLMLVNGGVKK

Mascot: http://www.matrixscience.com/

AT5G20830.1

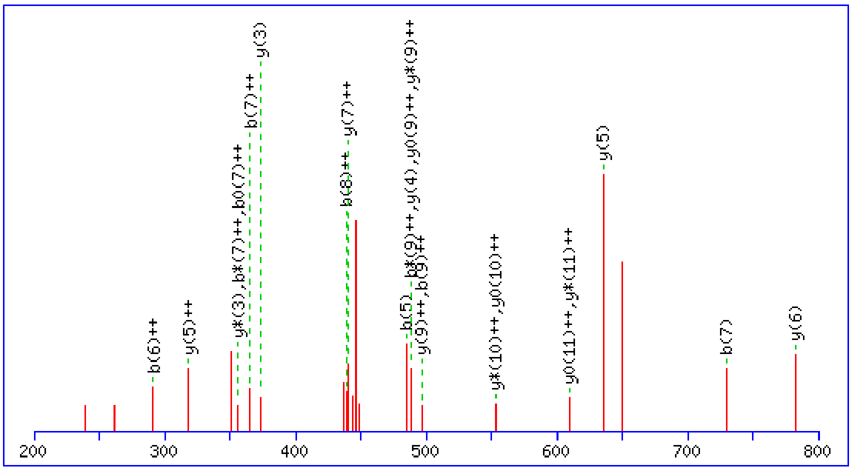
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLEGGPFFDLLK**
Found in **AT5G20830.1** in **TAIR_Arabidopsis**, Symbols: SUS1, ASUS1, ATSUS1 | SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase | chr5:7050601-7054034 REVERSE

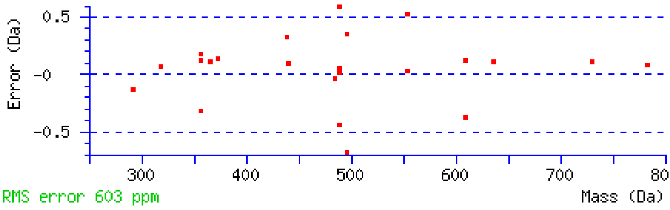
Match to Query 4961: 1362.756225 from(455.259351,3+) index(8314)
Title: Elution from: 74.830 to 74.830 scan no 11218 cid35.00 polarity:+
Data file D6h-2_3.mgf

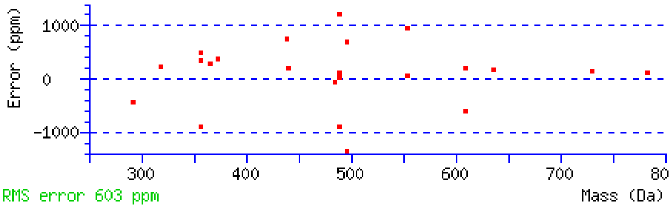
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1362.7547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00041
Matches : 25/122 fragment ions using 24 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**12**
2	242.1863	121.5968	225.1598	113.0835			**L**	1235.6671	618.3372	1218.6405	609.8239	1217.6565	609.3319	**11**
3	371.2289	186.1181	354.2023	177.6048	353.2183	177.1128	**E**	1122.5830	561.7951	1105.5564	553.2819	1104.5724	552.7898	**10**
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	**G**	993.5404	497.2738	976.5138	488.7606	975.5298	488.2686	**9**
5	**485.2718**	243.1395	468.2453	234.6263	467.2613	234.1343	**G**	936.5189	468.7631	919.4924	460.2498	918.5084	459.7578	**8**
6	582.3246	***291.6659***	565.2980	283.1527	564.3140	282.6606	**P**	879.4975	440.2524	862.4709	431.7391	861.4869	431.2471	**7**
7	**729.3930**	***365.2001***	712.3665	356.6869	711.3824	356.1949	**F**	**782.4447**	391.7260	765.4182	383.2127	764.4341	382.7207	**6**
8	876.4614	***438.7343***	859.4349	430.2211	858.4509	429.7291	**F**	**635.3763**	318.1918	618.3497	309.6785	617.3657	309.1865	**5**
9	991.4884	***496.2478***	974.4618	487.7345	973.4778	487.2425	**D**	**488.3079**	244.6576	471.2813	236.1443	470.2973	235.6523	**4**
10	1104.5724	***552.7898***	1087.5459	544.2766	1086.5619	543.7846	**L**	**373.2809**	187.1441	356.2544	178.6308			**3**
11	1217.6565	***609.3319***	1200.6299	600.8186	1199.6459	600.3266	**L**	260.1969	130.6021	243.1703	122.0888			**2**
12							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of KLEGGPFFDLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G20830.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.3	1362.7547	0.0015	KLEGGPFFDLLK
3.0	1362.7540	0.0022	VKSSAETLAKAMK

AT5G20890.1

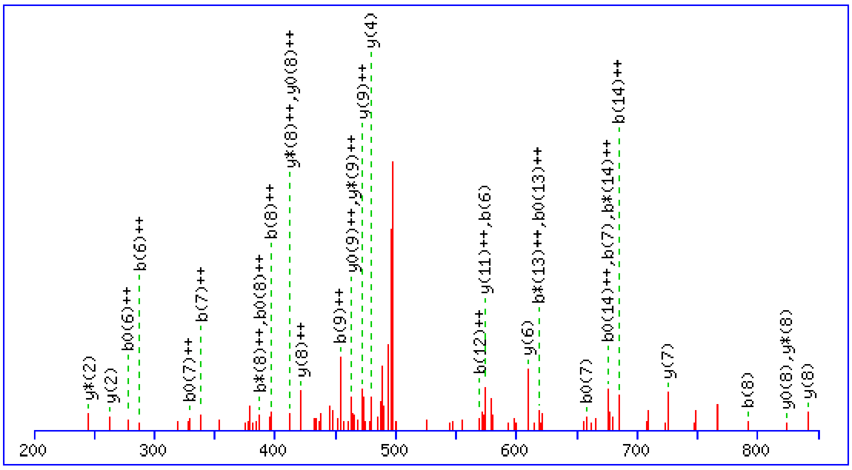
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHAVTVTNDGATILK**
Found in **AT5G20890.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr5:7087022-7089908 REVERSE

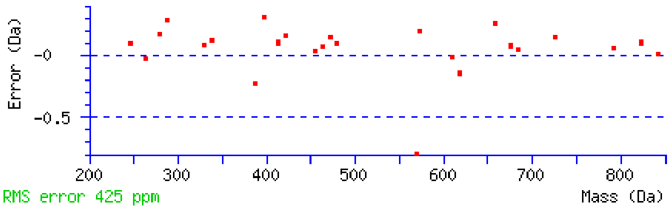
Match to Query 6764: 1514.744862 from(505.922230,3+) index(2899)
Title: Elution from: 29.120 to 29.120 scan no 3595 cid35.00 polarity:+
Data file C7-1_1.mgf

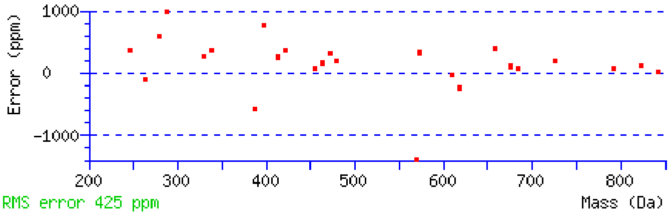
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1514.7431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.013
Matches : 33/140 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							15
2	199.0758	100.0415					H	1457.7319	729.3696	1439.7083	720.3578	1439.7213	720.3643	14
3	271.1099	136.0586					A	1317.6819	659.3446	1299.6583	650.3328	1299.6713	650.3393	13
4	371.1754	186.0913					V	1245.6477	623.3275	1227.6241	614.3157	1227.6372	614.3222	12
5	473.2201	237.1137			455.2095	228.1084	T	1145.5823	573.2948	1127.5587	564.2830	1127.5717	564.2895	11
6	***573.2856***	***287.1464***			555.2750	278.1411	V	1043.5376	522.2724	1025.5140	513.2606	1025.5270	513.2671	10
7	***675.3303***	***338.1688***			657.3197	329.1635	T	943.4721	472.2397	925.4485	463.2279	925.4616	463.2344	9
8	***791.3673***	***396.1873***	773.3437	387.1755	773.3567	387.1820	N	***841.4274***	421.2173	823.4038	412.2056	823.4168	412.2121	8
9	907.3912	***454.1993***	889.3677	445.1875	889.3807	445.1940	D	***725.3904***	363.1988	707.3668	354.1871	707.3798	354.1936	7
10	965.4097	483.2085	947.3862	474.1967	947.3992	474.2032	G	***609.3664***	305.1869	591.3428	296.1751	591.3559	296.1816	6
11	1037.4439	519.2256	1019.4203	510.2138	1019.4333	510.2203	A	551.3479	276.1776	533.3244	267.1658	533.3374	267.1723	5
12	1139.4886	***570.2479***	1121.4650	561.2361	1121.4780	561.2427	T	***479.3138***	240.1605	461.2902	231.1487	461.3032	231.1552	4
13	1253.5697	627.2885	1235.5461	618.2767	1235.5591	618.2832	I	377.2691	189.1382	359.2455	180.1264			3
14	1367.6508	***684.3290***	1349.6272	675.3172	1349.6402	675.3238	L	***263.1880***	132.0976	245.1644	123.0858			2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GHAVTVTNDGATILK

AT5G20890.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.5	1514.7431	0.0018	GHAVTVTNDGATILK
6.4	1514.7487	-0.0039	HVIMEGGEKKEIK
4.1	1514.7427	0.0022	ASLVYSPFTLSTSK
1.9	1514.7453	-0.0005	SSFQAFLEVVKSR
1.3	1514.7406	0.0042	YIPQAKMNFTRK
0.1	1514.7453	-0.0005	QWLADGPKNLVEK

AT5G20950.1

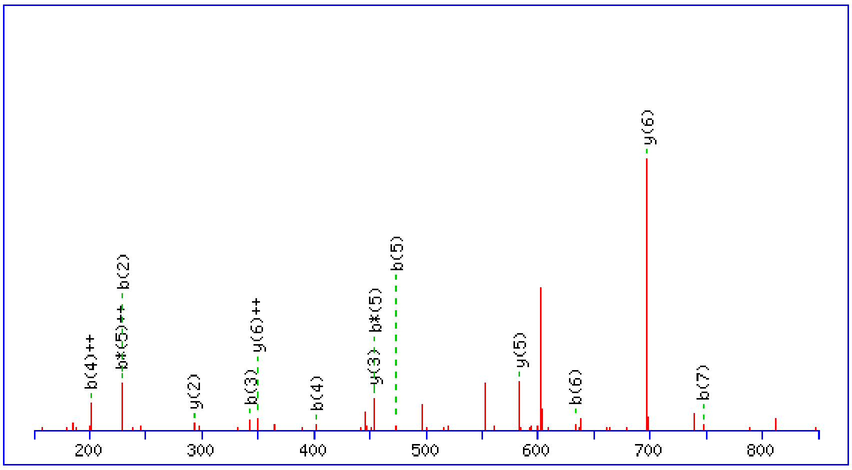
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPLGARIR**
Found in **AT5G20950.1** in **TAIR_Arabidopsis**, Symbols: | glycosyl hydrolase family 3 protein | chr5:7107611-7110777 REVERSE

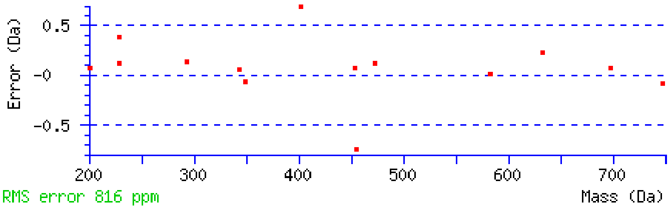
Match to Query 1778: 924.507922 from(463.261237,2+) index(4393)
Title: Elution from: 40.393 to 40.393 scan no 5525 cid35.00 polarity:+
Data file C7-3_3.mgf

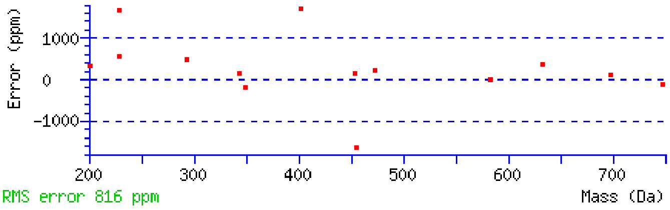
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 924.5063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0026
Matches : 14/56 fragment ions using 33 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	131.0599	66.0336	113.0363	57.0218	Q					8
2	***229.1097***	115.0585	211.0861	106.0467	P	795.4610	398.2341	777.4374	389.2223	7
3	***343.1908***	172.0990	325.1672	163.0873	L	**697.4112**	349.2092	679.3876	340.1974	6
4	***401.2093***	201.1083	383.1857	192.0965	G	**583.3301**	292.1687	565.3065	283.1569	5
5	***473.2435***	237.1254	455.2199	228.1136	A	525.3116	263.1594	507.2880	254.1476	4
6	***633.3327***	317.1700	615.3091	308.1582	R	**453.2774**	227.1424	435.2539	218.1306	3
7	***747.4138***	374.2105	729.3902	365.1988	I	**293.1882**	147.0977	275.1646	138.0859	2
8					R	179.1071	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of QPLGARIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.1	924.5063	0.0016	QPLGARIR
3.0	924.5093	-0.0014	LLGQKMPK

AT5G20950.1

2.4	924.5059	0.0020	IIEHFKK

Mascot: http://www.matrixscience.com/

AT5G20960.1

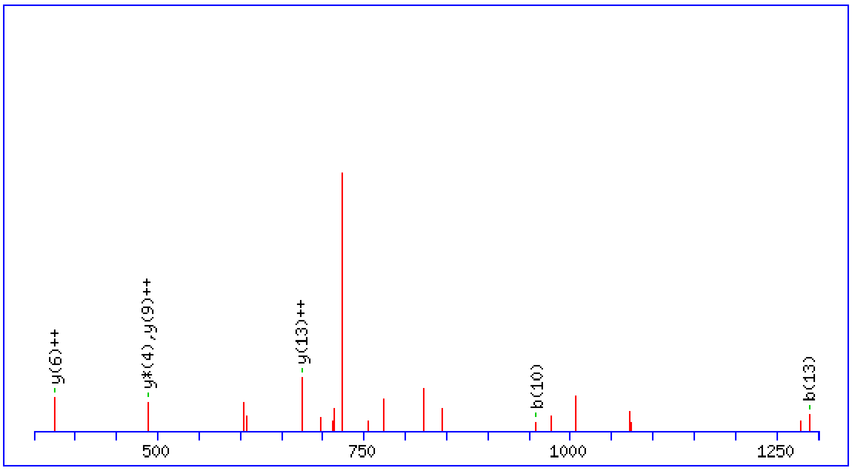
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTGTIGGNIMMAQR**
Found in **AT5G20960.1** in **TAIR_Arabidopsis**, Symbols: AO1, ATAO, ATAO1, AAO1 | AAO1 (ALDEHYDE OXIDASE 1) | chr5:7116785-7122340 FORWARD

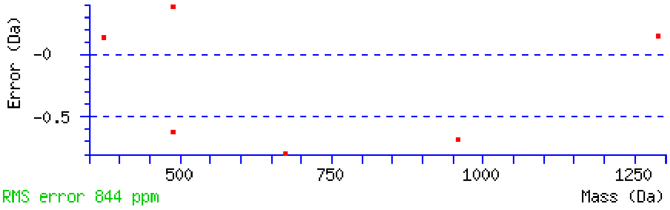
Match to Query 6037: 1462.699402 from(732.356977,2+) index(3872)
Title: Elution from: 35.721 to 35.721 scan no 4801 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

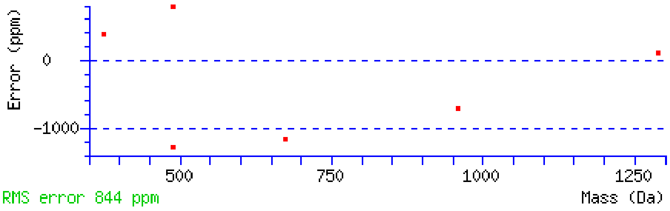


Monoisotopic mass of neutral peptide Mr(calc): 1462.7021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.04
Matches : 6/134 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							14
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	T	1349.6664	675.3368	1332.6399	666.8236	1331.6559	666.3316	13
3	273.1193	137.0633	256.0928	128.5500	255.1088	128.0580	G	1248.6187	624.8130	1231.5922	616.2997	1230.6082	615.8077	12
4	374.1670	187.5872	357.1405	179.0739	356.1565	178.5819	T	1191.5973	596.3023	1174.5707	587.7890	1173.5867	587.2970	11
5	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	I	1090.5496	545.7784	1073.5230	537.2652			10
6	544.2726	272.6399	527.2460	264.1266	526.2620	263.6346	G	977.4655	489.2364	960.4390	480.7231			9
7	601.2940	301.1506	584.2675	292.6374	583.2835	292.1454	G	920.4441	460.7257	903.4175	452.2124			8
8	715.3369	358.1721	698.3104	349.6588	697.3264	349.1668	N	863.4226	432.2149	846.3961	423.7017			7
9	828.4210	414.7141	811.3945	406.2009	810.4104	405.7089	I	749.3797	375.1935	732.3531	366.6802			6
10	***959.4615***	480.2344	942.4349	471.7211	941.4509	471.2291	M	636.2956	318.6514	619.2691	310.1382			5
11	1090.5020	545.7546	1073.4754	537.2414	1072.4914	536.7493	M	505.2551	253.1312	488.2286	244.6179			4
12	1161.5391	581.2732	1144.5125	572.7599	1143.5285	572.2679	A	374.2146	187.6110	357.1881	179.0977			3
13	***1289.5977***	645.3025	1272.5711	636.7892	1271.5871	636.2972	Q	303.1775	152.0924	286.1510	143.5791			2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 844 ppm



RMS error 844 ppm

NCBI **BLAST** search of NTGTIGGNIMMAQR

AT5G20960.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.6	1462.7021	-0.0027	NTGTIGGNIMMAQR
2.8	1462.6973	0.0021	SEEAEKIIEEMR
2.8	1462.6973	0.0021	TVEMTPEEVKER
2.2	1462.6987	0.0007	WAAAVCAQTTQTR
1.2	1462.6973	0.0021	KMEEEVDLVESR

AT5G21930.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WKEMVSK**
Found in **AT5G21930.1** in **TAIR_Arabidopsis**, Symbols: PAA2, HMA8 | HMA8/PAA2 (P-TYPE ATPASE OF ARABIDOPSIS 2); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / copper ion transmembrane transporter | chr5:7243132-7248724 FORWARD

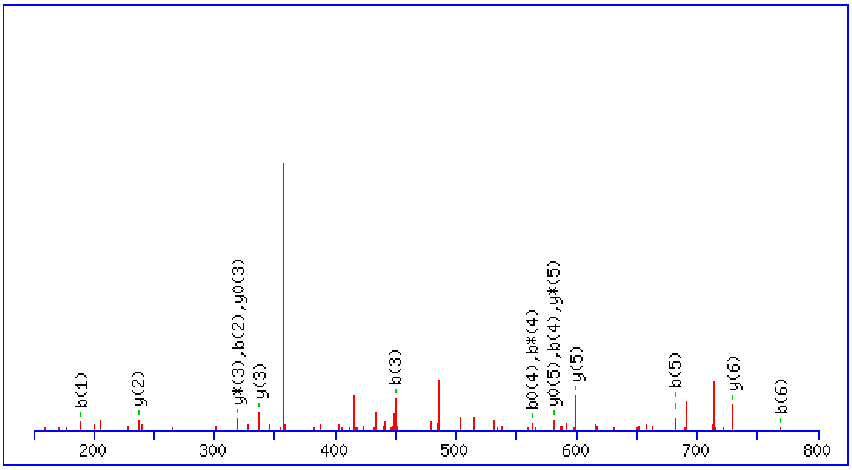
Match to Query 1419: 916.434194 from(459.224373,2+) index(2620)
Title: Elution from: 30.122 to 30.122 scan no 3388 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 800 Da Full range

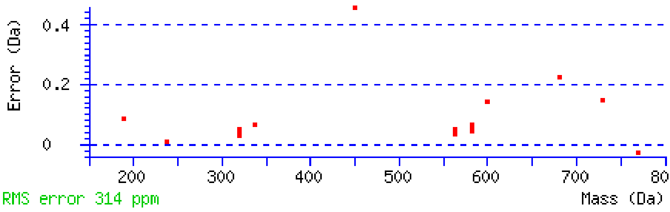
Label all possible matches ○ Label matches used for scoring ●

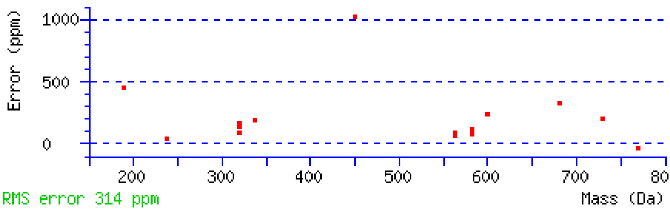
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 916.4337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0054
Matches : 16/64 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	***189.0807***	95.0440					**W**							7
2	***319.1697***	160.0885	301.1461	151.0767			**K**	**729.3676**	365.1874	711.3440	356.1756	711.3570	356.1821	6
3	***449.2093***	225.1083	431.1857	216.0965	431.1988	216.1030	**E**	**599.2785**	300.1429	581.2549	291.1311	581.2680	291.1376	5
4	***581.2468***	291.1271	563.2233	282.1153	563.2363	282.1218	**M**	469.2389	235.1231	451.2153	226.1113	451.2283	226.1178	4
5	***681.3123***	341.1598	663.2887	332.1480	663.3017	332.1545	**V**	**337.2014**	169.1043	319.1778	160.0925	319.1908	160.0990	3
6	***769.3414***	385.1743	751.3178	376.1625	751.3308	376.1690	**S**	**237.1359**	119.0716	219.1124	110.0598	219.1254	110.0663	2
7							**K**	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of WKEMVSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.4	916.4337	0.0005	WKEMVSK

AT5G21930.1

14.9	916.4337	0.0005	MPSLAGFGK
11.8	916.4359	-0.0017	AIMPFWK
7.9	916.4337	0.0005	WLEGMKK
6.6	916.4362	-0.0020	EGLSSLSSK
5.8	916.4330	0.0012	WKNPFGR
5.7	916.4362	-0.0020	ISLDSSASK
3.6	916.4337	0.0005	MLAFNPSK
2.7	916.4314	0.0028	MSLQNVSK
2.3	916.4362	-0.0020	TLTSSSPSK

AT5G22000.1

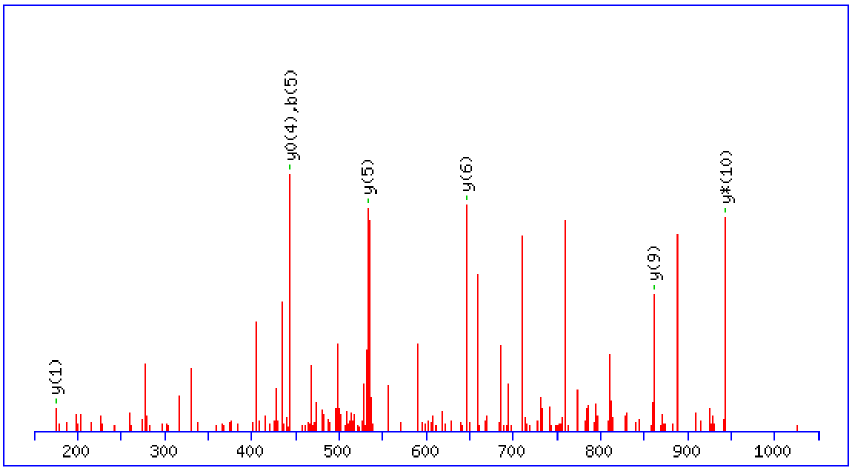
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVSAGIATVSR**
Found in **AT5G22000.1** in **TAIR_Arabidopsis**, Symbols: RHF2A, CIC7E11 | CIC7E11; protein binding / zinc ion binding | chr5:7277439-7279556 FORWARD

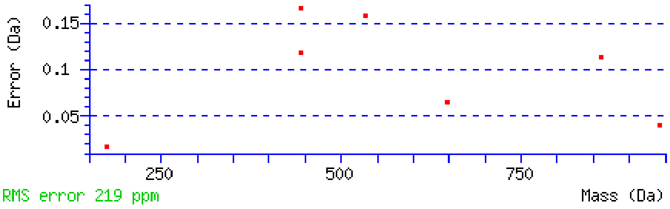
Match to Query 3363: 1088.584354 from(545.299453,2+) index(5371)
Title: Elution from: 48.395 to 48.395 scan no 6736 cid35.00 polarity:+
Data file D12h-3_1.mgf

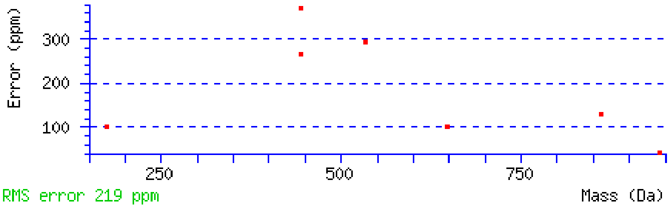
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1088.5826
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.029
Matches : 7/98 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							11
2	229.1183	115.0628	211.1077	106.0575	V	960.5473	480.7773	943.5207	472.2640	942.5367	471.7720	10
3	316.1503	158.5788	298.1397	149.5735	S	***861.4789***	431.2431	844.4523	422.7298	843.4683	422.2378	9
4	387.1874	194.0974	369.1769	185.0921	A	774.4468	387.7271	757.4203	379.2138	756.4363	378.7218	8
5	444.2089	222.6081	426.1983	213.6028	G	703.4097	352.2085	686.3832	343.6952	685.3991	343.2032	7
6	557.2930	279.1501	539.2824	270.1448	I	***646.3883***	323.6978	629.3617	315.1845	628.3777	314.6925	6
7	628.3301	314.6687	610.3195	305.6634	A	***533.3042***	267.1557	516.2776	258.6425	515.2936	258.1504	5
8	729.3777	365.1925	711.3672	356.1872	T	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
9	828.4462	414.7267	810.4356	405.7214	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	915.4782	458.2427	897.4676	449.2374	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11					R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EVSAGIATVSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G22000.1

Score	Mr(calc)	Delta	Sequence
23.2	1088.5826	0.0018	EVSAGIATVSR
15.8	1088.5873	-0.0029	IDMRNLRR
13.3	1088.5873	-0.0029	SERCIIRR
7.8	1088.5873	-0.0029	ECLRSLRR
6.9	1088.5826	0.0018	SSIREQELK
6.7	1088.5826	0.0018	DIDSVVGKTR
5.7	1088.5866	-0.0022	LYPAANEAIK
3.0	1088.5826	0.0018	GGSAAEKASALK
1.6	1088.5826	0.0018	DKSVDELRK
1.1	1088.5826	0.0018	EVIASSSLQR

AT5G22440.1

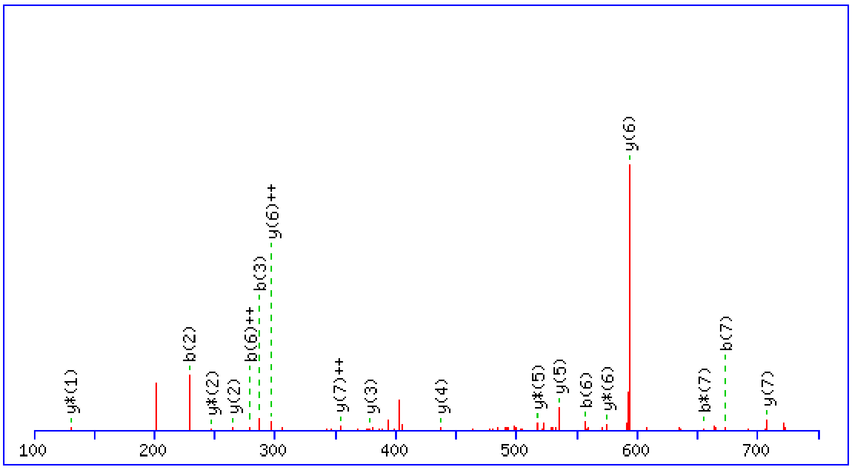
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLGPGLNK**
Found in **AT5G22440.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L10A (RPL10aC) | chr5:7435331-7436489 REVERSE

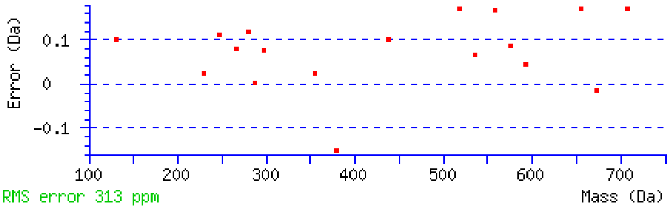
Match to Query 1088: 820.465720 from(411.240136,2+) index(2123)
Title: Elution from: 24.368 to 24.368 scan no 2713 cid35.00 polarity:+
Data file D6h-1_3.mgf

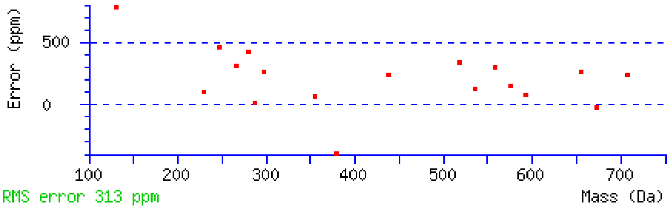
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 820.4667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.00079
Matches : 18/44 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	115.0884	58.0478			L					8
2	**229.1695**	115.0884			L	***707.3929***	354.2001	689.3693	345.1883	7
3	**287.1880**	144.0976			G	***593.3118***	297.1595	575.2882	288.1477	6
4	385.2378	193.1225			P	***535.2933***	268.1503	517.2697	259.1385	5
5	443.2563	222.1318			G	***437.2435***	219.1254	419.2199	210.1136	4
6	**557.3374**	279.1723			L	***379.2250***	190.1161	361.2014	181.1043	3
7	**673.3744**	337.1908	655.3508	328.1790	N	***265.1439***	133.0756	247.1203	124.0638	2
8					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LLGPGLNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.8	820.4667	-0.0010	LLGPGLNK
9.9	820.4667	-0.0010	LLPIAER

AT5G22440.1

Mascot: http://www.matrixscience.com/

AT5G22650.1

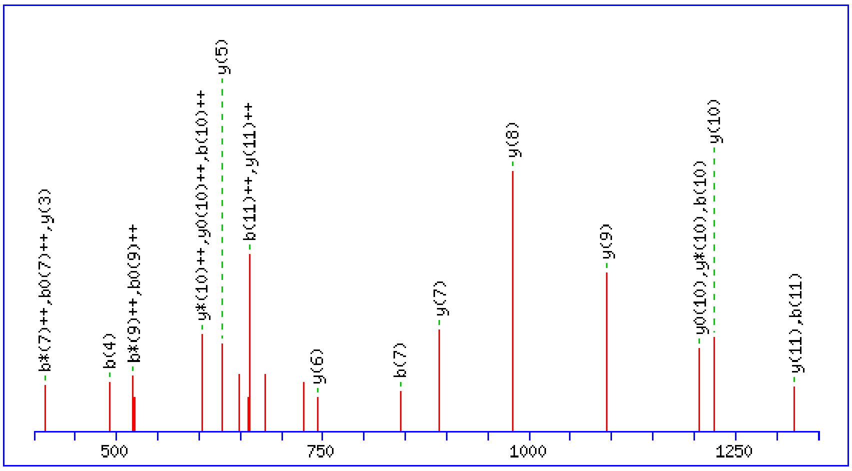
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPQISFDLVFDK**
Found in **AT5G22650.1** in **TAIR_Arabidopsis**, Symbols: HDT02, HDT2, ATHD2B, HDA4, HD2, HD2B | HD2B (HISTONE DEACETYLASE 2B) | chr5:7534123-7536057 FORWARD

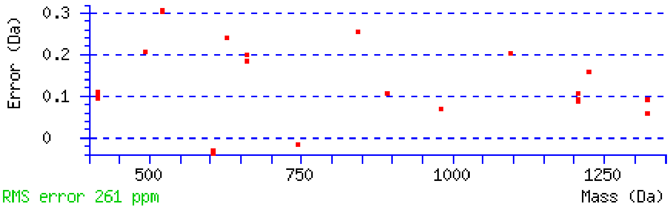
Match to Query 6111: 1468.701112 from(735.357832,2+) index(10670)
Title: Elution from: 102.882 to 102.882 scan no 15238 cid35.00 polarity:+
Data file D6h-2_1.mgf

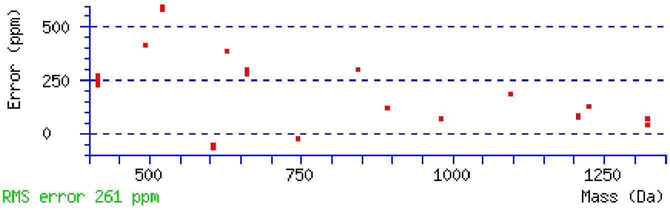
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.7030
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 2.4e-008
Matches : 23/118 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							12
2	247.1225	124.0649					P	***1321.6449***	661.3261	1303.6213	652.3143	1303.6343	652.3208	11
3	377.1752	189.0912	359.1516	180.0794			Q	***1223.5951***	612.3012	1205.5715	603.2894	1205.5845	603.2959	10
4	**491.2563**	246.1318	473.2327	237.1200			I	***1093.5424***	547.2749	1075.5189	538.2631	1075.5319	538.2696	9
5	579.2853	290.1463	561.2617	281.1345	561.2748	281.1410	S	***979.4613***	490.2343	961.4378	481.2225	961.4508	481.2290	8
6	727.3508	364.1790	709.3272	355.1672	709.3402	355.1737	F	***891.4323***	446.2198	873.4087	437.2080	873.4217	437.2145	7
7	**843.3748**	422.1910	825.3512	413.1792	825.3642	413.1857	D	***743.3668***	372.1871	725.3432	363.1753	725.3563	363.1818	6
8	957.4559	479.2316	939.4323	470.2198	939.4453	470.2263	L	***627.3428***	314.1751	609.3193	305.1633	609.3323	305.1698	5
9	1057.5213	529.2643	1039.4977	520.2525	1039.5107	520.2590	V	513.2617	257.1345	495.2382	248.1227	495.2512	248.1292	4
10	**1205.5868**	**603.2970**	1187.5632	594.2852	1187.5762	594.2917	F	***413.1963***	207.1018	395.1727	198.0900	395.1857	198.0965	3
11	**1321.6107**	**661.3090**	1303.5872	652.2972	1303.6002	652.3037	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FPQISFDLVFDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G22650.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
85.5	1468.7030	-0.0019	FPQISFDLVFDK
11.1	1468.6995	0.0016	MPIMLVSAYREK
10.3	1468.7035	-0.0024	FSYKATHNIKDK
9.6	1468.6990	0.0021	AVSTSSSIKGRDNK
4.4	1468.7012	-0.0001	EDDLTRRLASFK
3.8	1468.7042	-0.0031	MSAALSSSLYISPK
3.7	1468.7013	-0.0002	IEFERNVSKSNK
3.7	1468.7042	-0.0031	TFGVATKLDIMDK
3.7	1468.7008	0.0003	VLDLSYVQFEGGK
3.7	1468.7008	0.0003	YGIKFLVDEENK

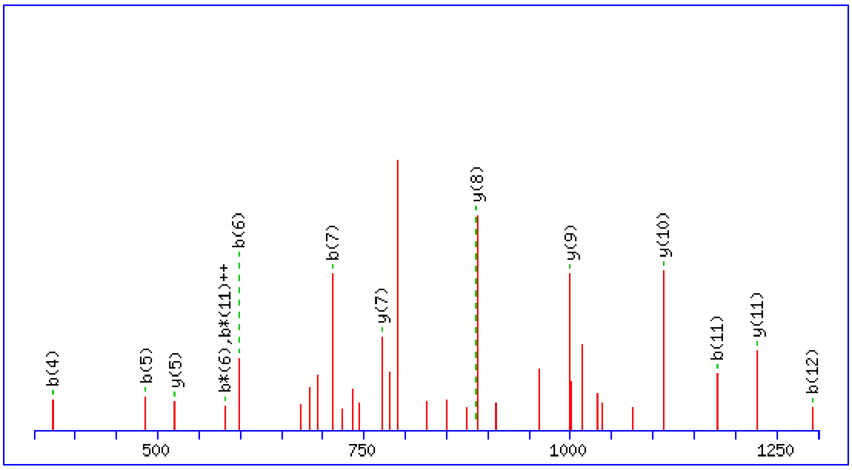
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSNIIILDSYTDSAK**
Found in **AT5G23060.1** in **TAIR_Arabidopsis**, Symbols: CAS | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G59780.1); similar to extracellular Ca2+ sensing receptor [Glycine max] (GB:ABY57763.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763) | chr5:7736763-7738415 R

Match to Query 6986: 1595.801990 from(798.908271,2+) index(6647)
Title: Elution from: 57.528 to 57.528 scan no 8568 cid35.00 polarity:+
Data file D1d-3_3.mgf

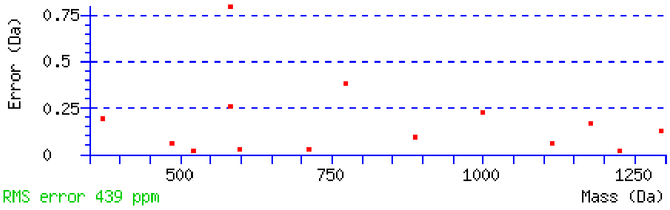
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

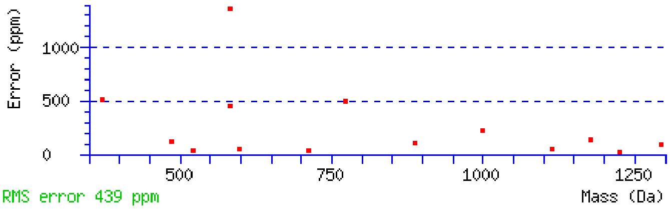


Monoisotopic mass of neutral peptide Mr(calc): 1595.8042
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 8.7e-006
Matches : 14/158 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	145.0608	73.0340			127.0502	64.0287	S	1539.7901	770.3987	1522.7635	761.8854	1521.7795	761.3934	14
3	259.1037	130.0555	242.0771	121.5422	241.0931	121.0502	N	1452.7581	726.8827	1435.7315	718.3694	1434.7475	717.8774	13
4	***372.1878***	186.5975	355.1612	178.0842	354.1772	177.5922	I	1338.7151	669.8612	1321.6886	661.3479	1320.7046	660.8559	12
5	***485.2718***	243.1395	468.2453	234.6263	467.2613	234.1343	I	***1225.6311***	613.3192	1208.6045	604.8059	1207.6205	604.3139	11
6	***598.3559***	299.6816	581.3293	291.1683	580.3453	290.6763	I	***1112.5470***	556.7771	1095.5204	548.2639	1094.5364	547.7719	10
7	***711.4400***	356.2236	694.4134	347.7103	693.4294	347.2183	L	***999.4629***	500.2351	982.4364	491.7218	981.4524	491.2298	9
8	826.4669	413.7371	809.4403	405.2238	808.4563	404.7318	D	***886.3789***	443.6931	869.3523	435.1798	868.3683	434.6878	8
9	913.4989	457.2531	896.4724	448.7398	895.4884	448.2478	S	***771.3519***	386.1796	754.3254	377.6663	753.3414	377.1743	7
10	1076.5623	538.7848	1059.5357	530.2715	1058.5517	529.7795	Y	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	6
11	***1177.6099***	589.3086	1160.5834	580.7953	1159.5994	580.3033	T	***521.2566***	261.1319	504.2300	252.6186	503.2460	252.1266	5
12	***1292.6369***	646.8221	1275.6103	638.3088	1274.6263	637.8168	D	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
13	1379.6689	690.3381	1362.6424	681.8248	1361.6583	681.3328	S	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
14	1450.7060	725.8566	1433.6795	717.3434	1432.6955	716.8514	A	218.1499	109.5786	201.1234	101.0653			2
15							K	147.1128	74.0600	130.0863	65.5468			1

AT5G23060.1





NCBI **BLAST** search of GSNIIILDSYTDSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.9	1595.8042	-0.0023	GSNIIILDSYTDSAK
7.7	1595.8056	-0.0036	RQYDFSGNLDLIR
5.0	1595.8042	-0.0022	KVSSILNEEYEASK

Mascot: http://www.matrixscience.com/

AT5G23120.1

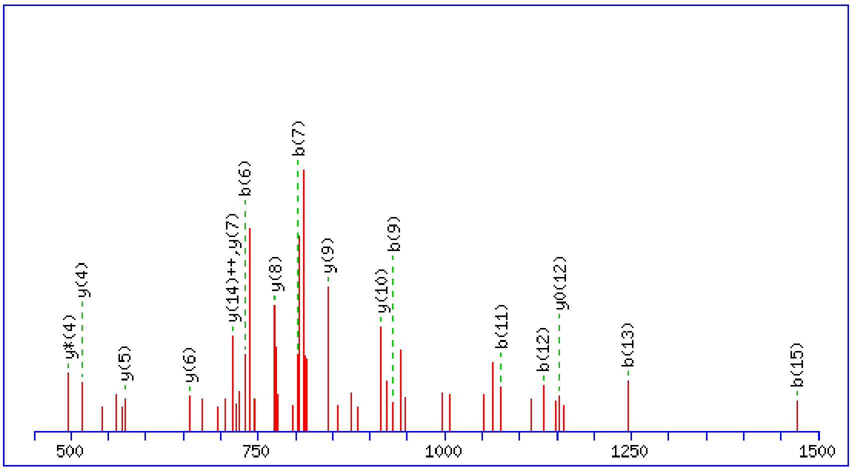
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEEEAWAAGGSGILLR**
Found in **AT5G23120.1** in **TAIR_Arabidopsis**, Symbols: HCF136 | HCF136 (High chlorophyll fluorescence 136) | chr5:7778157-7780466 FORWARD

Match to Query 7432: 1644.811736 from(823.413144,2+) index(7175)
Title: Elution from: 64.089 to 64.089 scan no 9410 cid35.00 polarity:+
Data file D6h-1_3.mgf

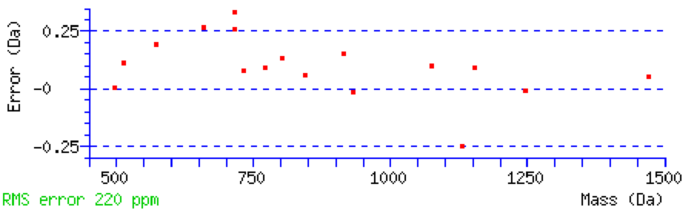
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

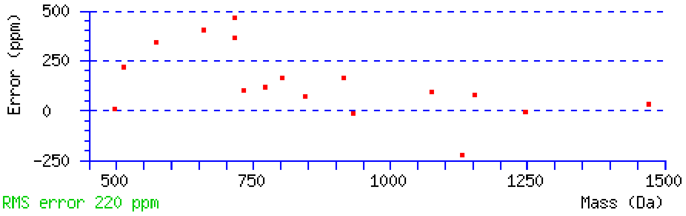


Monoisotopic mass of neutral peptide Mr(calc): 1644.8107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00032
Matches : 17/140 fragment ions using 35 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	70.0287	35.5180	S							16
2	217.0819	109.0446	199.0713	100.0393	E	1558.7860	779.8966	1541.7594	771.3834	1540.7754	770.8914	15
3	346.1245	173.5659	328.1139	164.5606	E	1429.7434	715.3753	1412.7169	706.8621	1411.7328	706.3701	14
4	475.1671	238.0872	457.1565	229.0819	E	1300.7008	650.8540	1283.6743	642.3408	1282.6902	641.8488	13
5	546.2042	273.6057	528.1936	264.6005	A	1171.6582	586.3327	1154.6317	577.8195	1153.6477	577.3275	12
6	***732.2835***	366.6454	714.2729	357.6401	W	1100.6211	550.8142	1083.5946	542.3009	1082.6105	541.8089	11
7	***803.3206***	402.1640	785.3101	393.1587	A	***914.5418***	457.7745	897.5152	449.2613	896.5312	448.7693	10
8	874.3577	437.6825	856.3472	428.6772	A	***843.5047***	422.2560	826.4781	413.7427	825.4941	413.2507	9
9	***931.3792***	466.1932	913.3686	457.1880	G	***772.4676***	386.7374	755.4410	378.2241	754.4570	377.7321	8
10	988.4007	494.7040	970.3901	485.6987	G	***715.4461***	358.2267	698.4196	349.7134	697.4355	349.2214	7
11	***1075.4327***	538.2200	1057.4221	529.2147	S	***658.4246***	329.7160	641.3981	321.2027	640.4141	320.7107	6
12	***1132.4542***	566.7307	1114.4436	557.7254	G	***571.3926***	286.1999	554.3661	277.6867			5
13	***1245.5382***	623.2727	1227.5277	614.2675	I	***514.3711***	257.6892	497.3446	249.1759			4
14	1358.6223	679.8148	1340.6117	670.8095	L	401.2871	201.1472	384.2605	192.6339			3
15	***1471.7063***	736.3568	1453.6958	727.3515	L	288.2030	144.6051	271.1765	136.0919			2
16					R	175.1190	88.0631	158.0924	79.5498			1

AT5G23120.1





NCBI **BLAST** search of SEEEAWAAGGSGILLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.6	1644.8107	0.0010	SEEEAWAAGGSGILLR
3.3	1644.8107	0.0011	EWAEAKKELQEER
2.6	1644.8154	-0.0037	DRSLVWGGSEPRMR

Mascot: http://www.matrixscience.com/

AT5G23140.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFGIIDEVIDERPLELVK**
Found in **AT5G23140.1** in **TAIR_Arabidopsis**, Symbols: NCLPP2, CLPP2 | CLPP2 (Clp protease proteolytic subunit 2); endopeptidase Clp | chr5:7783814-7784829 FORWARD

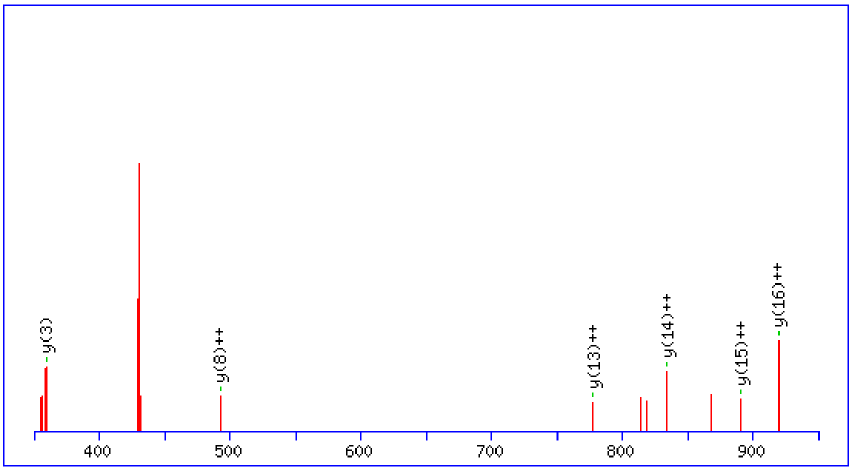
Match to Query 9853: 2055.123960 from(686.048596,3+) index(10869)
Title: Elution from: 103.166 to 103.166 scan no 15424 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 350 to 950 Da Full range

Label all possible matches ○ Label matches used for scoring ●

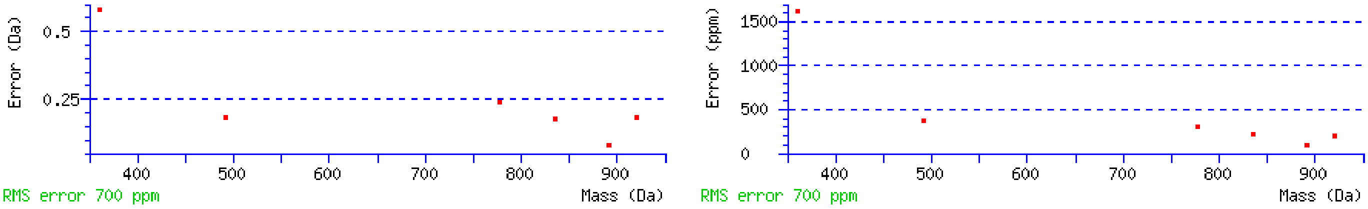
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2055.1252
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.022
Matches : 6/166 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							18
2	219.1128	110.0600					F	1985.0954	993.0513	1968.0688	984.5380	1967.0848	984.0460	17
3	276.1343	138.5708					G	1838.0270	919.5171	1821.0004	911.0038	1820.0164	910.5118	16
4	389.2183	195.1128					I	1781.0055	891.0064	1763.9789	882.4931	1762.9949	882.0011	15
5	502.3024	251.6548					I	1667.9214	834.4644	1650.8949	825.9511	1649.9109	825.4591	14
6	617.3293	309.1683			599.3188	300.1630	D	1554.8374	777.9223	1537.8108	769.4090	1536.8268	768.9170	13
7	746.3719	373.6896			728.3614	364.6843	E	1439.8104	720.4088	1422.7839	711.8956	1421.7999	711.4036	12
8	845.4403	423.2238			827.4298	414.2185	V	1310.7678	655.8876	1293.7413	647.3743	1292.7573	646.8823	11
9	958.5244	479.7658			940.5138	470.7606	I	1211.6994	606.3533	1194.6729	597.8401	1193.6888	597.3481	10
10	1073.5514	537.2793			1055.5408	528.2740	D	1098.6154	549.8113	1081.5888	541.2980	1080.6048	540.8060	9
11	1202.5939	601.8006			1184.5834	592.7953	E	983.5884	492.2978	966.5619	483.7846	965.5778	483.2926	8
12	1358.6951	679.8512	1341.6685	671.3379	1340.6845	670.8459	R	854.5458	427.7765	837.5193	419.2633	836.5352	418.7713	7
13	1455.7478	728.3775	1438.7213	719.8643	1437.7373	719.3723	P	698.4447	349.7260	681.4182	341.2127	680.4341	340.7207	6
14	1568.8319	784.9196	1551.8053	776.4063	1550.8213	775.9143	L	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
15	1697.8745	849.4409	1680.8479	840.9276	1679.8639	840.4356	E	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
16	1810.9585	905.9829	1793.9320	897.4696	1792.9480	896.9776	L	359.2653	180.1363	342.2387	171.6230			3
17	1910.0270	955.5171	1893.0004	947.0038	1892.0164	946.5118	V	246.1812	123.5942	229.1547	115.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1

AT5G23140.1



NCBI **BLAST** search of AFGIIDEVIDERPLELVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.6	2055.1252	-0.0012	AFGIIDEVIDERPLELVK
3.4	2055.1299	-0.0059	SLLQTLLMRAGHSPPKYK
2.0	2055.1285	-0.0046	IPDIEKCLEVVATLEAKK

Mascot: http://www.matrixscience.com/

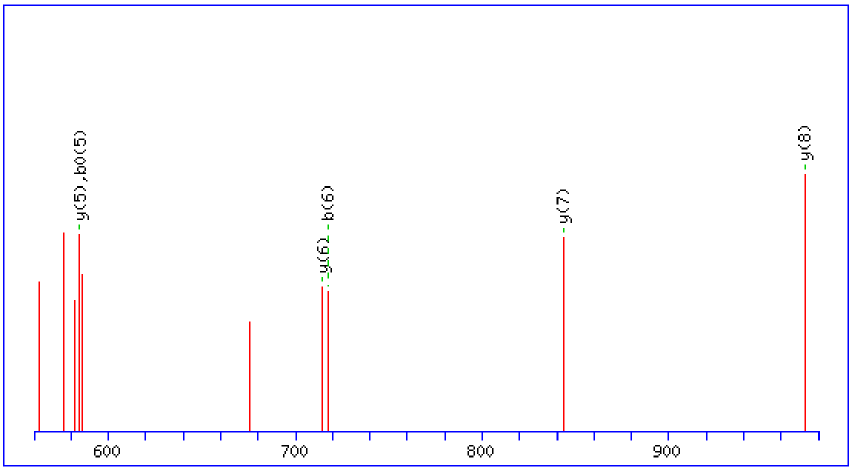
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEEEDPIIK**
Found in **AT5G23820.1** in **TAIR_Arabidopsis**, Symbols: | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein | chr5:8031389-8032812 FORWARD

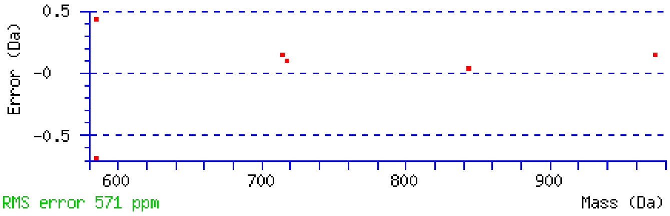
Match to Query 3913: 1185.613020 from(593.813786,2+) index(3789)
Title: Elution from: 35.849 to 35.849 scan no 4726 cid35.00 polarity:+
Data file 0-3_2.mgf

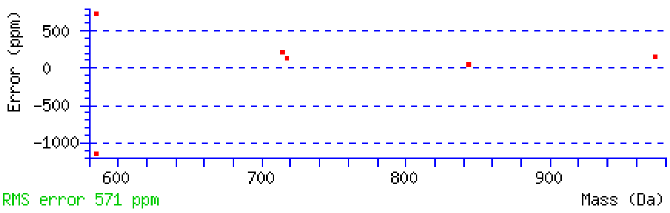
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 560 to 980 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1185.6129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0051
Matches : 6/82 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	**T**							**10**
2	215.1390	108.0731	197.1285	99.0679	**L**	1085.5725	543.2899	1068.5459	534.7766	1067.5619	534.2846	**9**
3	344.1816	172.5944	326.1710	163.5892	**E**	***972.4884***	486.7478	955.4619	478.2346	954.4779	477.7426	**8**
4	473.2242	237.1157	455.2136	228.1105	**E**	***843.4458***	422.2266	826.4193	413.7133	825.4353	413.2213	**7**
5	602.2668	301.6370	584.2562	292.6318	**E**	***714.4032***	357.7053	697.3767	349.1920	696.3927	348.7000	**6**
6	717.2937	359.1505	699.2832	350.1452	**D**	***585.3606***	293.1840	568.3341	284.6707	567.3501	284.1787	**5**
7	814.3465	407.6769	796.3359	398.6716	**P**	470.3337	235.6705	453.3071	227.1572			**4**
8	927.4306	464.2189	909.4200	455.2136	**I**	373.2809	187.1441	356.2544	178.6308			**3**
9	1040.5146	520.7610	1022.5041	511.7557	**I**	260.1969	130.6021	243.1703	122.0888			**2**
10					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of TLEEEDPIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G23820.1

Score	Mr(calc)	Delta	Sequence
28.3	1185.6129	0.0002	TLEEEDPIIK

Mascot: http://www.matrixscience.com/

AT5G23860.1

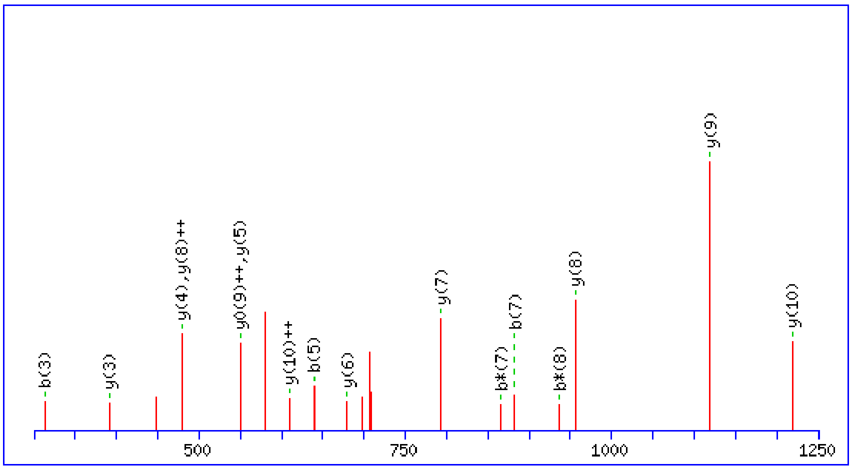
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNVYYNEASCGR**
Found in **AT5G23860.1** in **TAIR_Arabidopsis**, Symbols: TUB8 | TUB8 (tubulin beta-8) | chr5:8042965-8044531 FORWARD

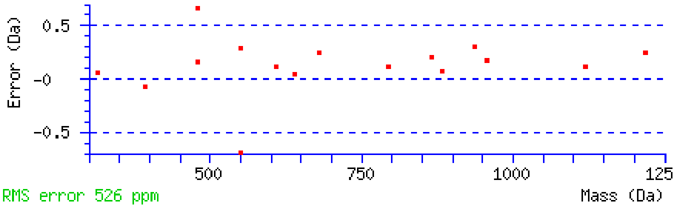
Match to Query 5536: 1430.624646 from(716.319599,2+) index(2123)
Title: Elution from: 26.298 to 26.298 scan no 2795 cid35.00 polarity:+
Data file D1d-2_1.mgf

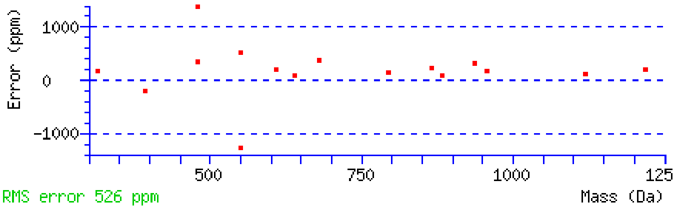
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1430.6248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 1.8e-008
Matches : 16/112 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							12
2	214.1186	107.5629	197.0921	99.0497			N	1332.5637	666.7855	1315.5372	658.2722	1314.5532	657.7802	11
3	**313.1870**	157.0972	296.1605	148.5839			V	***1218.5208***	609.7640	1201.4943	601.2508	1200.5102	600.7588	10
4	476.2504	238.6288	459.2238	230.1155			Y	***1119.4524***	560.2298	1102.4258	551.7166	1101.4418	551.2245	9
5	**639.3137**	320.1605	622.2871	311.6472			Y	***956.3891***	478.6982	939.3625	470.1849	938.3785	469.6929	8
6	753.3566	377.1819	736.3301	368.6687			N	***793.3257***	397.1665	776.2992	388.6532	775.3152	388.1612	7
7	**882.3992**	441.7032	865.3727	433.1900	864.3886	432.6980	E	***679.2828***	340.1450	662.2563	331.6318	661.2722	331.1398	6
8	953.4363	477.2218	936.4098	468.7085	935.4258	468.2165	A	***550.2402***	275.6237	533.2137	267.1105	532.2296	266.6185	5
9	1040.4684	520.7378	1023.4418	512.2245	1022.4578	511.7325	S	***479.2031***	240.1052	462.1765	231.5919	461.1925	231.0999	4
10	1200.4990	600.7531	1183.4725	592.2399	1182.4884	591.7479	C	***392.1711***	196.5892	375.1445	188.0759			3
11	1257.5205	629.2639	1240.4939	620.7506	1239.5099	620.2586	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VNVYYNEASCGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G23860.1

Score	Mr(calc)	Delta	Sequence
77.4	1430.6248	-0.0002	VNVYYNEASCGR

Mascot: http://www.matrixscience.com/

AT5G23900.1

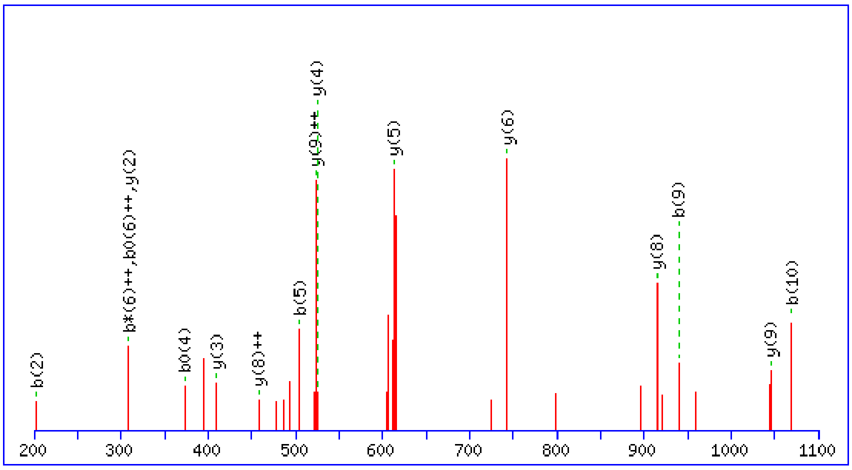
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLEGLQSNVQR**
Found in **AT5G23900.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L13 (RPL13D) | chr5:8064179-8065084 REVERSE

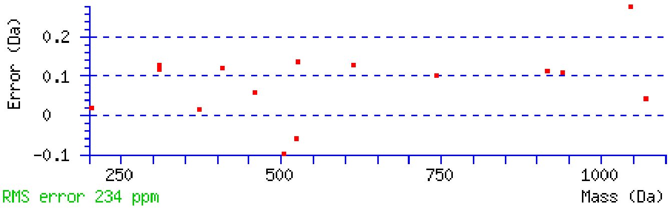
Match to Query 4483: 1246.586708 from(624.300630,2+) index(2443)
Title: Elution from: 26.082 to 26.082 scan no 3067 cid35.00 polarity:+
Data file C7-2_2.mgf

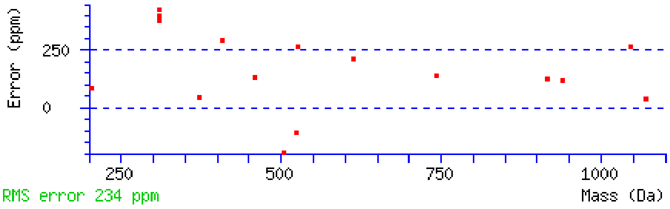
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1246.5860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 2.3e-005
Matches : 16/102 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							11
2	**203.1174**	102.0624			185.1069	93.0571	L	1159.5642	580.2857	1141.5406	571.2740	1141.5537	571.2805	10
3	333.1571	167.0822			315.1465	158.0769	E	***1045.4831***	523.2452	1027.4595	514.2334	1027.4726	514.2399	9
4	391.1756	196.0914			373.1650	187.0861	G	***915.4435***	458.2254	897.4199	449.2136	897.4329	449.2201	8
5	**505.2567**	253.1320			487.2461	244.1267	L	857.4250	429.2161	839.4014	420.2043	839.4144	420.2109	7
6	635.3093	318.1583	617.2857	309.1465	617.2987	309.1530	Q	***743.3439***	372.1756	725.3203	363.1638	725.3333	363.1703	6
7	723.3384	362.1728	705.3148	353.1610	705.3278	353.1675	S	***613.2912***	307.1493	595.2677	298.1375	595.2807	298.1440	5
8	839.3754	420.1913	821.3518	411.1795	821.3648	411.1860	N	***525.2622***	263.1347	507.2386	254.1229			4
9	**939.4408**	470.2240	921.4172	461.2123	921.4303	461.2188	V	***409.2252***	205.1162	391.2016	196.1044			3
10	**1069.4935**	535.2504	1051.4699	526.2386	1051.4829	526.2451	Q	***309.1597***	155.0835	291.1362	146.0717			2
11							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SLEGLQSNVQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G23900.1

Score	Mr(calc)	Delta	Sequence
57.0	1246.5860	0.0007	SLEGLQSNVQR
11.4	1246.5882	-0.0015	LSFDAPQAVQR
5.6	1246.5833	0.0034	KAESISDLENK
3.0	1246.5860	0.0007	QISQLNDEKR
2.9	1246.5860	0.0007	NVNGSVKDIER
1.2	1246.5860	0.0007	GEEVEKRVER

AT5G23940.1

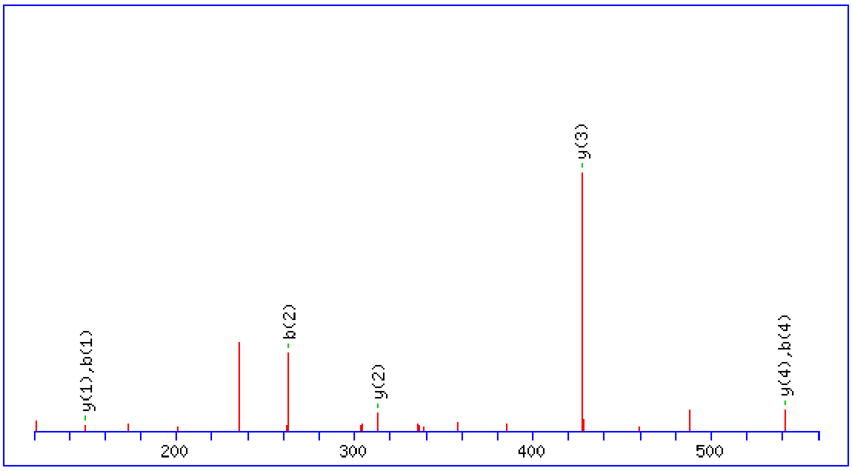
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLLYK**
Found in **AT5G23940.1** in **TAIR_Arabidopsis**, Symbols: EMB3009 | EMB3009 (EMBRYO DEFECTIVE 3009); transferase | chr5:8076619-8079680 REVERSE

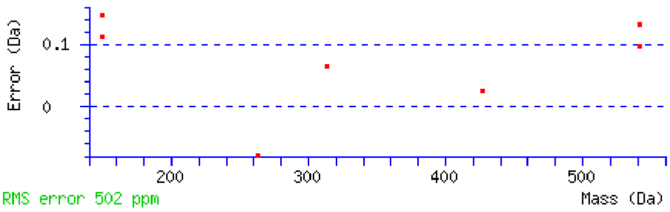
Match to Query 613: 688.387594 from(345.201073,2+) index(3204)
Title: Elution from: 32.275 to 32.275 scan no 3994 cid35.00 polarity:+
Data file D12h-3_1.mgf

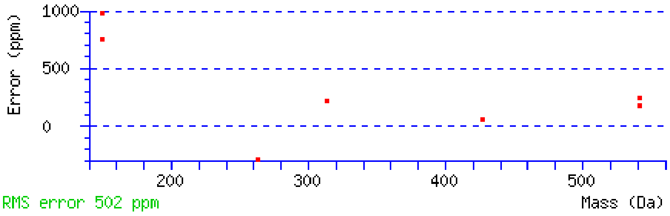
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 560 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 688.3876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.012
Matches : 7/24 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**149.0727**	75.0400	F					5
2	**263.1538**	132.0805	L	***541.3294***	271.1684	523.3059	262.1566	4
3	377.2349	189.1211	L	***427.2483***	214.1278	409.2248	205.1160	3
4	**541.2953**	271.1513	Y	***313.1672***	157.0873	295.1437	148.0755	2
5			K	***149.1069***	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of FLLYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.2	688.3876	-0.0000	FIIYK
24.2	688.3876	-0.0000	FLIYK
24.2	688.3876	-0.0000	FLLYK
24.2	688.3876	-0.0000	FYIIK

AT5G23940.1

22.6	688.3876	-0.0000	FLYLK
15.5	688.3876	-0.0000	IFLYK
15.5	688.3876	-0.0000	YFIIK
8.8	688.3876	-0.0000	YLFLK
7.8	688.3880	-0.0004	RTFKK
7.8	688.3880	-0.0004	TRKFK

AT5G23950.1

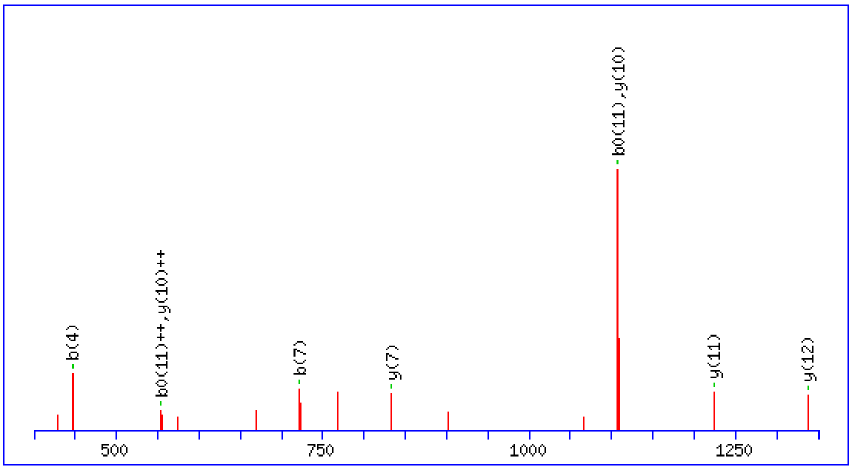
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVIDDVGFGVPFMK**
Found in **AT5G23950.1** in **TAIR_Arabidopsis**, Symbols: | C2 domain-containing protein | chr5:8082792-8083451 FORWARD

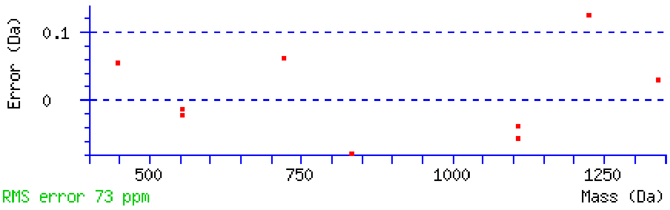
Match to Query 6351: 1552.703172 from(777.358862,2+) index(8685)
Title: Elution from: 81.386 to 81.386 scan no 11895 cid35.00 polarity:+
Data file D1d-2_2.mgf

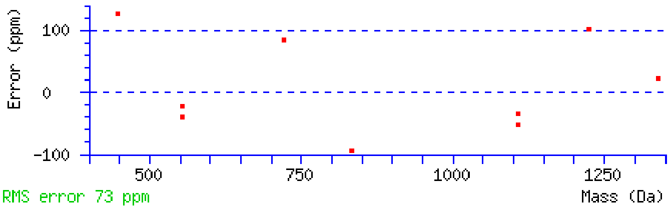
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1552.7041
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0022
Matches : 9/112 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193	99.0207	50.0140	D							14
2	217.0967	109.0520	199.0861	100.0467	V	1437.6875	719.3474	1419.6639	710.3356	1419.6769	710.3421	13
3	331.1778	166.0925	313.1672	157.0873	I	***1337.6220***	669.3147	1319.5985	660.3029	1319.6115	660.3094	12
4	**447.2018**	224.1045	429.1912	215.0992	D	***1223.5409***	612.2741	1205.5174	603.2623	1205.5304	603.2688	11
5	563.2258	282.1165	545.2152	273.1112	D	***1107.5170***	554.2621	1089.4934	545.2503	1089.5064	545.2568	10
6	663.2912	332.1492	645.2806	323.1440	V	991.4930	496.2501	973.4694	487.2383			9
7	**721.3097**	361.1585	703.2991	352.1532	G	891.4275	446.2174	873.4040	437.2056			8
8	869.3752	435.1912	851.3646	426.1859	F	***833.4090***	417.2082	815.3855	408.1964			7
9	927.3937	464.2005	909.3831	455.1952	G	685.3436	343.1754	667.3200	334.1636			6
10	1027.4591	514.2332	1009.4485	505.2279	V	627.3251	314.1662	609.3015	305.1544			5
11	1125.5089	563.2581	1107.4983	554.2528	P	527.2596	264.1335	509.2361	255.1217			4
12	1273.5744	637.2908	1255.5638	628.2855	F	429.2098	215.1086	411.1863	206.0968			3
13	1405.6119	703.3096	1387.6013	694.3043	M	281.1444	141.0758	263.1208	132.0640			2
14					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DVIDDVGFGVPFMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G23950.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.7	1552.7041	-0.0010	DVIDDVGFGVPFMK
32.6	1552.6986	0.0046	VNLDPEGVFDFSAK

AT5G24165.1

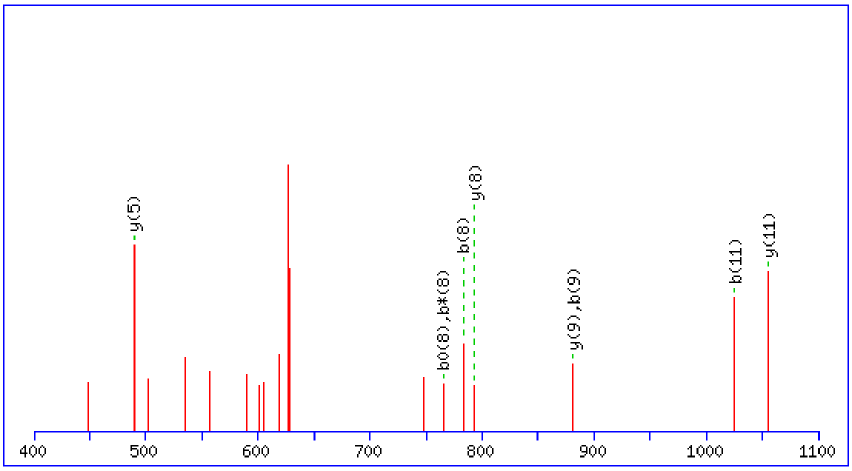
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVTASSDVPAAPK**
Found in **AT5G24165.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G23885.1); similar to unknown [Populus trichocarpa] (GB:ABK96174.1) | chr5:8188625-8189090 FORWARD

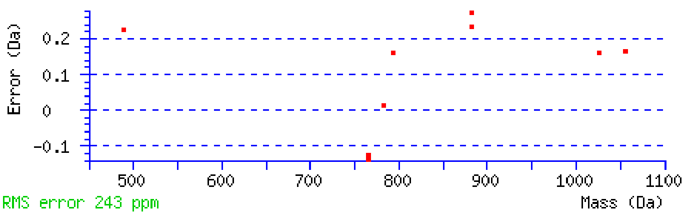
Match to Query 4767: 1270.594708 from(636.304630,2+) index(1662)
Title: Elution from: 21.023 to 21.023 scan no 2203 cid35.00 polarity:+
Data file C7-1_1.mgf

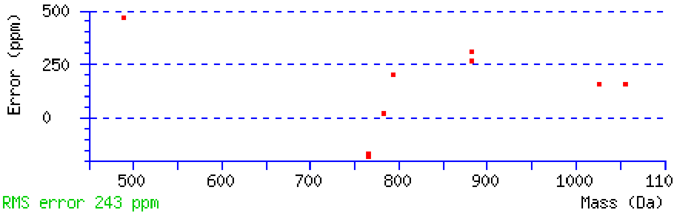
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1270.5964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0045
Matches : 9/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							13
2	217.1097	109.0585	199.0861	100.0467			V	1155.5666	578.2870	1137.5431	569.2752	1137.5561	569.2817	12
3	319.1544	160.0809	301.1309	151.0691	301.1439	151.0756	T	***1055.5012***	528.2542	1037.4776	519.2424	1037.4906	519.2489	11
4	391.1886	196.0979	373.1650	187.0861	373.1780	187.0926	A	953.4565	477.2319	935.4329	468.2201	935.4459	468.2266	10
5	479.2176	240.1125	461.1941	231.1007	461.2071	231.1072	S	***881.4223***	441.2148	863.3987	432.2030	863.4118	432.2095	9
6	567.2467	284.1270	549.2231	275.1152	549.2361	275.1217	S	***793.3933***	397.2003	775.3697	388.1885	775.3827	388.1950	8
7	683.2707	342.1390	665.2471	333.1272	665.2601	333.1337	D	705.3642	353.1857	687.3406	344.1739	687.3536	344.1805	7
8	***783.3361***	392.1717	765.3126	383.1599	765.3256	383.1664	V	589.3402	295.1737	571.3166	286.1620			6
9	***881.3859***	441.1966	863.3624	432.1848	863.3754	432.1913	P	***489.2748***	245.1410	471.2512	236.1292			5
10	953.4201	477.2137	935.3965	468.2019	935.4095	468.2084	A	391.2250	196.1161	373.2014	187.1043			4
11	***1025.4542***	513.2308	1007.4307	504.2190	1007.4437	504.2255	A	319.1908	160.0990	301.1672	151.0873			3
12	1123.5040	562.2557	1105.4804	553.2439	1105.4935	553.2504	P	247.1567	124.0820	229.1331	115.0702			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NVTASSDVPAAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G24165.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1270.5964	-0.0017	NVTASSDVPAAPK
8.6	1270.5916	0.0031	QQQPQAPMSLK
2.6	1270.5963	-0.0016	VNGGVAEGELPSK
1.0	1270.5937	0.0010	EELIEEIEQK
0.6	1270.5972	-0.0025	IPLCTMIGHSK

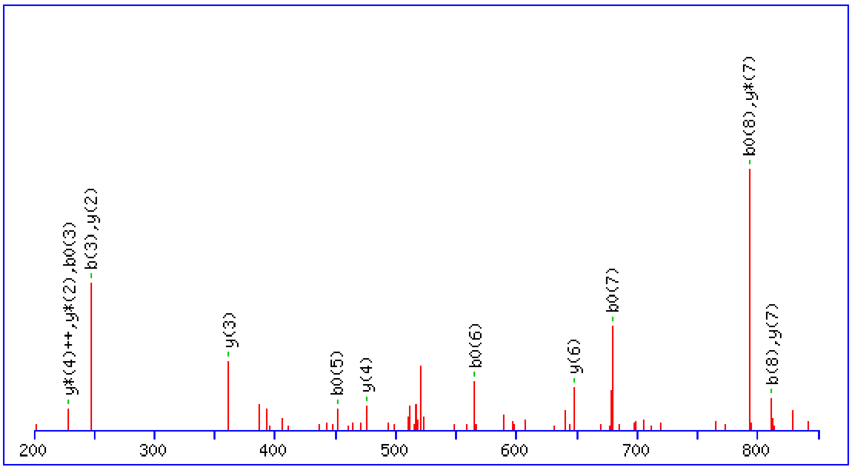
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGGYGLIIPK**
Found in **AT5G24490.1** in **TAIR_Arabidopsis**, Symbols: | 30S ribosomal protein, putative | chr5:8365693-8367181 FORWARD

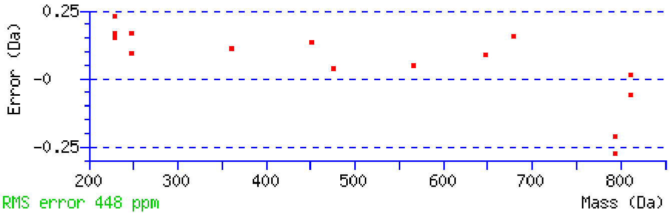
Match to Query 2892: 1056.547850 from(529.281201,2+) index(5367)
Title: Elution from: 48.968 to 48.968 scan no 6743 cid35.00 polarity:+
Data file D6h-2_2.mgf

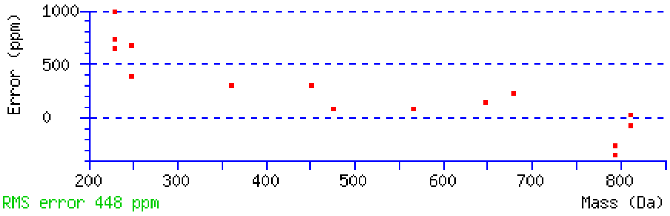
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1056.5482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.001
Matches : 15/72 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	131.0469	66.0271	113.0363	57.0218	E					10
2	189.0654	95.0363	171.0548	86.0311	G	927.5158	464.2616	909.4922	455.2498	9
3	**247.0839**	124.0456	229.0733	115.0403	G	869.4973	435.2523	851.4737	426.2405	8
4	411.1443	206.0758	393.1337	197.0705	Y	***811.4788***	406.2431	793.4552	397.2313	7
5	469.1628	235.0850	451.1522	226.0797	G	***647.4185***	324.2129	629.3949	315.2011	6
6	583.2439	292.1256	565.2333	283.1203	L	589.4000	295.2036	571.3764	286.1918	5
7	697.3250	349.1661	679.3144	340.1608	I	***475.3189***	238.1631	457.2953	229.1513	4
8	**811.4061**	406.2067	793.3955	397.2014	I	***361.2378***	181.1225	343.2142	172.1107	3
9	909.4559	455.2316	891.4453	446.2263	P	***247.1567***	124.0820	229.1331	115.0702	2
10					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of EGGYGLIIPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G24490.1

40.2	1056.5482	-0.0003	EGGYGLIIPK
14.1	1056.5460	0.0019	SSTSNVIIPK
2.2	1056.5482	-0.0003	LPSEVFLNK
1.4	1056.5482	-0.0003	VFITDNLPK
1.1	1056.5486	-0.0007	GLRTQKDPK
1.1	1056.5482	-0.0003	LFALDDKPK

AT5G24690.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAYEMGLVSSAQMVK**
Found in **AT5G24690.1** in **TAIR_Arabidopsis**, Symbols: | similar to RER1 (RETICULATA-RELATED 1) [Arabidopsis thaliana] (TAIR:AT5G22790.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24736.1) | chr5:8455786-8458516 REVERSE

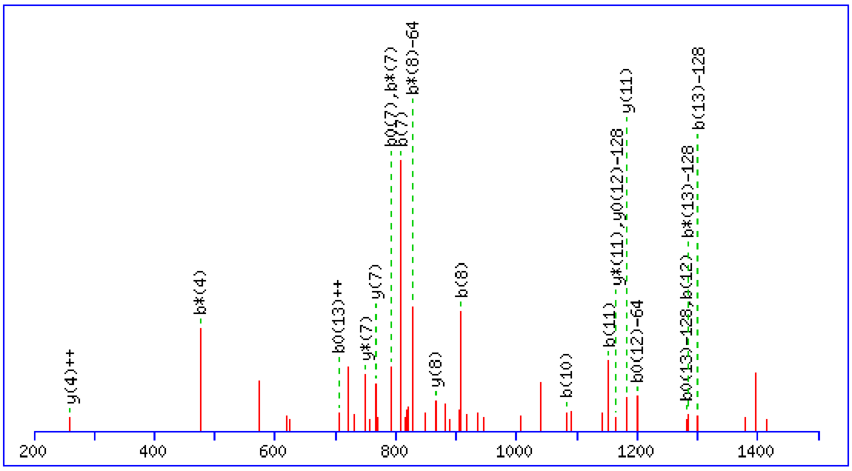
Match to Query 7533: 1672.783762 from(837.399157,2+) index(7360)
Title: Elution from: 65.386 to 65.386 scan no 9693 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

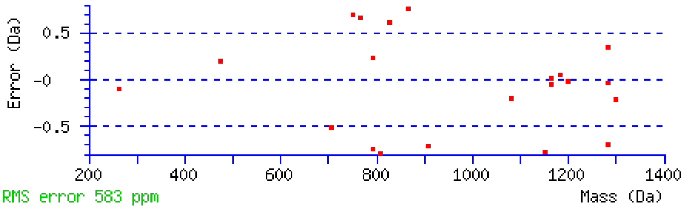
Show Y-axis ☐

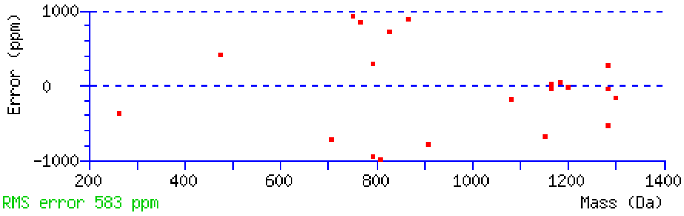


Monoisotopic mass of neutral peptide Mr(calc): 1672.7800
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 18 **Expect:** 0.042
Matches : 21/278 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	200.1030	100.5551	183.0764	92.0418			A	1545.7287	773.3680	1528.7022	764.8547	1527.7182	764.3627	14
3	363.1663	182.0868	346.1397	173.5735			Y	1474.6916	737.8495	1457.6651	729.3362	1456.6811	728.8442	13
4	492.2089	246.6081	475.1823	238.0948	474.1983	237.6028	E	1311.6283	656.3178	1294.6018	647.8045	1293.6177	647.3125	12
5	639.2443	320.1258	622.2177	311.6125	621.2337	311.1205	M	**1182.5857**	591.7965	1165.5592	583.2832	1164.5751	582.7912	11
6	696.2658	348.6365	679.2392	340.1232	678.2552	339.6312	G	1035.5503	518.2788	1018.5238	509.7655	1017.5397	509.2735	10
7	***809.3498***	405.1785	792.3233	396.6653	791.3393	396.1733	L	978.5288	489.7681	961.5023	481.2548	960.5183	480.7628	9
8	***908.4182***	454.7128	891.3917	446.1995	890.4077	445.7075	V	**865.4448**	433.2260	848.4182	424.7128	847.4342	424.2207	8
9	995.4503	498.2288	978.4237	489.7155	977.4397	489.2235	S	**766.3764**	383.6918	749.3498	375.1785	748.3658	374.6865	7
10	***1082.4823***	541.7448	1065.4557	533.2315	1064.4717	532.7395	S	679.3443	340.1758	662.3178	331.6625	661.3338	331.1705	6
11	***1153.5194***	577.2633	1136.4929	568.7501	1135.5088	568.2581	A	592.3123	296.6598	575.2858	288.1465			5
12	***1281.5780***	641.2926	1264.5514	632.7794	1263.5674	632.2873	Q	521.2752	261.1412	504.2486	252.6280			4
13	1428.6134	714.8103	1411.5868	706.2971	1410.6028	705.8050	M	393.2166	197.1119	376.1901	188.5987			3
14	1527.6818	764.3445	1510.6552	755.8313	1509.6712	755.3393	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1

AT5G24690.1





NCBI **BLAST** search of QAYEMGLVSSAQMVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.2	1672.7800	0.0037	QAYEMGLVSSAQMVK

Mascot: http://www.matrixscience.com/

Mascot Search Results

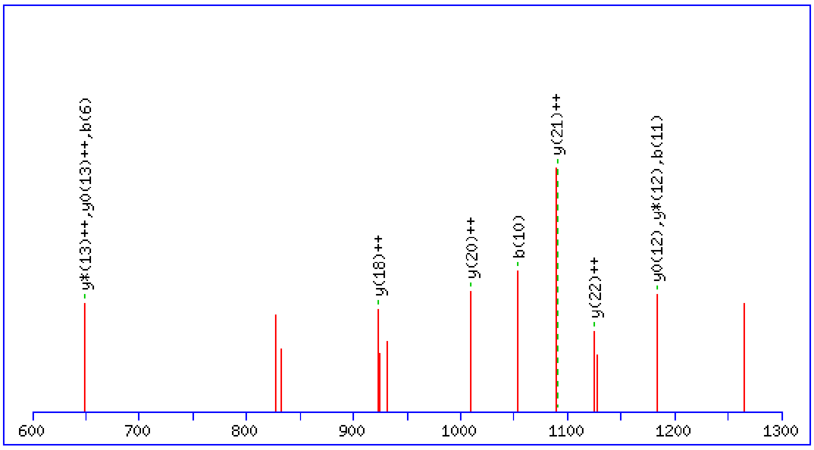
Peptide View

MS/MS Fragmentation of **LKEAQARAVAEHGELALITVEGSQAAK**
Found in **AT5G24710.1** in **TAIR_Arabidopsis**, Symbols: | similar to hypothetical protein OsI_003062 [Oryza sativa (indica cultivar-group)] (GB:EAY75215.1); similar to hypothetical protein OsJ_002759 [Oryza sativa (japonica cultivar-group)] (GB:EAZ12934.1); similar to unnamed protein product [

Match to Query 10445: 2825.393304 from(942.805044,3+) index(10438)
Title: Elution from: 105.843 to 105.843 scan no 15249 cid35.00 polarity:+
Data file D12h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

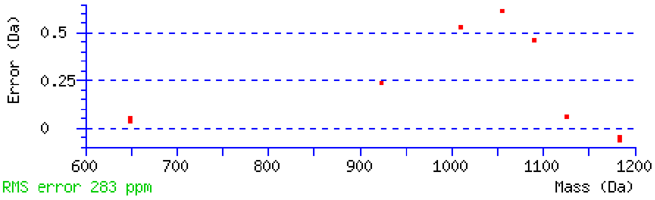
Or, Plot from 600 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

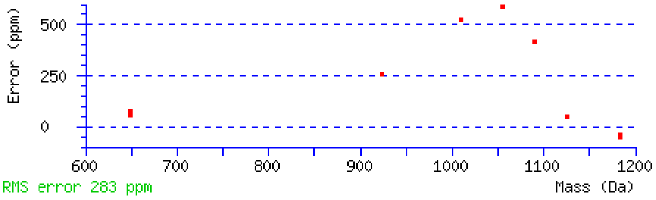


Monoisotopic mass of neutral peptide Mr(calc): 2825.3968
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.04
Matches : 11/298 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							27
2	245.1774	123.0923	227.1538	114.0805			K	2712.3230	1356.6651	2694.2994	1347.6533	2694.3124	1347.6599	26
3	375.2170	188.1122	357.1935	179.1004	357.2065	179.1069	E	2582.2340	1291.6206	2564.2104	1282.6088	2564.2234	1282.6153	25
4	447.2512	224.1292	429.2276	215.1174	429.2406	215.1239	A	2452.1943	1226.6008	2434.1707	1217.5890	2434.1838	1217.5955	24
5	577.3038	289.1556	559.2802	280.1438	559.2933	280.1503	Q	2380.1602	1190.5837	2362.1366	1181.5719	2362.1496	1181.5784	23
6	***649.3380***	325.1726	631.3144	316.1608	631.3274	316.1673	A	2250.1075	1125.5574	2232.0840	1116.5456	2232.0970	1116.5521	22
7	809.4272	405.2173	791.4036	396.2055	791.4167	396.2120	R	2178.0734	1089.5403	2160.0498	1080.5285	2160.0628	1080.5350	21
8	881.4614	441.2343	863.4378	432.2225	863.4508	432.2290	A	2017.9841	1009.4957	1999.9606	1000.4839	1999.9736	1000.4904	20
9	981.5268	491.2671	963.5032	482.2553	963.5163	482.2618	V	1945.9500	973.4786	1927.9264	964.4668	1927.9394	964.4733	19
10	***1053.5610***	527.2841	1035.5374	518.2723	1035.5504	518.2788	A	1845.8845	923.4459	1827.8610	914.4341	1827.8740	914.4406	18
11	***1183.6006***	592.3039	1165.5770	583.2921	1165.5900	583.2987	E	1773.8504	887.4288	1755.8268	878.4170	1755.8398	878.4236	17
12	1323.6506	662.3290	1305.6270	653.3172	1305.6401	653.3237	H	1643.8108	822.4090	1625.7872	813.3972	1625.8002	813.4037	16
13	1381.6691	691.3382	1363.6455	682.3264	1363.6586	682.3329	G	1503.7607	752.3840	1485.7372	743.3722	1485.7502	743.3787	15
14	1511.7088	756.3580	1493.6852	747.3462	1493.6982	747.3527	E	1445.7422	723.3748	1427.7187	714.3630	1427.7317	714.3695	14
15	1625.7899	813.3986	1607.7663	804.3868	1607.7793	804.3933	L	1315.7026	658.3549	1297.6790	649.3432	1297.6921	649.3497	13
16	1697.8240	849.4156	1679.8004	840.4038	1679.8134	840.4104	A	1201.6215	601.3144	1183.5979	592.3026	1183.6110	592.3091	12
17	1811.9051	906.4562	1793.8815	897.4444	1793.8945	897.4509	L	1129.5874	565.2973	1111.5638	556.2855	1111.5768	556.2920	11
18	1925.9862	963.4967	1907.9626	954.4849	1907.9756	954.4915	I	1015.5063	508.2568	997.4827	499.2450	997.4957	499.2515	10
19	2028.0309	1014.5191	2010.0073	1005.5073	2010.0203	1005.5138	T	901.4252	451.2162	883.4016	442.2044	883.4146	442.2109	9
20	2128.0964	1064.5518	2110.0728	1055.5400	2110.0858	1055.5465	V	799.3805	400.1939	781.3569	391.1821	781.3699	391.1886	8
21	2258.1360	1129.5716	2240.1124	1120.5598	2240.1254	1120.5663	E	699.3150	350.1611	681.2914	341.1494	681.3044	341.1559	7
22	2316.1545	1158.5809	2298.1309	1149.5691	2298.1439	1149.5756	G	569.2754	285.1413	551.2518	276.1295	551.2648	276.1360	6
23	2404.1835	1202.5954	2386.1600	1193.5836	2386.1730	1193.5901	S	511.2569	256.1321	493.2333	247.1203	493.2463	247.1268	5

24	2534.2362	1267.6217	2516.2126	1258.6099	2516.2256	1258.6165	**Q**	423.2278	212.1175	405.2042	203.1058			**4**
25	2606.2703	1303.6388	2588.2468	1294.6270	2588.2598	1294.6335	**A**	293.1752	147.0912	275.1516	138.0794			**3**
26	2678.3045	1339.6559	2660.2809	1330.6441	2660.2939	1330.6506	**A**	221.1410	111.0741	203.1174	102.0624			**2**
27							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of LKEAQARAVAEHGELALITVEGSQAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.9	2825.3968	-0.0035	LKEAQARAVAEHGELALITVEGSQAAK
2.9	2825.4013	-0.0080	FLLDLDIAAPKITIPTEFRPDNHR
0.7	2825.3858	0.0075	HVWSKTPHLSFEWLMVSPKLINK

Mascot: http://www.matrixscience.com/

AT5G24740.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQTDNIIR**
Found in **AT5G24740.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17140.1); similar to hypothetical protein OsI_026627 [Oryza sativa (indica cultivar-group)] (GB:EAZ05395.1); similar to C-5 cytosine-specific DNA methylase; Vacuolar protein so

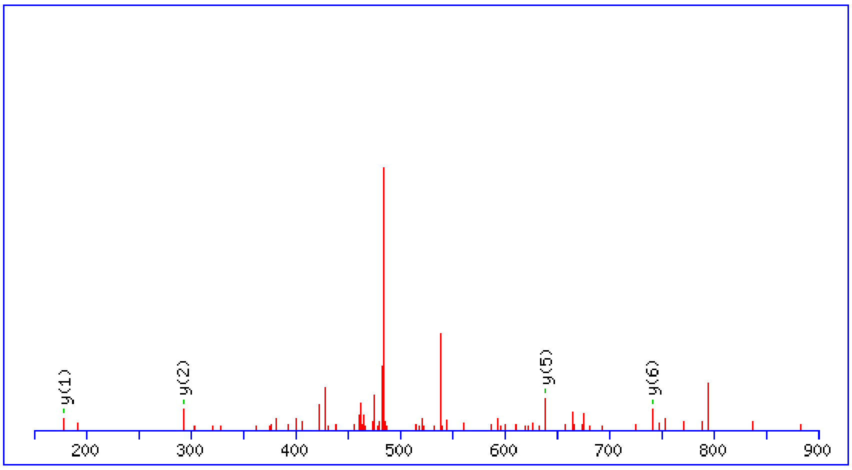
Match to Query 2329: 984.502472 from(493.258512,2+) index(3303)
Title: Elution from: 33.463 to 33.463 scan no 4155 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

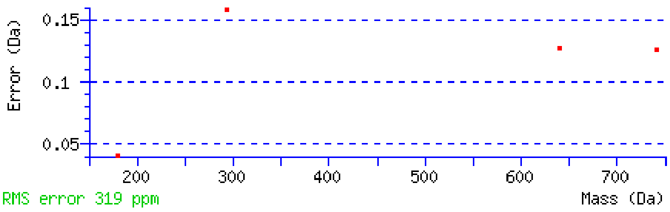
Label all possible matches ○ Label matches used for scoring ●

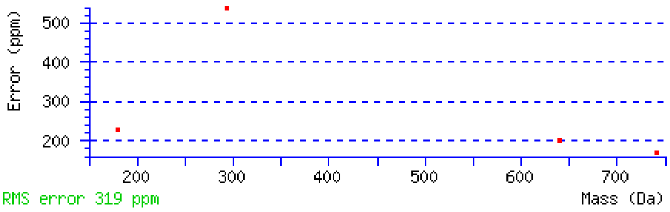
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 984.5014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.029
Matches : 4/70 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							8
2	245.1410	123.0741	227.1174	114.0624			Q	871.4276	436.2175	853.4040	427.2057	853.4171	427.2122	7
3	347.1857	174.0965	329.1622	165.0847	329.1752	165.0912	T	***741.3750***	371.1911	723.3514	362.1793	723.3644	362.1858	6
4	463.2097	232.1085	445.1861	223.0967	445.1991	223.1032	D	***639.3303***	320.1688	621.3067	311.1570	621.3197	311.1635	5
5	579.2467	290.1270	561.2231	281.1152	561.2361	281.1217	N	523.3063	262.1568	505.2827	253.1450			4
6	693.3278	347.1675	675.3042	338.1558	675.3172	338.1623	I	407.2693	204.1383	389.2457	195.1265			3
7	807.4089	404.2081	789.3853	395.1963	789.3983	395.2028	I	***293.1882***	147.0977	275.1646	138.0859			2
8							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LQTDNIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G24740.1

25.8	984.5014	0.0010	LQTDNIIR
15.5	984.5014	0.0010	LKQAEDLR
14.6	984.5014	0.0010	TSVGEKPVR
13.7	984.5014	0.0010	QITAALAER
13.6	984.5014	0.0010	ELENAKLR
13.6	984.5014	0.0010	IQINTDLR
13.6	984.5014	0.0010	LQLENSLR
13.6	984.5014	0.0010	QLQDLSIR
9.8	984.5037	-0.0012	FELVNVPR
8.9	984.5014	0.0010	EIAELNKR

AT5G24830.1

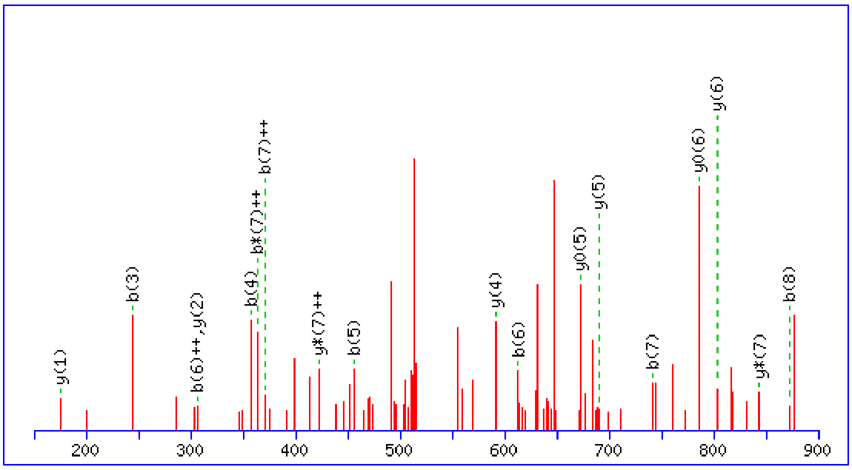
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADGLVREMR**
Found in **AT5G24830.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:8531229-8533269 FORWARD

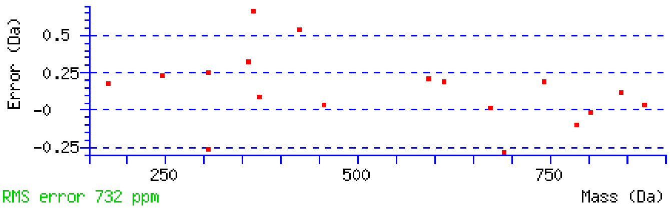
Match to Query 2833: 1045.532260 from(523.773406,2+) index(5213)
Title: Elution from: 47.063 to 47.063 scan no 6582 cid35.00 polarity:+
Data file D6h-1_3.mgf

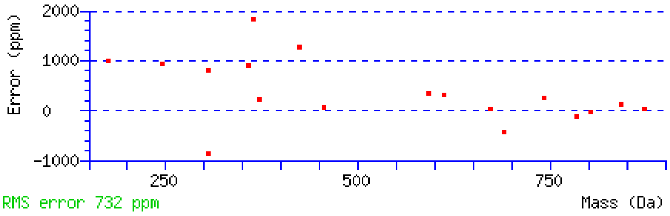
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1045.5338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.02
Matches : 18/80 fragment ions using 46 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							9
2	187.0713	94.0393			169.0608	85.0340	D	975.5040	488.2557	958.4775	479.7424	957.4935	479.2504	8
3	***244.0928***	122.5500			226.0822	113.5448	G	860.4771	430.7422	843.4505	422.2289	842.4665	421.7369	7
4	***357.1769***	179.0921			339.1663	170.0868	L	**803.4556**	402.2314	786.4291	393.7182	785.4451	393.2262	6
5	***456.2453***	228.6263			438.2347	219.6210	V	**690.3716**	345.6894	673.3450	337.1761	672.3610	336.6841	5
6	***612.3464***	306.6768	595.3198	298.1636	594.3358	297.6715	R	**591.3031**	296.1552	574.2766	287.6419	573.2926	287.1499	4
7	***741.3890***	371.1981	724.3624	362.6849	723.3784	362.1928	E	435.2020	218.1047	418.1755	209.5914	417.1915	209.0994	3
8	***872.4295***	436.7184	855.4029	428.2051	854.4189	427.7131	M	**306.1594**	153.5834	289.1329	145.0701			2
9							R	**175.1190**	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ADGLVREMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	1045.5338	-0.0016	ADGLVREMR

AT5G24830.1

10.1	1045.5305	0.0018	GWNALSKDR
7.1	1045.5338	-0.0016	DLGNNVMKR
4.4	1045.5339	-0.0016	TTKMVSSHR
4.0	1045.5339	-0.0016	VALACVGNSR
1.8	1045.5338	-0.0016	LNDLRMER
0.2	1045.5339	-0.0016	TCIVLGNNR

AT5G25460.1

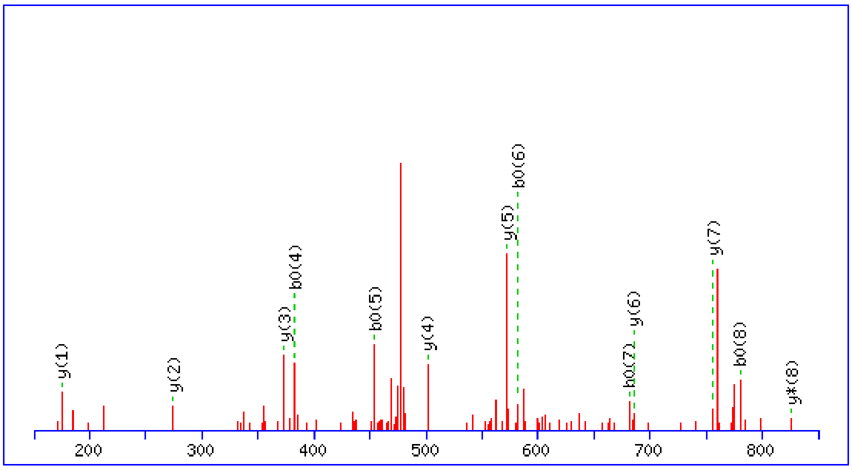
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESAIAQVVR**
Found in **AT5G25460.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11420.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Protein of unknown function DUF642 (InterPro:IPR006946) | chr5:8863433-8865397 FORWARD

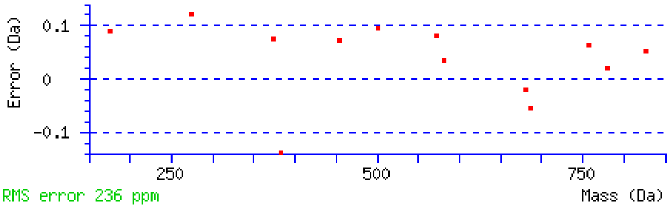
Match to Query 2180: 971.541240 from(486.777896,2+) index(2464)
Title: Elution from: 25.321 to 25.321 scan no 3062 cid35.00 polarity:+
Data file 0-2_3.mgf

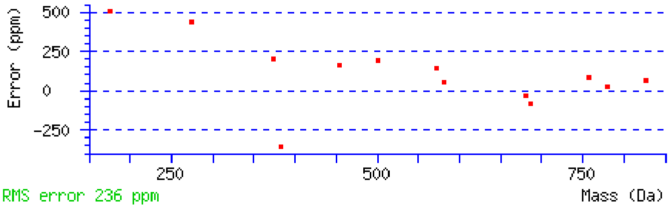
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 971.5400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0016
Matches : 13/72 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**9**
2	217.0819	109.0446			199.0713	100.0393	**S**	843.5047	422.2560	826.4781	413.7427	825.4941	413.2507	**8**
3	288.1190	144.5631			270.1084	135.5579	**A**	***756.4727***	378.7400	739.4461	370.2267			**7**
4	401.2031	201.1052			383.1925	192.0999	**I**	***685.4355***	343.2214	668.4090	334.7081			**6**
5	472.2402	236.6237			454.2296	227.6185	**A**	***572.3515***	286.6794	555.3249	278.1661			**5**
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	**Q**	***501.3144***	251.1608	484.2878	242.6475			**4**
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	**V**	***373.2558***	187.1315	356.2292	178.6183			**3**
8	798.4356	399.7214	781.4090	391.2082	780.4250	390.7162	**V**	***274.1874***	137.5973	257.1608	129.0840			**2**
9							**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of ESAIAQVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G25460.1

Score	Mr(calc)	Delta	Sequence
37.0	971.5400	0.0013	ESAIAQVVR
16.1	971.5400	0.0012	SSPVQTVVR
7.9	971.5400	0.0012	GKPSTEVVR
6.3	971.5400	0.0012	SSVPALGSVR
6.1	971.5400	0.0013	DKVENIVR
5.5	971.5400	0.0012	TSVGEKPVR
5.2	971.5400	0.0013	ATTISNLPR
4.8	971.5440	-0.0028	LAYELHVK
4.7	971.5400	0.0013	IQINTDLR
4.6	971.5400	0.0012	KQLVDDVR

AT5G25754.1

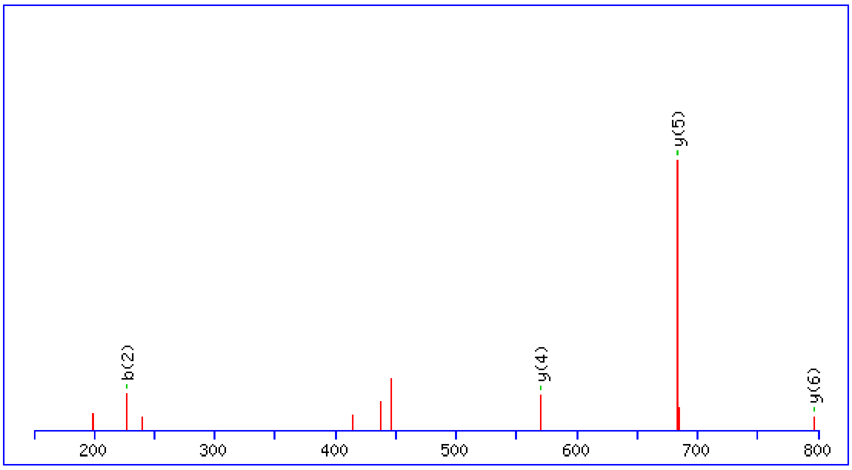
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLYIFK**
Found in **AT5G25754.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25757.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ51676.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAT77307.1

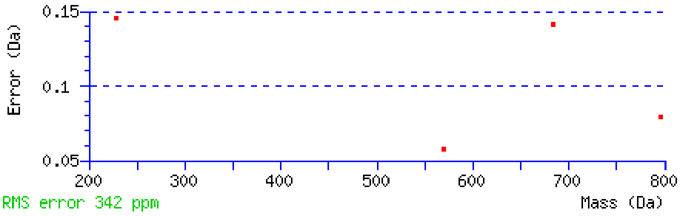
Match to Query 1411: 908.573648 from(455.294100,2+) index(8135)
Title: Elution from: 75.928 to 75.928 scan no 11015 cid35.00 polarity:+
Data file D1d-2_2.mgf

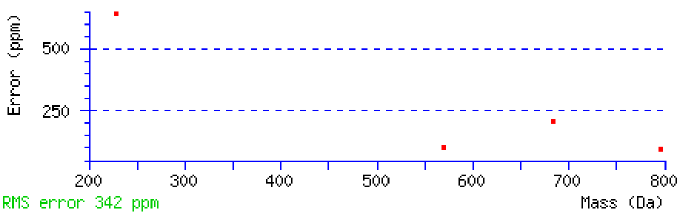
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 908.5735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.0078
Matches : 4/36 fragment ions using 5 most intense peaks (help)

#	b	b⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	#
1	114.0913	57.5493	I					7
2	227.1754	114.0913	L	***796.4967***	398.7520	779.4702	390.2387	6
3	340.2595	170.6334	L	***683.4127***	342.2100	666.3861	333.6967	5
4	503.3228	252.1650	Y	***570.3286***	285.6679	553.3021	277.1547	4
5	616.4069	308.7071	I	407.2653	204.1363	390.2387	195.6230	3
6	763.4753	382.2413	F	294.1812	147.5942	277.1547	139.0810	2
7			K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of ILLYIFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.1	908.5735	0.0001	ILLYIFK

AT5G25754.1

21.1	908.5735	0.0001	LLLFIYK

Mascot: http://www.matrixscience.com/

AT5G25770.1

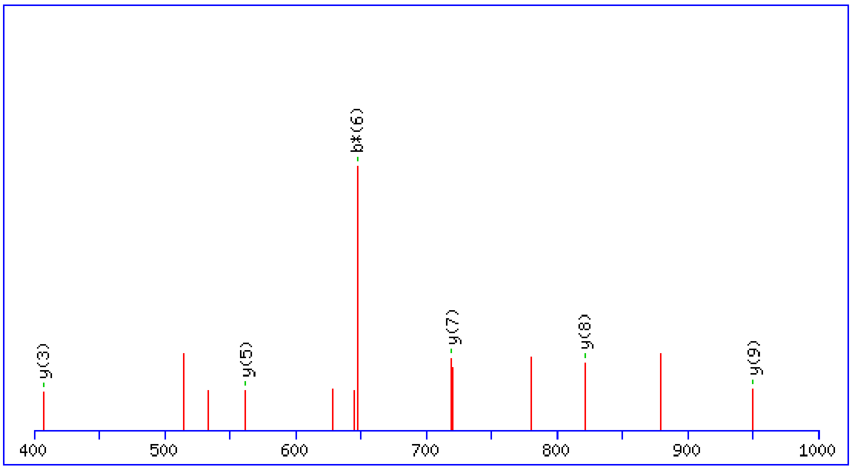
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYKETASPGNFK**
Found in **AT5G25770.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO44054.1); contains domain PTHR10992 (PTHR10992); contains domain SSF53474 (SSF53474); contains domain G3DSA:3.40.50.1820 (G3DSA:3.40.50.1820) | chr5:8969311-8971392 REVERSE

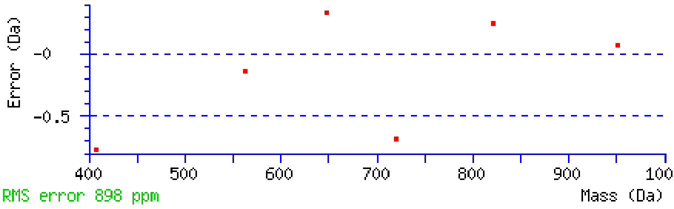
Match to Query 4343: 1311.644552 from(656.829552,2+) index(3676)
Title: Elution from: 37.978 to 37.978 scan no 4716 cid35.00 polarity:+
Data file D1d-2_2.mgf

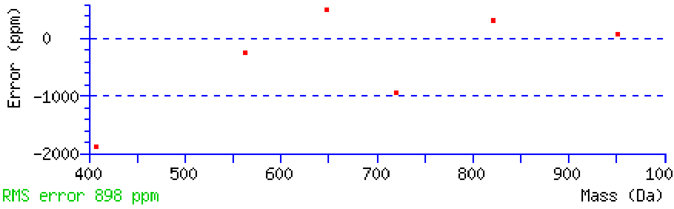
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1311.6459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0022
Matches : 6/112 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							12
2	235.1077	118.0575					Y	1241.6161	621.3117	1224.5895	612.7984	1223.6055	612.3064	11
3	363.2027	182.1050	346.1761	173.5917			K	1078.5528	539.7800	1061.5262	531.2667	1060.5422	530.7747	10
4	492.2453	246.6263	475.2187	238.1130	474.2347	237.6210	E	***950.4578***	475.7325	933.4312	467.2193	932.4472	466.7272	9
5	593.2930	297.1501	576.2664	288.6368	575.2824	288.1448	T	***821.4152***	411.2112	804.3886	402.6980	803.4046	402.2060	8
6	664.3301	332.6687	647.3035	324.1554	646.3195	323.6634	A	***720.3675***	360.6874	703.3410	352.1741	702.3569	351.6821	7
7	751.3621	376.1847	734.3355	367.6714	733.3515	367.1794	S	649.3304	325.1688	632.3039	316.6556	631.3198	316.1636	6
8	848.4149	424.7111	831.3883	416.1978	830.4043	415.7058	P	***562.2984***	281.6528	545.2718	273.1396			5
9	905.4363	453.2218	888.4098	444.7085	887.4258	444.2165	G	465.2456	233.1264	448.2191	224.6132			4
10	1019.4793	510.2433	1002.4527	501.7300	1001.4687	501.2380	N	***408.2241***	204.6157	391.1976	196.1024			3
11	1166.5477	583.7775	1149.5211	575.2642	1148.5371	574.7722	F	294.1812	147.5942	277.1547	139.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AYKETASPGNFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G25770.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.0	1311.6459	-0.0013	AYKETASPGNFK
17.9	1311.6459	-0.0013	SFGAAVIYNNEK
3.5	1311.6414	0.0031	MSSVVLMLGSEK
2.6	1311.6459	-0.0014	ATEAGYWKTTGK
2.5	1311.6419	0.0027	TSSAANLFTGSTR
0.5	1311.6428	0.0018	MMRDVFRPTK
0.3	1311.6427	0.0018	GHINPMLNLCK

AT5G25980.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGPVMITR**
Found in **AT5G25980.1** in **TAIR_Arabidopsis**, Symbols: TGG2 | TGG2 (GLUCOSIDE GLUCOHYDROLASE 2); hydrolase, hydrolyzing O-glycosyl compounds | chr5:9072733-9075146 FORWARD

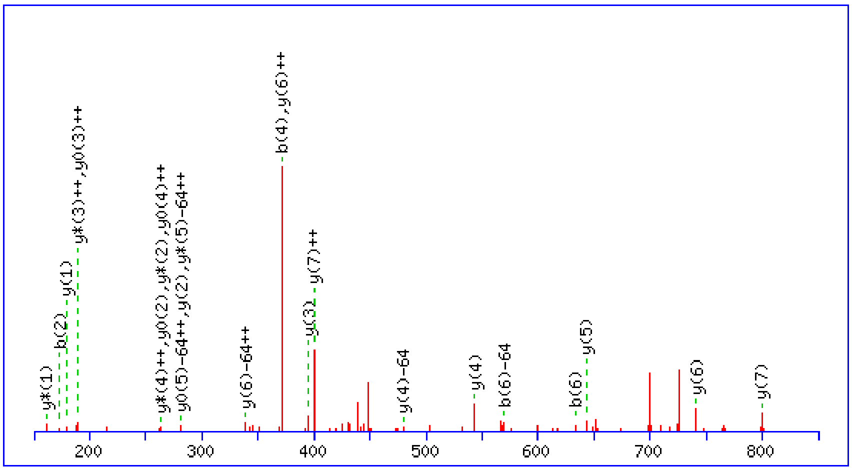
Match to Query 1665: 912.472214 from(457.243383,2+) index(2609)
Title: Elution from: 26.627 to 26.627 scan no 3261 cid35.00 polarity:+
Data file D12h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

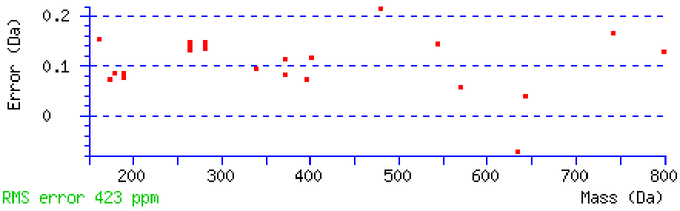
Label all possible matches ○ Label matches used for scoring ●

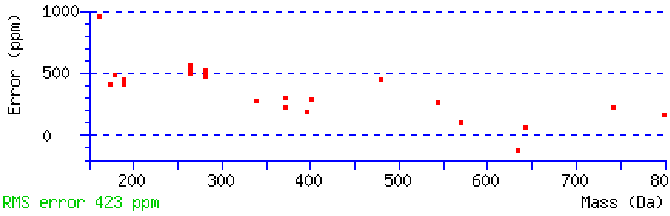
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 912.4729
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 41 **Expect:** 0.00054
Matches : 24/88 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							8
2	**173.1069**	87.0571			G	***799.3991***	400.2032	781.3755	391.1914	781.3885	391.1979	7
3	271.1567	136.0820			P	***741.3806***	371.1939	723.3570	362.1821	723.3700	362.1886	6
4	**371.2221**	186.1147			V	***643.3308***	322.1690	625.3072	313.1572	625.3202	313.1637	5
5	519.2546	260.1309			M	***543.2653***	272.1363	525.2418	263.1245	525.2548	263.1310	4
6	**633.3357**	317.1715			I	***395.2329***	198.1201	377.2093	189.1083	377.2223	189.1148	3
7	735.3804	368.1938	717.3698	359.1885	T	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	2
8					R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IGPVMITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G25980.1

41.2	912.4729	-0.0007	IGPVMITR
9.8	912.4695	0.0027	LVIWDTR
7.6	912.4729	-0.0007	IVEIICR
5.9	912.4729	-0.0007	NAPTKLMK
5.3	912.4695	0.0027	IAQWSGLK
2.6	912.4695	0.0027	LLVDWTR
2.5	912.4722	0.0000	LAHFQKR
2.3	912.4695	0.0027	LFSHTLGK
2.2	912.4722	0.0000	LFHAAGRK
1.8	912.4729	-0.0007	LDMAALLR

AT5G25980.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASGLWYQSFLR**
Found in **AT5G25980.2** in **TAIR_Arabidopsis**, Symbols: TGG2 | TGG2 (GLUCOSIDE GLUCOHYDROLASE 2); hydrolase, hydrolyzing O-glycosyl compounds | chr5:9072733-9075480 FORWARD

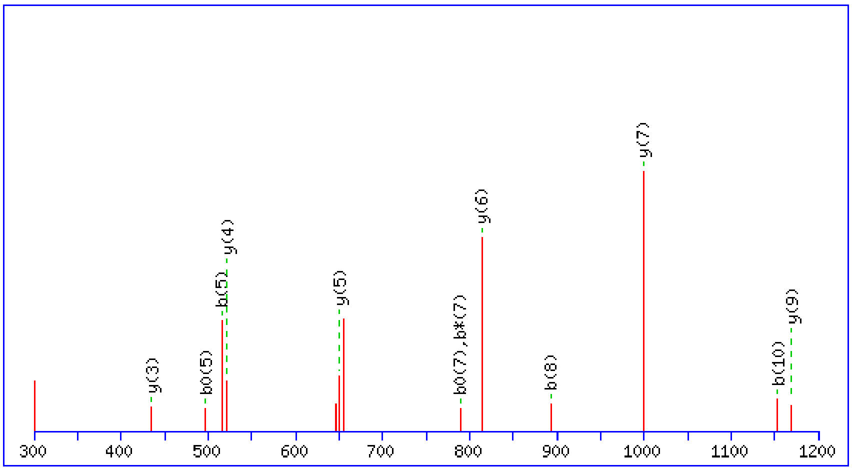
Match to Query 4859: 1326.669956 from(664.342254,2+) index(8957)
Title: Elution from: 81.104 to 81.104 scan no 12187 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1200 Da Full range

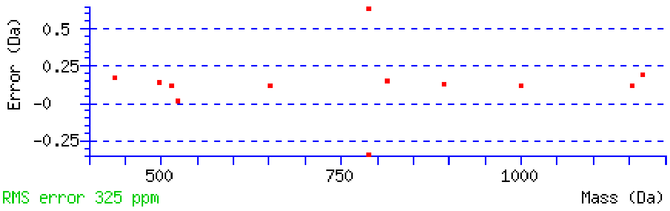
Label all possible matches ○ Label matches used for scoring ●

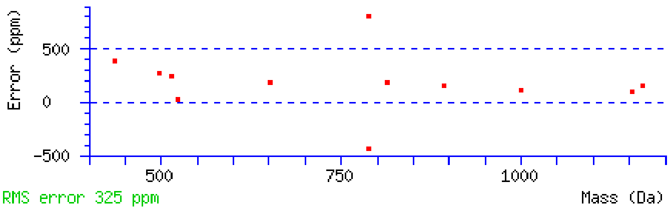
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1326.6721
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 6.5e-006
Matches : 12/100 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**11**
2	159.0764	80.0418			141.0659	71.0366	**S**	1256.6422	628.8248	1239.6157	620.3115	1238.6317	619.8195	**10**
3	216.0979	108.5526			198.0873	99.5473	**G**	***1169.6102***	585.3087	1152.5837	576.7955	1151.5996	576.3035	**9**
4	329.1819	165.0946			311.1714	156.0893	**L**	1112.5887	556.7980	1095.5622	548.2847	1094.5782	547.7927	**8**
5	**515.2613**	258.1343			497.2507	249.1290	**W**	***999.5047***	500.2560	982.4781	491.7427	981.4941	491.2507	**7**
6	678.3246	339.6659			660.3140	330.6606	**Y**	***813.4254***	407.2163	796.3988	398.7030	795.4148	398.2110	**6**
7	806.3832	403.6952	789.3566	395.1819	788.3726	394.6899	**Q**	***650.3620***	325.6847	633.3355	317.1714	632.3515	316.6794	**5**
8	**893.4152**	447.2112	876.3886	438.6980	875.4046	438.2060	**S**	***522.3035***	261.6554	505.2769	253.1421	504.2929	252.6501	**4**
9	1040.4836	520.7454	1023.4571	512.2322	1022.4730	511.7402	**F**	***435.2714***	218.1394	418.2449	209.6261			**3**
10	**1153.5677**	577.2875	1136.5411	568.7742	1135.5571	568.2822	**L**	288.2030	144.6051	271.1765	136.0919			**2**
11							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of ASGLWYQSFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G25980.2

Score	Mr(calc)	Delta	Sequence
57.6	1326.6721	-0.0021	ASGLWYQSFLR
3.9	1326.6714	-0.0015	ACGDQLVVVGGPR

AT5G26000.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLNVWDSFTHR**
Found in **AT5G26000.1** in **TAIR_Arabidopsis**, Symbols: TGG1 | TGG1 (THIOGLUCOSIDE GLUCOHYDROLASE 1); hydrolase, hydrolyzing O-glycosyl compounds | chr5:9079681-9082350 REVERSE

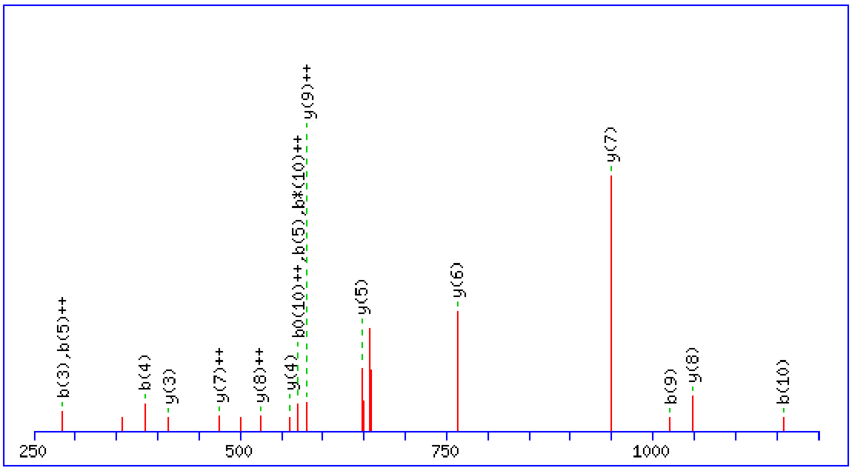
Match to Query 4999: 1330.641386 from(666.327969,2+) index(7190)
Title: Elution from: 64.284 to 64.284 scan no 9325 cid35.00 polarity:+
Data file 0-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1200 Da Full range

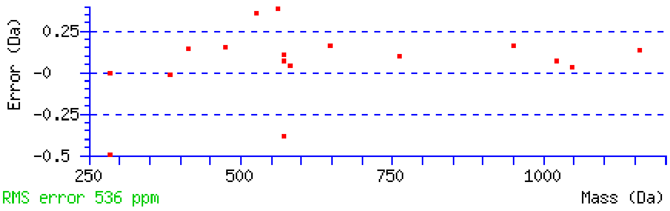
Label all possible matches ○ Label matches used for scoring ●

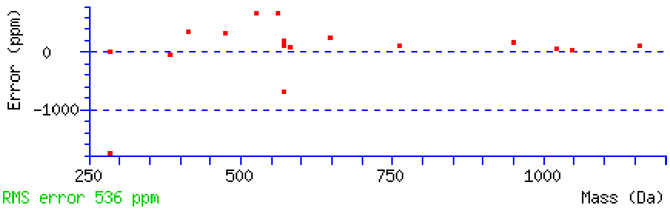
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1330.6418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 1.6e-006
Matches : 17/102 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							11
2	171.1128	86.0600					L	1274.6276	637.8175	1257.6011	629.3042	1256.6171	628.8122	10
3	***285.1557***	143.0815	268.1292	134.5682			N	1161.5436	581.2754	1144.5170	572.7622	1143.5330	572.2701	9
4	***384.2241***	192.6157	367.1976	184.1024			V	***1047.5007***	524.2540	1030.4741	515.7407	1029.4901	515.2487	8
5	***570.3035***	285.6554	553.2769	277.1421			W	***948.4322***	474.7198	931.4057	466.2065	930.4217	465.7145	7
6	685.3304	343.1688	668.3039	334.6556	667.3198	334.1636	D	***762.3529***	381.6801	745.3264	373.1668	744.3424	372.6748	6
7	772.3624	386.6849	755.3359	378.1716	754.3519	377.6796	S	***647.3260***	324.1666	630.2994	315.6534	629.3154	315.1613	5
8	919.4308	460.2191	902.4043	451.7058	901.4203	451.2138	F	***560.2940***	280.6506	543.2674	272.1373	542.2834	271.6453	4
9	***1020.4785***	510.7429	1003.4520	502.2296	1002.4680	501.7376	T	***413.2255***	207.1164	396.1990	198.6031	395.2150	198.1111	3
10	***1157.5374***	579.2724	1140.5109	570.7591	1139.5269	570.2671	H	312.1779	156.5926	295.1513	148.0793			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GLNVWDSFTHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G26000.1

Score	Mr(calc)	Delta	Sequence
62.3	1330.6418	-0.0005	GLNVWDSFTHR
5.5	1330.6378	0.0036	KRSYNGGSGSYR

AT5G26360.1

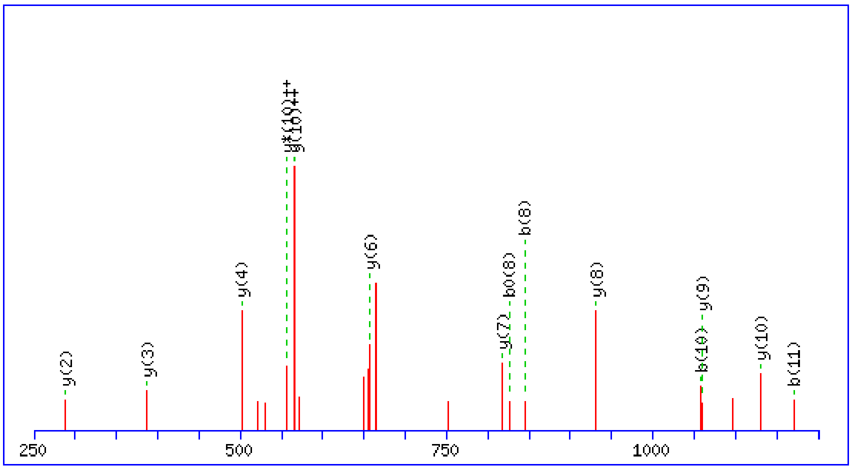
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLAQNCGVNVIR**
Found in **AT5G26360.1** in **TAIR_Arabidopsis**, Symbols: | chaperonin, putative | chr5:9255564-9258894 REVERSE

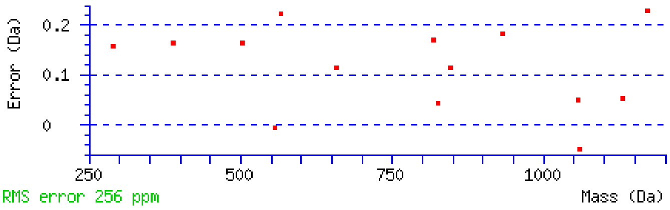
Match to Query 4867: 1343.697050 from(672.855801,2+) index(2816)
Title: Elution from: 31.141 to 31.141 scan no 3622 cid35.00 polarity:+
Data file D1d-2_1.mgf

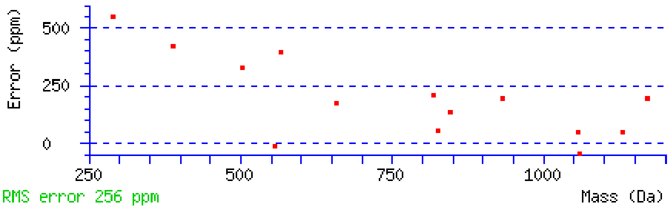
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1343.6980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 2.9e-007
Matches : 14/104 fragment ions using 18 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	102.0550	51.5311			84.0444	42.5258	T					12
2	215.1390	108.0731			197.1285	99.0679	L	1243.6576	622.3324	1226.6310	613.8191	11
3	286.1761	143.5917			268.1656	134.5864	A	***1130.5735***	565.7904	1113.5470	557.2771	10
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	Q	***1059.5364***	530.2718	1042.5098	521.7586	9
5	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	N	***931.4778***	466.2425	914.4513	457.7293	8
6	688.3083	344.6578	671.2817	336.1445	670.2977	335.6525	C	***817.4349***	409.2211	800.4083	400.7078	7
7	745.3298	373.1685	728.3032	364.6552	727.3192	364.1632	G	***657.4042***	329.2058	640.3777	320.6925	6
8	**844.3982**	422.7027	827.3716	414.1894	826.3876	413.6974	V	600.3828	300.6950	583.3562	292.1817	5
9	958.4411	479.7242	941.4145	471.2109	940.4305	470.7189	N	***501.3144***	251.1608	484.2878	242.6475	4
10	**1057.5095**	529.2584	1040.4830	520.7451	1039.4989	520.2531	V	***387.2714***	194.1394	370.2449	185.6261	3
11	**1170.5936**	585.8004	1153.5670	577.2871	1152.5830	576.7951	I	***288.2030***	144.6051	271.1765	136.0919	2
12							R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of TLAQNCGVNVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G26360.1

Score	Mr(calc)	Delta	Sequence
72.9	1343.6980	-0.0009	TLAQNCGVNVIR
12.1	1343.6980	-0.0009	VMGKGGGNLENIR
9.0	1343.6946	0.0025	ENVASHLQKYR
8.5	1343.6979	-0.0009	SASRSAPMTAPLR
5.3	1343.6946	0.0024	KSGHFQVTDLGR
4.2	1343.6986	-0.0015	VKWSYTYNRK
3.8	1343.6933	0.0038	VSVEEDIDGLIR
3.3	1343.6946	0.0025	YKHVAGTVAENR
3.0	1343.6946	0.0025	HQKVDSQAYLR
0.8	1343.6932	0.0038	EGAEIDDITLIR

AT5G26730.1

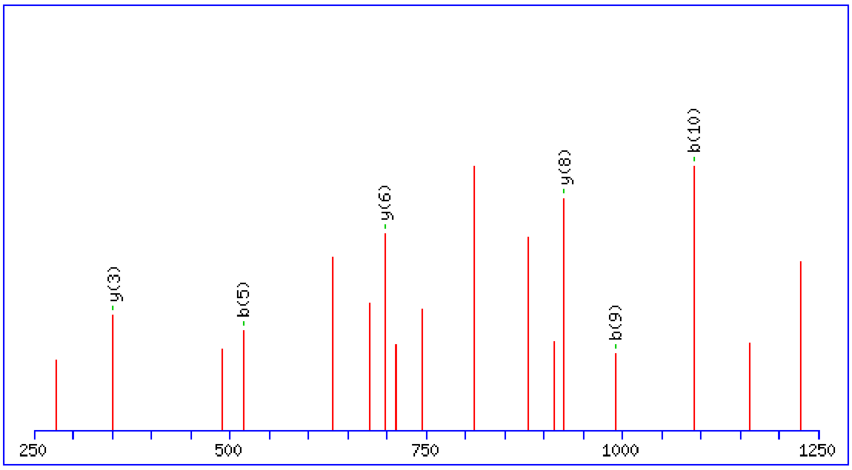
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGDSHKPMLVKAK**
Found in **AT5G26730.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16920.1); similar to hypothetical protein OsI_036632 [Oryza sativa (indica cultivar-group)] (GB:EAY82673.1); similar to Os12g0233900 [Oryza sativa (japonica cultivar-group)] (G

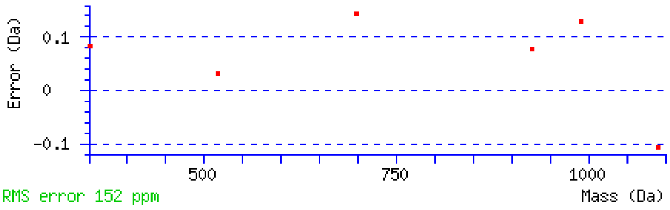
Match to Query 5692: 1440.744286 from(721.379419,2+) index(9070)
Title: Elution from: 81.791 to 81.791 scan no 12319 cid35.00 polarity:+
Data file 0-1_3.mgf

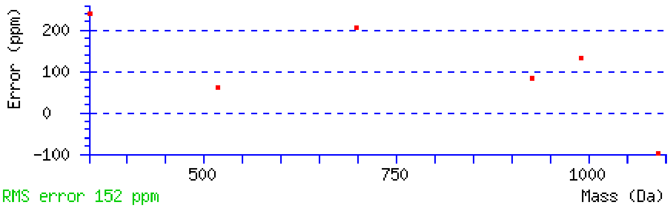
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1440.7483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.047
Matches : 6/112 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							13
2	173.1069	87.0571					G	1327.6745	664.3409	1309.6509	655.3291	1309.6639	655.3356	12
3	289.1309	145.0691			271.1203	136.0638	D	1269.6560	635.3316	1251.6324	626.3199	1251.6454	626.3264	11
4	377.1599	189.0836			359.1493	180.0783	S	1153.6320	577.3197	1135.6085	568.3079	1135.6215	568.3144	10
5	***517.2099***	259.1086			499.1994	250.1033	H	1065.6030	533.3051	1047.5794	524.2933			9
6	647.2990	324.1531	629.2754	315.1413	629.2884	315.1478	K	***925.5530***	463.2801	907.5294	454.2683			8
7	745.3488	373.1780	727.3252	364.1662	727.3382	364.1727	P	795.4639	398.2356	777.4403	389.2238			7
8	877.3863	439.1968	859.3627	430.1850	859.3757	430.1915	M	***697.4141***	349.2107	679.3905	340.1989			6
9	***991.4674***	496.2373	973.4438	487.2255	973.4568	487.2320	L	565.3766	283.1919	547.3530	274.1801			5
10	***1091.5328***	546.2701	1073.5092	537.2583	1073.5223	537.2648	V	451.2955	226.1514	433.2719	217.1396			4
11	1221.6219	611.3146	1203.5983	602.3028	1203.6113	602.3093	K	***351.2301***	176.1187	333.2065	167.1069			3
12	1293.6560	647.3316	1275.6324	638.3199	1275.6454	638.3264	A	221.1410	111.0741	203.1174	102.0624			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LGDSHKPMLVKAK

AT5G26730.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.4	1440.7483	-0.0041	LGDSHKPMLVKAK
3.9	1440.7423	0.0020	QFAEYKTVISLK
2.5	1440.7445	-0.0002	LVYKSFLFGPEK
0.7	1440.7483	-0.0041	RMALQSLPQPLVA
0.3	1440.7423	0.0020	GYLQDLVYKLSK

AT5G26742.1

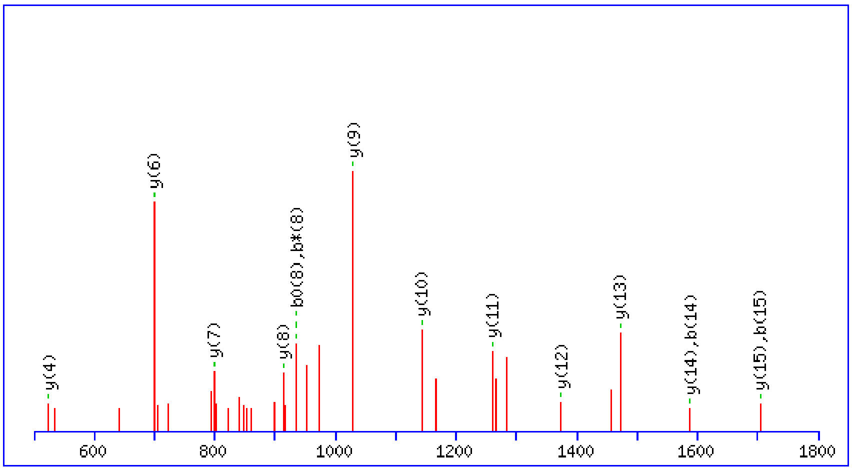
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLDNPLNIDLVGDQDEK**
Found in **AT5G26742.1** in **TAIR_Arabidopsis**, Symbols: EMB1138 | EMB1138 (EMBRYO DEFECTIVE 1138); ATP binding / ATP-dependent helicase | chr5:9285543-9288874 REVERSE

Match to Query 8738: 1980.880104 from(991.447328,2+) index(8468)
Title: Elution from: 77.894 to 77.894 scan no 11479 cid35.00 polarity:+
Data file D1d-1_3.mgf

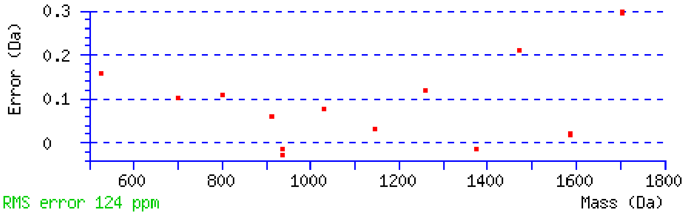
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

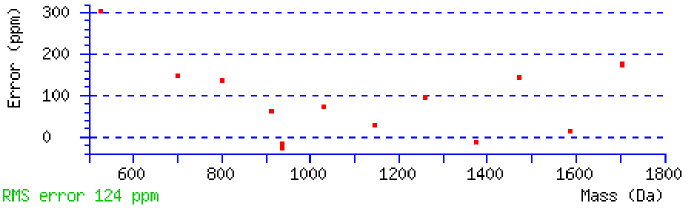


Monoisotopic mass of neutral peptide Mr(calc): 1980.8803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 1.4e-011
Matches : 15/180 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	165.0676	83.0375					Y							17
2	279.1487	140.0780					L	1817.8272	909.4172	1799.8036	900.4054	1799.8166	900.4120	16
3	395.1727	198.0900			377.1622	189.0847	D	***1703.7461***	852.3767	1685.7225	843.3649	1685.7355	843.3714	15
4	511.2097	256.1085	493.1861	247.0967	493.1991	247.1032	N	***1587.7221***	794.3647	1569.6985	785.3529	1569.7116	785.3594	14
5	609.2595	305.1334	591.2359	296.1216	591.2489	296.1281	P	***1471.6851***	736.3462	1453.6615	727.3344	1453.6746	727.3409	13
6	723.3406	362.1739	705.3170	353.1622	705.3300	353.1687	L	***1373.6353***	687.3213	1355.6117	678.3095	1355.6248	678.3160	12
7	839.3776	420.1924	821.3540	411.1807	821.3670	411.1872	N	***1259.5542***	630.2808	1241.5306	621.2690	1241.5437	621.2755	11
8	953.4587	477.2330	935.4351	468.2212	935.4481	468.2277	I	***1143.5172***	572.2623	1125.4936	563.2505	1125.5067	563.2570	10
9	1069.4827	535.2450	1051.4591	526.2332	1051.4721	526.2397	D	***1029.4361***	515.2217	1011.4125	506.2099	1011.4256	506.2164	9
10	1183.5638	592.2855	1165.5402	583.2737	1165.5532	583.2802	L	***913.4122***	457.2097	895.3886	448.1979	895.4016	448.2044	8
11	1283.6292	642.3183	1265.6057	633.3065	1265.6187	633.3130	V	***799.3311***	400.1692	781.3075	391.1574	781.3205	391.1639	7
12	1341.6477	671.3275	1323.6241	662.3157	1323.6372	662.3222	G	***699.2656***	350.1364	681.2420	341.1246	681.2550	341.1312	6
13	1457.6717	729.3395	1439.6481	720.3277	1439.6611	720.3342	D	641.2471	321.1272	623.2235	312.1154	623.2365	312.1219	5
14	**1587.7244**	794.3658	1569.7008	785.3540	1569.7138	785.3605	Q	***525.2231***	263.1152	507.1995	254.1034	507.2126	254.1099	4
15	**1703.7483**	852.3778	1685.7248	843.3660	1685.7378	843.3725	D	395.1705	198.0889	377.1469	189.0771	377.1599	189.0836	3
16	1833.7880	917.3976	1815.7644	908.3858	1815.7774	908.3923	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT5G26742.1





NCBI **BLAST** search of YLDNPLNIDLVGDQDEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
117.1	1980.8803	-0.0002	YLDNPLNIDLVGDQDEK
20.1	1980.8755	0.0046	MGEVEVVADLPGFPDNVR
0.4	1980.8766	0.0035	YFFAFVPNLDFDDPVR

Mascot: http://www.matrixscience.com/

AT5G26742.2

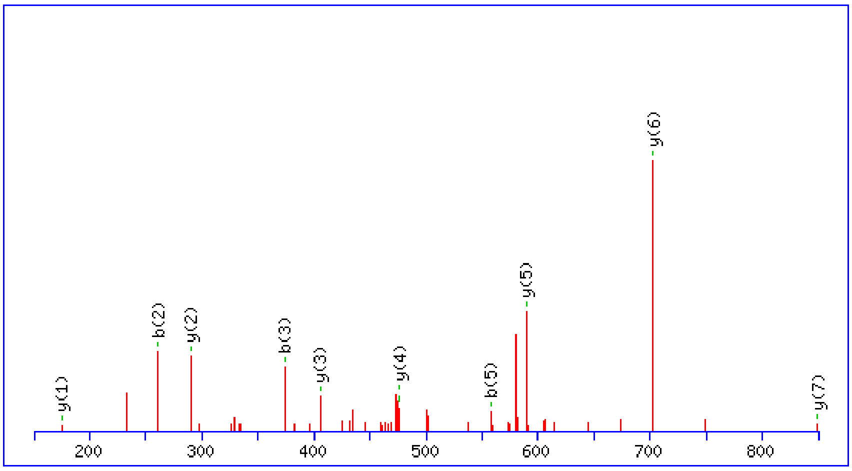
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFLIADDR**
Found in **AT5G26742.2** in **TAIR_Arabidopsis**, Symbols: EMB1138 | EMB1138 (EMBRYO DEFECTIVE 1138); ATP binding / ATP-dependent helicase | chr5:9285543-9288874 REVERSE

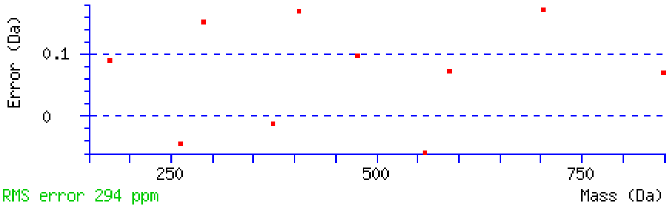
Match to Query 2286: 961.523632 from(481.769092,2+) index(6034)
Title: Elution from: 53.340 to 53.340 scan no 7606 cid35.00 polarity:+
Data file C7-2_1.mgf

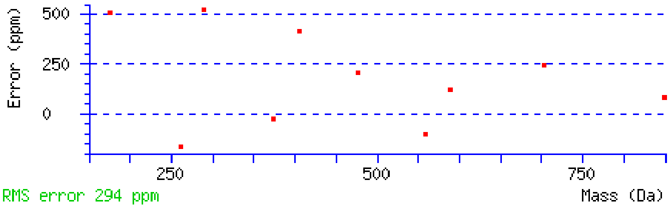
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 961.5233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 8.4e-006
Matches : 10/58 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			**I**							**8**
2	**261.1598**	131.0835			**F**	***849.4465***	425.2269	832.4199	416.7136	831.4359	416.2216	**7**
3	**374.2438**	187.6255			**L**	***702.3781***	351.6927	685.3515	343.1794	684.3675	342.6874	**6**
4	487.3279	244.1676			**I**	***589.2940***	295.1506	572.2675	286.6374	571.2835	286.1454	**5**
5	**558.3650**	279.6861			**A**	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	**4**
6	673.3919	337.1996	655.3814	328.1943	**D**	***405.1728***	203.0901	388.1463	194.5768	387.1623	194.0848	**3**
7	788.4189	394.7131	770.4083	385.7078	**D**	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
8					**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IFLIADDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.1	961.5233	0.0004	IFLIADDR

AT5G26742.2

11.2	961.5233	0.0004	SDSWLKVK
8.9	961.5233	0.0004	IPSSFGNLK
6.3	961.5233	0.0004	FLVELADR
5.6	961.5233	0.0004	KEFSLPNK
4.2	961.5233	0.0004	KESPFLNK
2.7	961.5233	0.0004	LFDIIDAR
2.7	961.5233	0.0004	LFQNAIEK
2.0	961.5233	0.0004	YPPDSKKK
1.5	961.5246	-0.0010	LRSFFHR

AT5G27020.1

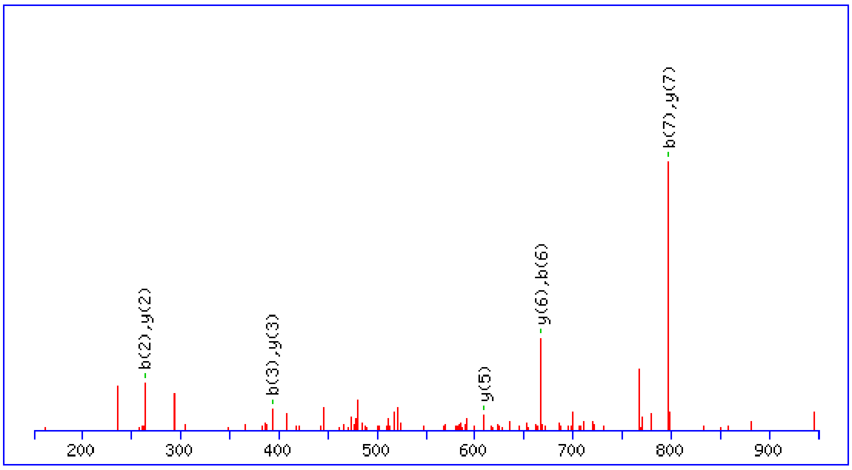
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEQGTIKIK**
Found in **AT5G27020.1** in **TAIR_Arabidopsis**, Symbols: | unknown protein | chr5:9508190-9508684 FORWARD

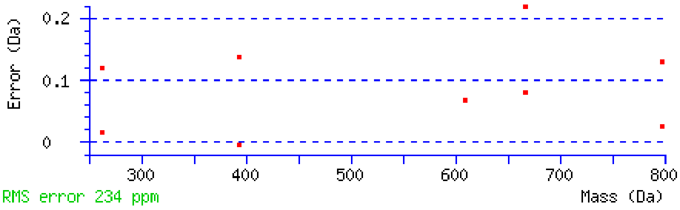
Match to Query 2494: 1058.545550 from(530.280051,2+) index(5549)
Title: Elution from: 53.265 to 53.265 scan no 7214 cid35.00 polarity:+
Data file D1d-1-2.mgf

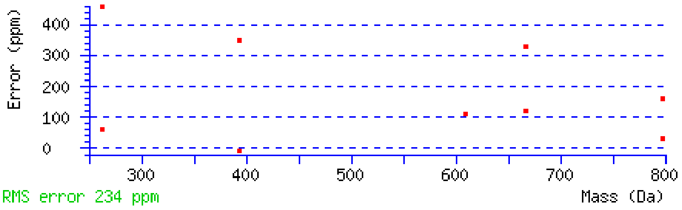
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1058.5438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.039
Matches : 9/82 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					M							9
2	**263.0844**	132.0458			245.0739	123.0406	E	927.5136	464.2604	909.4900	455.2486	909.5030	455.2552	8
3	**393.1371**	197.0722	375.1135	188.0604	375.1265	188.0669	Q	***797.4740***	399.2406	779.4504	390.2288	779.4634	390.2353	7
4	451.1556	226.0814	433.1320	217.0696	433.1450	217.0761	G	***667.4213***	334.2143	649.3977	325.2025	649.4108	325.2090	6
5	553.2003	277.1038	535.1767	268.0920	535.1897	268.0985	T	***609.4028***	305.2050	591.3792	296.1933	591.3923	296.1998	5
6	**667.2814**	334.1443	649.2578	325.1325	649.2708	325.1390	I	507.3581	254.1827	489.3345	245.1709			4
7	**797.3704**	399.1888	779.3468	390.1771	779.3598	390.1836	K	***393.2770***	197.1421	375.2534	188.1303			3
8	911.4515	456.2294	893.4279	447.2176	893.4409	447.2241	I	***263.1880***	132.0976	245.1644	123.0858			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MEQGTIKIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	1058.5438	0.0017	MEQGTIKIK

AT5G27020.1

14.2	1058.5438	0.0017	KCLGLESIK
13.0	1058.5438	0.0017	LGTVMELLR
11.1	1058.5438	0.0017	LMAQNLLTK
11.1	1058.5465	-0.0009	MQKPKVGTR
9.9	1058.5465	-0.0010	KAGAMNALIR
9.4	1058.5431	0.0024	RIHYSQLK
9.2	1058.5438	0.0017	KEMEAAKIK
9.0	1058.5465	-0.0009	EMRLVGALR
7.8	1058.5438	0.0017	LSEVTVMLR

AT5G27410.1

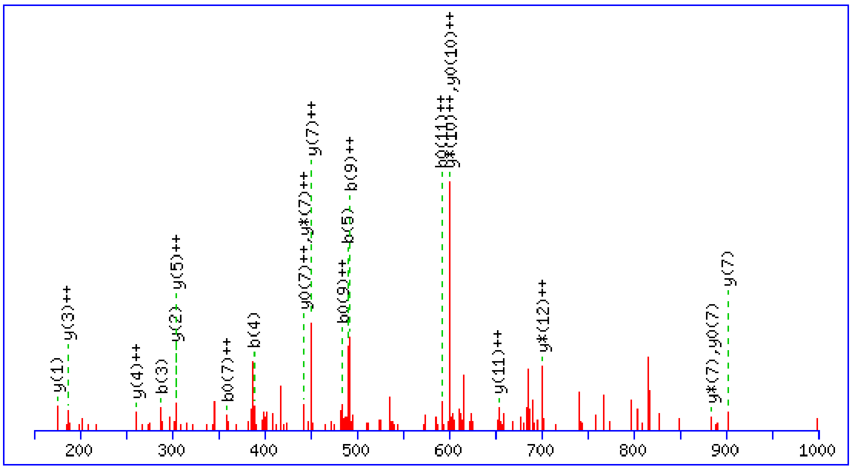
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLSTTLMYSFAQR**
Found in **AT5G27410.1** in **TAIR_Arabidopsis**, Symbols: | aminotransferase class IV family protein | chr5:9678824-9682471 FORWARD

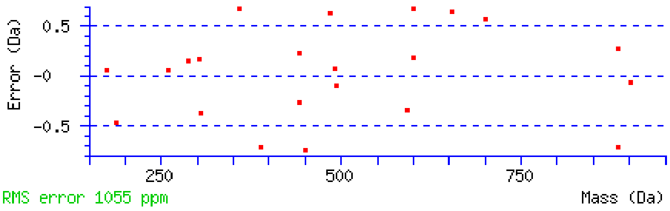
Match to Query 6319: 1503.738369 from(502.253399,3+) index(4571)
Title: Elution from: 42.401 to 42.401 scan no 5766 cid35.00 polarity:+
Data file D6h-1_2.mgf

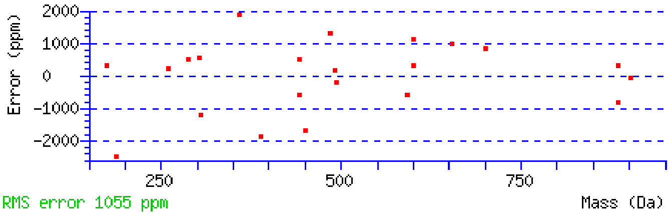
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1503.7392
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.018
Matches : 22/114 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	201.1234	101.0653			183.1128	92.0600	L	1417.7144	709.3608	1400.6879	700.8476	1399.7038	700.3556	12
3	***288.1554***	144.5813			270.1448	135.5761	S	1304.6303	652.8188	1287.6038	644.3055	1286.6198	643.8135	11
4	***389.2031***	195.1052			371.1925	186.0999	T	1217.5983	609.3028	1200.5718	600.7895	1199.5878	600.2975	10
5	***490.2508***	245.6290			472.2402	236.6237	T	1116.5506	558.7790	1099.5241	550.2657	1098.5401	549.7737	9
6	603.3348	302.1710			585.3243	293.1658	L	1015.5030	508.2551	998.4764	499.7418	997.4924	499.2498	8
7	734.3753	367.6913			716.3647	358.6860	M	***902.4189***	451.7131	885.3924	443.1998	884.4083	442.7078	7
8	897.4386	449.2230			879.4281	440.2177	Y	771.3784	386.1928	754.3519	377.6796	753.3678	377.1876	6
9	984.4707	492.7390			966.4601	483.7337	S	608.3151	304.6612	591.2885	296.1479	590.3045	295.6559	5
10	1131.5391	566.2732			1113.5285	557.2679	F	521.2831	261.1452	504.2565	252.6319			4
11	1202.5762	601.7917			1184.5656	592.7864	A	374.2146	187.6110	357.1881	179.0977			3
12	1330.6348	665.8210	1313.6082	657.3077	1312.6242	656.8157	Q	***303.1775***	152.0924	286.1510	143.5791			2
13							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SLSTTLMYSFAQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G27410.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	1503.7392	-0.0008	SLSTTLMYSFAQR
10.3	1503.7416	-0.0033	EISKDEISDALER
5.7	1503.7425	-0.0042	CDIVDILLEMQR

AT5G27470.1

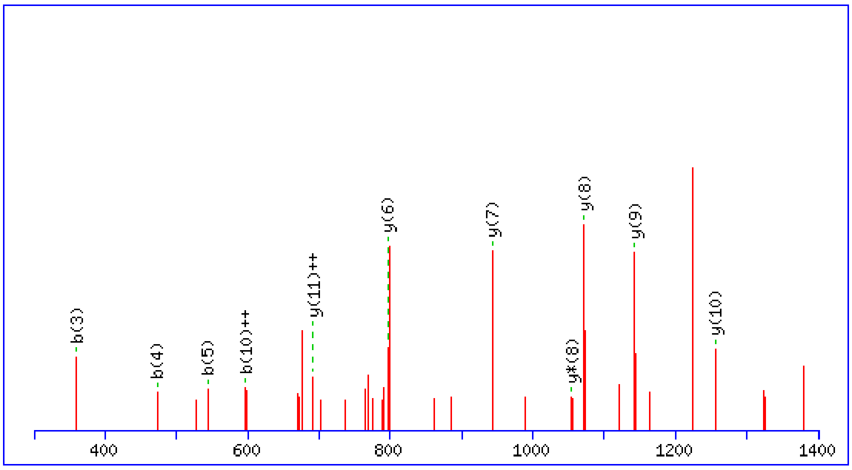
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CAQLAQFDEELYK**
Found in **AT5G27470.1** in **TAIR_Arabidopsis**, Symbols: | seryl-tRNA synthetase / serine--tRNA ligase | chr5:9695090-9697157 FORWARD

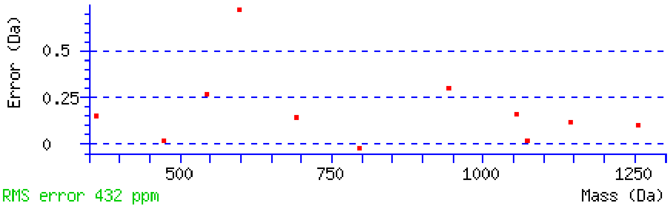
Match to Query 7400: 1613.738950 from(807.876751,2+) index(6815)
Title: Elution from: 61.259 to 61.259 scan no 8786 cid35.00 polarity:+
Data file D6h-2_1.mgf

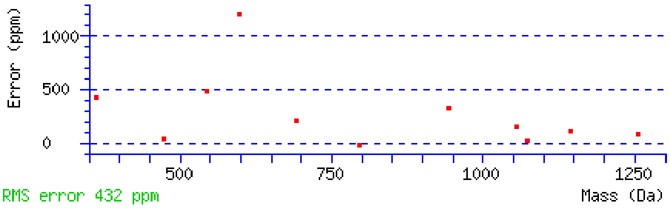
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1613.7395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.014
Matches : 11/120 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	161.0379	81.0226					C							13
2	232.0750	116.5412					A	1454.7162	727.8617	1437.6896	719.3485	1436.7056	718.8564	12
3	**360.1336**	180.5704	343.1071	172.0572			Q	1383.6791	692.3432	1366.6525	683.8299	1365.6685	683.3379	11
4	**473.2177**	237.1125	456.1911	228.5992			L	***1255.6205***	628.3139	1238.5939	619.8006	1237.6099	619.3086	10
5	**544.2548**	272.6310	527.2282	264.1178			A	***1142.5364***	571.7719	1125.5099	563.2586	1124.5259	562.7666	9
6	672.3134	336.6603	655.2868	328.1471			Q	***1071.4993***	536.2533	1054.4728	527.7400	1053.4888	527.2480	8
7	819.3818	410.1945	802.3552	401.6813			F	***943.4407***	472.2240	926.4142	463.7107	925.4302	463.2187	7
8	934.4087	467.7080	917.3822	459.1947	916.3982	458.7027	D	***796.3723***	398.6898	779.3458	390.1765	778.3618	389.6845	6
9	1063.4513	532.2293	1046.4248	523.7160	1045.4408	523.2240	E	681.3454	341.1763	664.3188	332.6631	663.3348	332.1710	5
10	1192.4939	596.7506	1175.4674	588.2373	1174.4834	587.7453	E	552.3028	276.6550	535.2762	268.1418	534.2922	267.6498	4
11	1305.5780	653.2926	1288.5514	644.7794	1287.5674	644.2873	L	423.2602	212.1337	406.2336	203.6205			3
12	1468.6413	734.8243	1451.6148	726.3110	1450.6307	725.8190	Y	310.1761	155.5917	293.1496	147.0784			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of CAQLAQFDEELYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G27470.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.9	1613.7395	-0.0006	CAQLAQFDEELYK

Mascot: http://www.matrixscience.com/

AT5G27620.1

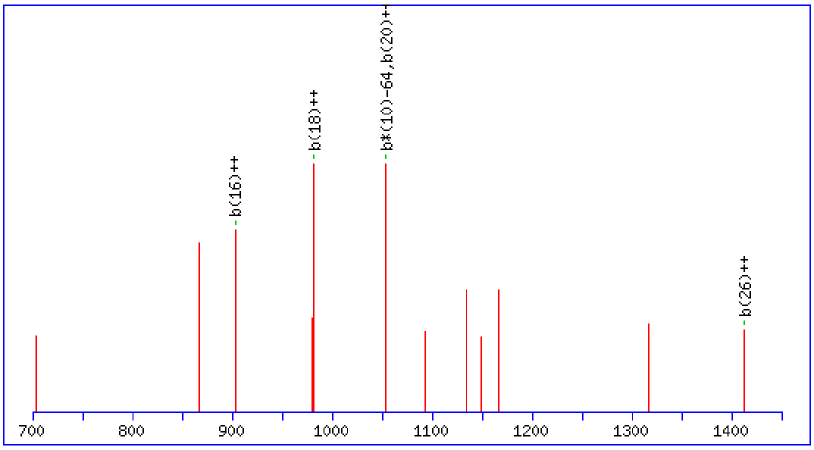
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVQMLEKCGTTQVEVDASGSLTYPKDK**
Found in **AT5G27620.1** in **TAIR_Arabidopsis**, Symbols: CYCH;1 | CYCH;1 (CYCLIN H;1); cyclin-dependent protein kinase/ protein binding / protein kinase | chr5:9771765-9774687 FORWARD

Match to Query 10738: 2970.425673 from(991.149167,3+) index(9935)
Title: Elution from: 90.268 to 90.268 scan no 13751 cid35.00 polarity:+
Data file D1d-3_2.mgf

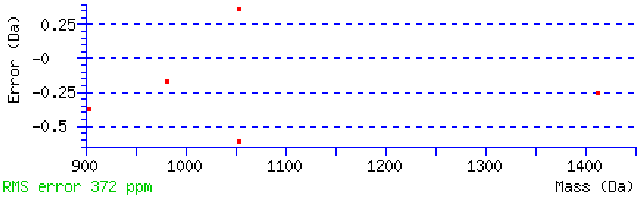
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 700 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

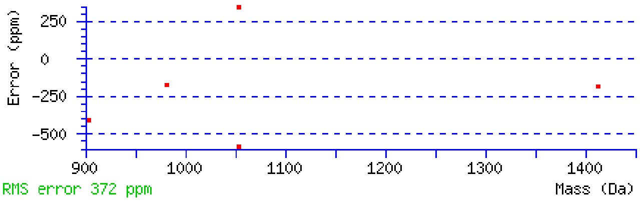


Monoisotopic mass of neutral peptide Mr(calc): 2970.4314
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 19 **Expect:** 0.027
Matches : 5/448 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							27
2	171.1128	86.0600					V	2900.4016	1450.7044	2883.3751	1442.1912	2882.3910	1441.6992	26
3	299.1714	150.0893	282.1448	141.5761			Q	2801.3332	1401.1702	2784.3066	1392.6570	2783.3226	1392.1650	25
4	446.2068	223.6070	429.1802	215.0938			M	2673.2746	1337.1409	2656.2481	1328.6277	2655.2640	1328.1357	24
5	559.2908	280.1491	542.2643	271.6358			L	2526.2392	1263.6232	2509.2127	1255.1100	2508.2286	1254.6180	23
6	688.3334	344.6704	671.3069	336.1571	670.3229	335.6651	E	2413.1551	1207.0812	2396.1286	1198.5679	2395.1446	1198.0759	22
7	816.4284	408.7178	799.4019	400.2046	798.4178	399.7126	K	2284.1126	1142.5599	2267.0860	1134.0466	2266.1020	1133.5546	21
8	976.4591	488.7332	959.4325	480.2199	958.4485	479.7279	C	2156.0176	1078.5124	2138.9910	1069.9992	2138.0070	1069.5072	20
9	1033.4805	517.2439	1016.4540	508.7306	1015.4699	508.2386	G	1995.9869	998.4971	1978.9604	989.9838	1977.9764	989.4918	19
10	1134.5282	567.7677	1117.5016	559.2545	1116.5176	558.7625	T	1938.9655	969.9864	1921.9389	961.4731	1920.9549	960.9811	18
11	1235.5759	618.2916	1218.5493	609.7783	1217.5653	609.2863	T	1837.9178	919.4625	1820.8913	910.9493	1819.9072	910.4573	17
12	1363.6345	682.3209	1346.6079	673.8076	1345.6239	673.3156	Q	1736.8701	868.9387	1719.8436	860.4254	1718.8596	859.9334	16
13	1462.7029	731.8551	1445.6763	723.3418	1444.6923	722.8498	V	1608.8115	804.9094	1591.7850	796.3961	1590.8010	795.9041	15
14	1591.7455	796.3764	1574.7189	787.8631	1573.7349	787.3711	E	1509.7431	755.3752	1492.7166	746.8619	1491.7326	746.3699	14
15	1690.8139	845.9106	1673.7873	837.3973	1672.8033	836.9053	V	1380.7005	690.8539	1363.6740	682.3406	1362.6900	681.8486	13
16	1805.8408	***903.4240***	1788.8143	894.9108	1787.8303	894.4188	D	1281.6321	641.3197	1264.6056	632.8064	1263.6216	632.3144	12
17	1876.8779	938.9426	1859.8514	930.4293	1858.8674	929.9373	A	1166.6052	583.8062	1149.5786	575.2930	1148.5946	574.8009	11
18	1963.9100	***982.4586***	1946.8834	973.9453	1945.8994	973.4533	S	1095.5681	548.2877	1078.5415	539.7744	1077.5575	539.2824	10
19	2020.9314	1010.9693	2003.9049	1002.4561	2002.9209	1001.9641	G	1008.5360	504.7717	991.5095	496.2584	990.5255	495.7664	9
20	2107.9634	***1054.4854***	2090.9369	1045.9721	2089.9529	1045.4801	S	951.5146	476.2609	934.4880	467.7477	933.5040	467.2556	8
21	2221.0475	1111.0274	2204.0210	1102.5141	2203.0369	1102.0221	L	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	7
22	2322.0952	1161.5512	2305.0686	1153.0380	2304.0846	1152.5460	T	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	6
23	2485.1585	1243.0829	2468.1320	1234.5696	2467.1480	1234.0776	Y	650.3508	325.6790	633.3243	317.1658	632.3402	316.6738	5

24	2582.2113	1291.6093	2565.1847	1283.0960	2564.2007	1282.6040	**P**	487.2875	244.1474	470.2609	235.6341	469.2769	235.1421	**4**
25	2710.3062	1355.6568	2693.2797	1347.1435	2692.2957	1346.6515	**K**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**3**
26	2825.3332	***1413.1702***	2808.3066	1404.6570	2807.3226	1404.1650	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
27							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of AVQMLEKCGTTQVEVDASGSLTYPKDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.5	2970.4314	-0.0058	AVQMLEKCGTTQVEVDASGSLTYPKDK
2.0	2970.4201	0.0056	YSRPESMELVEAEKVEEEKIMTAEK
1.0	2970.4290	-0.0033	SVDGLFCLYSGVDMKQPIMVINPDTR

Mascot: http://www.matrixscience.com/

AT5G27770.1

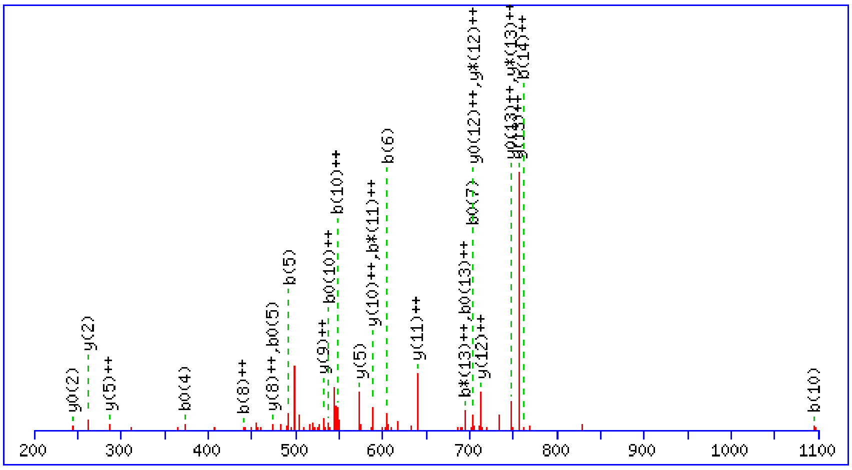
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVSFTIDCSKPVDDK**
Found in **AT5G27770.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L22 (RPL22C) | chr5:9836170-9837117 FORWARD

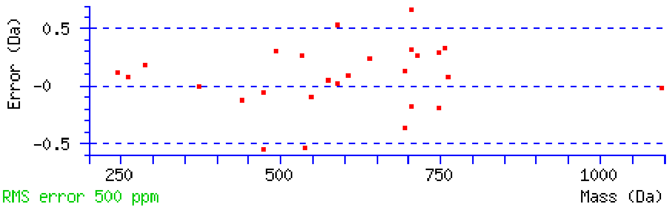
Match to Query 8029: 1666.786623 from(556.602817,3+) index(4027)
Title: Elution from: 38.411 to 38.411 scan no 5048 cid35.00 polarity:+
Data file D12h-3_1.mgf

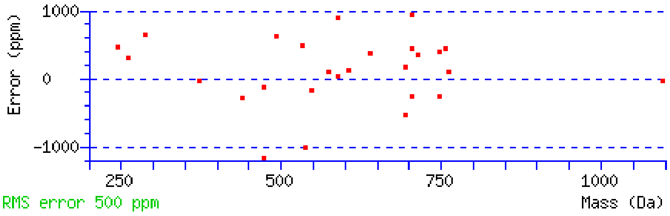
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1666.7873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.002
Matches : 29/144 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							15
2	157.0972	79.0522					V	1610.7731	805.8902	1593.7465	797.3769	1592.7625	796.8849	14
3	**244.1292**	122.5682			226.1186	113.5629	S	1511.7046	756.3560	1494.6781	747.8427	1493.6941	747.3507	13
4	391.1976	196.1024			373.1870	187.0972	F	1424.6726	712.8399	1407.6461	704.3267	1406.6620	703.8347	12
5	**492.2453**	246.6263			474.2347	237.6210	T	1277.6042	639.3057	1260.5776	630.7925	1259.5936	630.3005	11
6	**605.3293**	303.1683			587.3188	294.1630	I	1176.5565	588.7819	1159.5300	580.2686	1158.5460	579.7766	10
7	720.3563	360.6818			702.3457	351.6765	D	1063.4725	532.2399	1046.4459	523.7266	1045.4619	523.2346	9
8	880.3869	***440.6971***			862.3764	431.6918	C	948.4455	474.7264	931.4190	466.2131	930.4349	465.7211	8
9	967.4190	484.2131			949.4084	475.2078	S	788.4149	394.7111	771.3883	386.1978	770.4043	385.7058	7
10	**1095.5139**	***548.2606***	1078.4874	539.7473	1077.5034	539.2553	K	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	6
11	1192.5667	596.7870	1175.5401	588.2737	1174.5561	587.7817	P	573.2879	287.1476	556.2613	278.6343	555.2773	278.1423	5
12	1291.6351	646.3212	1274.6086	637.8079	1273.6245	637.3159	V	476.2351	238.6212	459.2086	230.1079	458.2245	229.6159	4
13	1406.6620	***703.8347***	1389.6355	695.3214	1388.6515	694.8294	D	377.1667	189.0870	360.1401	180.5737	359.1561	180.0817	3
14	1521.6890	***761.3481***	1504.6624	752.8349	1503.6784	752.3428	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GVSFTIDCSKPVDDK

AT5G27770.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.9	1666.7873	-0.0006	GVSFTIDCSKPVDDK
10.6	1666.7841	0.0026	QLMISSMNCTTPLR
7.5	1666.7910	-0.0044	DDRSVTYEELRER
2.6	1666.7832	0.0034	GVQSTTSERMAEDLK
2.1	1666.7881	-0.0015	EAMCFLMDPQIGKK
1.2	1666.7886	-0.0020	VGPDSVGAHPGPVCYR

AT5G28060.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSGYGLIYDTVENAK**
Found in **AT5G28060.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S24 (RPS24B) | chr5:10069795-10070796 REVERSE

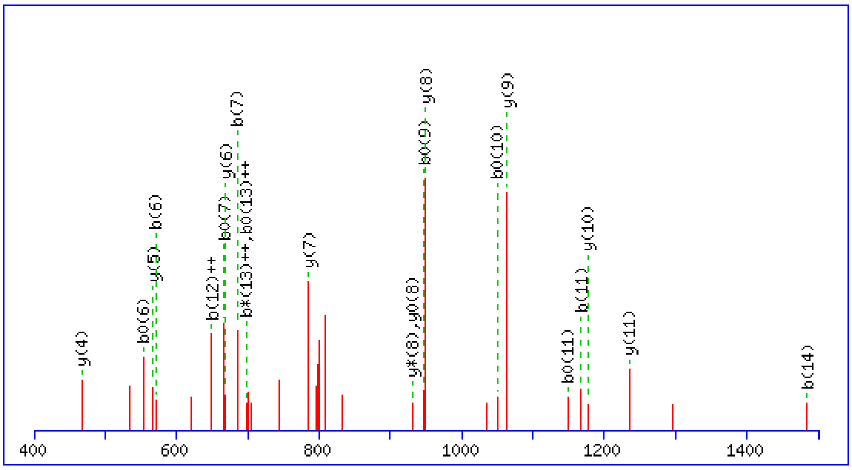
Match to Query 7497: 1632.721130 from(817.367841,2+) index(7515)
Title: Elution from: 66.386 to 66.386 scan no 9841 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1500 Da Full range

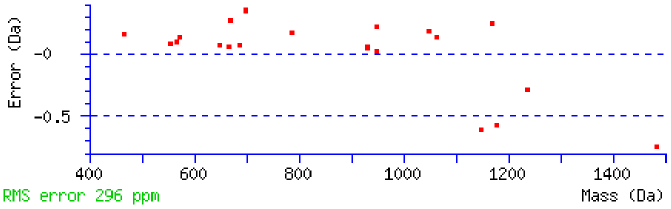
Label all possible matches ○ Label matches used for scoring ●

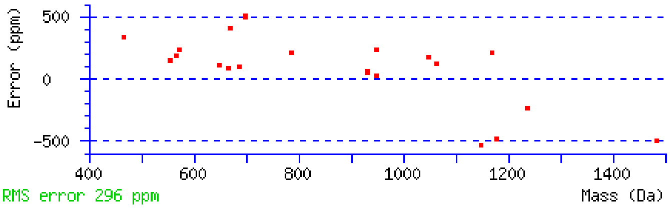
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1632.7225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 7.2e-006
Matches : 22/138 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	**S**							**15**
2	177.0654	89.0363			159.0548	80.0311	**S**	1545.7008	773.3540	1527.6772	764.3422	1527.6902	764.3487	**14**
3	235.0839	118.0456			217.0733	109.0403	**G**	1457.6717	729.3395	1439.6481	720.3277	1439.6611	720.3342	**13**
4	399.1443	200.0758			381.1337	191.0705	**Y**	1399.6532	700.3302	1381.6296	691.3185	1381.6426	691.3250	**12**
5	457.1628	229.0850			439.1522	220.0797	**G**	***1235.5928***	618.3001	1217.5693	609.2883	1217.5823	609.2948	**11**
6	**571.2439**	286.1256			553.2333	277.1203	**L**	***1177.5744***	589.2908	1159.5508	580.2790	1159.5638	580.2855	**10**
7	**685.3250**	343.1661			667.3144	334.1608	**I**	***1063.4933***	532.2503	1045.4697	523.2385	1045.4827	523.2450	**9**
8	849.3853	425.1963			831.3748	416.1910	**Y**	***949.4122***	475.2097	931.3886	466.1979	931.4016	466.2044	**8**
9	965.4093	483.2083			947.3987	474.2030	**D**	***785.3518***	393.1795	767.3282	384.1677	767.3412	384.1742	**7**
10	1067.4540	534.2306			1049.4435	525.2254	**T**	***669.3278***	335.1675	651.3042	326.1558	651.3172	326.1623	**6**
11	**1167.5195**	584.2634			1149.5089	575.2581	**V**	***567.2831***	284.1452	549.2595	275.1334	549.2725	275.1399	**5**
12	1297.5591	649.2832			1279.5485	640.2779	**E**	***467.2176***	234.1125	449.1941	225.1007	449.2071	225.1072	**4**
13	1413.5961	707.3017	1395.5725	698.2899	1395.5855	698.2964	**N**	337.1780	169.0926	319.1544	160.0809			**3**
14	**1485.6302**	743.3188	1467.6067	734.3070	1467.6197	734.3135	**A**	221.1410	111.0741	203.1174	102.0624			**2**
15							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of SSGYGLIYDTVENAK

AT5G28060.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.7	1632.7225	-0.0014	SSGYGLIYDTVENAK
18.4	1632.7239	-0.0027	LSCFGLMKNSRDGK
8.4	1632.7183	0.0029	YRDNSRAASEMALK
3.6	1632.7164	0.0047	MSDMAADAFLRMKK
2.4	1632.7209	0.0002	QFVSQSRARMENR

AT5G28500.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WVVLPGWDPVVAVR**
Found in **AT5G28500.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04550.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1) | chr5:10477814-10479118 FORWARD

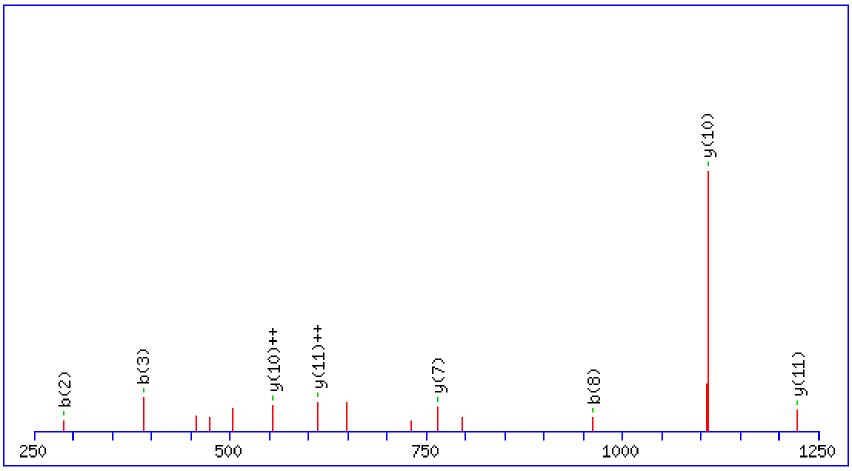
Match to Query 7139: 1610.830796 from(806.422674,2+) index(10080)
Title: Elution from: 95.816 to 95.816 scan no 14311 cid35.00 polarity:+
Data file D12h-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1250 Da Full range

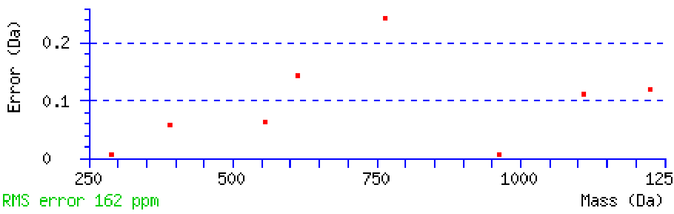
Label all possible matches ○ Label matches used for scoring ●

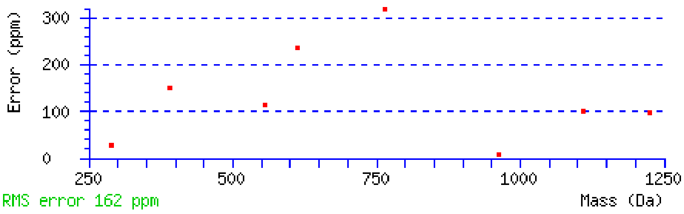
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1610.8311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0014
Matches : 8/104 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440			**W**							**14**
2	***289.1461***	145.0767			**V**	1423.7650	712.3862	1405.7415	703.3744	1405.7545	703.3809	**13**
3	***389.2116***	195.1094			**V**	1323.6996	662.3534	1305.6760	653.3416	1305.6890	653.3482	**12**
4	503.2927	252.1500			**L**	***1223.6341***	612.3207	1205.6106	603.3089	1205.6236	603.3154	**11**
5	601.3425	301.1749			**P**	***1109.5530***	555.2802	1091.5295	546.2684	1091.5425	546.2749	**10**
6	659.3610	330.1841			**G**	1011.5032	506.2553	993.4797	497.2435	993.4927	497.2500	**9**
7	847.4343	424.2208			**W**	953.4847	477.2460	935.4612	468.2342	935.4742	468.2407	**8**
8	***963.4583***	482.2328	945.4478	473.2275	**D**	***765.4114***	383.2093	747.3878	374.1975	747.4008	374.2040	**7**
9	1061.5081	531.2577	1043.4975	522.2524	**P**	649.3874	325.1973	631.3638	316.1855			**6**
10	1161.5736	581.2904	1143.5630	572.2851	**V**	551.3376	276.1724	533.3140	267.1606			**5**
11	1261.6390	631.3231	1243.6284	622.3179	**V**	451.2721	226.1397	433.2486	217.1279			**4**
12	1333.6732	667.3402	1315.6626	658.3349	**A**	351.2067	176.1070	333.1831	167.0952			**3**
13	1433.7386	717.3729	1415.7280	708.3677	**V**	279.1725	140.0899	261.1490	131.0781			**2**
14					**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of WVVLPGWDPVVAVR

AT5G28500.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.0	1610.8311	-0.0003	WVVLPGWDPVVAVR

Mascot: http://www.matrixscience.com/

AT5G28540.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSQEEIDR**
Found in **AT5G28540.1** in **TAIR_Arabidopsis**, Symbols: BIP1 | BIP1; ATP binding | chr5:10540669-10543278 REVERSE

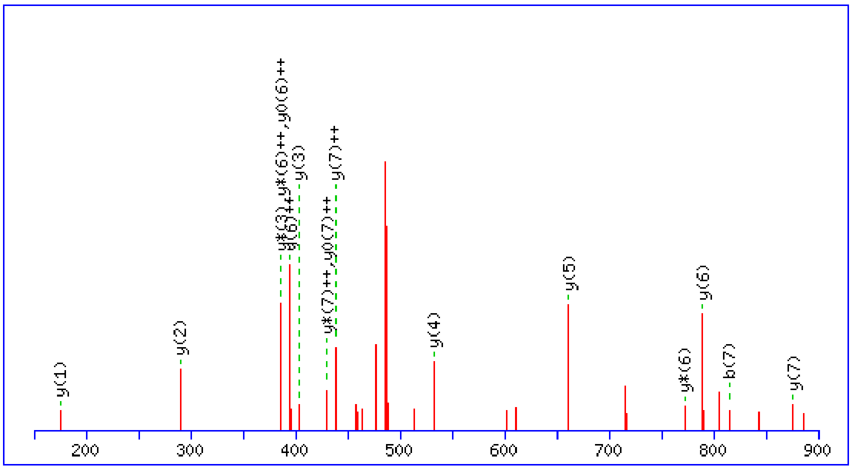
Match to Query 2485: 988.482484 from(495.248518,2+) index(808)
Title: Elution from: 14.211 to 14.211 scan no 1182 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range

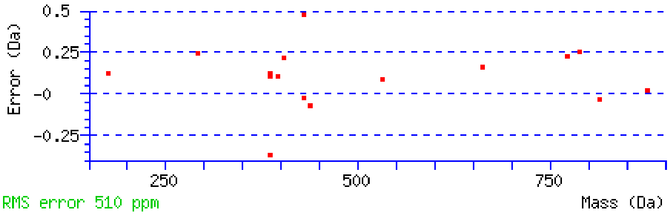
Label all possible matches ○ Label matches used for scoring ●

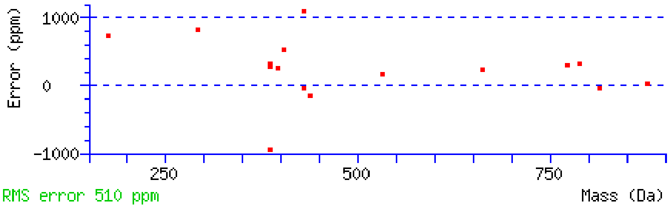
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 988.4825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 3.6e-005
Matches : 16/76 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							8
2	201.1234	101.0653			183.1128	92.0600	S	***876.4058***	438.7065	859.3792	430.1932	858.3952	429.7012	7
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	***789.3737***	395.1905	772.3472	386.6772	771.3632	386.1852	6
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	E	***661.3151***	331.1612	644.2886	322.6479	643.3046	322.1559	5
5	587.2671	294.1372	570.2406	285.6239	569.2566	285.1319	E	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
6	700.3512	350.6792	683.3246	342.1660	682.3406	341.6740	I	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
7	815.3781	408.1927	798.3516	399.6794	797.3676	399.1874	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LSQEEIDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.3	988.4825	-0.0000	LSQEEIDR
14.5	988.4825	-0.0000	AKEDEIER

AT5G28540.1

13.8	988.4825	-0.0000	LSEDLEQR
10.4	988.4825	-0.0000	EAEKQQEK
9.9	988.4825	-0.0000	EAENGVVSGK
8.8	988.4825	-0.0000	AEQESQIGK
6.3	988.4825	-0.0000	IDAEASDLR
5.9	988.4825	-0.0000	EEVKDDVR
5.5	988.4825	-0.0000	TQEVEDLR
4.6	988.4825	-0.0000	IVGSEEEAR

AT5G28840.1

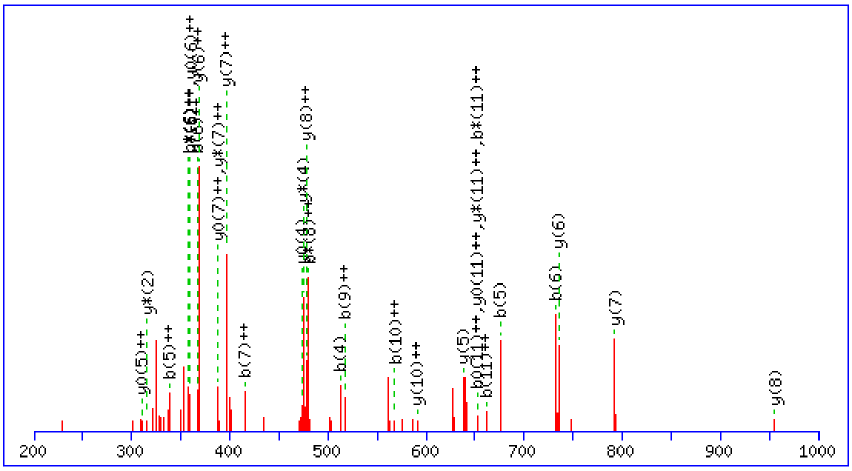
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FHNIYGPFGTWK**
Found in **AT5G28840.1** in **TAIR_Arabidopsis**, Symbols: GME | GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD binding / catalytic | chr5:10862476-10864028 REVERSE

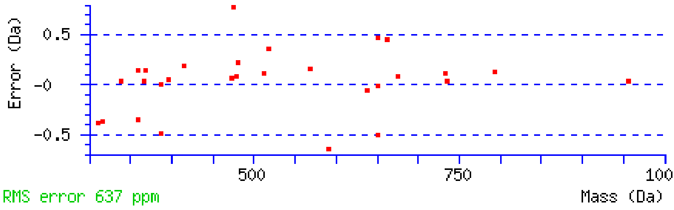
Match to Query 5541: 1465.715637 from(489.579155,3+) index(6355)
Title: Elution from: 59.616 to 59.616 scan no 8350 cid35.00 polarity:+
Data file D1d-2_2.mgf

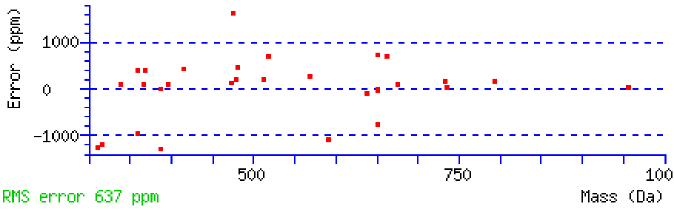
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1465.7143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.003
Matches : 31/106 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							12
2	285.1346	143.0709					H	1319.6531	660.3302	1302.6266	651.8169	1301.6426	651.3249	11
3	399.1775	200.0924	382.1510	191.5791			N	1182.5942	591.8007	1165.5677	583.2875	1164.5837	582.7955	10
4	**512.2616**	256.6344	495.2350	248.1212			I	1068.5513	534.7793	1051.5247	526.2660	1050.5407	525.7740	9
5	**675.3249**	***338.1661***	658.2984	329.6528			Y	**955.4672**	478.2373	938.4407	469.7240	937.4567	469.2320	8
6	**732.3464**	***366.6768***	715.3198	358.1636			G	**792.4039**	396.7056	775.3774	388.1923	774.3933	387.7003	7
7	829.3992	***415.2032***	812.3726	406.6899			P	**735.3824**	368.1949	718.3559	359.6816	717.3719	359.1896	6
8	976.4676	488.7374	959.4410	480.2241			F	**638.3297**	319.6685	621.3031	311.1552	620.3191	310.6632	5
9	1033.4890	***517.2482***	1016.4625	508.7349			G	491.2613	246.1343	474.2347	237.6210	473.2507	237.1290	4
10	1134.5367	***567.7720***	1117.5102	559.2587	1116.5261	558.7667	T	434.2398	217.6235	417.2132	209.1103	416.2292	208.6183	3
11	1320.6160	***660.8116***	1303.5895	652.2984	1302.6055	651.8064	W	333.1921	167.0997	316.1656	158.5864			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FHNIYGPFGTWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G28840.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.5	1465.7143	0.0014	FHNIYGPFGTWK
4.0	1465.7195	-0.0039	CGDVATTGSTTLRK
0.5	1465.7161	-0.0004	EFSNDAKSAAASLR

AT5G30510.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDANGALVDISAK**
Found in **AT5G30510.1** in **TAIR_Arabidopsis**, Symbols: ARRPS1, RPS1 | RPS1 (ribosomal protein S1); RNA binding | chr5:11636492-11638453 REVERSE

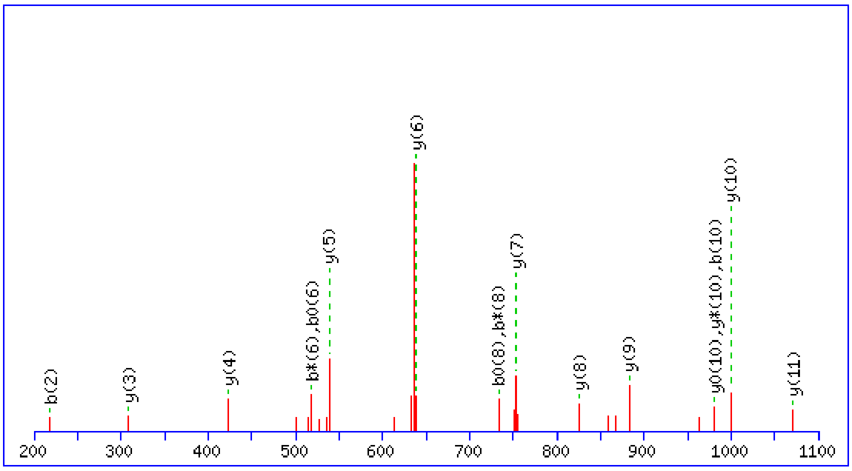
Match to Query 4598: 1288.607174 from(645.310863,2+) index(3634)
Title: Elution from: 36.097 to 36.097 scan no 4559 cid35.00 polarity:+
Data file D6h-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1100 Da Full range

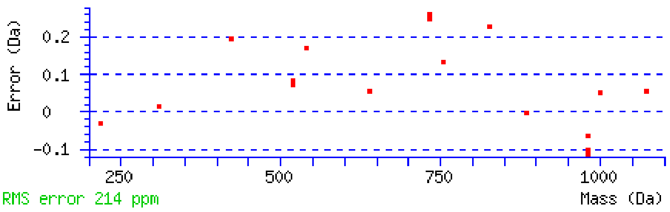
Label all possible matches ○ Label matches used for scoring ●

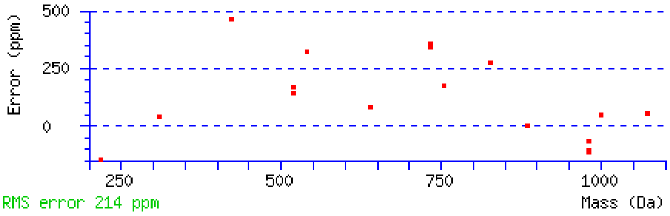
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1288.6069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 2.5e-009
Matches : 17/134 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							13
2	**219.0760**	110.0416			201.0654	101.0363	D	1187.5695	594.2884	1169.5459	585.2766	1169.5589	585.2831	12
3	291.1101	146.0587			273.0996	137.0534	A	***1071.5455***	536.2764	1053.5219	527.2646	1053.5349	527.2711	11
4	407.1471	204.0772	389.1235	195.0654	389.1365	195.0719	N	***999.5114***	500.2593	981.4878	491.2475	981.5008	491.2540	10
5	465.1656	233.0864	447.1420	224.0747	447.1550	224.0812	G	***883.4744***	442.2408	865.4508	433.2290	865.4638	433.2355	9
6	537.1998	269.1035	519.1762	260.0917	519.1892	260.0982	A	***825.4559***	413.2316	807.4323	404.2198	807.4453	404.2263	8
7	651.2809	326.1441	633.2573	317.1323	633.2703	317.1388	L	***753.4217***	377.2145	735.3981	368.2027	735.4111	368.2092	7
8	751.3463	376.1768	733.3227	367.1650	733.3357	367.1715	V	***639.3406***	320.1739	621.3170	311.1622	621.3300	311.1687	6
9	867.3703	434.1888	849.3467	425.1770	849.3597	425.1835	D	***539.2752***	270.1412	521.2516	261.1294	521.2646	261.1359	5
10	**981.4514**	491.2293	963.4278	482.2175	963.4408	482.2240	I	***423.2512***	212.1292	405.2276	203.1174	405.2406	203.1239	4
11	1069.4804	535.2439	1051.4569	526.2321	1051.4699	526.2386	S	***309.1701***	155.0887	291.1465	146.0769	291.1595	146.0834	3
12	1141.5146	571.2609	1123.4910	562.2491	1123.5040	562.2557	A	221.1410	111.0741	203.1174	102.0624			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TDANGALVDISAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G30510.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.4	1288.6069	0.0003	TDANGALVDISAK
14.3	1288.6096	-0.0024	DRGAELEVVQR
13.8	1288.6096	-0.0024	RQEVLDNELR
12.7	1288.6069	0.0003	EDSVVDDVIKR
12.1	1288.6048	0.0023	GRILAGTCHSAK
4.0	1288.6096	-0.0024	DAGRIAGLDVER
3.8	1288.6069	0.0003	ESVQVSDEILR
3.0	1288.6096	-0.0024	NISSPDEVVRR
2.9	1288.6069	0.0003	SLGEVISGDEIR
2.6	1288.6069	0.0003	AISEEEAKLER

AT5G34850.1

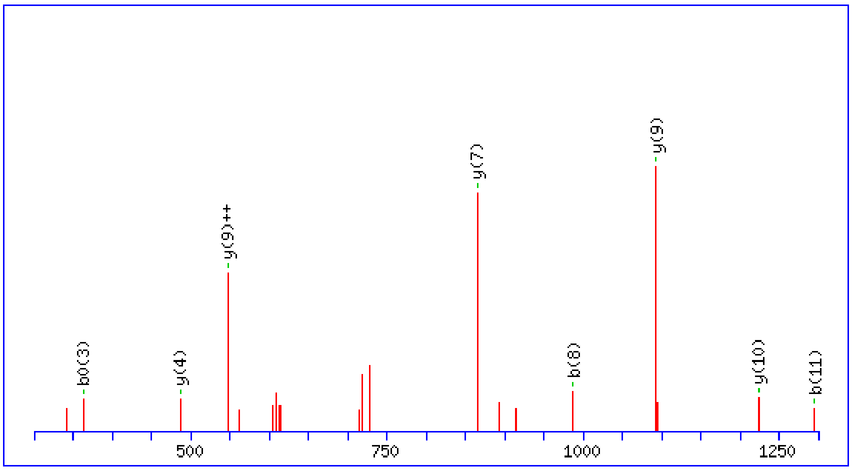
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTEPQPDYSAFR**
Found in **AT5G34850.1** in **TAIR_Arabidopsis**, Symbols: ATPAP26, PAP26 | ATPAP26/PAP26 (purple acid phosphatase 26); acid phosphatase/ protein serine/threonine phosphatase | chr5:13125705-13128447 REVERSE

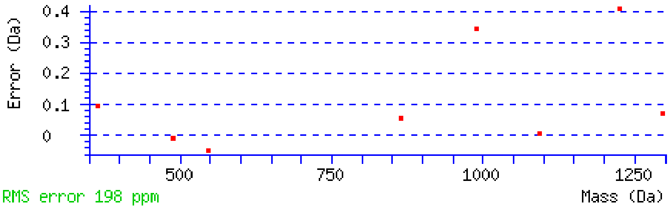
Match to Query 6029: 1472.611450 from(737.313001,2+) index(5235)
Title: Elution from: 47.209 to 47.209 scan no 6627 cid35.00 polarity:+
Data file 0-2_2.mgf

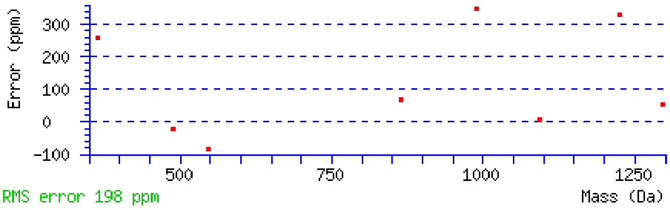
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1472.6148
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0033
Matches : 8/116 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							12
2	251.1174	126.0624			233.1069	117.0571	T	1325.5567	663.2820	1307.5331	654.2702	1307.5461	654.2767	11
3	381.1571	191.0822			363.1465	182.0769	E	***1223.5120***	612.2596	1205.4884	603.2478	1205.5014	603.2543	10
4	479.2069	240.1071			461.1963	231.1018	P	***1093.4723***	547.2398	1075.4488	538.2280	1075.4618	538.2345	9
5	609.2595	305.1334	591.2359	296.1216	591.2489	296.1281	Q	995.4225	498.2149	977.3990	489.2031	977.4120	489.2096	8
6	707.3093	354.1583	689.2857	345.1465	689.2987	345.1530	P	***865.3699***	433.1886	847.3463	424.1768	847.3593	424.1833	7
7	823.3333	412.1703	805.3097	403.1585	805.3227	403.1650	D	767.3201	384.1637	749.2965	375.1519	749.3095	375.1584	6
8	**987.3937**	494.2005	969.3701	485.1887	969.3831	485.1952	Y	651.2961	326.1517	633.2725	317.1399	633.2856	317.1464	5
9	1075.4227	538.2150	1057.3991	529.2032	1057.4122	529.2097	S	***487.2358***	244.1215	469.2122	235.1097	469.2252	235.1162	4
10	1147.4569	574.2321	1129.4333	565.2203	1129.4463	565.2268	A	399.2067	200.1070	381.1831	191.0952			3
11	**1295.5223**	648.2648	1277.4987	639.2530	1277.5117	639.2595	F	327.1725	164.0899	309.1490	155.0781			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of FTEPQPDYSAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G34850.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.5	1472.6148	-0.0034	FTEPQPDYSAFR
5.9	1472.6071	0.0043	YTGGYWEARGHR
2.3	1472.6104	0.0011	NHEIESDLVDER
2.0	1472.6079	0.0036	AAHFEESMKYAR
1.7	1472.6126	-0.0011	SFGFDTAVEEAQR
1.5	1472.6099	0.0015	FETQELAYDESK

AT5G35170.1

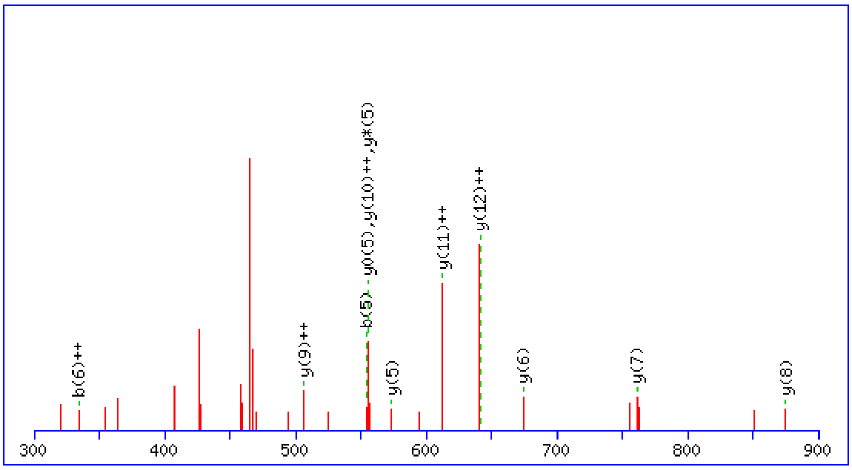
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGLVHISTGDLLR**
Found in **AT5G35170.1** in **TAIR_Arabidopsis**, Symbols: | adenylate kinase family protein | chr5:13436508-13440712 FORWARD

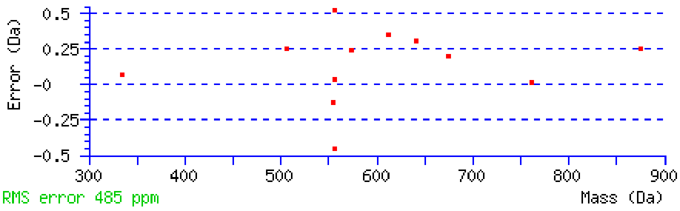
Match to Query 5578: 1426.792581 from(476.604803,3+) index(7700)
Title: Elution from: 68.254 to 68.254 scan no 10141 cid35.00 polarity:+
Data file 0-1_3.mgf

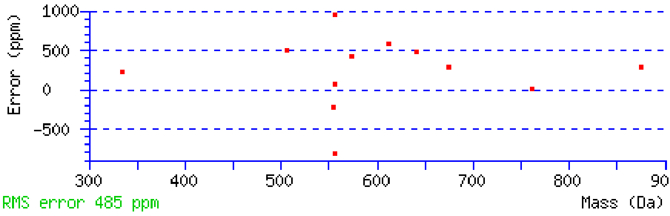
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1426.7933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.015
Matches : 12/102 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							13
2	205.0972	103.0522			G	1280.7321	640.8697	1263.7056	632.3564	1262.7215	631.8644	12
3	318.1812	159.5942			L	1223.7106	612.3590	1206.6841	603.8457	1205.7001	603.3537	11
4	417.2496	209.1285			V	1110.6266	555.8169	1093.6000	547.3037	1092.6160	546.8116	10
5	554.3085	277.6579			H	1011.5582	506.2827	994.5316	497.7694	993.5476	497.2774	9
6	667.3926	334.1999			I	***874.4993***	437.7533	857.4727	429.2400	856.4887	428.7480	8
7	754.4246	377.7160	736.4141	368.7107	S	***761.4152***	381.2112	744.3886	372.6980	743.4046	372.2060	7
8	855.4723	428.2398	837.4618	419.2345	T	***674.3832***	337.6952	657.3566	329.1819	656.3726	328.6899	6
9	912.4938	456.7505	894.4832	447.7452	G	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	5
10	1027.5207	514.2640	1009.5102	505.2587	D	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
11	1140.6048	570.8060	1122.5942	561.8007	L	401.2871	201.1472	384.2605	192.6339			3
12	1253.6889	627.3481	1235.6783	618.3428	L	288.2030	144.6051	271.1765	136.0919			2
13					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FGLVHISTGDLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G35170.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.6	1426.7933	-0.0007	FGLVHISTGDLLR
2.3	1426.7892	0.0034	SERKLSLSPPGTR
0.9	1426.7894	0.0032	IMSLLSGYFLVGK
0.2	1426.7932	-0.0006	EDAVSLLHLKFR

AT5G35360.1

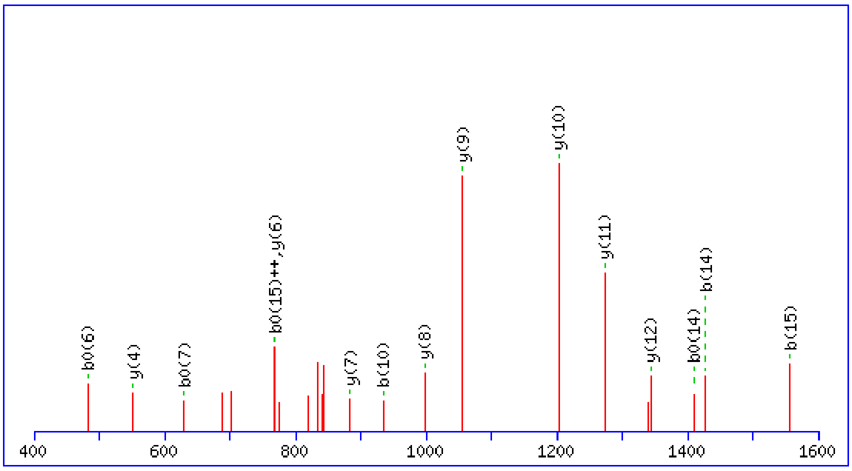
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEAAAAFGNDGCYLEK**
Found in **AT5G35360.1** in **TAIR_Arabidopsis**, Symbols: CAC2 | CAC2 (acetyl co-enzyme A carboxylase biotin carboxylase subunit) | chr5:13601530-13605498 FORWARD

Match to Query 7479: 1701.732410 from(851.873481,2+) index(4241)
Title: Elution from: 41.493 to 41.493 scan no 5458 cid35.00 polarity:+
Data file D1d-1_3.mgf

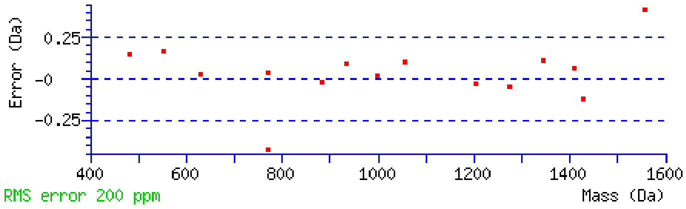
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

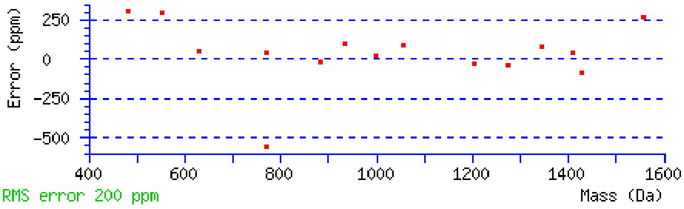


Monoisotopic mass of neutral peptide Mr(calc): 1701.7304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 6e-008
Matches : 15/162 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**16**
2	217.0819	109.0446			199.0713	100.0393	**E**	1615.7057	808.3565	1598.6792	799.8432	1597.6951	799.3512	**15**
3	288.1190	144.5631			270.1084	135.5579	**A**	1486.6631	743.8352	1469.6366	735.3219	1468.6525	734.8299	**14**
4	359.1561	180.0817			341.1456	171.0764	**A**	1415.6260	708.3166	1398.5994	699.8034	1397.6154	699.3114	**13**
5	430.1932	215.6003			412.1827	206.5950	**A**	***1344.5889***	672.7981	1327.5623	664.2848	1326.5783	663.7928	**12**
6	501.2304	251.1188			483.2198	242.1135	**A**	***1273.5518***	637.2795	1256.5252	628.7662	1255.5412	628.2742	**11**
7	648.2988	324.6530			630.2882	315.6477	**F**	***1202.5147***	601.7610	1185.4881	593.2477	1184.5041	592.7557	**10**
8	705.3202	353.1638			687.3097	344.1585	**G**	***1055.4462***	528.2268	1038.4197	519.7135	1037.4357	519.2215	**9**
9	819.3632	410.1852	802.3366	401.6719	801.3526	401.1799	**N**	***998.4248***	499.7160	981.3982	491.2027	980.4142	490.7107	**8**
10	**934.3901**	467.6987	917.3636	459.1854	916.3795	458.6934	**D**	***884.3818***	442.6946	867.3553	434.1813	866.3713	433.6893	**7**
11	991.4116	496.2094	974.3850	487.6961	973.4010	487.2041	**G**	***769.3549***	385.1811	752.3284	376.6678	751.3443	376.1758	**6**
12	1151.4422	576.2247	1134.4157	567.7115	1133.4316	567.2195	**C**	712.3334	356.6704	695.3069	348.1571	694.3229	347.6651	**5**
13	1314.5055	657.7564	1297.4790	649.2431	1296.4950	648.7511	**Y**	***552.3028***	276.6550	535.2762	268.1418	534.2922	267.6498	**4**
14	**1427.5896**	714.2984	1410.5631	705.7852	1409.5790	705.2932	**L**	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	**3**
15	**1556.6322**	778.8197	1539.6057	770.3065	1538.6216	769.8145	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT5G35360.1





NCBI **BLAST** search of SEAAAAFGNDGCYLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.2	1701.7304	0.0020	SEAAAAFGNDGCYLEK

Mascot: http://www.matrixscience.com/

AT5G35590.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTYGYEMPVDILAK**
Found in **AT5G35590.1** in **TAIR_Arabidopsis**, Symbols: PAA1 | PAA1 (20S proteasome alpha subunit A1); peptidase | chr5:13782647-13784998 REVERSE

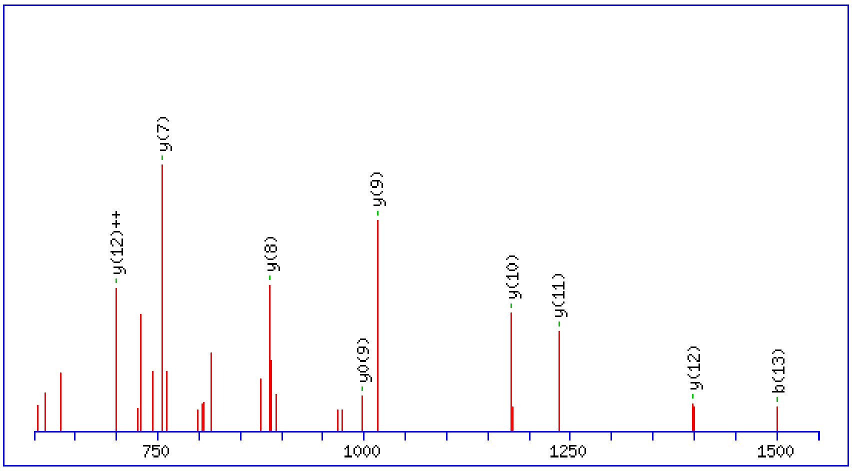
Match to Query 8030: 1645.807868 from(823.911210,2+) index(9696)
Title: Elution from: 86.234 to 86.234 scan no 13084 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 600 to 1550 Da Full range

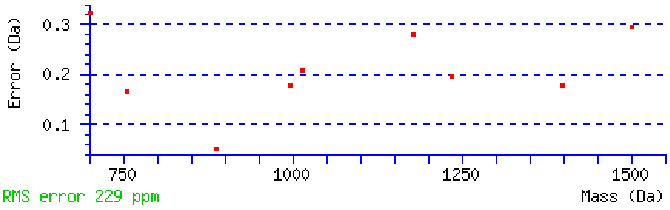
Label all possible matches ○ Label matches used for scoring ●

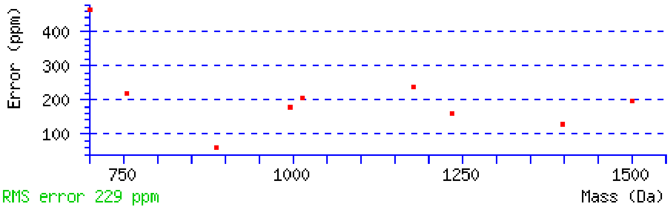
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1645.8062
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 6.9e-005
Matches : 9/120 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							14
2	249.1234	125.0653	231.1128	116.0600	T	1499.7450	750.3762	1482.7185	741.8629	1481.7345	741.3709	13
3	412.1867	206.5970	394.1761	197.5917	Y	***1398.6974***	699.8523	1381.6708	691.3390	1380.6868	690.8470	12
4	469.2082	235.1077	451.1976	226.1024	G	***1235.6340***	618.3207	1218.6075	609.8074	1217.6235	609.3154	11
5	632.2715	316.6394	614.2609	307.6341	Y	***1178.6126***	589.8099	1161.5860	581.2967	1160.6020	580.8046	10
6	761.3141	381.1607	743.3035	372.1554	E	***1015.5492***	508.2783	998.5227	499.7650	997.5387	499.2730	9
7	892.3546	446.6809	874.3440	437.6756	M	***886.5067***	443.7570	869.4801	435.2437	868.4961	434.7517	8
8	989.4073	495.2073	971.3968	486.2020	P	***755.4662***	378.2367	738.4396	369.7234	737.4556	369.2314	7
9	1088.4757	544.7415	1070.4652	535.7362	V	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
10	1203.5027	602.2550	1185.4921	593.2497	D	559.3450	280.1761	542.3184	271.6629	541.3344	271.1708	5
11	1316.5868	658.7970	1298.5762	649.7917	I	444.3180	222.6627	427.2915	214.1494			4
12	1429.6708	715.3390	1411.6603	706.3338	L	331.2340	166.1206	314.2074	157.6074			3
13	1500.7079	750.8576	1482.6974	741.8523	A	218.1499	109.5786	201.1234	101.0653			2
14					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FTYGYEMPVDILAK

AT5G35590.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.7	1645.8062	0.0017	FTYGYEMPVDILAK
0.1	1645.8107	-0.0028	MSRQIQESGWRPR
0.1	1645.8107	-0.0028	MSRQLQESGWRPR

Mascot: http://www.matrixscience.com/

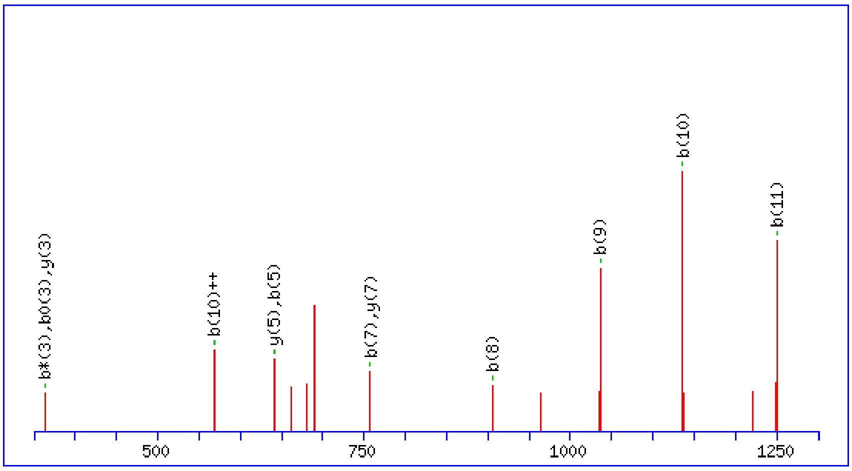
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMREEGGFEVIK**
Found in **AT5G35630.1** in **TAIR_Arabidopsis**, Symbols: GLN2, ATGSL1, GS2 | GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase | chr5:13848450-13850469 FORWARD

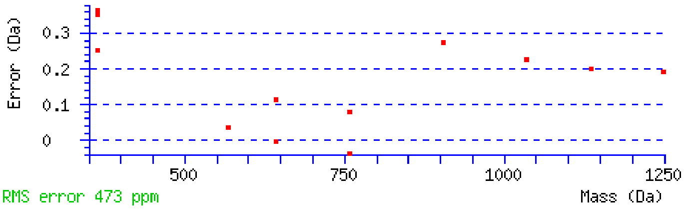
Match to Query 5361: 1396.625338 from(699.319945,2+) index(3103)
Title: Elution from: 31.145 to 31.145 scan no 3892 cid35.00 polarity:+
Data file 0-2_2.mgf

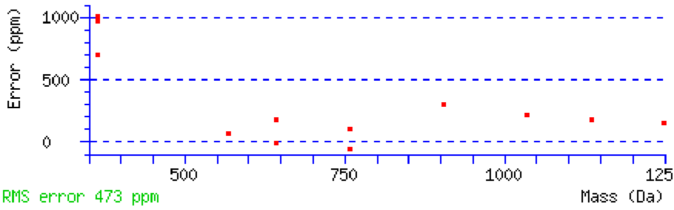
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1396.6233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 6.5e-005
Matches : 12/122 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							12
2	221.0739	111.0406			203.0633	102.0353	M	1309.6015	655.3044	1291.5779	646.2926	1291.5910	646.2991	11
3	381.1631	191.0852	363.1395	182.0734	363.1525	182.0799	R	1177.5640	589.2856	1159.5404	580.2738	1159.5534	580.2804	10
4	511.2027	256.1050	493.1792	247.0932	493.1922	247.0997	E	1017.4748	509.2410	999.4512	500.2292	999.4642	500.2357	9
5	***641.2424***	321.1248	623.2188	312.1130	623.2318	312.1195	E	887.4351	444.2212	869.4115	435.2094	869.4246	435.2159	8
6	699.2609	350.1341	681.2373	341.1223	681.2503	341.1288	G	**757.3955**	379.2014	739.3719	370.1896	739.3849	370.1961	7
7	***757.2794***	379.1433	739.2558	370.1315	739.2688	370.1380	G	699.3770	350.1921	681.3534	341.1803	681.3664	341.1869	6
8	***905.3448***	453.1760	887.3212	444.1643	887.3342	444.1708	F	**641.3585**	321.1829	623.3349	312.1711	623.3479	312.1776	5
9	***1035.3844***	518.1959	1017.3609	509.1841	1017.3739	509.1906	E	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
10	***1135.4499***	568.2286	1117.4263	559.2168	1117.4393	559.2233	V	**363.2534**	182.1303	345.2298	173.1186			3
11	***1249.5310***	625.2691	1231.5074	616.2573	1231.5204	616.2638	I	263.1880	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SMREEGGFEVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G35630.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.3	1396.6233	0.0020	SMREEGGFEVIK
25.8	1396.6280	-0.0027	DAATPPLTQEDPK
15.1	1396.6233	0.0020	TEERMTPQVYK
14.3	1396.6233	0.0020	QYKQADCELVK
13.1	1396.6240	0.0013	LESMSMSVDILK
12.3	1396.6285	-0.0031	TEEESSSLGKRR
8.3	1396.6237	0.0016	ENGEGMRTSRLK
5.1	1396.6220	0.0034	MGLMRSMLPNAK
3.7	1396.6237	0.0016	RKASTAMGIDGDR
3.3	1396.6233	0.0020	LMSSRETDWIK

AT5G35730.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSLLNALK**
Found in **AT5G35730.1** in **TAIR_Arabidopsis**, Symbols: | EXS family protein / ERD1/XPR1/SYG1 family protein | chr5:13911171-13914051 FORWARD

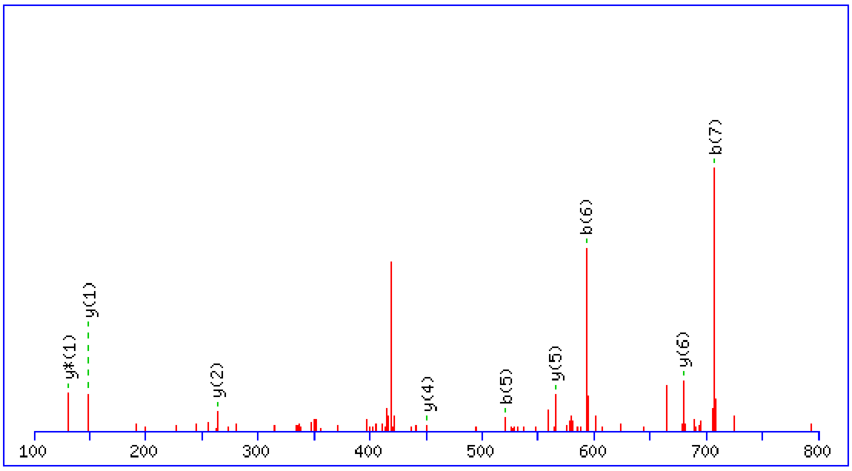
Match to Query 1480: 854.474512 from(428.244532,2+) index(3103)
Title: Elution from: 30.553 to 30.553 scan no 3863 cid35.00 polarity:+
Data file D1d-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

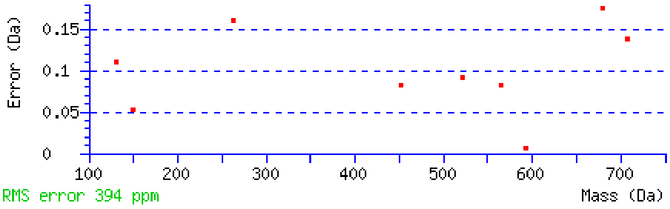
Label all possible matches ○ Label matches used for scoring ●

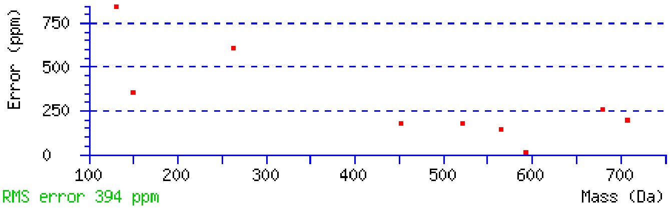
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 854.4722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00092
Matches : 9/64 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							8
2	177.0654	89.0363			159.0548	80.0311	S	767.4504	384.2288	749.4268	375.2170	749.4398	375.2235	7
3	291.1465	146.0769			273.1359	137.0716	L	***679.4213***	340.2143	661.3977	331.2025			6
4	405.2276	203.1174			387.2170	194.1122	L	***565.3402***	283.1737	547.3166	274.1620			5
5	**521.2646**	261.1359	503.2410	252.1241	503.2540	252.1307	N	***451.2591***	226.1332	433.2355	217.1214			4
6	**593.2987**	297.1530	575.2752	288.1412	575.2882	288.1477	A	335.2221	168.1147	317.1985	159.1029			3
7	**707.3798**	354.1936	689.3563	345.1818	689.3693	345.1883	L	***263.1880***	132.0976	245.1644	123.0858			2
8							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of SSLLNALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.7	854.4722	0.0023	SSLLNALK

AT5G35730.1

28.1	854.4748	-0.0003	QRLQGLK
28.0	854.4722	0.0023	EKEKALK
28.0	854.4722	0.0024	TLAQTALK
20.9	854.4744	0.0001	YPVLNLK
19.2	854.4771	-0.0026	QIRWIK
15.7	854.4748	-0.0003	AQRVGALK
15.7	854.4748	-0.0003	GNALRALK
15.7	854.4771	-0.0026	RGLWAIK
15.6	854.4722	0.0023	EAEKKLK

AT5G35753.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGEVGFKLEGDLAFR**
Found in **AT5G35753.1** in **TAIR_Arabidopsis**, Symbols: | similar to DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G05230.1); similar to DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G05250.1); similar to hypothetica

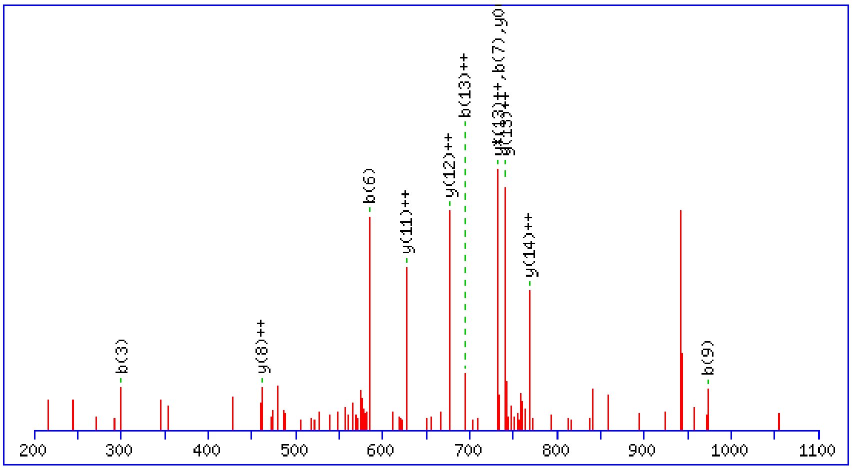
Match to Query 8193: 1778.918388 from(593.980072,3+) index(6354)
Title: Elution from: 55.693 to 55.693 scan no 8218 cid35.00 polarity:+
Data file 0-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●

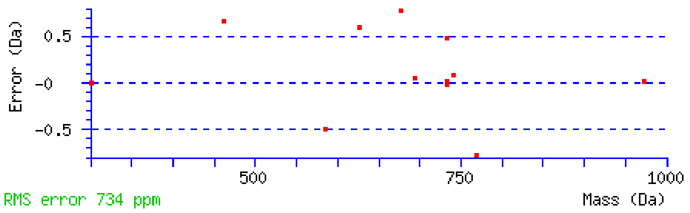
Show Y-axis ☐

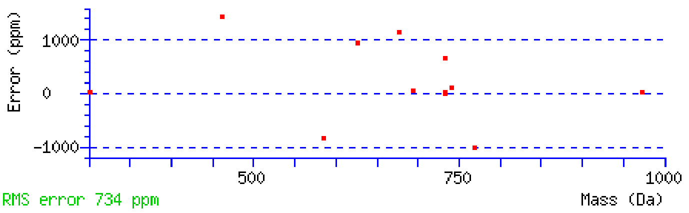


Monoisotopic mass of neutral peptide Mr(calc): 1778.9203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.022
Matches : 12/158 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	243.1339	122.0706			225.1234	113.0653	L	1650.8850	825.9461	1633.8584	817.4329	1632.8744	816.9408	15
3	***300.1554***	150.5813			282.1448	141.5761	G	1537.8009	769.4041	1520.7744	760.8908	1519.7904	760.3988	14
4	429.1980	215.1026			411.1874	206.0974	E	1480.7795	740.8934	1463.7529	732.3801	1462.7689	731.8881	13
5	528.2664	264.6368			510.2558	255.6316	V	1351.7369	676.3721	1334.7103	667.8588	1333.7263	667.3668	12
6	***585.2879***	293.1476			567.2773	284.1423	G	1252.6684	626.8379	1235.6419	618.3246	1234.6579	617.8326	11
7	***732.3563***	366.6818			714.3457	357.6765	F	1195.6470	598.3271	1178.6204	589.8139	1177.6364	589.3218	10
8	860.4512	430.7293	843.4247	422.2160	842.4407	421.7240	K	1048.5786	524.7929	1031.5520	516.2796	1030.5680	515.7876	9
9	***973.5353***	487.2713	956.5088	478.7580	955.5247	478.2660	L	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	8
10	1102.5779	551.7926	1085.5514	543.2793	1084.5673	542.7873	E	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	7
11	1159.5994	580.3033	1142.5728	571.7900	1141.5888	571.2980	G	678.3570	339.6821	661.3304	331.1688	660.3464	330.6768	6
12	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	D	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	5
13	1387.7104	694.3588	1370.6838	685.8456	1369.6998	685.3535	L	506.3085	253.6579	489.2820	245.1446			4
14	1458.7475	729.8774	1441.7209	721.3641	1440.7369	720.8721	A	393.2245	197.1159	376.1979	188.6026			3
15	1605.8159	803.4116	1588.7894	794.8983	1587.8053	794.4063	F	322.1874	161.5973	305.1608	153.0840			2
16							R	175.1190	88.0631	158.0924	79.5498			1

AT5G35753.1





NCBI **BLAST** search of ELGEVGFKLEGDLAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.9	1778.9203	-0.0019	ELGEVGFKLEGDLAFR
11.3	1778.9236	-0.0052	LQGEKALLAMEASQYK
5.8	1778.9236	-0.0052	VAEERLPTLKMYSDK
1.9	1778.9209	-0.0026	IHLPSNTPNEMRKAR
0.2	1778.9203	-0.0019	LWQVPETLHEEALSK
0.1	1778.9163	0.0021	GLEDIGKEQAGGIVEHK

Mascot: http://www.matrixscience.com/

AT5G36000.1

MATRIX SCIENCE

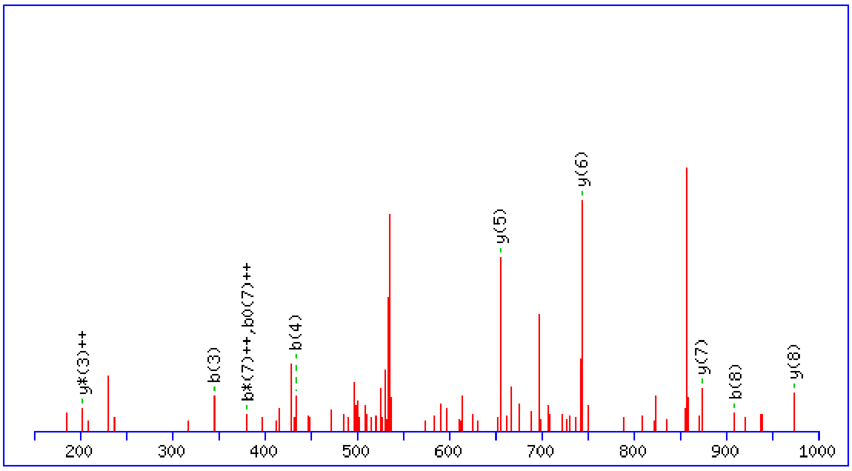
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVQSNDIQR**
Found in **AT5G36000.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G61730.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39758.1); contains domain F-box domain (SSF81383) | chr5:14157226-14159122 FORWARD

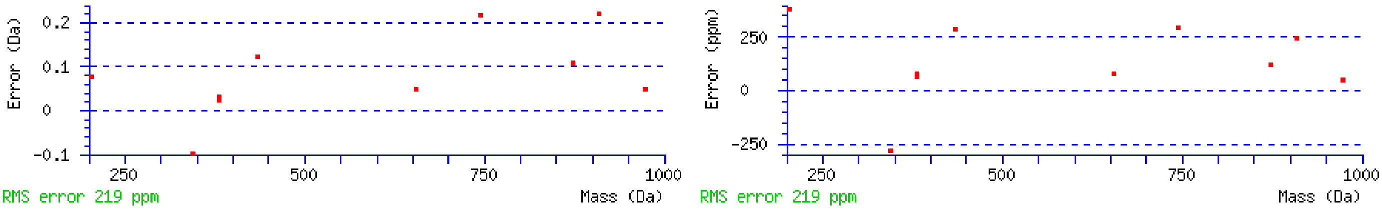
Match to Query 2773: 1086.523638 from(544.269095,2+) index(2301)
Title: Elution from: 26.213 to 26.213 scan no 2961 cid35.00 polarity:+
Data file D12h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1086.5228
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.029
Matches : 10/80 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							9
2	215.1538	108.0805					V	***973.4490***	487.2281	955.4254	478.2163	955.4384	478.2228	8
3	***345.2065***	173.1069	327.1829	164.0951			Q	***873.3835***	437.1954	855.3599	428.1836	855.3730	428.1901	7
4	***433.2355***	217.1214	415.2120	208.1096	415.2250	208.1161	S	***743.3309***	372.1691	725.3073	363.1573	725.3203	363.1638	6
5	549.2725	275.1399	531.2489	266.1281	531.2620	266.1346	N	***655.3018***	328.1545	637.2782	319.1428	637.2912	319.1493	5
6	665.2965	333.1519	647.2729	324.1401	647.2859	324.1466	D	539.2648	270.1360	521.2412	261.1243	521.2543	261.1308	4
7	779.3776	390.1924	761.3540	381.1807	761.3670	381.1872	I	423.2408	212.1241	405.2173	203.1123			3
8	***909.4303***	455.2188	891.4067	446.2070	891.4197	446.2135	Q	309.1597	155.0835	291.1362	146.0717			2
9							R	179.1071	90.0572	161.0835	81.0454			1



NCBI **BLAST** search of LVQSNDIQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G36000.1

24.9	1086.5228	0.0009	LVQSNDIQR
10.6	1086.5257	-0.0021	VQLTEDLMK
10.0	1086.5228	0.0008	DLLRPESSR
6.8	1086.5257	-0.0021	VLEGMGVVEK
6.2	1086.5250	-0.0014	IVEYHREK
5.5	1086.5228	0.0009	EVARLEAER
5.3	1086.5228	0.0008	QVSSGAAPLSR
4.7	1086.5228	0.0008	INNTKETPR
4.7	1086.5250	-0.0014	LDHLYIGSR
4.4	1086.5257	-0.0021	LSSTTLMGGLP

AT5G36880.2

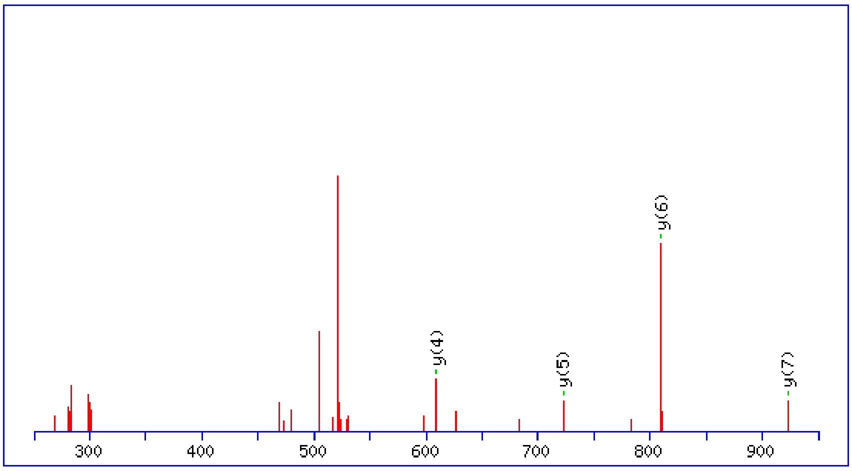
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPISIEWFK**
Found in **AT5G36880.2** in **TAIR_Arabidopsis**, Symbols: | acetyl-CoA synthetase, putative / acetate-CoA ligase, putative | chr5:14552191-14557526 REVERSE

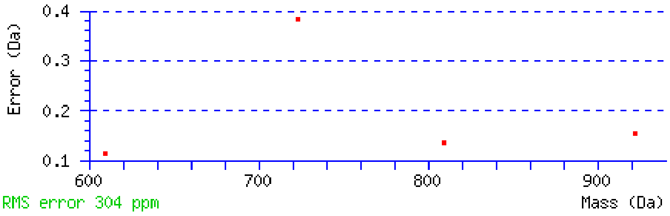
Match to Query 3123: 1075.570082 from(538.792317,2+) index(8598)
Title: Elution from: 77.288 to 77.288 scan no 11445 cid35.00 polarity:+
Data file 0-3_1.mgf

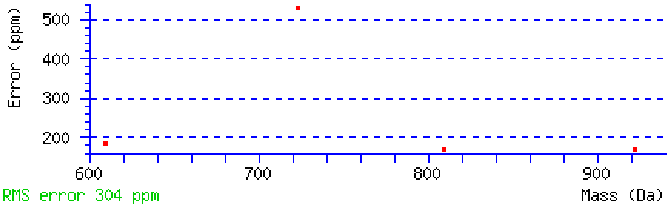
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1075.5702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0072
Matches : 4/68 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							9
2	155.0815	78.0444			P	1019.5560	510.2817	1002.5295	501.7684	1001.5455	501.2764	8
3	268.1656	134.5864			I	***922.5033***	461.7553	905.4767	453.2420	904.4927	452.7500	7
4	355.1976	178.1024	337.1870	169.0972	S	***809.4192***	405.2132	792.3927	396.7000	791.4087	396.2080	6
5	468.2817	234.6445	450.2711	225.6392	I	***722.3872***	361.6972	705.3606	353.1840	704.3766	352.6919	5
6	597.3243	299.1658	579.3137	290.1605	E	***609.3031***	305.1552	592.2766	296.6419	591.2926	296.1499	4
7	783.4036	392.2054	765.3930	383.2001	W	480.2605	240.6339	463.2340	232.1206			3
8	930.4720	465.7396	912.4614	456.7343	F	294.1812	147.5942	277.1547	139.0810			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GPISIEWFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G36880.2

28.7	1075.5702	-0.0001	GPISIEWFK

Mascot: http://www.matrixscience.com/

AT5G37010.1

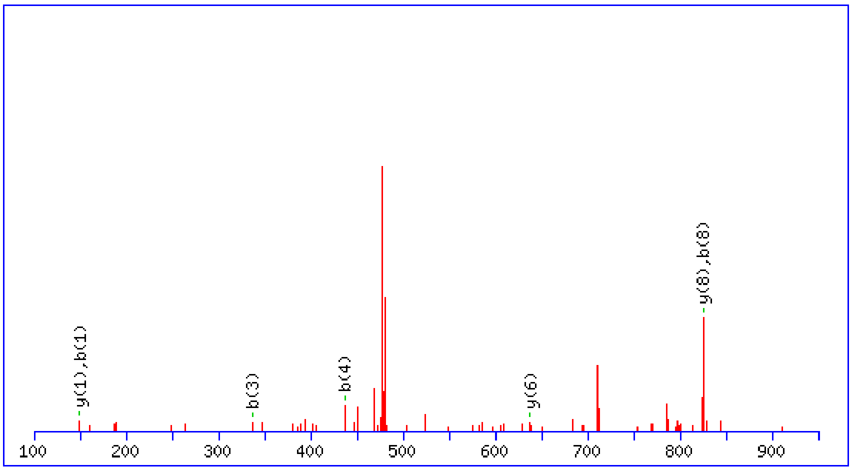
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVSVPATDK**
Found in **AT5G37010.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65710.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN76723.1) | chr5:14638083-14640109 REVERSE

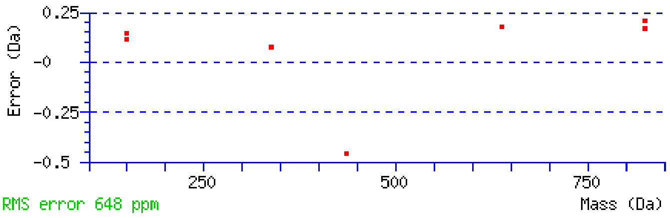
Match to Query 1976: 972.477046 from(487.245799,2+) index(1112)
Title: Elution from: 19.421 to 19.421 scan no 1660 cid35.00 polarity:+
Data file D1d-2_1.mgf

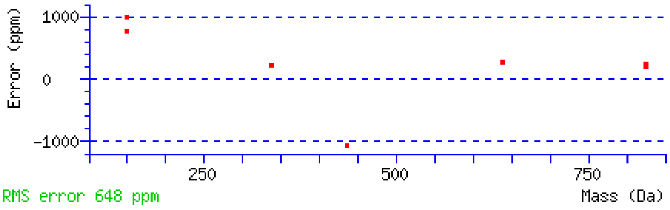
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.4776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.015
Matches : 7/74 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***149.0727***	75.0400			F							9
2	249.1382	125.0727			V	**825.4195**	413.2134	807.3959	404.2016	807.4089	404.2081	8
3	***337.1672***	169.0873	319.1567	160.0820	S	725.3540	363.1807	707.3304	354.1689	707.3435	354.1754	7
4	***437.2327***	219.1200	419.2221	210.1147	V	**637.3250**	319.1661	619.3014	310.1543	619.3144	310.1608	6
5	535.2825	268.1449	517.2719	259.1396	P	537.2595	269.1334	519.2359	260.1216	519.2489	260.1281	5
6	607.3166	304.1620	589.3061	295.1567	A	439.2097	220.1085	421.1861	211.0967	421.1991	211.1032	4
7	709.3613	355.1843	691.3508	346.1790	T	367.1756	184.0914	349.1520	175.0796	349.1650	175.0861	3
8	***825.3853***	413.1963	807.3748	404.1910	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
9					K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FVSVPATDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G37010.1

29.1	972.4776	-0.0006	FVSVPATDK
20.8	972.4776	-0.0006	GFDIVVGEK
19.2	972.4754	0.0016	GSTSQEILK
17.0	972.4799	-0.0028	LFEEWLK
16.3	972.4754	0.0017	EGTDSVVKK
16.2	972.4781	-0.0010	GSLVNREGK
14.4	972.4776	-0.0006	FLGLDVGDK
14.3	972.4754	0.0016	DSKDKELK
12.6	972.4781	-0.0010	RREELEK
12.3	972.4754	0.0016	ASSISAAEVK

AT5G37510.1

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FASEVAGVQDLGILGR**
Found in **AT5G37510.1** in **TAIR_Arabidopsis**, Symbols: EMB1467 | EMB1467 (EMBRYO DEFECTIVE 1467); NADH dehydrogenase | chr5:14914720-14917582 FORWARD

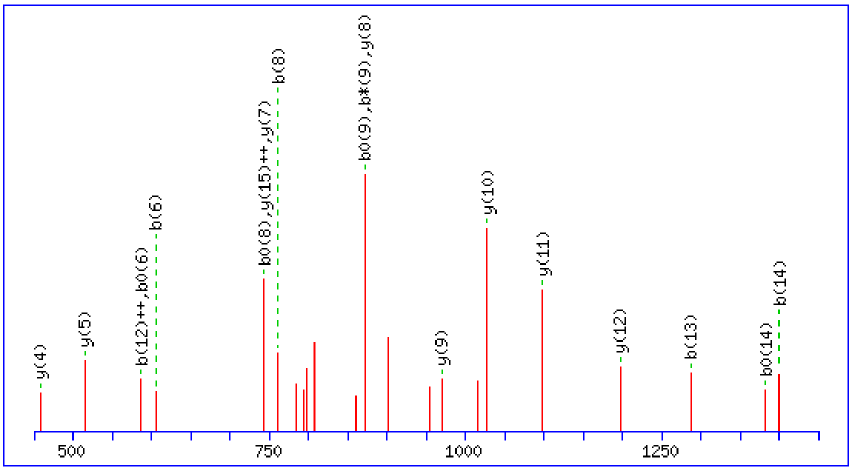
Match to Query 7467: 1630.867584 from(816.441068,2+) index(8475)
Title: Elution from: 75.938 to 75.938 scan no 11317 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1450 Da Full range

Label all possible matches ○ Label matches used for scoring ●

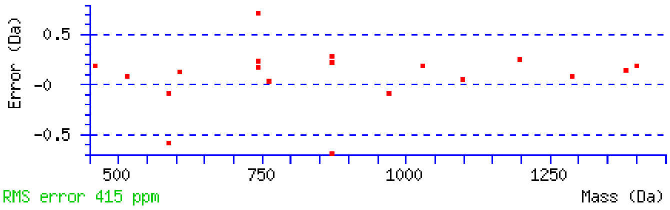
Show Y-axis ☐

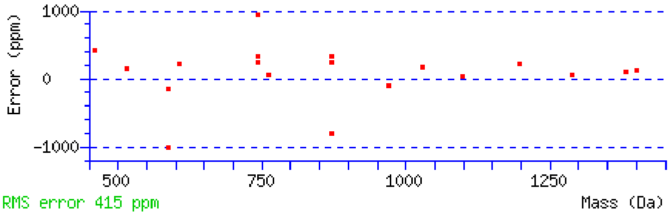


Monoisotopic mass of neutral peptide Mr(calc): 1630.8679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.2e-007
Matches : 19/148 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							16
2	219.1128	110.0600					A	1484.8067	742.9070	1467.7802	734.3937	1466.7962	733.9017	15
3	306.1448	153.5761			288.1343	144.5708	S	1413.7696	707.3884	1396.7431	698.8752	1395.7591	698.3832	14
4	435.1874	218.0974			417.1769	209.0921	E	1326.7376	663.8724	1309.7110	655.3592	1308.7270	654.8672	13
5	534.2558	267.6316			516.2453	258.6263	V	***1197.6950***	599.3511	1180.6684	590.8379	1179.6844	590.3459	12
6	**605.2930**	303.1501			587.2824	294.1448	A	***1098.6266***	549.8169	1081.6000	541.3037	1080.6160	540.8116	11
7	662.3144	331.6608			644.3039	322.6556	G	***1027.5895***	514.2984	1010.5629	505.7851	1009.5789	505.2931	10
8	**761.3828**	381.1951			743.3723	372.1898	V	***970.5680***	485.7876	953.5415	477.2744	952.5574	476.7824	9
9	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	Q	***871.4996***	436.2534	854.4730	427.7402	853.4890	427.2482	8
10	1004.4684	502.7378	987.4418	494.2245	986.4578	493.7325	D	***743.4410***	372.2241	726.4145	363.7109	725.4304	363.2189	7
11	1117.5524	559.2798	1100.5259	550.7666	1099.5419	550.2746	L	628.4141	314.7107	611.3875	306.1974			6
12	1174.5739	587.7906	1157.5473	579.2773	1156.5633	578.7853	G	***515.3300***	258.1686	498.3035	249.6554			5
13	**1287.6579**	644.3326	1270.6314	635.8193	1269.6474	635.3273	I	***458.3085***	229.6579	441.2820	221.1446			4
14	**1400.7420**	700.8746	1383.7155	692.3614	1382.7314	691.8694	L	345.2245	173.1159	328.1979	164.6026			3
15	1457.7635	729.3854	1440.7369	720.8721	1439.7529	720.3801	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1

AT5G37510.1





NCBI **BLAST** search of FASEVAGVQDLGILGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.9	1630.8679	-0.0003	FASEVAGVQDLGILGR
2.5	1630.8719	-0.0043	SAEDIAFHVALFIAK
2.2	1630.8712	-0.0036	ISSGMEGIARIEIQK
1.2	1630.8638	0.0038	LNGNGVTERSSSIAVK

Mascot: http://www.matrixscience.com/

AT5G37530.1

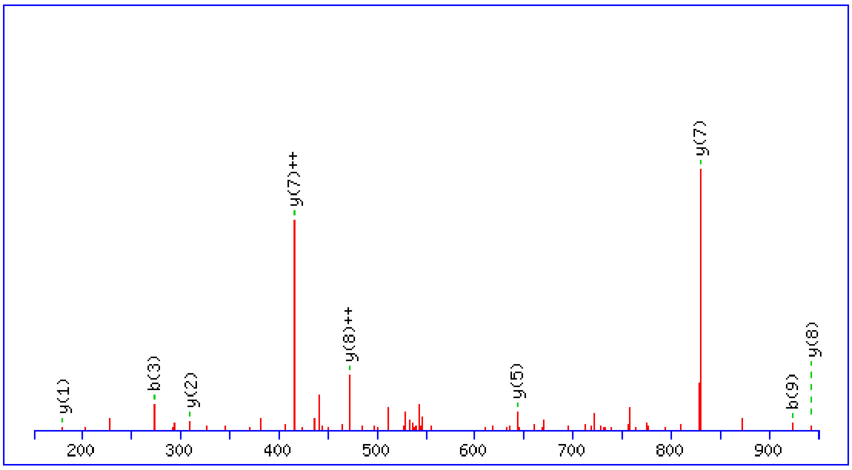
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGLLAACVKR**
Found in **AT5G37530.1** in **TAIR_Arabidopsis**, Symbols: | thiF family protein | chr5:14923735-14926250 FORWARD

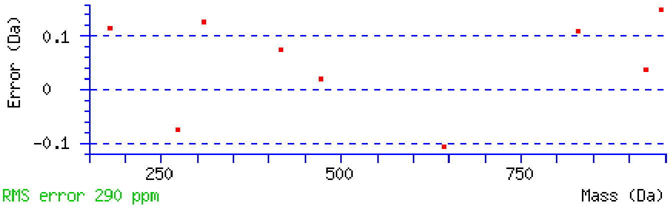
Match to Query 3360: 1100.592732 from(551.303642,2+) index(6598)
Title: Elution from: 58.526 to 58.526 scan no 8526 cid35.00 polarity:+
Data file 0-2_2.mgf

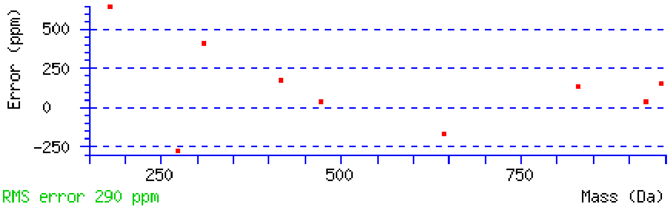
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1100.5934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.012
Matches : 9/56 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	101.0727	51.0400			V					10
2	159.0912	80.0492			G	1001.5353	501.2713	983.5117	492.2595	9
3	**273.1723**	137.0898			L	***943.5168***	472.2620	925.4932	463.2502	8
4	387.2534	194.1303			L	***829.4357***	415.2215	811.4121	406.2097	7
5	459.2876	230.1474			A	715.3546	358.1809	697.3310	349.1691	6
6	531.3217	266.1645			A	***643.3204***	322.1639	625.2969	313.1521	5
7	693.3464	347.1769			C	571.2863	286.1468	553.2627	277.1350	4
8	793.4119	397.2096			V	409.2616	205.1344	391.2380	196.1226	3
9	**923.5009**	462.2541	905.4773	453.2423	K	***309.1961***	155.1017	291.1725	146.0899	2
10					R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of VGLLAACVKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G37530.1

26.1	1100.5934	-0.0007	VGLLAACVKR
2.1	1100.5927	-0.0000	RKIHVFQR

AT5G37770.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISVDELK**
Found in **AT5G37770.1** in **TAIR_Arabidopsis**, Symbols: CML24, TCH2 | TCH2 (TOUCH 2); calcium ion binding | chr5:15016305-15016790 REVERSE

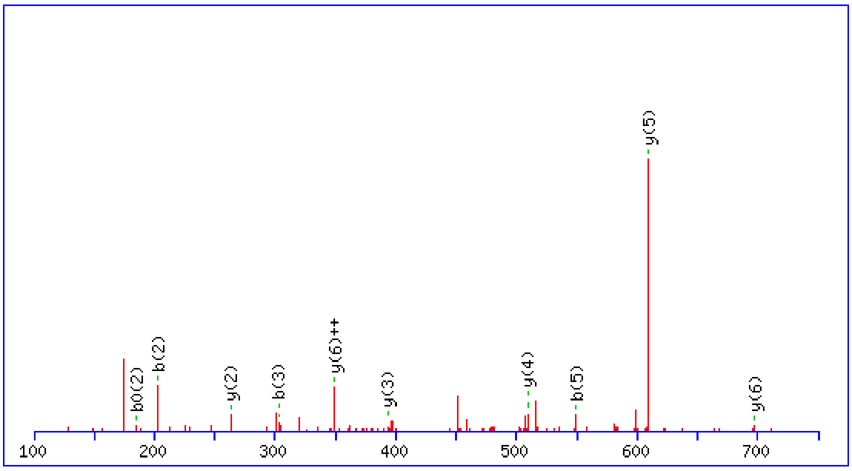
Match to Query 1143: 810.418238 from(406.216395,2+) index(2921)
Title: Elution from: 30.244 to 30.244 scan no 3644 cid35.00 polarity:+
Data file 0-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 750 Da Full range

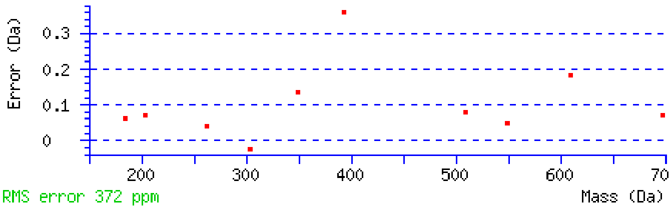
Label all possible matches ○ Label matches used for scoring ●

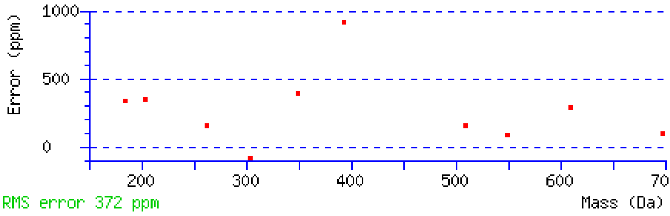
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 810.4199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.012
Matches : 10/54 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							7
2	**203.1174**	102.0624	185.1069	93.0571	S	***697.3461***	349.1767	679.3225	340.1649	679.3355	340.1714	6
3	**303.1829**	152.0951	285.1723	143.0898	V	***609.3170***	305.1622	591.2934	296.1504	591.3065	296.1569	5
4	419.2069	210.1071	401.1963	201.1018	D	***509.2516***	255.1294	491.2280	246.1176	491.2410	246.1241	4
5	**549.2465**	275.1269	531.2359	266.1216	E	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	3
6	663.3276	332.1674	645.3170	323.1622	L	***263.1880***	132.0976	245.1644	123.0858			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ISVDELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.8	810.4199	-0.0017	ISVDELK
15.8	810.4199	-0.0017	SIVDEIK

AT5G37770.1

13.4	810.4199	-0.0017	SIVEDLK
10.4	810.4199	-0.0017	ATELELK
8.0	810.4199	-0.0017	DLEVSLK
4.5	810.4199	-0.0017	LDSIDLK
3.4	810.4199	-0.0017	ISEDLVK
2.4	810.4199	-0.0017	LLSDDIK
1.0	810.4199	-0.0017	VIDSELK
0.7	810.4199	-0.0017	SVLDELK

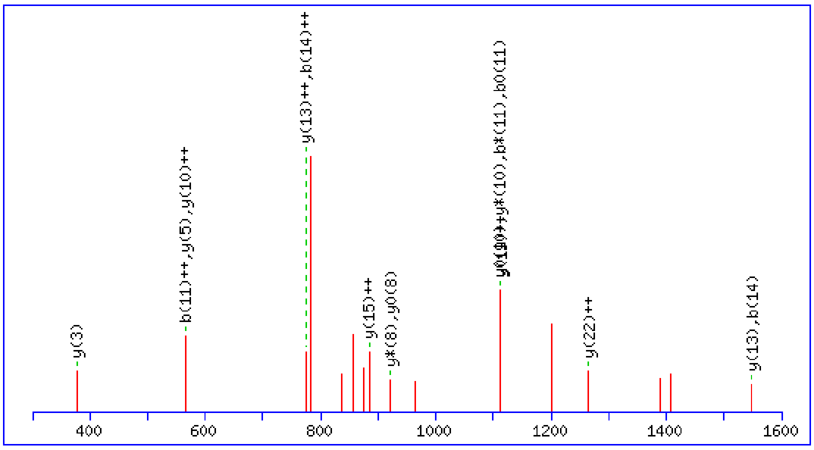
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAAACVINEESRRPGMEEIVSILK**
Found in **AT5G37790.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr5:15025663-15028255 REVERSE

Match to Query 10615: 2675.262111 from(892.761313,3+) index(10684)
Title: Elution from: 104.656 to 104.656 scan no 15424 cid35.00 polarity:+
Data file 0-1_2.mgf

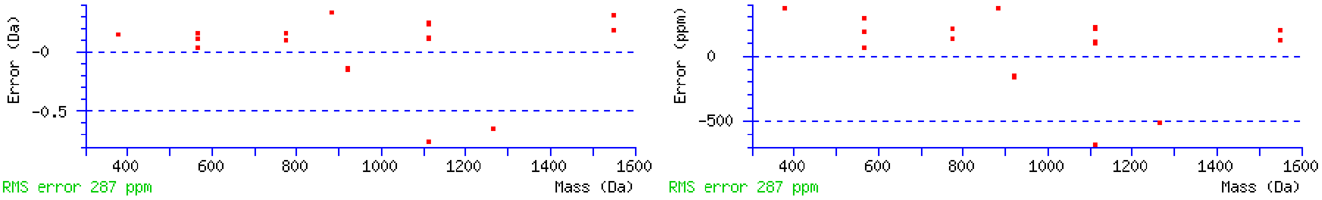
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2675.2542
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.023
Matches : 17/240 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							24
2	145.0756	73.0414					A	2604.2273	1302.6173	2586.2037	1293.6055	2586.2167	1293.6120	23
3	217.1097	109.0585					A	2532.1931	1266.6002	2514.1696	1257.5884	2514.1826	1257.5949	22
4	289.1439	145.0756					A	2460.1590	1230.5831	2442.1354	1221.5713	2442.1484	1221.5779	21
5	451.1686	226.0879					C	2388.1248	1194.5661	2370.1013	1185.5543	2370.1143	1185.5608	20
6	551.2340	276.1207					V	2226.1001	1113.5537	2208.0765	1104.5419	2208.0896	1104.5484	19
7	665.3151	333.1612					I	2126.0347	1063.5210	2108.0111	1054.5092	2108.0241	1054.5157	18
8	781.3521	391.1797	763.3286	382.1679			N	2011.9536	1006.4804	1993.9300	997.4686	1993.9430	997.4751	17
9	911.3918	456.1995	893.3682	447.1877	893.3812	447.1942	E	1895.9166	948.4619	1877.8930	939.4501	1877.9060	939.4566	16
10	1041.4314	521.2193	1023.4078	512.2075	1023.4208	512.2141	E	1765.8770	883.4421	1747.8534	874.4303	1747.8664	874.4368	15
11	1129.4605	**565.2339**	1111.4369	556.2221	1111.4499	556.2286	S	1635.8373	818.4223	1617.8137	809.4105	1617.8268	809.4170	14
12	1289.5497	645.2785	1271.5261	636.2667	1271.5391	636.2732	R	**1547.8083**	774.4078	1529.7847	765.3960	1529.7977	765.4025	13
13	1449.6390	725.3231	1431.6154	716.3113	1431.6284	716.3178	R	1387.7190	694.3631	1369.6954	685.3514	1369.7084	685.3579	12
14	1547.6888	**774.3480**	1529.6652	765.3362	1529.6782	765.3427	P	1227.6298	614.3185	1209.6062	605.3067	1209.6192	605.3132	11
15	1605.7073	803.3573	1587.6837	794.3455	1587.6967	794.3520	G	1129.5800	565.2936	1111.5564	556.2818	1111.5694	556.2883	10
16	1737.7448	869.3760	1719.7212	860.3642	1719.7342	860.3707	M	1071.5615	536.2844	1053.5379	527.2726	1053.5509	527.2791	9
17	1867.7844	934.3958	1849.7608	925.3840	1849.7738	925.3906	E	939.5239	470.2656	921.5004	461.2538	921.5134	461.2603	8
18	1997.8240	999.4157	1979.8004	990.4039	1979.8135	990.4104	E	809.4843	405.2458	791.4607	396.2340	791.4737	396.2405	7
19	2111.9051	1056.4562	2093.8815	1047.4444	2093.8946	1047.4509	I	679.4447	340.2260	661.4211	331.2142	661.4341	331.2207	6
20	2211.9706	1106.4889	2193.9470	1097.4771	2193.9600	1097.4836	V	**565.3636**	283.1854	547.3400	274.1736	547.3530	274.1801	5
21	2299.9996	1150.5035	2281.9761	1141.4917	2281.9891	1141.4982	S	465.2981	233.1527	447.2746	224.1409	447.2876	224.1474	4
22	2414.0807	1207.5440	2396.0572	1198.5322	2396.0702	1198.5387	I	**377.2691**	189.1382	359.2455	180.1264			3
23	2528.1618	1264.5846	2510.1383	1255.5728	2510.1513	1255.5793	L	263.1880	132.0976	245.1644	123.0858			2
24							K	149.1069	75.0571	131.0833	66.0453			1

AT5G37790.1



NCBI **BLAST** search of AAAACVINEESRRPGMEEIVSILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.5	2675.2542	0.0079	AAAACVINEESRRPGMEEIVSILK
11.4	2675.2627	-0.0005	ENKWKQGGWLNQSAQDWLTLIK
3.1	2675.2645	-0.0024	DESEIMNPAILCAVRAGDKVSLLK
0.5	2675.2616	0.0005	FWDNSGFKIVVSMSMLMLVVVSK
0.1	2675.2661	-0.0040	WAELHSGPIKLALMQSPSNHVAEK

Mascot: http://www.matrixscience.com/

AT5G38410.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHGNTPGYYDGR**
Found in **AT5G38410.1** in **TAIR_Arabidopsis**, Symbols: | ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B) | chr5:15394731-15395536 REVERSE

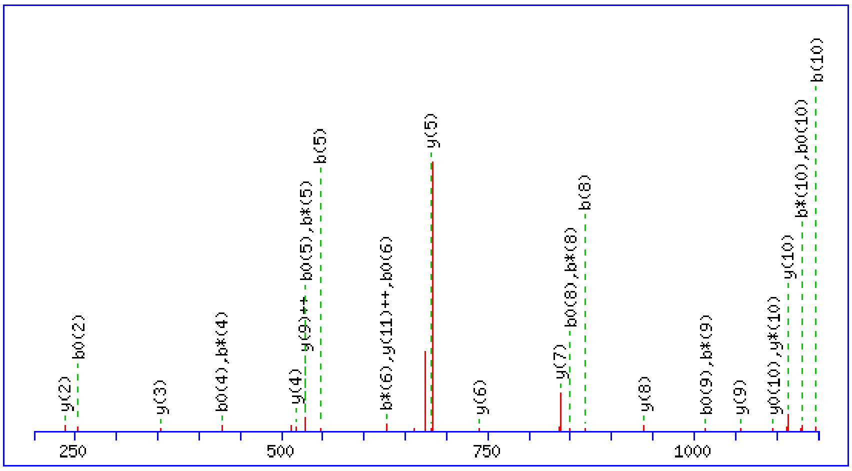
Match to Query 5233: 1382.521124 from(692.267838,2+) index(436)
Title: Elution from: 10.496 to 10.496 scan no 719 cid35.00 polarity:+
Data file D6h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1150 Da Full range

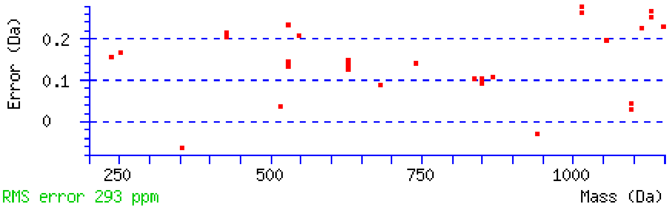
Label all possible matches ○ Label matches used for scoring ●

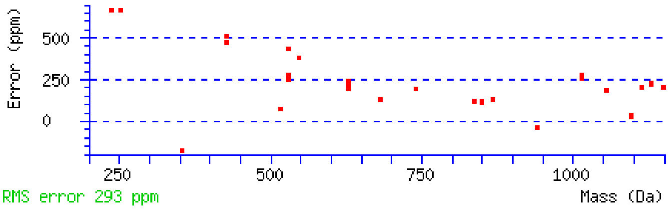
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1382.5211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 1.2e-008
Matches : 29/122 fragment ions using 34 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	131.0469	66.0271			113.0363	57.0218	E							12
2	271.0969	136.0521			253.0864	127.0468	H	1253.4888	627.2480	1235.4652	618.2363	1235.4783	618.2428	11
3	329.1154	165.0613			311.1049	156.0561	G	***1113.4388***	557.2230	1095.4152	548.2112	1095.4282	548.2178	10
4	445.1524	223.0798	427.1288	214.0681	427.1419	214.0746	N	***1055.4203***	528.2138	1037.3967	519.2020	1037.4097	519.2085	9
5	**547.1971**	274.1022	529.1735	265.0904	529.1866	265.0969	T	***939.3833***	470.1953	921.3597	461.1835	921.3727	461.1900	8
6	645.2469	323.1271	627.2233	314.1153	627.2364	314.1218	P	***837.3386***	419.1729	819.3150	410.1611	819.3280	410.1677	7
7	703.2654	352.1364	685.2418	343.1246	685.2549	343.1311	G	***739.2888***	370.1480	721.2652	361.1362	721.2782	361.1428	6
8	**867.3258**	434.1665	849.3022	425.1547	849.3152	425.1613	Y	***681.2703***	341.1388	663.2467	332.1270	663.2597	332.1335	5
9	1031.3862	516.1967	1013.3626	507.1849	1013.3756	507.1914	Y	***517.2099***	259.1086	499.1863	250.0968	499.1994	250.1033	4
10	**1147.4101**	574.2087	1129.3865	565.1969	1129.3996	565.2034	D	***353.1496***	177.0784	335.1260	168.0666	335.1390	168.0731	3
11	1205.4286	603.2180	1187.4050	594.2062	1187.4181	594.2127	G	***237.1256***	119.0664	219.1020	110.0546			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of EHGNTPGYYDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G38410.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
80.0	1382.5211	-0.0000	EHGNTPGYYDGR
0.9	1382.5219	-0.0007	YPGENCIEGDSK

Mascot: http://www.matrixscience.com/

AT5G38420.1

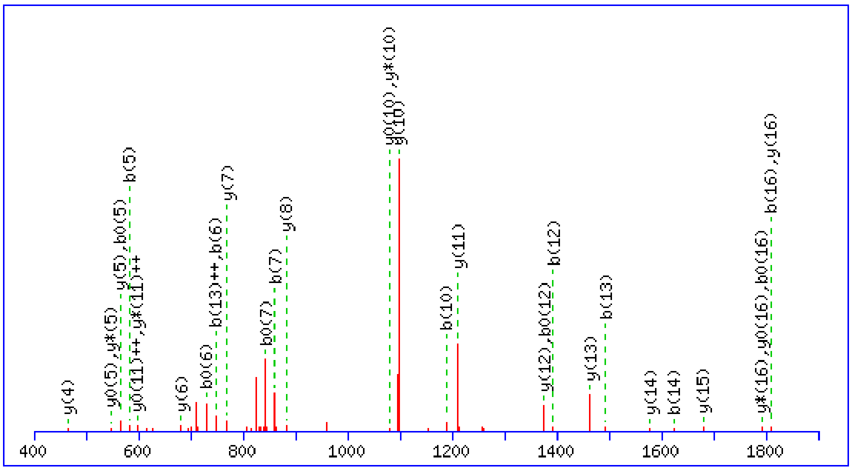
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FETLSYLPDLSDVELAK**
Found in **AT5G38420.1** in **TAIR_Arabidopsis**, Symbols: | ribulose bisphosphate carboxylase small chain 2B / RuBisCO small subunit 2B (RBCS-2B) (ATS2B) | chr5:15398433-15399208 REVERSE

Match to Query 8822: 1956.929528 from(979.472040,2+) index(9878)
Title: Elution from: 96.101 to 96.101 scan no 14170 cid35.00 polarity:+
Data file D1d-2_2.mgf

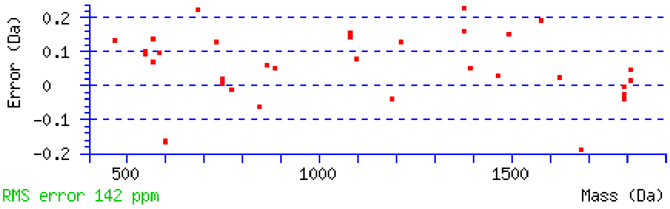
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

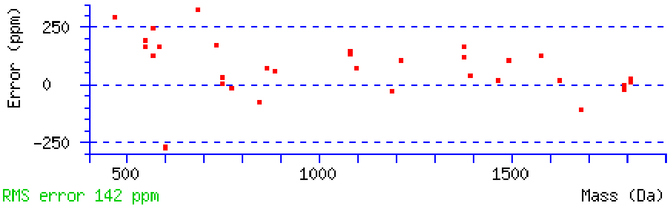


Monoisotopic mass of neutral peptide Mr(calc): 1956.9292
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 110 **Expect:** 8.8e-011
Matches : 34/152 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400			**F**							**17**
2	279.1124	140.0598	261.1018	131.0545	**E**	***1809.8711***	905.4392	1791.8475	896.4274	1791.8605	896.4339	**16**
3	381.1571	191.0822	363.1465	182.0769	**T**	***1679.8315***	840.4194	1661.8079	831.4076	1661.8209	831.4141	**15**
4	495.2382	248.1227	477.2276	239.1174	**L**	***1577.7867***	789.3970	1559.7632	780.3852	1559.7762	780.3917	**14**
5	**583.2672**	292.1373	565.2567	283.1320	**S**	***1463.7056***	732.3565	1445.6821	723.3447	1445.6951	723.3512	**13**
6	**747.3276**	374.1674	729.3170	365.1622	**Y**	***1375.6766***	688.3419	1357.6530	679.3301	1357.6660	679.3366	**12**
7	**861.4087**	431.2080	843.3981	422.2027	**L**	***1211.6162***	606.3117	1193.5926	597.3000	1193.6057	597.3065	**11**
8	959.4585	480.2329	941.4479	471.2276	**P**	***1097.5351***	549.2712	1079.5115	540.2594	1079.5246	540.2659	**10**
9	1075.4825	538.2449	1057.4719	529.2396	**D**	999.4853	500.2463	981.4617	491.2345	981.4748	491.2410	**9**
10	**1189.5636**	595.2854	1171.5530	586.2801	**L**	***883.4613***	442.2343	865.4378	433.2225	865.4508	433.2290	**8**
11	1277.5926	639.3000	1259.5821	630.2947	**S**	***769.3802***	385.1938	751.3567	376.1820	751.3697	376.1885	**7**
12	**1393.6166**	697.3119	1375.6060	688.3067	**D**	***681.3512***	341.1792	663.3276	332.1674	663.3406	332.1739	**6**
13	**1493.6821**	747.3447	1475.6715	738.3394	**V**	***565.3272***	283.1672	547.3036	274.1554	547.3166	274.1620	**5**
14	**1623.7217**	812.3645	1605.7111	803.3592	**E**	***465.2618***	233.1345	447.2382	224.1227	447.2512	224.1292	**4**
15	1737.8028	869.4050	1719.7922	860.3997	**L**	335.2221	168.1147	317.1985	159.1029			**3**
16	**1809.8369**	905.4221	1791.8264	896.4168	**A**	221.1410	111.0741	203.1174	102.0624			**2**
17					**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT5G38420.1





NCBI **BLAST** search of FETLSYLPDLSDVELAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
110.3	1956.9292	0.0003	FETLSYLPDLSDVELAK
21.6	1956.9332	-0.0037	MKIAVGAARGIEYLHCK
16.7	1956.9346	-0.0050	GSQWFEVNRDLAATIVK
13.6	1956.9299	-0.0003	GFRPMNLEWEAIRGIK
12.3	1956.9272	0.0023	HGLMSGYLNKFVEALEK
8.5	1956.9276	0.0019	RGGGFNKICQLSPQLEK
6.1	1956.9245	0.0050	FNAFEMVEELGLAVEIK
5.3	1956.9353	-0.0058	SSLTEPTDRPLIVYSMK
4.5	1956.9353	-0.0058	IYDASVLGEPMAVGKDKK
1.6	1956.9346	-0.0051	EVPAYFTHRASGGSLTIK

Mascot: http://www.matrixscience.com/

AT5G38430.1

Mascot Search Results

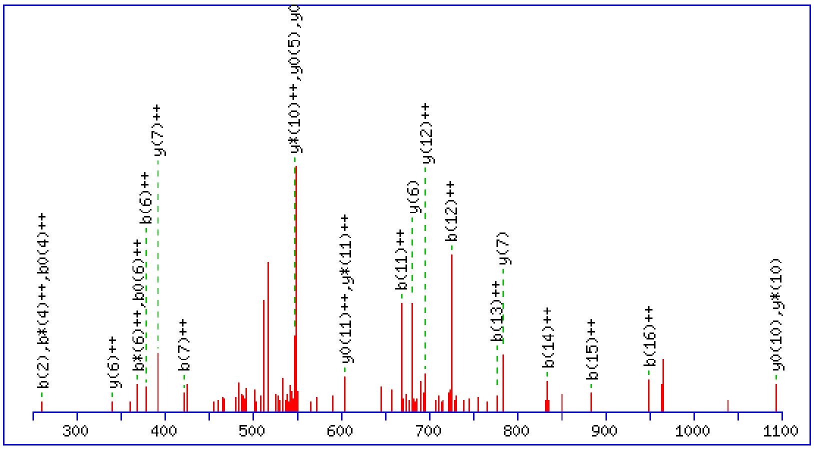
Peptide View

MS/MS Fragmentation of **KKFETLSYLPDLTDVELAK**
Found in **AT5G38430.1** in **TAIR_Arabidopsis**, Symbols: | ribulose bisphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B) | chr5:15401580-15402385 REVERSE

Match to Query 10024: 2231.120676 from(558.787445,4+) index(8768)
Title: Elution from: 77.386 to 77.386 scan no 11622 cid35.00 polarity:+
Data file C7-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

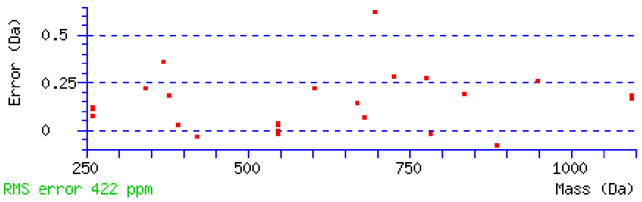
Or, Plot from 250 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

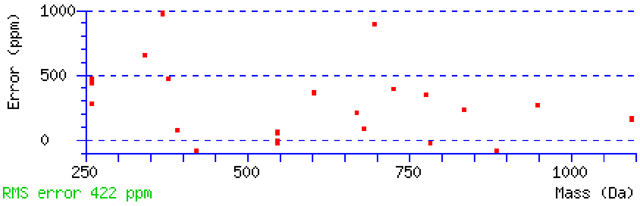


`Monoisotopic mass of neutral peptide Mr(calc):` 2231.1230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.011
Matches : 26/204 fragment ions using 35 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	131.0963	66.0518	113.0727	57.0400			K							19
2	261.1853	131.0963	243.1618	122.0845			K	2102.0412	1051.5242	2084.0176	1042.5125	2084.0306	1042.5190	18
3	409.2508	205.1290	391.2272	196.1172			F	1971.9522	986.4797	1953.9286	977.4679	1953.9416	977.4744	17
4	539.2904	270.1488	521.2668	261.1371	521.2799	261.1436	E	1823.8867	912.4470	1805.8631	903.4352	1805.8762	903.4417	16
5	641.3351	321.1712	623.3115	312.1594	623.3246	312.1659	T	1693.8471	847.4272	1675.8235	838.4154	1675.8365	838.4219	15
6	755.4162	***378.2118***	737.3926	369.2000	737.4057	369.2065	L	1591.8024	796.4048	1573.7788	787.3930	1573.7918	787.3996	14
7	843.4453	***422.2263***	825.4217	413.2145	825.4347	413.2210	S	1477.7213	739.3643	1459.6977	730.3525	1459.7107	730.3590	13
8	1007.5057	504.2565	989.4821	495.2447	989.4951	495.2512	Y	1389.6922	695.3498	1371.6686	686.3380	1371.6817	686.3445	12
9	1121.5868	561.2970	1103.5632	552.2852	1103.5762	552.2917	L	1225.6319	613.3196	1207.6083	604.3078	1207.6213	604.3143	11
10	1219.6366	610.3219	1201.6130	601.3101	1201.6260	601.3166	P	1111.5508	556.2790	1093.5272	547.2672	1093.5402	547.2737	10
11	1335.6605	***668.3339***	1317.6369	659.3221	1317.6500	659.3286	D	1013.5010	507.2541	995.4774	498.2423	995.4904	498.2488	9
12	1449.7416	***725.3745***	1431.7180	716.3627	1431.7311	716.3692	L	897.4770	449.2421	879.4534	440.2303	879.4664	440.2369	8
13	1551.7863	***776.3968***	1533.7628	767.3850	1533.7758	767.3915	T	783.3959	392.2016	765.3723	383.1898	765.3853	383.1963	7
14	1667.8103	***834.4088***	1649.7867	825.3970	1649.7998	825.4035	D	681.3512	341.1792	663.3276	332.1674	663.3406	332.1739	6
15	1767.8758	***884.4415***	1749.8522	875.4297	1749.8652	875.4362	V	565.3272	283.1672	547.3036	274.1554	547.3166	274.1620	5
16	1897.9154	***949.4613***	1879.8918	940.4495	1879.9048	940.4561	E	465.2618	233.1345	447.2382	224.1227	447.2512	224.1292	4
17	2011.9965	1006.5019	1993.9729	997.4901	1993.9859	997.4966	L	335.2221	168.1147	317.1985	159.1029			3
18	2084.0306	1042.5190	2066.0071	1033.5072	2066.0201	1033.5137	A	221.1410	111.0741	203.1174	102.0624			2
19							K	149.1069	75.0571	131.0833	66.0453			1

AT5G38430.1





NCBI **BLAST** search of KKFETLSYLPDLTDVELAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	2231.1230	-0.0023	KKFETLSYLPDLTDVELAK
0.1	2231.1160	0.0047	IQLKYLAEEMQAISKGLEK

Mascot: http://www.matrixscience.com/

AT5G38480.1

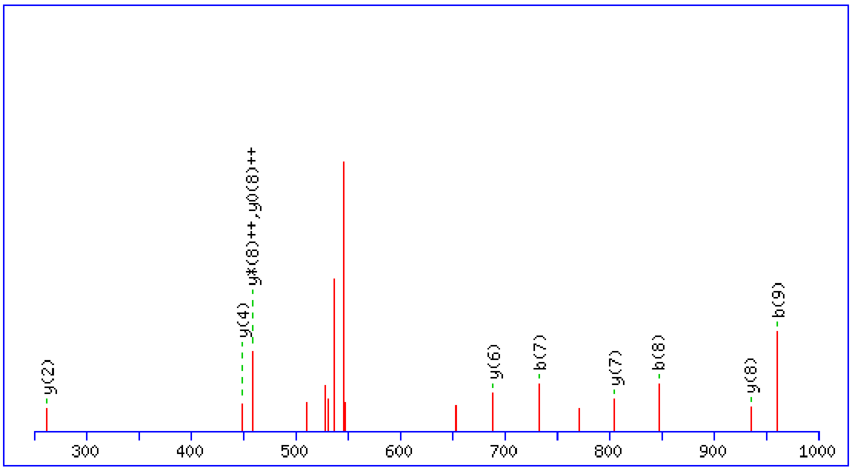
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNEDHVAIIK**
Found in **AT5G38480.1** in **TAIR_Arabidopsis**, Symbols: RCI1, GRF3 | GRF3 (GENERAL REGULATORY FACTOR 3); protein phosphorylated amino acid binding | chr5:15427507-15428515 FORWARD

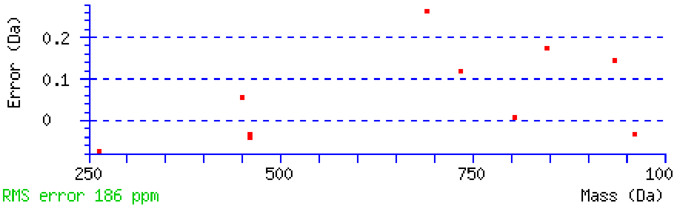
Match to Query 3434: 1108.532236 from(555.273394,2+) index(1073)
Title: Elution from: 18.136 to 18.136 scan no 1584 cid35.00 polarity:+
Data file 0-3_1.mgf

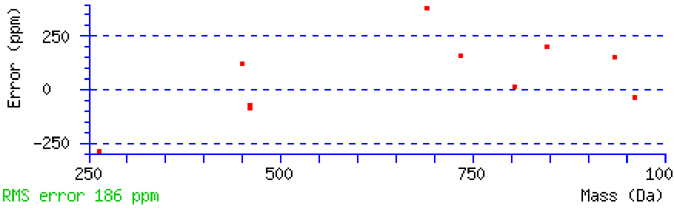
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [250] to [1000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1108.5305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 6.6e-005
Matches : 10/90 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							10
2	175.0628	88.0350	157.0392	79.0232			N	1051.5193	526.2633	1033.4957	517.2515	1033.5087	517.2580	9
3	305.1024	153.0548	287.0788	144.0430	287.0918	144.0496	E	***935.4823***	468.2448	917.4587	459.2330	917.4717	459.2395	8
4	421.1264	211.0668	403.1028	202.0550	403.1158	202.0615	D	***805.4427***	403.2250	787.4191	394.2132	787.4321	394.2197	7
5	561.1764	281.0918	543.1528	272.0800	543.1658	272.0866	H	***689.4187***	345.2130	671.3951	336.2012			6
6	661.2418	331.1246	643.2183	322.1128	643.2313	322.1193	V	549.3687	275.1880	531.3451	266.1762			5
7	***733.2760***	367.1416	715.2524	358.1298	715.2654	358.1364	A	***449.3032***	225.1552	431.2796	216.1435			4
8	***847.3571***	424.1822	829.3335	415.1704	829.3465	415.1769	I	377.2691	189.1382	359.2455	180.1264			3
9	***961.4382***	481.2227	943.4146	472.2109	943.4276	472.2175	I	***263.1880***	132.0976	245.1644	123.0858			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GNEDHVAIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G38480.1

Score	Mr(calc)	Delta	Sequence
51.0	1108.5305	0.0017	GNEDHVAIIK
15.8	1108.5332	-0.0009	SGDRFNRLK
13.7	1108.5305	0.0017	EHNDVQILK
13.7	1108.5301	0.0022	GLDYYDILK
11.3	1108.5339	-0.0017	MISSSSRSLK
9.9	1108.5305	0.0017	NSVSERYIK
9.4	1108.5305	0.0017	FESRTQSLK
5.9	1108.5332	-0.0009	DSGRLFRNK
5.1	1108.5332	-0.0009	SDGVFRQRK
4.1	1108.5354	-0.0032	AHFNLHNLK

AT5G39130.1

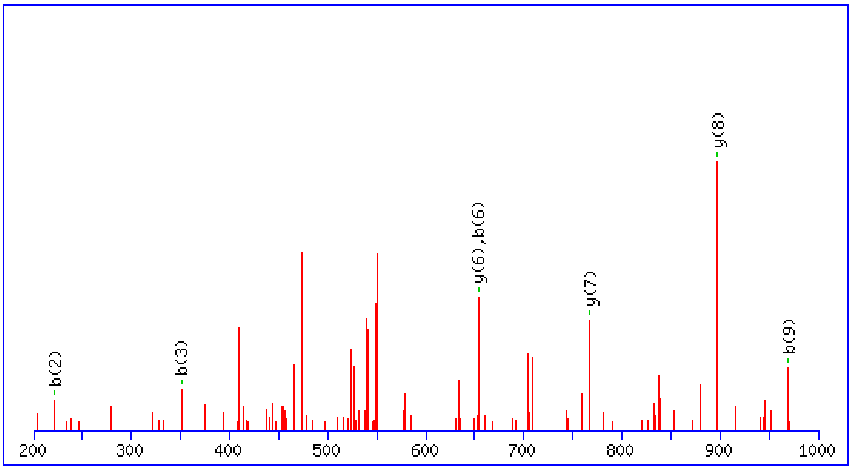
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFQLDANVVK**
Found in **AT5G39130.1** in **TAIR_Arabidopsis**, Symbols: | germin-like protein, putative | chr5:15682866-15683641 REVERSE

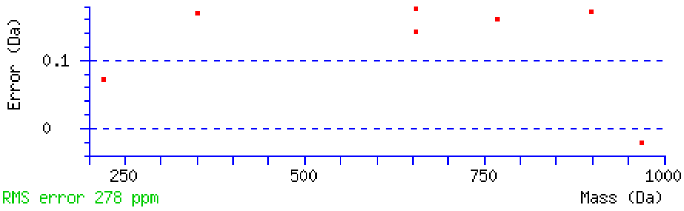
Match to Query 3532: 1116.556746 from(559.285649,2+) index(3192)
Title: Elution from: 33.204 to 33.204 scan no 4037 cid35.00 polarity:+
Data file D6h-2_1.mgf

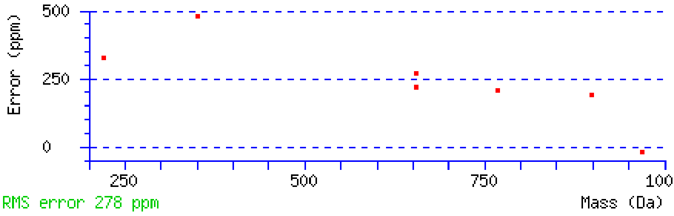
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5589
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.013
Matches : 7/86 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							10
2	***221.1069***	111.0571					F	1045.5321	523.2697	1027.5085	514.2579	1027.5215	514.2644	9
3	***351.1595***	176.0834	333.1359	167.0716			Q	**897.4666**	449.2370	879.4431	440.2252	879.4561	440.2317	8
4	465.2406	233.1239	447.2170	224.1122			L	**767.4140**	384.2106	749.3904	375.1988	749.4034	375.2054	7
5	581.2646	291.1359	563.2410	282.1241	563.2540	282.1307	D	**653.3329**	327.1701	635.3093	318.1583	635.3223	318.1648	6
6	***653.2987***	327.1530	635.2752	318.1412	635.2882	318.1477	A	537.3089	269.1581	519.2853	260.1463			5
7	769.3357	385.1715	751.3122	376.1597	751.3252	376.1662	N	465.2748	233.1410	447.2512	224.1292			4
8	869.4012	435.2042	851.3776	426.1924	851.3906	426.1990	V	349.2378	175.1225	331.2142	166.1107			3
9	***969.4666***	485.2370	951.4431	476.2252	951.4561	476.2317	V	249.1723	125.0898	231.1487	116.0780			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AFQLDANVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G39130.1

29.6	1116.5589	-0.0022	AFQLDANVVK
10.1	1116.5542	0.0025	FLSLTMVHR
9.8	1116.5567	0.0000	GLSKDEKAQK
8.0	1116.5590	-0.0022	HTTFASLLSK
5.4	1116.5542	0.0025	LSLMWGKPR
4.6	1116.5590	-0.0022	FSPEKLLDR
3.1	1116.5594	-0.0026	LREEARAQK
3.0	1116.5567	0.0000	TEKNDLKAGK
2.3	1116.5567	0.0000	SDEVIRKEK
2.3	1116.5567	0.0000	SAVTVNSNLAK

AT5G39210.1

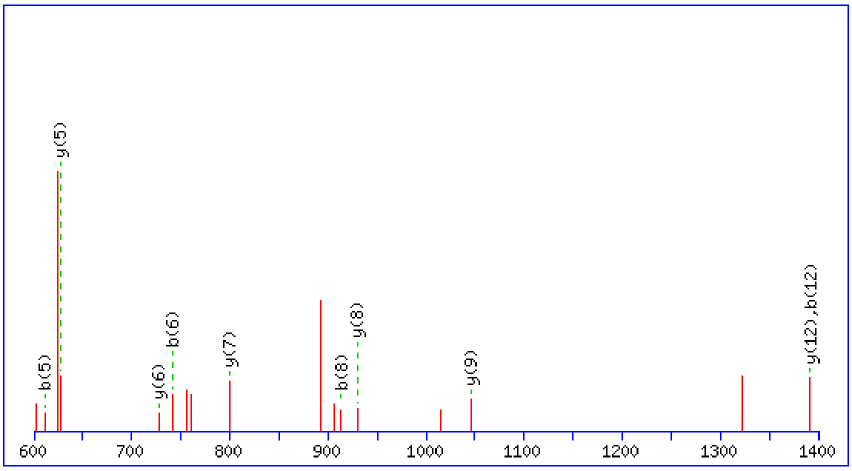
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDDLDEAVDFLVK**
Found in **AT5G39210.1** in **TAIR_Arabidopsis**, Symbols: CRR7 | CRR7 (CHLORORESPIRATORY REDUCTION 7) | chr5:15720459-15721227 FORWARD

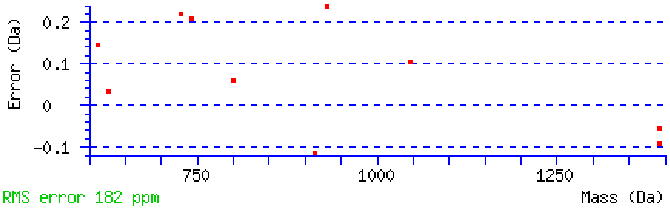
Match to Query 6748: 1538.695222 from(770.354887,2+) index(10619)
Title: Elution from: 100.935 to 100.935 scan no 15070 cid35.00 polarity:+
Data file C7-2_2.mgf

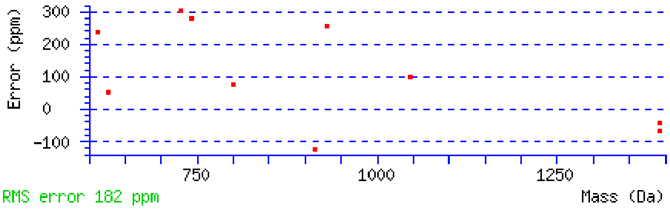
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1538.6932
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0071
Matches : 10/110 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400			F							13
2	265.0967	133.0520	247.0861	124.0467	D	***1391.6351***	696.3212	1373.6115	687.3094	1373.6245	687.3159	12
3	381.1207	191.0640	363.1101	182.0587	D	1275.6111	638.3092	1257.5875	629.2974	1257.6006	629.3039	11
4	495.2018	248.1045	477.1912	239.0992	L	1159.5872	580.2972	1141.5636	571.2854	1141.5766	571.2919	10
5	**611.2258**	306.1165	593.2152	297.1112	D	***1045.5061***	523.2567	1027.4825	514.2449	1027.4955	514.2514	9
6	**741.2654**	371.1363	723.2548	362.1310	E	***929.4821***	465.2447	911.4585	456.2329	911.4715	456.2394	8
7	813.2995	407.1534	795.2890	398.1481	A	***799.4424***	400.2249	781.4189	391.2131	781.4319	391.2196	7
8	**913.3650**	457.1861	895.3544	448.1808	V	***727.4083***	364.2078	709.3847	355.1960	709.3977	355.2025	6
9	1029.3890	515.1981	1011.3784	506.1928	D	***627.3428***	314.1751	609.3193	305.1633	609.3323	305.1698	5
10	1177.4544	589.2308	1159.4438	580.2256	F	511.3189	256.1631	493.2953	247.1513			4
11	1291.5355	646.2714	1273.5249	637.2661	L	363.2534	182.1303	345.2298	173.1186			3
12	**1391.6010**	696.3041	1373.5904	687.2988	V	249.1723	125.0898	231.1487	116.0780			2
13					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FDDLDEAVDFLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G39210.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	1538.6932	0.0020	FDDLDEAVDFLVK
14.0	1538.6937	0.0015	KVKDFEDGDNNIK
3.9	1538.6998	-0.0045	MNVDELRREAAAK
3.8	1538.6993	-0.0041	DTVSWNSMLGGLVK
3.0	1538.6979	-0.0027	LMDMLMDREVIR
1.6	1538.6937	0.0015	ALEGNYEEKAAAQK
1.5	1538.6915	0.0038	DSGSEQSKSVGNVVK
1.1	1538.6993	-0.0041	FDNDVSLEIIAMR
0.3	1538.6993	-0.0041	SDCLAKAEGTFVPK
0.1	1538.6968	-0.0016	KNAGKDGGNGRPSTR

Mascot: http://www.matrixscience.com/

AT5G39380.1

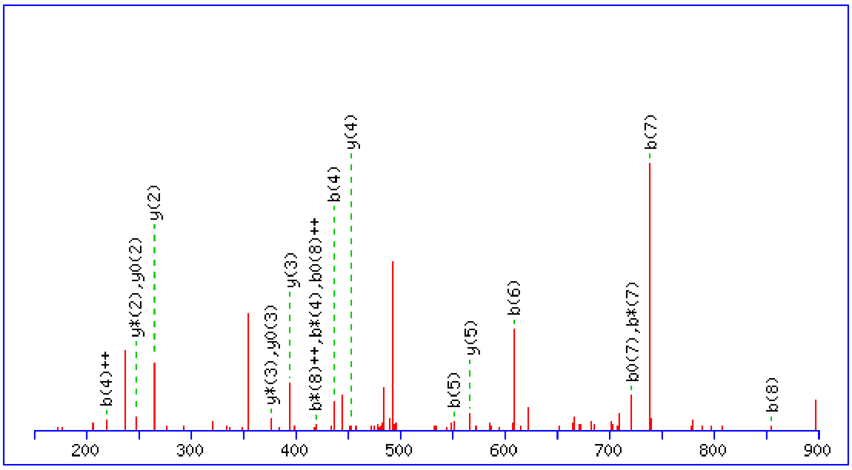
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RGRGLGEDK**
Found in **AT5G39380.1** in **TAIR_Arabidopsis**, Symbols: | calmodulin-binding protein-related | chr5:15776391-15777914 REVERSE

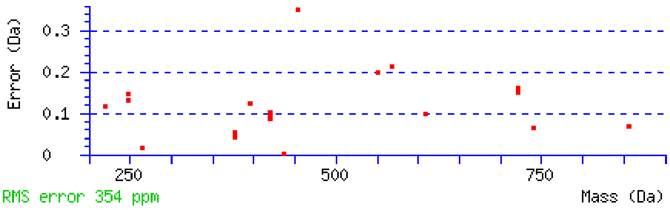
Match to Query 2468: 1002.480164 from(502.247358,2+) index(5186)
Title: Elution from: 47.360 to 47.360 scan no 6587 cid35.00 polarity:+
Data file 0-1_2.mgf

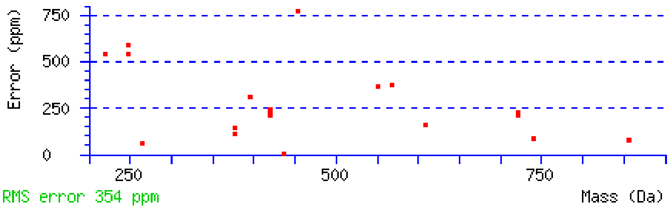
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1002.4783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27  Expect: 0.028
Matches : 20/82 fragment ions using 43 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	161.0965	81.0519	143.0729	72.0401			R							9
2	***219.1150***	110.0612	201.0914	101.0494			G	843.3963	422.2018	825.3727	413.1900	825.3858	413.1965	8
3	379.2043	190.1058	361.1807	181.0940			R	785.3778	393.1926	767.3542	384.1808	767.3673	384.1873	7
4	***437.2228***	219.1150	419.1992	210.1032			G	625.2886	313.1479	607.2650	304.1361	607.2780	304.1426	6
5	***551.3039***	276.1556	533.2803	267.1438			L	**567.2701**	284.1387	549.2465	275.1269	549.2595	275.1334	5
6	***609.3224***	305.1648	591.2988	296.1530			G	**453.1890**	227.0981	435.1654	218.0863	435.1784	218.0928	4
7	***739.3620***	370.1846	721.3384	361.1728	721.3514	361.1794	E	**395.1705**	198.0889	377.1469	189.0771	377.1599	189.0836	3
8	***855.3860***	428.1966	837.3624	419.1848	837.3754	419.1913	D	**265.1309**	133.0691	247.1073	124.0573	247.1203	124.0638	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RGRGLGEDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.7	1002.4783	0.0019	RGRGLGEDK

AT5G39380.1

21.1	1002.4778	0.0023	FQNLGDIGK
20.4	1002.4812	-0.0011	KDIMGVSNK
19.6	1002.4812	-0.0011	DMKNILNK
11.6	1002.4778	0.0023	DFKGQTPAK
9.5	1002.4812	-0.0011	LEVKGGMGGK
9.0	1002.4778	0.0023	VIQFQDNK
7.5	1002.4812	-0.0011	VALGMASTGGK
7.4	1002.4778	0.0023	LLFDDVNR
5.9	1002.4812	-0.0011	TVMSKSPNK

AT5G39650.1

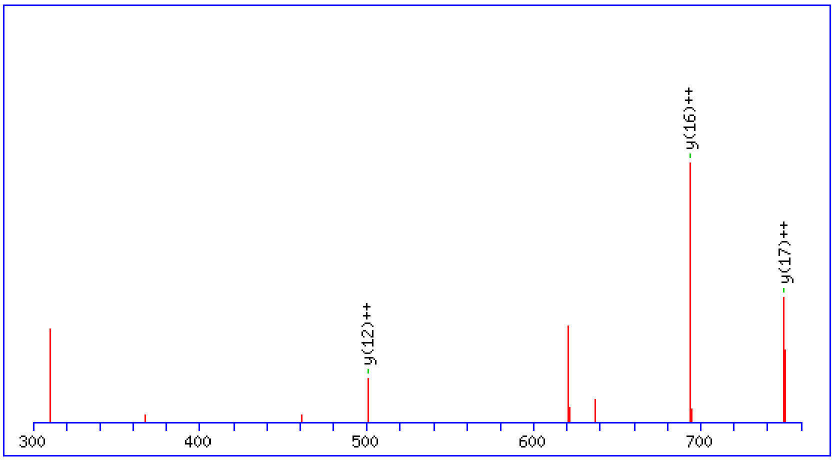
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPKPVLISSLPSLPSGAAAGGGR**
Found in **AT5G39650.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G09157.1); similar to 52O08_3 [Brassica rapa subsp. pekinensis] (GB:AAZ67548.1); contains InterPro domain Protein of unknown function DUF679 (InterPro:IPR007770) | chr5:15892493

Match to Query 9729: 2118.174432 from(530.550884,4+) index(10323)
Title: Elution from: 96.583 to 96.583 scan no 14595 cid35.00 polarity:+
Data file C7-1_2.mgf

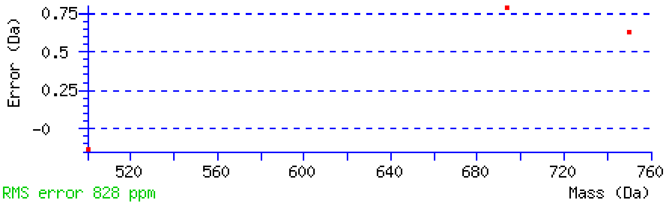
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 760 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

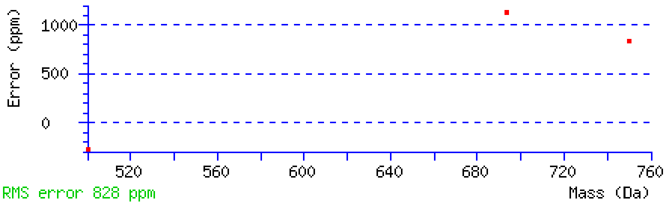


Monoisotopic mass of neutral peptide Mr(calc): 2118.1797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.021
Matches : 3/244 fragment ions using 4 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							23
2	185.0921	93.0497			167.0815	84.0444	P	2032.1550	1016.5811	2015.1284	1008.0678	2014.1444	1007.5758	22
3	313.1870	157.0972	296.1605	148.5839	295.1765	148.0919	K	1935.1022	968.0547	1918.0756	959.5415	1917.0916	959.0494	21
4	410.2398	205.6235	393.2132	197.1103	392.2292	196.6183	P	1807.0072	904.0072	1789.9807	895.4940	1788.9967	895.0020	20
5	509.3082	255.1577	492.2817	246.6445	491.2976	246.1525	V	1709.9545	855.4809	1692.9279	846.9676	1691.9439	846.4756	19
6	622.3923	311.6998	605.3657	303.1865	604.3817	302.6945	L	1610.8860	805.9467	1593.8595	797.4334	1592.8755	796.9414	18
7	735.4763	368.2418	718.4498	359.7285	717.4658	359.2365	I	1497.8020	749.4046	1480.7754	740.8914	1479.7914	740.3993	17
8	822.5084	411.7578	805.4818	403.2445	804.4978	402.7525	S	1384.7179	692.8626	1367.6914	684.3493	1366.7074	683.8573	16
9	909.5404	455.2738	892.5138	446.7606	891.5298	446.2686	S	1297.6859	649.3466	1280.6593	640.8333	1279.6753	640.3413	15
10	1022.6245	511.8159	1005.5979	503.3026	1004.6139	502.8106	L	1210.6539	605.8306	1193.6273	597.3173	1192.6433	596.8253	14
11	1119.6772	560.3422	1102.6507	551.8290	1101.6667	551.3370	P	1097.5698	549.2885	1080.5432	540.7753	1079.5592	540.2833	13
12	1206.7092	603.8583	1189.6827	595.3450	1188.6987	594.8530	S	1000.5170	500.7622	983.4905	492.2489	982.5065	491.7569	12
13	1319.7933	660.4003	1302.7668	651.8870	1301.7827	651.3950	L	913.4850	457.2461	896.4585	448.7329	895.4744	448.2409	11
14	1416.8461	708.9267	1399.8195	700.4134	1398.8355	699.9214	P	800.4009	400.7041	783.3744	392.1908	782.3904	391.6988	10
15	1503.8781	752.4427	1486.8516	743.9294	1485.8675	743.4374	S	703.3482	352.1777	686.3216	343.6645	685.3376	343.1724	9
16	1560.8996	780.9534	1543.8730	772.4401	1542.8890	771.9481	G	616.3161	308.6617	599.2896	300.1484			8
17	1631.9367	816.4720	1614.9101	807.9587	1613.9261	807.4667	A	559.2947	280.1510	542.2681	271.6377			7
18	1702.9738	851.9905	1685.9472	843.4773	1684.9632	842.9853	A	488.2576	244.6324	471.2310	236.1191			6
19	1774.0109	887.5091	1756.9844	878.9958	1756.0003	878.5038	A	417.2205	209.1139	400.1939	200.6006			5
20	1831.0324	916.0198	1814.0058	907.5066	1813.0218	907.0145	G	346.1833	173.5953	329.1568	165.0820			4
21	1888.0538	944.5306	1871.0273	936.0173	1870.0433	935.5253	G	289.1619	145.0846	272.1353	136.5713			3
22	1945.0753	973.0413	1928.0488	964.5280	1927.0647	964.0360	G	232.1404	116.5738	215.1139	108.0606			2

23							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SPKPVLISSLPSLPSGAAAGGGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.2	2118.1797	-0.0053	SPKPVLISSLPSLPSGAAAGGGR
6.3	2118.1698	0.0046	FFKRNGGLLLQQQLNTNK
2.7	2118.1806	-0.0061	VLREGLMLIVQCRQFLK

Mascot: http://www.matrixscience.com/

AT5G39730.1

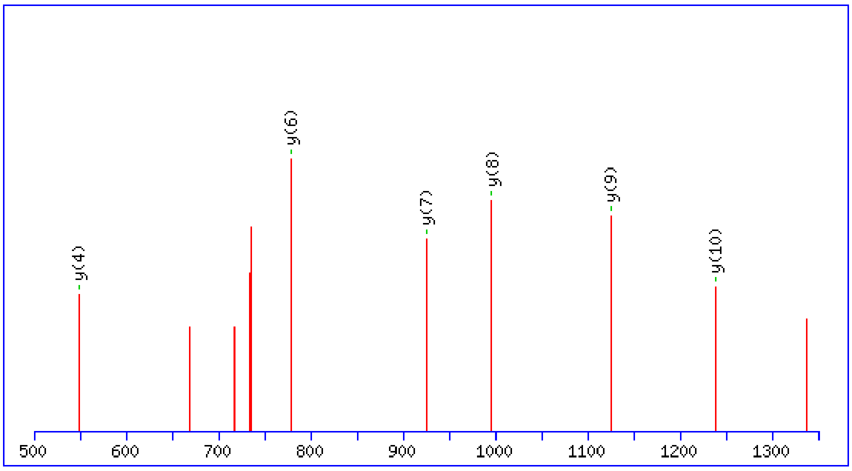
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFIEAFTEIMER**
Found in **AT5G39730.1** in **TAIR_Arabidopsis**, Symbols: | avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related | chr5:15918968-15919852 FORWARD

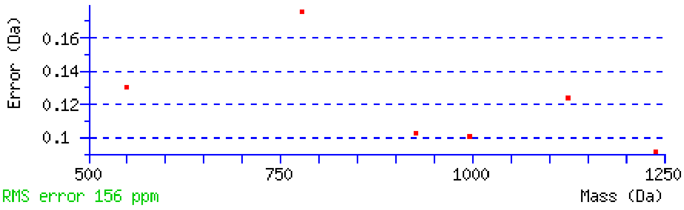
Match to Query 6078: 1485.714844 from(743.864698,2+) index(10526)
Title: Elution from: 105.057 to 105.057 scan no 15357 cid35.00 polarity:+
Data file D6h-1_3.mgf

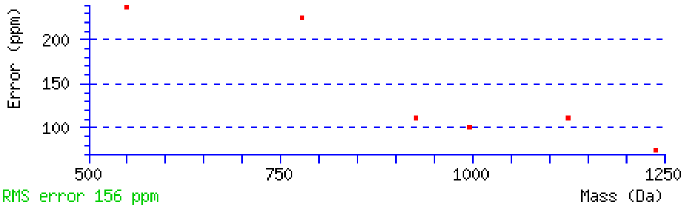
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1485.7173
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 1e-005
Matches : 6/108 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							12
2	249.1234	125.0653	231.1128	116.0600	F	1385.6770	693.3421	1368.6504	684.8288	1367.6664	684.3368	11
3	362.2074	181.6074	344.1969	172.6021	I	***1238.6086***	619.8079	1221.5820	611.2946	1220.5980	610.8026	10
4	491.2500	246.1287	473.2395	237.1234	E	***1125.5245***	563.2659	1108.4979	554.7526	1107.5139	554.2606	9
5	562.2871	281.6472	544.2766	272.6419	A	***996.4819***	498.7446	979.4553	490.2313	978.4713	489.7393	8
6	709.3556	355.1814	691.3450	346.1761	F	***925.4448***	463.2260	908.4182	454.7128	907.4342	454.2207	7
7	810.4032	405.7053	792.3927	396.7000	T	***778.3764***	389.6918	761.3498	381.1785	760.3658	380.6865	6
8	939.4458	470.2266	921.4353	461.2213	E	677.3287	339.1680	660.3021	330.6547	659.3181	330.1627	5
9	1052.5299	526.7686	1034.5193	517.7633	I	***548.2861***	274.6467	531.2595	266.1334	530.2755	265.6414	4
10	1183.5704	592.2888	1165.5598	583.2835	M	435.2020	218.1047	418.1755	209.5914	417.1915	209.0994	3
11	1312.6130	656.8101	1294.6024	647.8048	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TFIEAFTEIMER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G39730.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.6	1485.7173	-0.0025	TFIEAFTEIMER

Mascot: http://www.matrixscience.com/

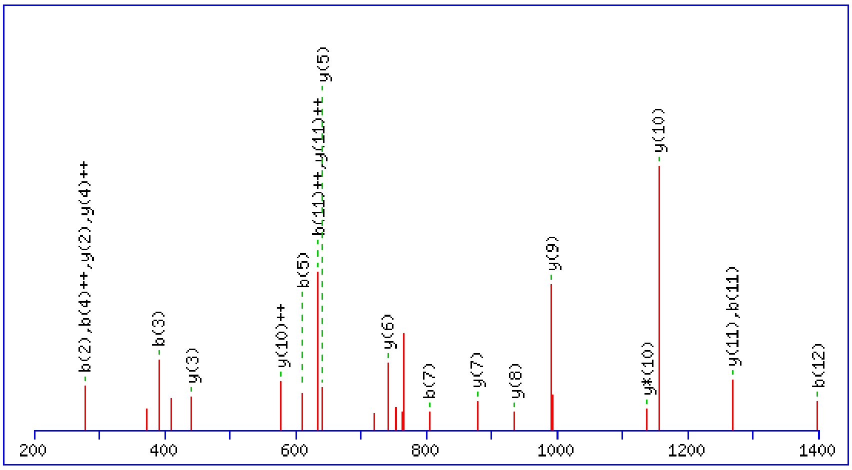
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NYIYGGHVSNYMK**
Found in **AT5G39740.1** in **TAIR_Arabidopsis**, Symbols: | 60S ribosomal protein L5 (RPL5B) | chr5:15920593-15922413 FORWARD

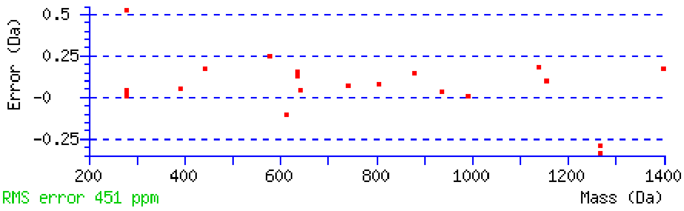
Match to Query 6285: 1544.707368 from(773.360960,2+) index(3105)
Title: Elution from: 33.517 to 33.517 scan no 3961 cid35.00 polarity:+
Data file D12h-2_2.mgf

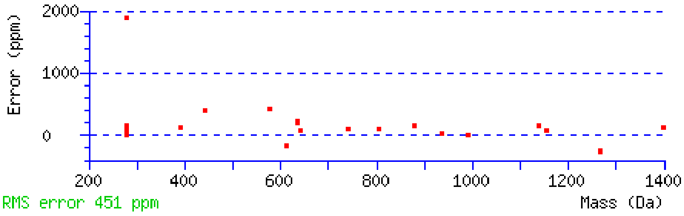
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1544.7082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 2.4e-008
Matches : 21/120 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	**278.1135**	139.5604	261.0870	131.0471			Y	1431.6725	716.3399	1414.6460	707.8266	1413.6620	707.3346	12
3	**391.1976**	196.1024	374.1710	187.5892			I	***1268.6092***	634.8082	1251.5827	626.2950	1250.5987	625.8030	11
4	554.2609	**277.6341**	537.2344	269.1208			Y	***1155.5252***	578.2662	1138.4986	569.7529	1137.5146	569.2609	10
5	**611.2824**	306.1448	594.2558	297.6316			G	***992.4618***	496.7346	975.4353	488.2213	974.4513	487.7293	9
6	668.3039	334.6556	651.2773	326.1423			G	***935.4404***	468.2238	918.4138	459.7105	917.4298	459.2185	8
7	**805.3628**	403.1850	788.3362	394.6717			H	***878.4189***	439.7131	861.3923	431.1998	860.4083	430.7078	7
8	904.4312	452.7192	887.4046	444.2060			V	***741.3600***	371.1836	724.3334	362.6704	723.3494	362.1783	6
9	991.4632	496.2352	974.4367	487.7220	973.4526	487.2300	S	***642.2916***	321.6494	625.2650	313.1362	624.2810	312.6441	5
10	1105.5061	553.2567	1088.4796	544.7434	1087.4956	544.2514	N	555.2595	278.1334	538.2330	269.6201			4
11	**1268.5695**	**634.7884**	1251.5429	626.2751	1250.5589	625.7831	Y	***441.2166***	221.1119	424.1901	212.5987			3
12	**1399.6099**	700.3086	1382.5834	691.7953	1381.5994	691.3033	M	***278.1533***	139.5803	261.1267	131.0670			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NYIYGGHVSNYMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G39740.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.8	1544.7082	-0.0008	NYIYGGHVSNYMK
10.9	1544.7075	-0.0002	CTEHNVALADLMR
6.5	1544.7050	0.0023	MMQRNCFGFNLK
6.4	1544.7107	-0.0033	DFRDTYKTEQDK
1.7	1544.7107	-0.0033	FLSYSRSGQEDEK

AT5G39960.1

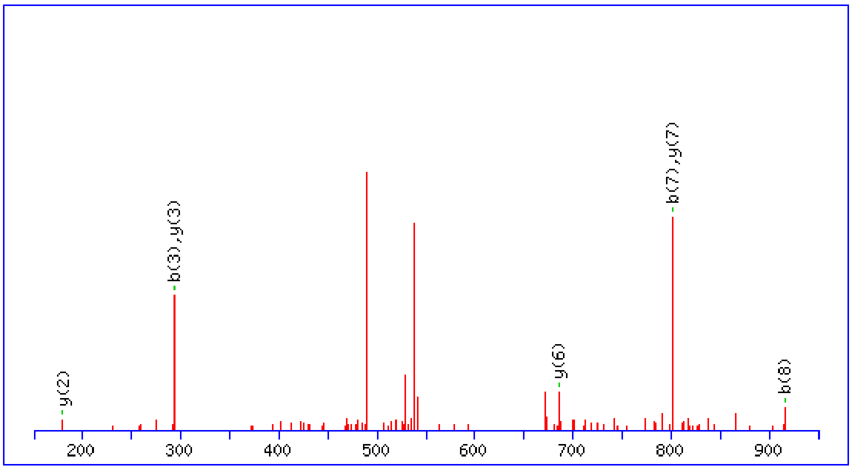
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTSDKRTLSA**
Found in **AT5G39960.1** in **TAIR_Arabidopsis**, Symbols: | GTP-binding family protein | chr5:16011423-16014048 FORWARD

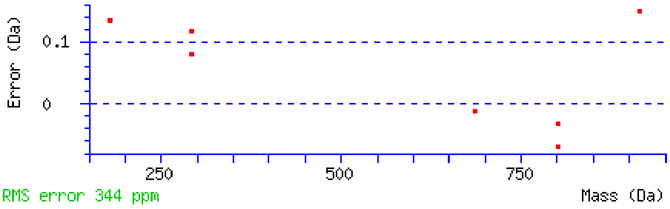
Match to Query 3198: 1092.517432 from(547.265992,2+) index(2509)
Title: Elution from: 26.384 to 26.384 scan no 3131 cid35.00 polarity:+
Data file D6h-2_3.mgf

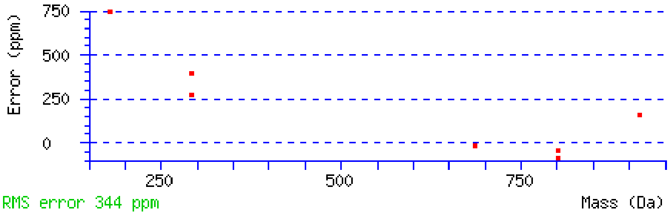
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1092.5203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.046
Matches : 7/90 fragment ions using 8 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	103.0520	52.0296			85.0414	43.0244	T							10
2	205.0967	103.0520			187.0861	94.0467	T	991.4829	496.2451	973.4593	487.2333	973.4723	487.2398	9
3	**293.1258**	147.0665			275.1152	138.0612	S	889.4382	445.2227	871.4146	436.2109	871.4276	436.2175	8
4	409.1497	205.0785			391.1392	196.0732	D	***801.4091***	401.2082	783.3855	392.1964	783.3986	392.2029	7
5	539.2388	270.1230	521.2152	261.1112	521.2282	261.1177	K	***685.3851***	343.1962	667.3616	334.1844	667.3746	334.1909	6
6	699.3280	350.1677	681.3044	341.1559	681.3175	341.1624	R	555.2961	278.1517	537.2725	269.1399	537.2856	269.1464	5
7	**801.3727**	401.1900	783.3492	392.1782	783.3622	392.1847	T	395.2069	198.1071			377.1963	189.1018	4
8	**915.4538**	458.2306	897.4303	449.2188	897.4433	449.2253	L	***293.1622***	147.0847			275.1516	138.0794	3
9	1003.4829	502.2451	985.4593	493.2333	985.4723	493.2398	S	***179.0811***	90.0442			161.0705	81.0389	2
10							A	91.0520	46.0296					1





NCBI **BLAST** search of TTSDKRTLSA
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G39960.1

23.4	1092.5203	-0.0029	TTSDKRTLSA
22.0	1092.5178	-0.0004	RMELFIDR
16.0	1092.5167	0.0007	YYRYFLR
14.2	1092.5183	-0.0008	TMERRNIR
9.6	1092.5149	0.0025	NHKSHSPLR
8.2	1092.5156	0.0018	SNNKSMLLR
8.0	1092.5194	-0.0019	LRFYHWR
5.7	1092.5178	-0.0004	DMERIFIR
3.4	1092.5178	-0.0004	MLDERFIR
3.4	1092.5178	-0.0004	TDMIPPHLR

AT5G40140.1

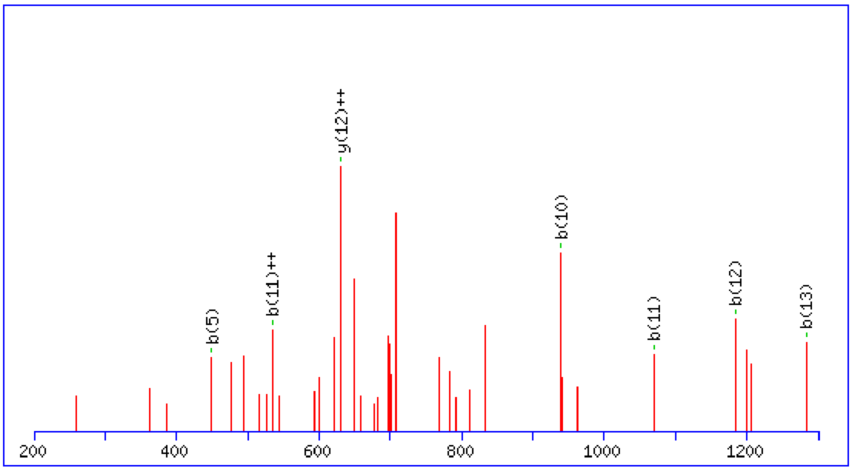
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLAMAANAVEELVK**
Found in **AT5G40140.1** in **TAIR_Arabidopsis**, Symbols: | armadillo/beta-catenin repeat family protein / U-box domain-containing protein | chr5:16074575-16076227 FORWARD

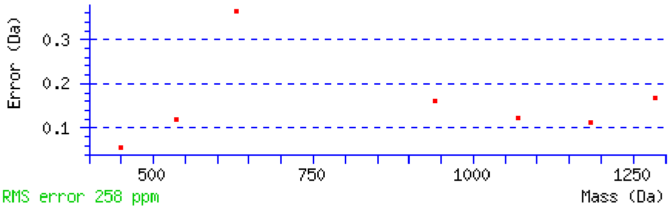
Match to Query 5644: 1430.701444 from(716.357998,2+) index(4113)
Title: Elution from: 39.415 to 39.415 scan no 5241 cid35.00 polarity:+
Data file 0-1_2.mgf

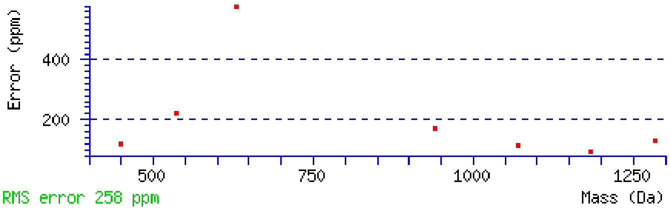
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1430.7016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.022
Matches : 7/120 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							14
2	173.1069	87.0571					L	1373.6903	687.3488	1355.6668	678.3370	1355.6798	678.3435	13
3	245.1410	123.0741					A	1259.6092	630.3083	1241.5857	621.2965	1241.5987	621.3030	12
4	377.1785	189.0929					M	1187.5751	594.2912	1169.5515	585.2794	1169.5645	585.2859	11
5	***449.2127***	225.1100					A	1055.5376	528.2724	1037.5140	519.2606	1037.5270	519.2671	10
6	521.2468	261.1271					A	983.5034	492.2553	965.4798	483.2436	965.4929	483.2501	9
7	637.2838	319.1456	619.2603	310.1338			N	911.4693	456.2383	893.4457	447.2265	893.4587	447.2330	8
8	709.3180	355.1626	691.2944	346.1508			A	795.4323	398.2198	777.4087	389.2080	777.4217	389.2145	7
9	809.3834	405.1954	791.3599	396.1836			V	723.3981	362.2027	705.3745	353.1909	705.3876	353.1974	6
10	***939.4231***	470.2152	921.3995	461.2034	921.4125	461.2099	E	623.3327	312.1700	605.3091	303.1582	605.3221	303.1647	5
11	***1069.4627***	535.2350	1051.4391	526.2232	1051.4521	526.2297	E	493.2930	247.1502	475.2695	238.1384	475.2825	238.1449	4
12	***1183.5438***	592.2755	1165.5202	583.2637	1165.5332	583.2703	L	363.2534	182.1303	345.2298	173.1186			3
13	***1283.6092***	642.3083	1265.5857	633.2965	1265.5987	633.3030	V	249.1723	125.0898	231.1487	116.0780			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GLAMAANAVEELVK

AT5G40140.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.8	1430.7016	-0.0001	GLAMAANAVEELVK
9.7	1430.7016	-0.0001	MADPEVAAAGIVKK
5.2	1430.7038	-0.0023	MDLATFHDILLK
5.2	1430.6982	0.0033	SHIFDDDKVIVK
4.7	1430.6982	0.0032	KSAISSSLFFNSK
2.3	1430.7016	-0.0001	EKTQEMLPQIAK
0.8	1430.7016	-0.0001	MAAEPKAATAEVVK

AT5G40950.1

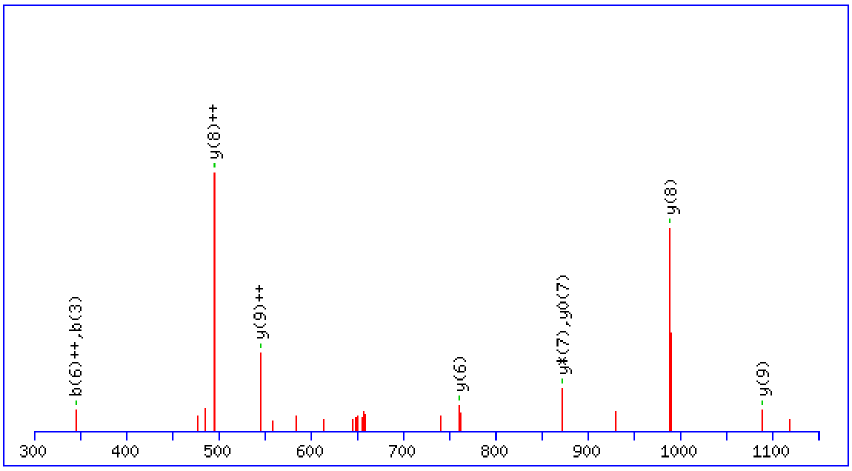
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIVPENPNSYR**
Found in **AT5G40950.1** in **TAIR_Arabidopsis**, Symbols: RPL27 | RPL27; structural constituent of ribosome | chr5:16428094-16429073 FORWARD

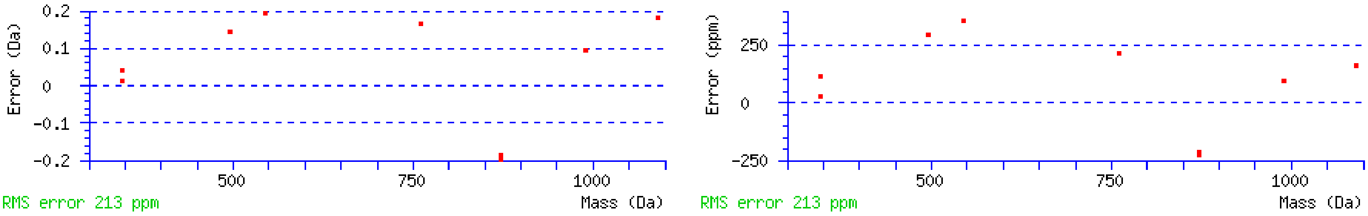
Match to Query 5005: 1332.591008 from(667.302780,2+) index(2978)
Title: Elution from: 30.311 to 30.311 scan no 3736 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1332.5887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.039
Matches : 9/106 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							11
2	245.1280	123.0676			227.1174	114.0624	I	1203.5563	602.2818	1185.5327	593.2700	1185.5457	593.2765	10
3	345.1935	173.1004			327.1829	164.0951	V	***1089.4752***	545.2412	1071.4516	536.2294	1071.4646	536.2359	9
4	443.2433	222.1253			425.2327	213.1200	P	***989.4097***	495.2085	971.3862	486.1967	971.3992	486.2032	8
5	573.2829	287.1451			555.2723	278.1398	E	891.3599	446.1836	873.3364	437.1718	873.3494	437.1783	7
6	689.3199	345.1636	671.2963	336.1518	671.3093	336.1583	N	***761.3203***	381.1638	743.2967	372.1520	743.3097	372.1585	6
7	787.3697	394.1885	769.3461	385.1767	769.3591	385.1832	P	645.2833	323.1453	627.2597	314.1335	627.2727	314.1400	5
8	903.4067	452.2070	885.3831	443.1952	885.3961	443.2017	N	547.2335	274.1204	529.2099	265.1086	529.2230	265.1151	4
9	991.4357	496.2215	973.4122	487.2097	973.4252	487.2162	S	431.1965	216.1019	413.1729	207.0901	413.1860	207.0966	3
10	1155.4961	578.2517	1137.4725	569.2399	1137.4855	569.2464	Y	343.1675	172.0874	325.1439	163.0756			2
11							R	179.1071	90.0572	161.0835	81.0454			1



NCBI **BLAST** search of EIVPENPNSYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G40950.1

Score	Mr(calc)	Delta	Sequence
21.6	1332.5887	0.0024	EIVPENPNSYR
1.8	1332.5909	0.0001	NPEGTGYPIGWK

AT5G41140.1

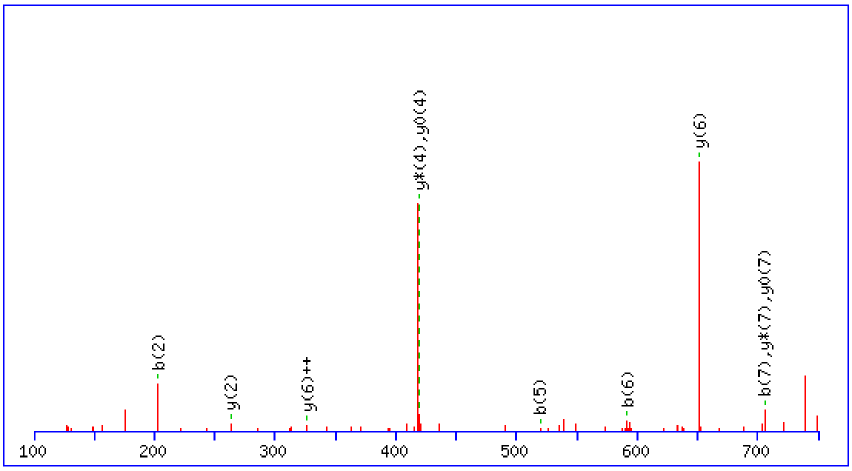
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAVITALK**
Found in **AT5G41140.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G63300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62788.1); contains domain PTHR23160 (PTHR23160) | chr5:16485954-16489774 FORWARD

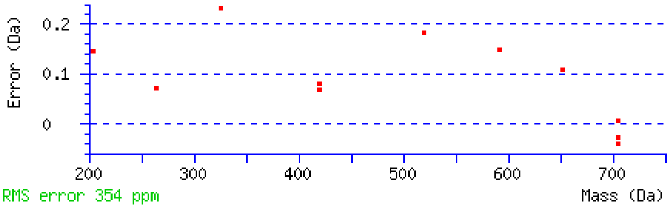
Match to Query 1324: 852.478034 from(427.246293,2+) index(2062)
Title: Elution from: 25.503 to 25.503 scan no 2716 cid35.00 polarity:+
Data file D6h-2_1.mgf

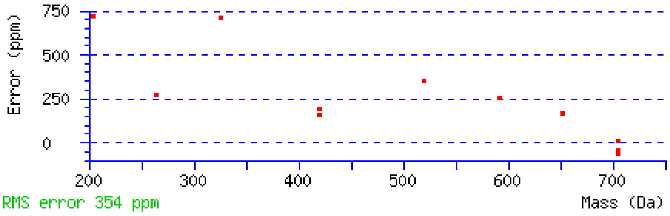
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 852.4799
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.039
Matches : 11/64 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	E							8
2	***203.0811***	102.0442	185.0705	93.0389	A	723.4475	362.2274	705.4239	353.2156	705.4370	353.2221	7
3	303.1465	152.0769	285.1359	143.0716	V	**651.4134**	326.2103	633.3898	317.1985	633.4028	317.2050	6
4	417.2276	209.1174	399.2170	200.1122	I	551.3479	276.1776	533.3243	267.1658	533.3374	267.1723	5
5	***519.2723***	260.1398	501.2617	251.1345	T	437.2668	219.1371	419.2433	210.1253	419.2563	210.1318	4
6	***591.3065***	296.1569	573.2959	287.1516	A	335.2221	168.1147	317.1985	159.1029			3
7	***705.3876***	353.1974	687.3770	344.1921	L	**263.1880**	132.0976	245.1644	123.0858			2
8					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EAVITALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.8	852.4799	-0.0018	EAVITALK

AT5G41140.1

19.3	852.4799	-0.0019	ISISSPLK
17.2	852.4799	-0.0018	EAVTIIAK
11.0	852.4799	-0.0018	VIESGVLK
9.7	852.4799	-0.0018	LSLVIDGK
9.2	852.4799	-0.0018	IVVKEEK
8.4	852.4799	-0.0018	VSEAVVLK
8.3	852.4799	-0.0018	LLVDEKK
7.5	852.4799	-0.0018	KVEEVLK
7.3	852.4799	-0.0018	VTGVVIEK

AT5G41670.1

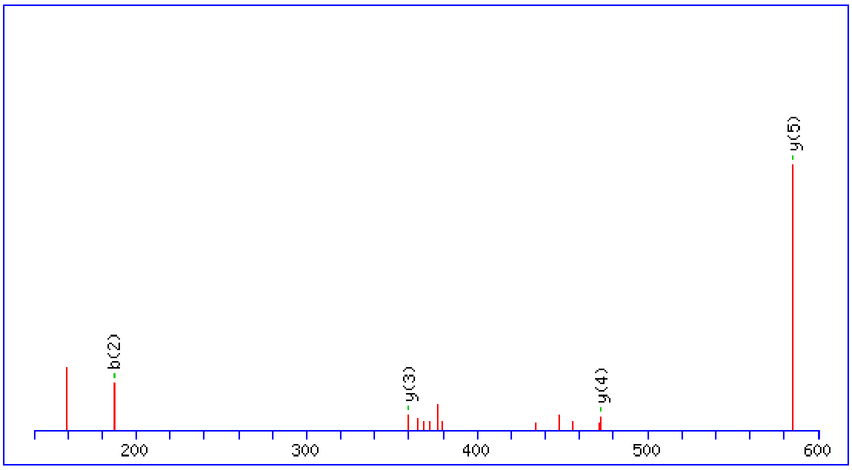
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVIILVK**
Found in **AT5G41670.1** in **TAIR_Arabidopsis**, Symbols: | 6-phosphogluconate dehydrogenase family protein | chr5:16682875-16684338 REVERSE

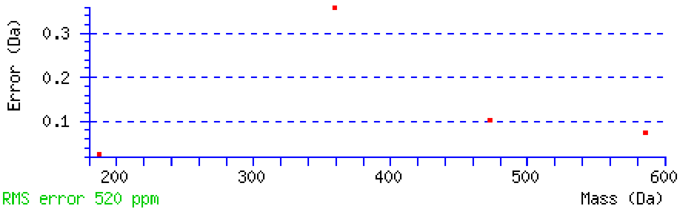
Match to Query 885: 770.526564 from(386.270558,2+) index(4078)
Title: Elution from: 36.596 to 36.596 scan no 5045 cid35.00 polarity:+
Data file D1d-3_3.mgf

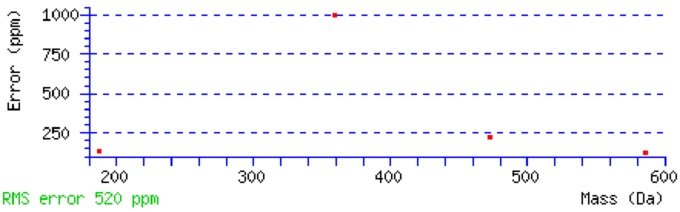
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.5266
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.0048
Matches : 4/48 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	88.0393	44.5233	70.0287	35.5180	S					7
2	187.1077	94.0575	169.0972	85.0522	V	684.5018	342.7546	667.4753	334.2413	6
3	300.1918	150.5995	282.1812	141.5942	I	***585.4334***	293.2203	568.4069	284.7071	5
4	413.2758	207.1416	395.2653	198.1363	I	***472.3493***	236.6783	455.3228	228.1650	4
5	526.3599	263.6836	508.3493	254.6783	L	***359.2653***	180.1363	342.2387	171.6230	3
6	625.4283	313.2178	607.4178	304.2125	V	246.1812	123.5942	229.1547	115.0810	2
7					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of SVIILVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	770.5266	-0.0000	SVIILVK
3.8	770.5266	-0.0000	VLSLIVK

AT5G41670.1

Mascot: http://www.matrixscience.com/

AT5G41700.1

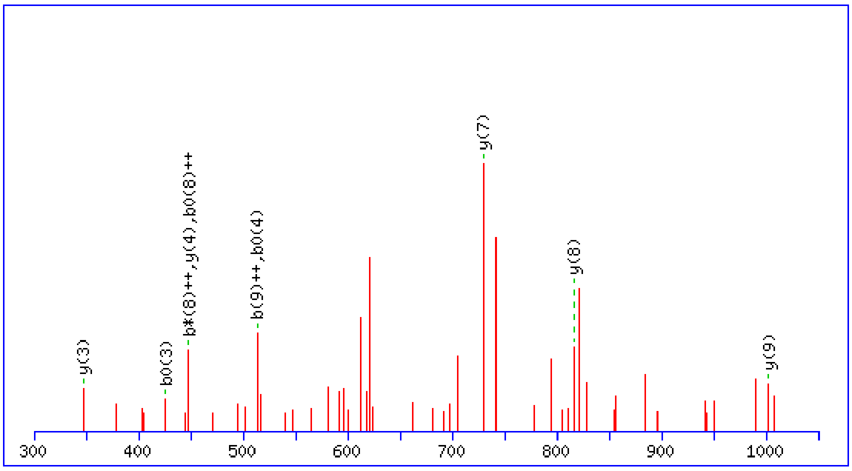
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQWSPALTISK**
Found in **AT5G41700.1** in **TAIR_Arabidopsis**, Symbols: ATUBC8, UBC8 | UBC8 (UBIQUITIN CONJUGATING ENZYME 8); ubiquitin-protein ligase | chr5:16693300-16694451 FORWARD

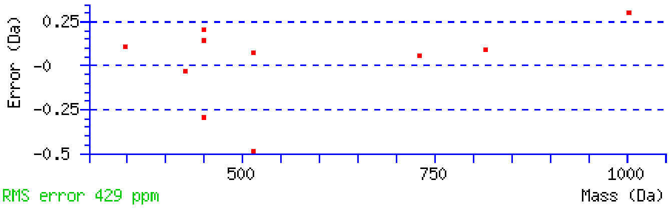
Match to Query 4368: 1258.653588 from(630.334070,2+) index(5456)
Title: Elution from: 48.584 to 48.584 scan no 6889 cid35.00 polarity:+
Data file 0-3_2.mgf

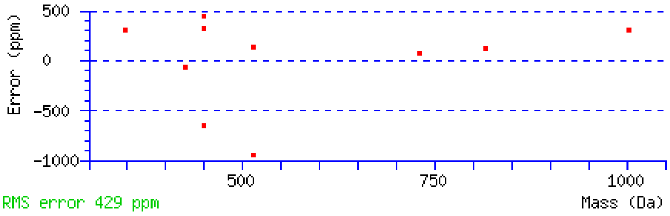
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1258.6557
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.017
Matches : 10/116 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**11**
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	**Q**	1130.6204	565.8139	1113.5939	557.3006	1112.6099	556.8086	**10**
3	444.1878	222.5975	427.1612	214.0842	426.1772	213.5922	**W**	***1002.5619***	501.7846	985.5353	493.2713	984.5513	492.7793	**9**
4	531.2198	266.1135	514.1932	257.6003	513.2092	257.1082	**S**	***816.4825***	408.7449	799.4560	400.2316	798.4720	399.7396	**8**
5	628.2726	314.6399	611.2460	306.1266	610.2620	305.6346	**P**	***729.4505***	365.2289	712.4240	356.7156	711.4400	356.2236	**7**
6	699.3097	350.1585	682.2831	341.6452	681.2991	341.1532	**A**	632.3978	316.7025	615.3712	308.1892	614.3872	307.6972	**6**
7	812.3937	406.7005	795.3672	398.1872	794.3832	397.6952	**L**	561.3606	281.1840	544.3341	272.6707	543.3501	272.1787	**5**
8	913.4414	457.2243	896.4149	448.7111	895.4308	448.2191	**T**	***448.2766***	224.6419	431.2500	216.1287	430.2660	215.6366	**4**
9	1026.5255	513.7664	1009.4989	505.2531	1008.5149	504.7611	**I**	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	**3**
10	1113.5575	557.2824	1096.5310	548.7691	1095.5469	548.2771	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
11							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EQWSPALTISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G41700.1

Score	Mr(calc)	Delta	Sequence
25.5	1258.6557	-0.0021	EQWSPALTISK

Mascot: http://www.matrixscience.com/

AT5G41750.1

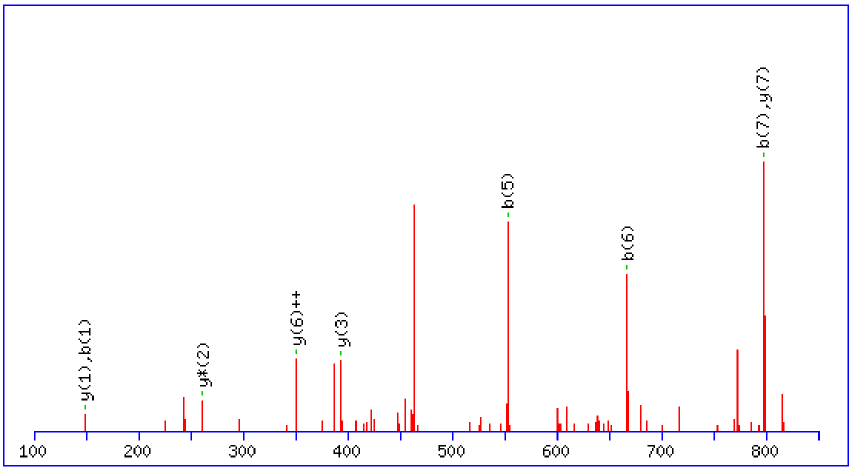
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPSSKLKK**
Found in **AT5G41750.1** in **TAIR_Arabidopsis**, Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr5:16711275-16714755 FORWARD

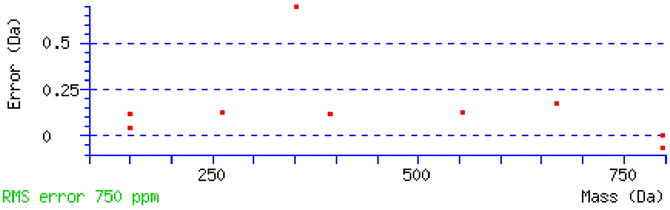
Match to Query 2164: 944.500148 from(473.257350,2+) index(2246)
Title: Elution from: 24.779 to 24.779 scan no 2865 cid35.00 polarity:+
Data file D1d-3_1.mgf

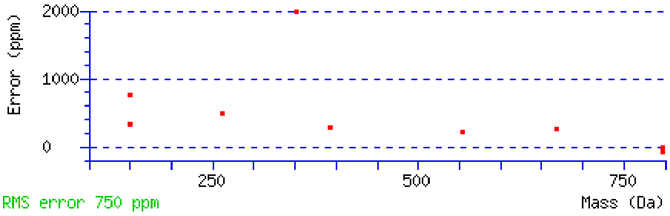
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 944.4991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.032
Matches : 9/94 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***149.0397***	75.0235					M							8
2	247.0895	124.0484					P	**797.4740**	399.2406	779.4504	390.2288	779.4634	390.2353	7
3	335.1186	168.0629			317.1080	159.0576	S	699.4242	350.2157	681.4006	341.2039	681.4136	341.2104	6
4	423.1476	212.0775			405.1371	203.0722	S	611.3951	306.2012	593.3715	297.1894	593.3845	297.1959	5
5	***553.2367***	277.1220	535.2131	268.1102	535.2261	268.1167	K	523.3660	262.1867	505.3425	253.1749			4
6	***667.3178***	334.1625	649.2942	325.1507	649.3072	325.1572	L	**393.2770**	197.1421	375.2534	188.1303			3
7	***797.4068***	399.2070	779.3832	390.1952	779.3962	390.2018	K	279.1959	140.1016	261.1723	131.0898			2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MPSSKLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

23.5	944.4991	0.0010	MPSSKLKK
20.3	944.4991	0.0010	MKVVDAKK
14.7	944.4991	0.0010	KMPSSKLK
14.7	944.4984	0.0017	SNRWLKK
14.3	944.4991	0.0010	SGVLVGMKK
12.2	944.5018	-0.0016	KCVRGALK
10.6	944.4991	0.0010	MKDKLGVK
10.3	944.4991	0.0010	KMKETGLK
10.2	944.4991	0.0010	QVITSMKK
8.5	944.4991	0.0010	MVVKNSIK

AT5G41780.1

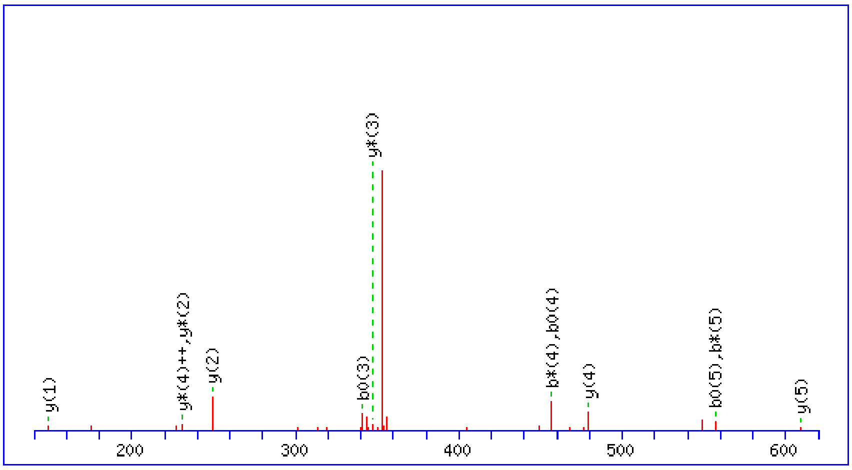
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEINVK**
Found in **AT5G41780.1** in **TAIR_Arabidopsis**, Symbols: | myosin heavy chain-related | chr5:16740303-16742061 FORWARD

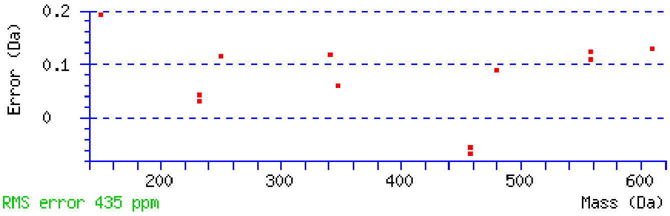
Match to Query 553: 722.404310 from(362.209431,2+) index(1087)
Title: Elution from: 20.452 to 20.452 scan no 1645 cid35.00 polarity:+
Data file D1d-1-2.mgf

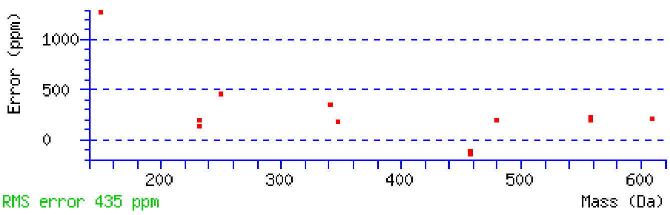
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 620 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 722.4039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.043
Matches : 12/44 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					L							6
2	245.1280	123.0676			227.1174	114.0624	E	***609.3300***	305.1687	591.3065	296.1569	591.3195	296.1634	5
3	359.2091	180.1082			341.1985	171.1029	I	***479.2904***	240.1488	461.2668	231.1371			4
4	475.2461	238.1267	457.2225	229.1149	457.2355	229.1214	N	365.2093	183.1083	347.1857	174.0965			3
5	575.3115	288.1594	557.2880	279.1476	557.3010	279.1541	V	***249.1723***	125.0898	231.1487	116.0780			2
6							K	***149.1069***	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LEINVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	722.4039	0.0004	LEINVK
16.7	722.4039	0.0005	LDLQVK
13.9	722.4039	0.0004	EIINVK
13.5	722.4039	0.0004	LDNLLK

AT5G41780.1

13.4	722.4039	0.0005	LGAIVDK
12.4	722.4039	0.0005	AAVEVVK
12.2	722.4039	0.0005	IDQIVK
12.2	722.4039	0.0005	IVEQVK
12.2	722.4039	0.0005	LDQLVK
12.2	722.4039	0.0005	LTPGTVK

AT5G41790.1

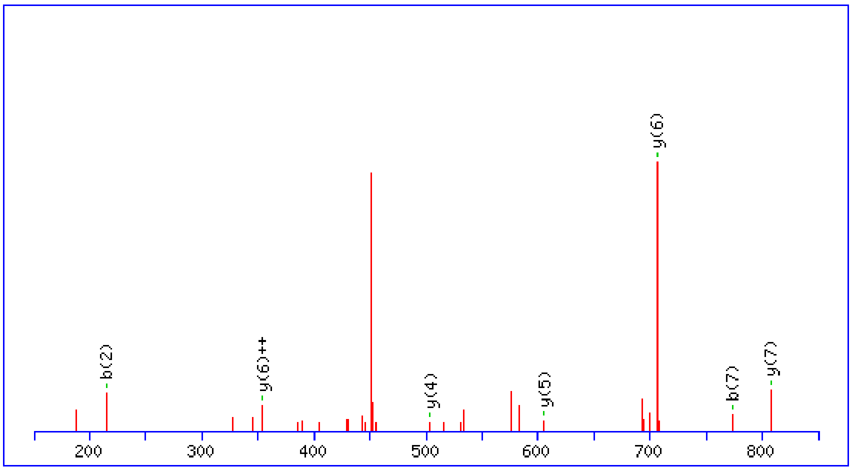
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTTTVEEK**
Found in **AT5G41790.1** in **TAIR_Arabidopsis**, Symbols: CIP1 | CIP1 (COP1-INTERACTIVE PROTEIN 1) | chr5:16744758-16749619 FORWARD

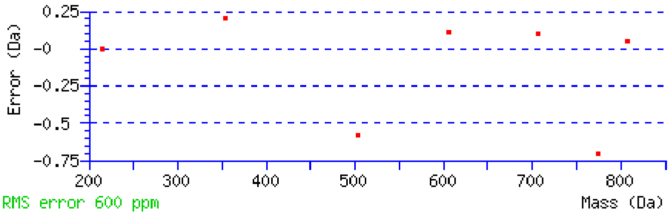
Match to Query 1945: 919.484142 from(460.749347,2+) index(5906)
Title: Elution from: 51.245 to 51.245 scan no 7387 cid35.00 polarity:+
Data file D1d-3_1.mgf

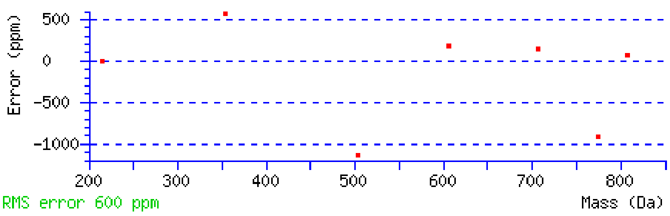
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 919.4862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.019
Matches : 7/66 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							8
2	**215.1390**	108.0731	197.1285	99.0679	T	***807.4094***	404.2084	790.3829	395.6951	789.3989	395.2031	7
3	316.1867	158.5970	298.1761	149.5917	T	***706.3618***	353.6845	689.3352	345.1712	688.3512	344.6792	6
4	417.2344	209.1208	399.2238	200.1155	T	***605.3141***	303.1607	588.2875	294.6474	587.3035	294.1554	5
5	516.3028	258.6550	498.2922	249.6498	V	***504.2664***	252.6368	487.2399	244.1236	486.2558	243.6316	4
6	645.3454	323.1763	627.3348	314.1710	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
7	**774.3880**	387.6976	756.3774	378.6923	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LTTTVEEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.4	919.4862	-0.0021	LTTTVEEK

AT5G41790.1

18.6	919.4837	0.0004	ITMIWEK
8.5	919.4835	0.0006	SGNSGKSRK

Mascot: http://www.matrixscience.com/

AT5G41820.1

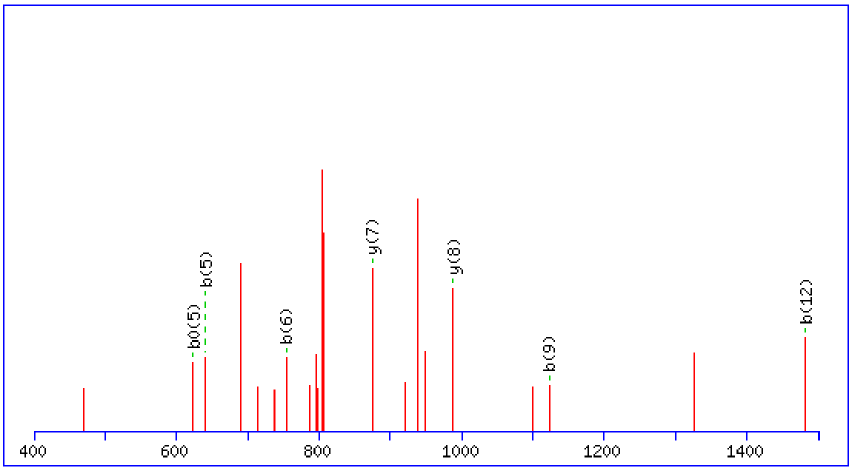
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQDAYLVLRDLMK**
Found in **AT5G41820.1** in **TAIR_Arabidopsis**, Symbols: | geranylgeranyl transferase alpha subunit-related / RAB geranylgeranyltransferase alpha subunit-related | chr5:16758032-16760661 FORWARD

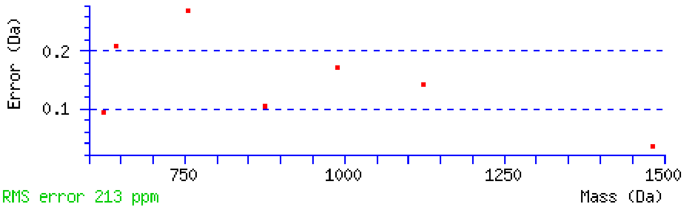
Match to Query 7808: 1626.840266 from(814.427409,2+) index(9359)
Title: Elution from: 82.914 to 82.914 scan no 12545 cid35.00 polarity:+
Data file D1d-3_1.mgf

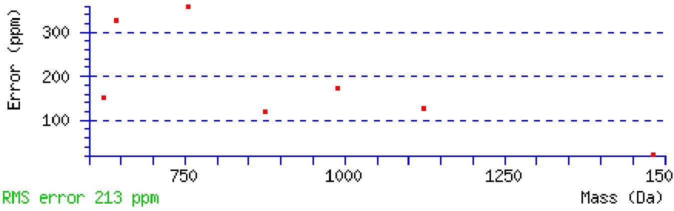
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1626.8439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.028
Matches : 7/132 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							13
2	292.1292	146.5682	275.1026	138.0550			Q	1464.7879	732.8976	1447.7614	724.3843	1446.7773	723.8923	12
3	407.1561	204.0817	390.1296	195.5684	389.1456	195.0764	D	1336.7293	668.8683	1319.7028	660.3550	1318.7188	659.8630	11
4	478.1932	239.6003	461.1667	231.0870	460.1827	230.5950	A	1221.7024	611.3548	1204.6758	602.8416	1203.6918	602.3496	10
5	***641.2566***	321.1319	624.2300	312.6186	623.2460	312.1266	Y	1150.6653	575.8363	1133.6387	567.3230	1132.6547	566.8310	9
6	***754.3406***	377.6740	737.3141	369.1607	736.3301	368.6687	L	**987.6019**	494.3046	970.5754	485.7913	969.5914	485.2993	8
7	853.4090	427.2082	836.3825	418.6949	835.3985	418.2029	V	**874.5179**	437.7626	857.4913	429.2493	856.5073	428.7573	7
8	966.4931	483.7502	949.4666	475.2369	948.4825	474.7449	L	775.4495	388.2284	758.4229	379.7151	757.4389	379.2231	6
9	***1122.5942***	561.8007	1105.5677	553.2875	1104.5837	552.7955	R	662.3654	331.6863	645.3389	323.1731	644.3548	322.6811	5
10	1237.6212	619.3142	1220.5946	610.8009	1219.6106	610.3089	D	506.2643	253.6358	489.2377	245.1225	488.2537	244.6305	4
11	1350.7052	675.8563	1333.6787	667.3430	1332.6947	666.8510	L	391.2374	196.1223	374.2108	187.6090			3
12	***1481.7457***	741.3765	1464.7192	732.8632	1463.7351	732.3712	M	278.1533	139.5803	261.1267	131.0670			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YQDAYLVLRDLMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G41820.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.9	1626.8439	-0.0037	YQDAYLVLRDLMK
12.2	1626.8440	-0.0037	AMSSTFLFSGVVPLR
8.9	1626.8365	0.0037	ALFSRESFENTKAK
2.3	1626.8439	-0.0037	AEAGFTLFCDLKKK
1.0	1626.8365	0.0037	LLNFSSSGNEYRLK

AT5G41850.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **RVAPKAEK**
Found in **AT5G41850.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO65820.1); contains domain PTHR13136 (PTHR13136); contains domain SSF53474 (SSF53474); contains domain G3DSA:3.40.50.1820 (G3DSA:3.40.50.1820) | chr5:16773926-16775019 REVERSE

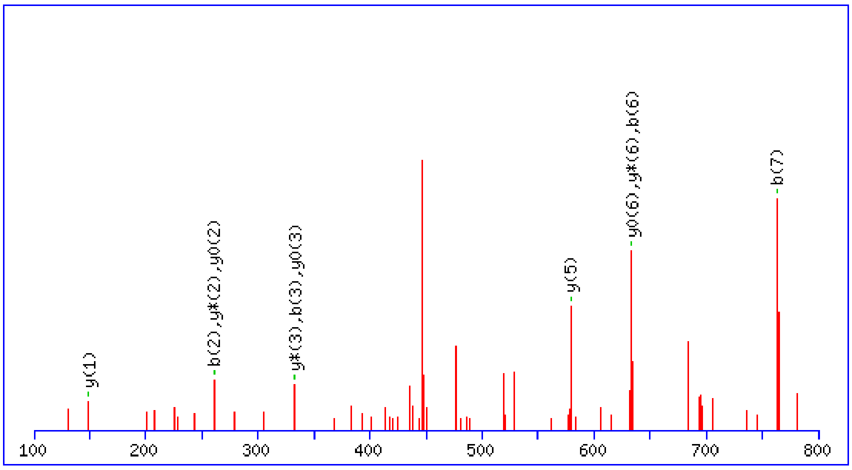
Match to Query 1691: 910.498318 from(456.256435,2+) index(1576)
Title: Elution from: 19.444 to 19.444 scan no 2049 cid35.00 polarity:+
Data file C7-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 800 Da Full range

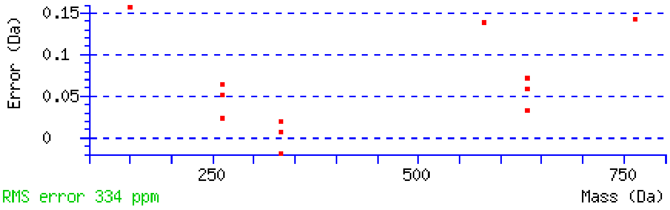
Label all possible matches ○ Label matches used for scoring ●

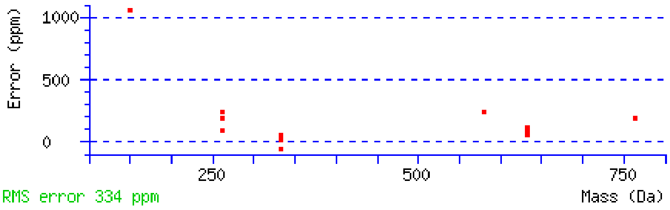
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 910.5011
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0014
Matches : 12/70 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							8
2	***261.1620***	131.0846	243.1384	122.0728			V	751.4191	376.2132	733.3955	367.2014	733.4085	367.2079	7
3	***333.1961***	167.1017	315.1725	158.0899			A	651.3536	326.1805	633.3300	317.1687	633.3431	317.1752	6
4	431.2459	216.1266	413.2223	207.1148			P	**579.3195**	290.1634	561.2959	281.1516	561.3089	281.1581	5
5	561.3350	281.1711	543.3114	272.1593			K	481.2697	241.1385	463.2461	232.1267	463.2591	232.1332	4
6	***633.3691***	317.1882	615.3455	308.1764			A	351.1807	176.0940	333.1571	167.0822	333.1701	167.0887	3
7	***763.4087***	382.2080	745.3851	373.1962	745.3982	373.2027	E	279.1465	140.0769	261.1229	131.0651	261.1359	131.0716	2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RVAPKAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G41850.1

37.6	910.5011	-0.0027	RVAPKAEK
25.7	910.4984	-0.0001	AKEAILEK
25.7	910.4984	-0.0001	EKAELALK
25.7	910.4984	-0.0001	KEAAEIIK
18.2	910.5011	-0.0027	KKGPVNQK
15.9	910.4984	-0.0001	AGLLSLAEK
15.6	910.4984	-0.0000	KVGEVIEK
13.4	910.4984	-0.0000	TIADIIQK
13.4	910.4984	-0.0000	LTVAQLEK
10.3	910.4984	-0.0001	IKSESLPK

AT5G41900.1

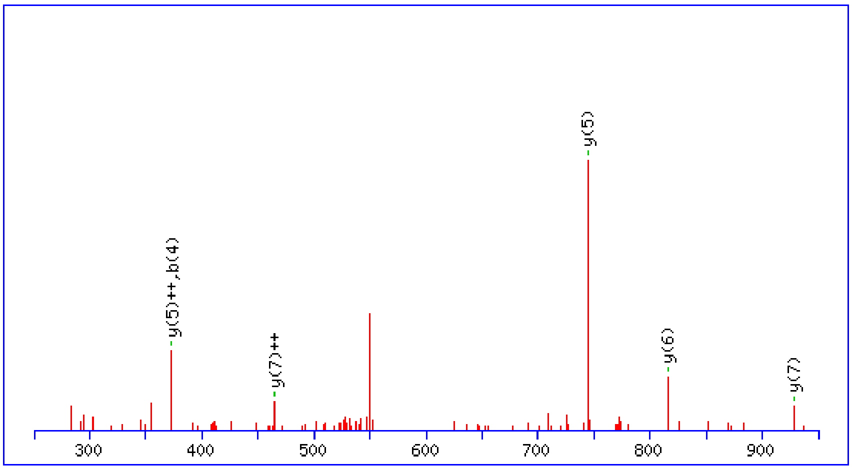
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGIARWLNR**
Found in **AT5G41900.1** in **TAIR_Arabidopsis**, Symbols: | hydrolase, alpha/beta fold family protein | chr5:16786260-16788795 FORWARD

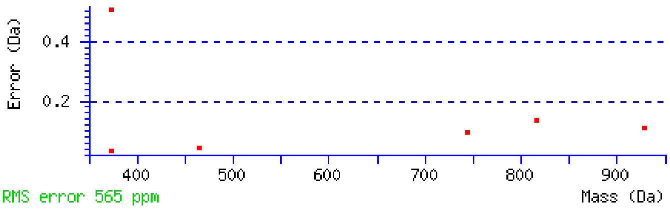
Match to Query 3433: 1115.602196 from(558.808374,2+) index(1870)
Title: Elution from: 22.639 to 22.639 scan no 2437 cid35.00 polarity:+
Data file C7-1_2.mgf

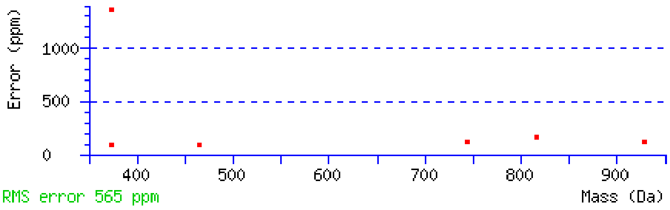
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1115.6022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.029
Matches : 6/56 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	132.0478	66.5275			M					9
2	189.0692	95.0383			G	985.5690	493.2881	968.5425	484.7749	8
3	302.1533	151.5803			I	***928.5475***	464.7774	911.5210	456.2641	7
4	373.1904	187.0988			A	***815.4635***	408.2354	798.4369	399.7221	6
5	529.2915	265.1494	512.2650	256.6361	R	***744.4264***	372.7168	727.3998	364.2035	5
6	715.3708	358.1891	698.3443	349.6758	W	588.3253	294.6663	571.2987	286.1530	4
7	828.4549	414.7311	811.4283	406.2178	L	402.2459	201.6266	385.2194	193.1133	3
8	942.4978	471.7525	925.4713	463.2393	N	289.1619	145.0846	272.1353	136.5713	2
9					R	175.1190	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of MGIARWLNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	1115.6022	0.0000	MGIARWLNR

AT5G41900.1

1.4	1115.6047	-0.0025	LGSDVREGKR

Mascot: http://www.matrixscience.com/

AT5G42020.1

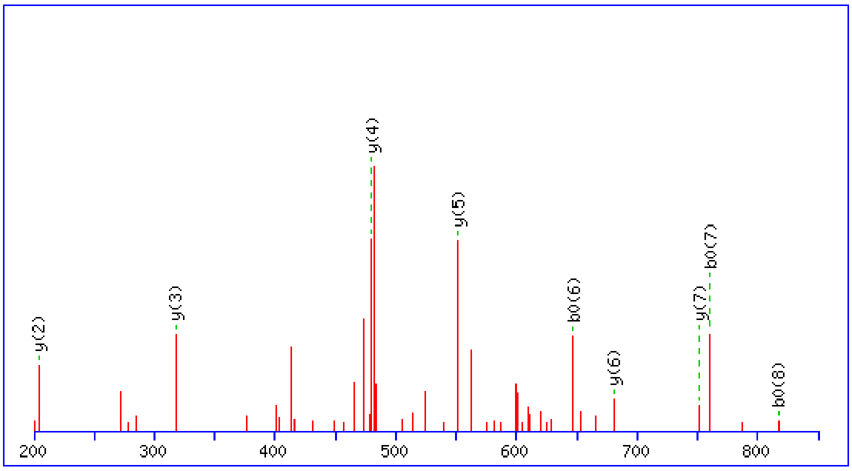
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAEAYLGK**
Found in **AT5G42020.1** in **TAIR_Arabidopsis**, Symbols: BIP2, BIP | BIP (LUMINAL BINDING PROTEIN); ATP binding | chr5:16824925-16827708 REVERSE

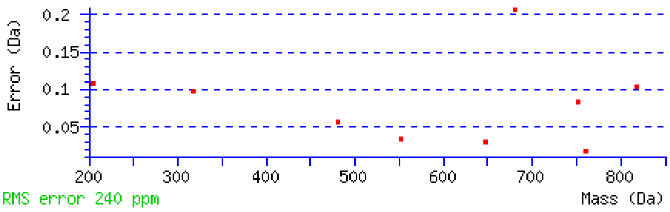
Match to Query 1959: 980.478918 from(491.246735,2+) index(1642)
Title: Elution from: 23.930 to 23.930 scan no 2271 cid35.00 polarity:+
Data file D1d-1_1.mgf

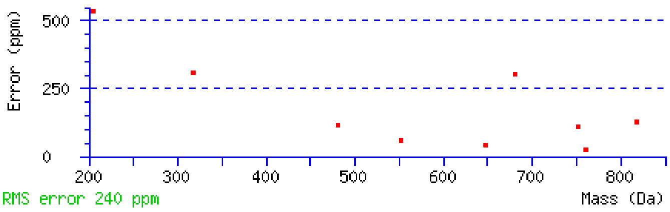
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 980.4814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00026
Matches : 9/70 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							9
2	231.0975	116.0524	213.0870	107.0471	T	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	8
3	302.1347	151.5710	284.1241	142.5657	A	***751.3985***	376.2029	734.3719	367.6896	733.3879	367.1976	7
4	431.1773	216.0923	413.1667	207.0870	E	***680.3614***	340.6843	663.3348	332.1710	662.3508	331.6790	6
5	502.2144	251.6108	484.2038	242.6055	A	***551.3188***	276.1630	534.2922	267.6498			5
6	665.2777	333.1425	647.2671	324.1372	Y	***480.2817***	240.6445	463.2551	232.1312			4
7	778.3618	389.6845	760.3512	380.6792	L	***317.2183***	159.1128	300.1918	150.5995			3
8	835.3832	418.1953	817.3727	409.1900	G	***204.1343***	102.5708	187.1077	94.0575			2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ETAEAYLGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G42020.1

42.4	980.4814	-0.0025	ETAEAYLGK
0.1	980.4815	-0.0026	GETITFEGK

AT5G42270.1

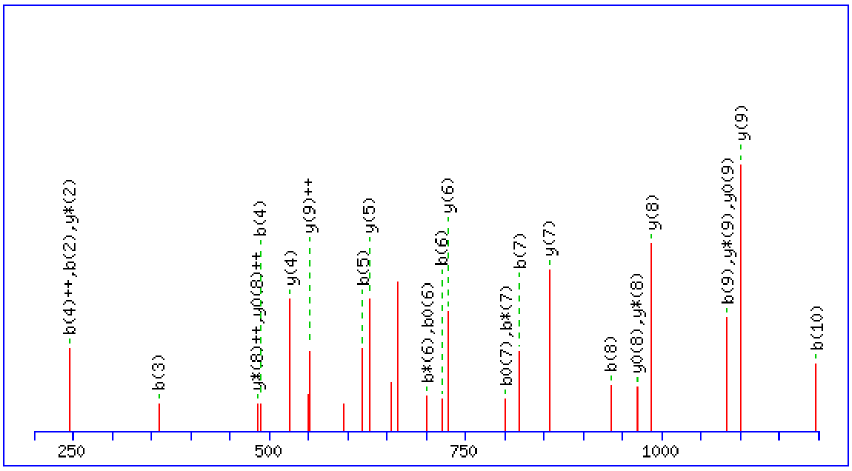
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LELQEVVDFLK**
Found in **AT5G42270.1** in **TAIR_Arabidopsis**, Symbols: FTSH5, VAR1 | VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase | chr5:16919887-16922330 FORWARD

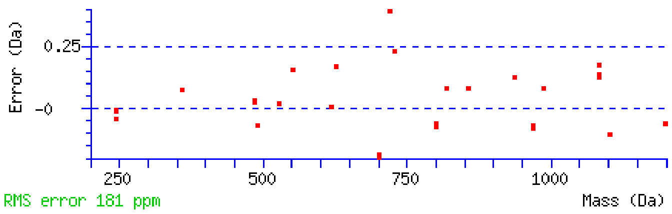
Match to Query 4983: 1344.697782 from(673.356167,2+) index(10304)
Title: Elution from: 98.850 to 98.850 scan no 14785 cid35.00 polarity:+
Data file 0-1_3.mgf

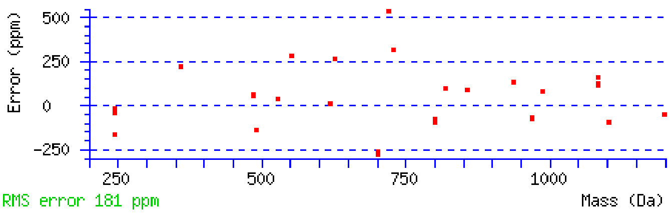
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1344.6951
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 3e-008
Matches : 28/106 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							11
2	***245.1280***	123.0676			227.1174	114.0624	E	1231.6213	616.3143	1213.5977	607.3025	1213.6107	607.3090	10
3	***359.2091***	180.1082			341.1985	171.1029	L	**1101.5817**	551.2945	1083.5581	542.2827	1083.5711	542.2892	9
4	***489.2617***	245.1345	471.2382	236.1227	471.2512	236.1292	Q	**987.5006**	494.2539	969.4770	485.2421	969.4900	485.2486	8
5	***619.3014***	310.1543	601.2778	301.1425	601.2908	301.1490	E	**857.4479**	429.2276	839.4243	420.2158	839.4374	420.2223	7
6	***719.3668***	360.1871	701.3432	351.1753	701.3563	351.1818	V	**727.4083**	364.2078	709.3847	355.1960	709.3977	355.2025	6
7	***819.4323***	410.2198	801.4087	401.2080	801.4217	401.2145	V	**627.3428**	314.1751	609.3193	305.1633	609.3323	305.1698	5
8	***935.4563***	468.2318	917.4327	459.2200	917.4457	459.2265	D	**527.2774**	264.1423	509.2538	255.1305	509.2668	255.1371	4
9	***1083.5217***	542.2645	1065.4981	533.2527	1065.5111	533.2592	F	411.2534	206.1303	393.2298	197.1186			3
10	***1197.6028***	599.3050	1179.5792	590.2932	1179.5922	590.2998	L	263.1880	132.0976	245.1644	123.0858			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LELQEVVDFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G42270.1

Score	Mr(calc)	Delta	Sequence
84.6	1344.6951	0.0027	LELQEVVDFLK
20.4	1344.6955	0.0022	EILKGILTGNDR
15.9	1344.6956	0.0022	IIKEDINNNKK
14.9	1344.7012	-0.0034	LKEINIKSCPK
13.3	1344.6955	0.0022	AVALREAELQTK
13.3	1344.6956	0.0022	ELRIPSLASQSK
7.5	1344.7012	-0.0034	ILRVEMSPLQK
7.3	1344.6978	-0.0000	LKPNTQYIPQK
4.4	1344.6978	-0.0000	LIEANPLFREK
3.2	1344.6955	0.0022	QDEKRTTLPLK

AT5G42390.1

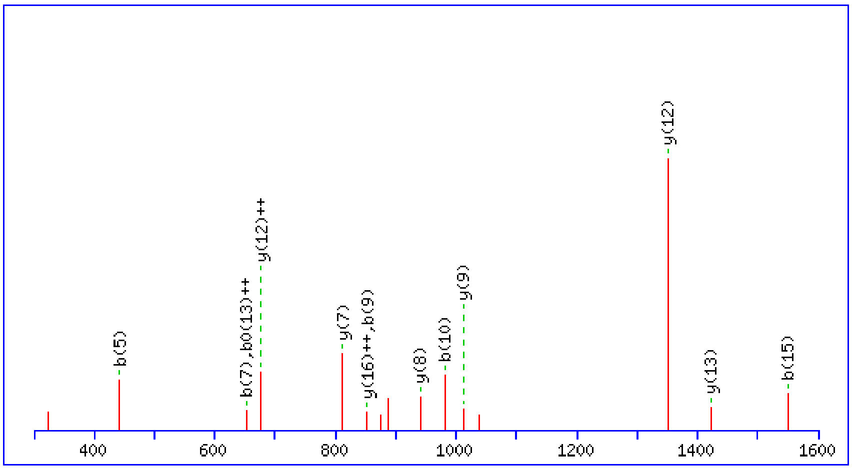
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGLLAPIEAEPELEVPK**
Found in **AT5G42390.1** in **TAIR_Arabidopsis**, Symbols: | metalloendopeptidase | chr5:16962536-16969875 FORWARD

Match to Query 8553: 1790.963486 from(896.489019,2+) index(8571)
Title: Elution from: 75.157 to 75.157 scan no 11382 cid35.00 polarity:+
Data file D1d-3_2.mgf

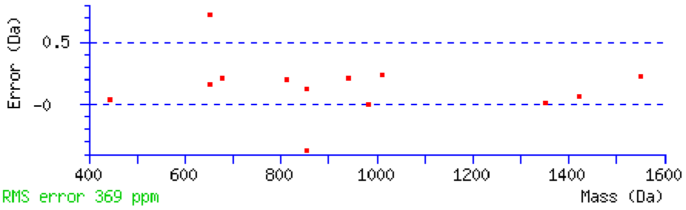
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

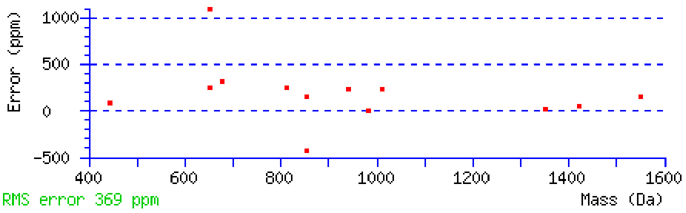


Monoisotopic mass of neutral peptide Mr(calc): 1790.9665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00021
Matches : 13/154 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	**S**							**17**
2	145.0608	73.0340	127.0502	64.0287	**G**	1704.9418	852.9746	1687.9153	844.4613	1686.9313	843.9693	**16**
3	258.1448	129.5761	240.1343	120.5708	**L**	1647.9204	824.4638	1630.8938	815.9505	1629.9098	815.4585	**15**
4	371.2289	186.1181	353.2183	177.1128	**L**	1534.8363	767.9218	1517.8098	759.4085	1516.8257	758.9165	**14**
5	***442.2660***	221.6366	424.2554	212.6314	**A**	***1421.7522***	711.3798	1404.7257	702.8665	1403.7417	702.3745	**13**
6	539.3188	270.1630	521.3082	261.1577	**P**	***1350.7151***	675.8612	1333.6886	667.3479	1332.7046	666.8559	**12**
7	***652.4028***	326.7051	634.3923	317.6998	**I**	1253.6624	627.3348	1236.6358	618.8215	1235.6518	618.3295	**11**
8	781.4454	391.2264	763.4349	382.2211	**E**	1140.5783	570.7928	1123.5517	562.2795	1122.5677	561.7875	**10**
9	***852.4825***	426.7449	834.4720	417.7396	**A**	***1011.5357***	506.2715	994.5092	497.7582	993.5251	497.2662	**9**
10	***981.5251***	491.2662	963.5146	482.2609	**E**	***940.4986***	470.7529	923.4720	462.2397	922.4880	461.7476	**8**
11	1078.5779	539.7926	1060.5673	530.7873	**P**	***811.4560***	406.2316	794.4294	397.7184	793.4454	397.2264	**7**
12	1207.6205	604.3139	1189.6099	595.3086	**E**	714.4032	357.7053	697.3767	349.1920	696.3927	348.7000	**6**
13	1320.7046	660.8559	1302.6940	651.8506	**L**	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	**5**
14	1449.7472	725.3772	1431.7366	716.3719	**E**	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	**4**
15	***1548.8156***	774.9114	1530.8050	765.9061	**V**	343.2340	172.1206	326.2074	163.6074			**3**
16	1645.8683	823.4378	1627.8578	814.4325	**P**	244.1656	122.5864	227.1390	114.0731			**2**
17					**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT5G42390.1





NCBI **BLAST** search of SGLLAPIEAEPELEVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.8	1790.9665	-0.0031	SGLLAPIEAEPELEVPK
3.0	1790.9601	0.0034	QDVVLVMALAFLDVSR
1.2	1790.9666	-0.0031	SLLKVDDIVGAEEIYK
0.5	1790.9634	0.0001	MTKELNALVPSSMKVK

Mascot: http://www.matrixscience.com/

AT5G42570.1

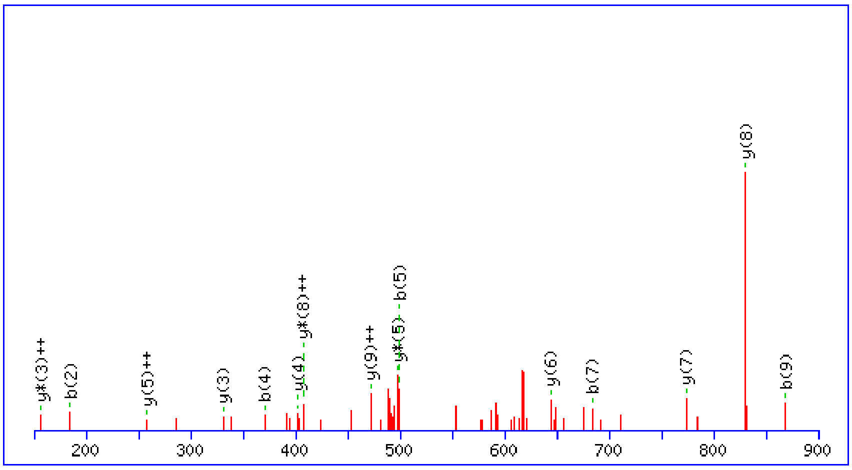
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGEEIAALK**
Found in **AT5G42570.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G11905.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24012.1); contains InterPro domain B-cell receptor-associated 31-like; (InterPro:IPR008417) | chr5:17038687

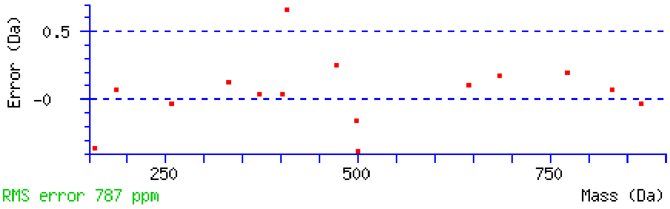
Match to Query 2570: 1013.576636 from(507.795594,2+) index(5217)
Title: Elution from: 47.054 to 47.054 scan no 6586 cid35.00 polarity:+
Data file D6h-3_1.mgf

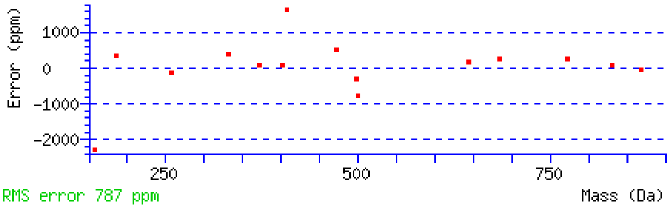
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1013.5757
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.013
Matches : 15/74 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			A							10
2	***185.1285***	93.0679			L	943.5459	472.2766	926.5193	463.7633	925.5353	463.2713	9
3	242.1499	121.5786			G	***830.4618***	415.7345	813.4353	407.2213	812.4512	406.7293	8
4	***371.1925***	186.0999	353.1819	177.0946	E	***773.4403***	387.2238	756.4138	378.7105	755.4298	378.2185	7
5	***500.2351***	250.6212	482.2245	241.6159	E	***644.3978***	322.7025	627.3712	314.1892	626.3872	313.6972	6
6	613.3192	307.1632	595.3086	298.1579	I	515.3552	258.1812	498.3286	249.6679			5
7	***684.3563***	342.6818	666.3457	333.6765	A	***402.2711***	201.6392	385.2445	193.1259			4
8	755.3934	378.2003	737.3828	369.1951	A	***331.2340***	166.1206	314.2074	157.6074			3
9	***868.4775***	434.7424	850.4669	425.7371	L	260.1969	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ALGEEIAALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G42570.1

Score	Mr(calc)	Delta	Sequence
24.7	1013.5757	0.0010	ALGEEIAALK
4.5	1013.5757	0.0010	EKIPSEIAK
4.3	1013.5757	0.0010	LETKDPAIK
1.0	1013.5757	0.0010	ALAALAIEDK
1.0	1013.5770	-0.0004	ALKRDHFK

AT5G42650.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEMLYGYQPLATR**
Found in **AT5G42650.1** in **TAIR_Arabidopsis**, Symbols: CYP74A, AOS | AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding | chr5:17115031-17116587 REVERSE

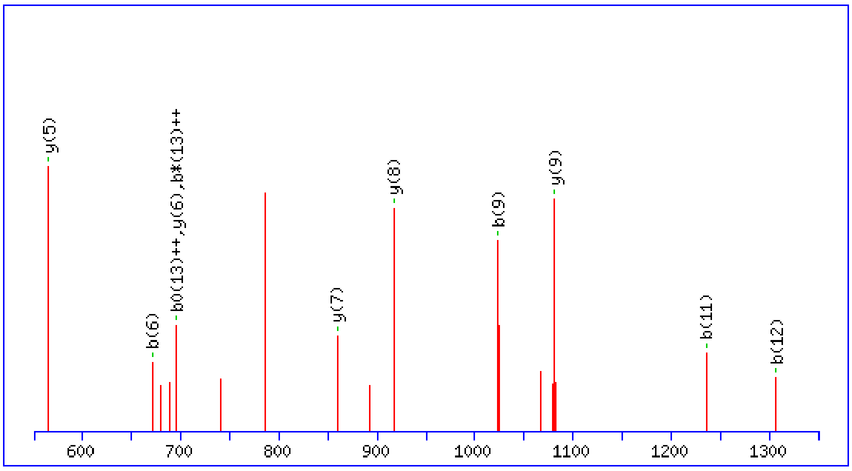
Match to Query 7398: 1586.712800 from(794.363676,2+) index(6723)
Title: Elution from: 59.344 to 59.344 scan no 8613 cid35.00 polarity:+
Data file 0-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 550 to 1350 Da Full range

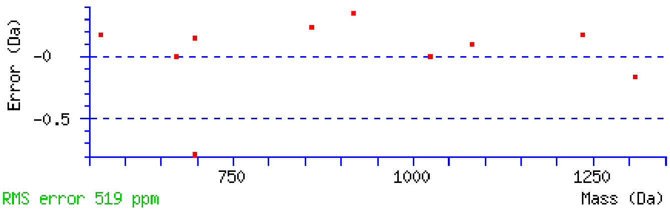
Label all possible matches ○ Label matches used for scoring ●

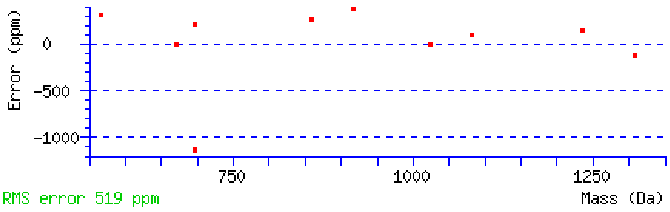
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1586.7123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00018
Matches : 11/134 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							14
2	131.0599	66.0336					G	1515.6855	758.3464	1497.6619	749.3346	1497.6749	749.3411	13
3	261.0996	131.0534			243.0890	122.0481	E	1457.6670	729.3371	1439.6434	720.3253	1439.6564	720.3318	12
4	393.1371	197.0722			375.1265	188.0669	M	1327.6273	664.3173	1309.6038	655.3055	1309.6168	655.3120	11
5	507.2182	254.1127			489.2076	245.1074	L	1195.5898	598.2986	1177.5662	589.2868	1177.5793	589.2933	10
6	***671.2785***	336.1429			653.2680	327.1376	Y	***1081.5087***	541.2580	1063.4851	532.2462	1063.4982	532.2527	9
7	729.2970	365.1522			711.2865	356.1469	G	***917.4484***	459.2278	899.4248	450.2160	899.4378	450.2225	8
8	893.3574	447.1823			875.3468	438.1771	Y	***859.4299***	430.2186	841.4063	421.2068	841.4193	421.2133	7
9	***1023.4100***	512.2087	1005.3865	503.1969	1005.3995	503.2034	Q	***695.3695***	348.1884	677.3459	339.1766	677.3589	339.1831	6
10	1121.4598	561.2336	1103.4363	552.2218	1103.4493	552.2283	P	***565.3169***	283.1621	547.2933	274.1503	547.3063	274.1568	5
11	***1235.5409***	618.2741	1217.5174	609.2623	1217.5304	609.2688	L	467.2671	234.1372	449.2435	225.1254	449.2565	225.1319	4
12	***1307.5751***	654.2912	1289.5515	645.2794	1289.5645	645.2859	A	353.1860	177.0966	335.1624	168.0848	335.1754	168.0913	3
13	1409.6198	705.3135	1391.5962	696.3017	1391.6092	696.3083	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AGEMLYGYQPLATR

AT5G42650.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.7	1586.7123	0.0005	AGEMLYGYQPLATR
3.3	1586.7101	0.0027	CGGNIGDDVNIPIPK
0.7	1586.7171	-0.0043	ERLVSTSPYYPTSA

AT5G42700.1

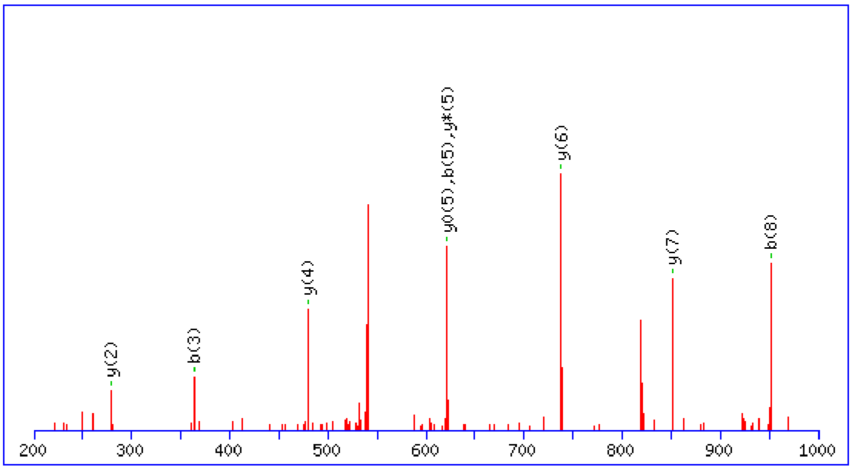
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RSIPRTPEK**
Found in **AT5G42700.1** in **TAIR_Arabidopsis**, Symbols: | transcriptional factor B3 family protein | chr5:17139399-17141405 FORWARD

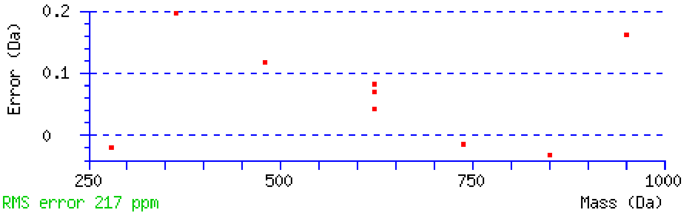
Match to Query 3356: 1098.574544 from(550.294548,2+) index(2623)
Title: Elution from: 27.711 to 27.711 scan no 3291 cid35.00 polarity:+
Data file D6h-3_1.mgf

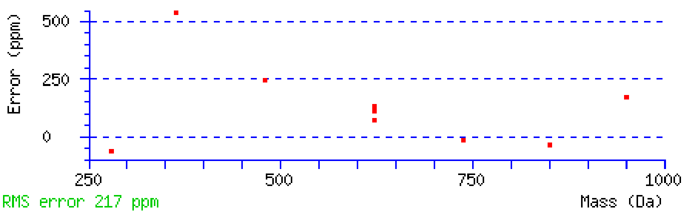
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1098.5722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00052
Matches : 9/92 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							9
2	249.1256	125.0664	231.1020	116.0546	231.1150	116.0612	S	939.4902	470.2488	921.4666	461.2370	921.4797	461.2435	8
3	***363.2067***	182.1070	345.1831	173.0952	345.1961	173.1017	I	***851.4612***	426.2342	833.4376	417.2224	833.4506	417.2289	7
4	461.2565	231.1319	443.2329	222.1201	443.2459	222.1266	P	***737.3801***	369.1937	719.3565	360.1819	719.3695	360.1884	6
5	***621.3457***	311.1765	603.3222	302.1647	603.3352	302.1712	R	639.3303	320.1688	621.3067	311.1570	621.3197	311.1635	5
6	723.3905	362.1989	705.3669	353.1871	705.3799	353.1936	T	***479.2410***	240.1241	461.2174	231.1124	461.2304	231.1189	4
7	821.4403	411.2238	803.4167	402.2120	803.4297	402.2185	P	377.1963	189.1018	359.1727	180.0900	359.1857	180.0965	3
8	***951.4799***	476.2436	933.4563	467.2318	933.4693	467.2383	E	***279.1465***	140.0769	261.1229	131.0651	261.1359	131.0716	2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RSIPRTPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	1098.5722	0.0023	RSIPRTPEK

19.3	1098.5722	0.0023	KTKDPNRPK
9.8	1098.5740	0.0006	FYFKGSVLK
7.2	1098.5722	0.0023	KVSPSGAPRGK
3.8	1098.5717	0.0028	IDEIWGKVK
3.3	1098.5722	0.0023	NLLGLGNINR
1.5	1098.5778	-0.0033	AQRLVPLCK
1.5	1098.5774	-0.0028	KYMYKVIK
1.5	1098.5774	-0.0028	MVKPFLEPK
1.5	1098.5722	0.0023	RADAALKNPK

AT5G42880.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEEMEKGVANEASVAVK**
Found in **AT5G42880.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G45545.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61337.1); contains InterPro domain Protein of unknown function DUF827, plant (InterPro:IPR008545) | chr5:17

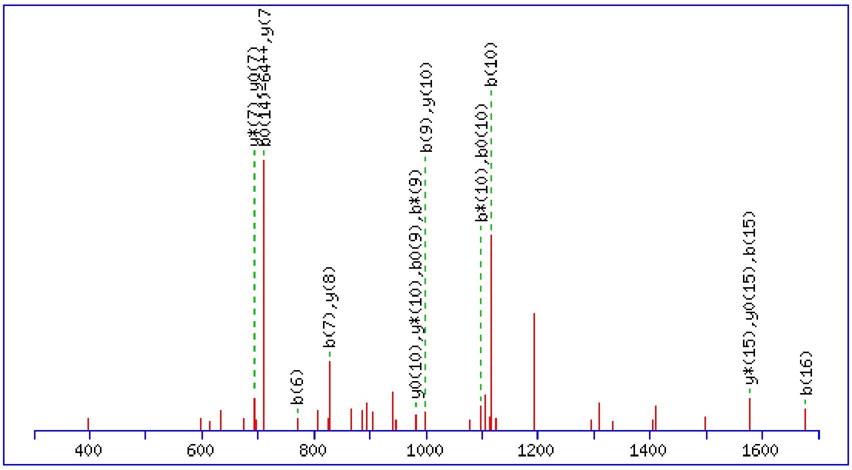
Match to Query 8116: 1824.823608 from(913.419080,2+) index(6578)
Title: Elution from: 60.737 to 60.737 scan no 8675 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

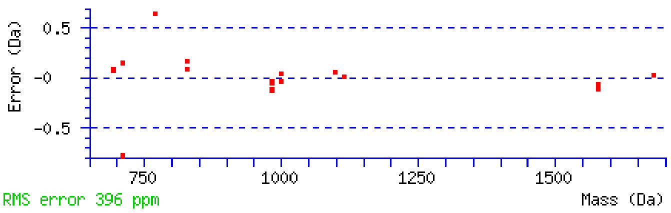
Show Y-axis ☐

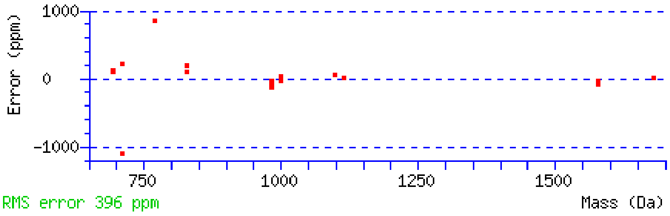


Monoisotopic mass of neutral peptide Mr(calc): 1824.8284
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.044
Matches : 21/264 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0727	51.0400					V							17
2	231.1124	116.0598			213.1018	107.0545	E	1725.7702	863.3887	1707.7466	854.3769	1707.7596	854.3835	16
3	361.1520	181.0796			343.1414	172.0743	E	1595.7306	798.3689	1577.7070	789.3571	1577.7200	789.3636	15
4	509.1844	255.0958			491.1739	246.0906	M	1465.6910	733.3491	1447.6674	724.3373	1447.6804	724.3438	14
5	639.2240	320.1157			621.2135	311.1104	E	1317.6585	659.3329	1299.6349	650.3211	1299.6480	650.3276	13
6	***769.3131***	385.1602	751.2895	376.1484	751.3025	376.1549	K	1187.6189	594.3131	1169.5953	585.3013	1169.6083	585.3078	12
7	***827.3316***	414.1694	809.3080	405.1576	809.3210	405.1641	G	1057.5299	529.2686	1039.5063	520.2568	1039.5193	520.2633	11
8	927.3970	464.2022	909.3734	455.1904	909.3865	455.1969	V	**999.5114**	500.2593	981.4878	491.2475	981.5008	491.2540	10
9	***999.4312***	500.2192	981.4076	491.2074	981.4206	491.2139	A	899.4459	450.2266	881.4223	441.2148	881.4353	441.2213	9
10	***1115.4682***	558.2377	1097.4446	549.2259	1097.4576	549.2324	N	**827.4118**	414.2095	809.3882	405.1977	809.4012	405.2042	8
11	1245.5078	623.2575	1227.4842	614.2457	1227.4972	614.2523	E	**711.3748**	356.1910	693.3512	347.1792	693.3642	347.1857	7
12	1317.5419	659.2746	1299.5184	650.2628	1299.5314	650.2693	A	581.3351	291.1712	563.3115	282.1594	563.3246	282.1659	6
13	1405.5710	703.2891	1387.5474	694.2774	1387.5604	694.2839	S	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	5
14	1505.6365	753.3219	1487.6129	744.3101	1487.6259	744.3166	V	421.2719	211.1396	403.2483	202.1278			4
15	***1577.6706***	789.3389	1559.6470	780.3272	1559.6600	780.3337	A	321.2065	161.1069	303.1829	152.0951			3
16	***1677.7361***	839.3717	1659.7125	830.3599	1659.7255	830.3664	V	249.1723	125.0898	231.1487	116.0780			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT5G42880.1





NCBI **BLAST** search of VEEMEKGVANEASVAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.8	1824.8284	-0.0048	VEEMEKGVANEASVAVK
11.9	1824.8228	0.0009	LEVSSSDQQQLETNVK
11.1	1824.8272	-0.0036	YYATKYADQGTDLLGK
6.5	1824.8284	-0.0048	LGNIESMIDLELSNNK
4.4	1824.8272	-0.0036	EVPSSWDSAALAGFIEK
4.4	1824.8259	-0.0023	FHLNTVAELLMCDVK
1.4	1824.8279	-0.0043	LHPFLSRYSICNHR
1.1	1824.8225	0.0011	GYNSMPLDLPGTLFHK
0.9	1824.8203	0.0034	QAFQSEVVTLAHSEMK

AT5G42970.1

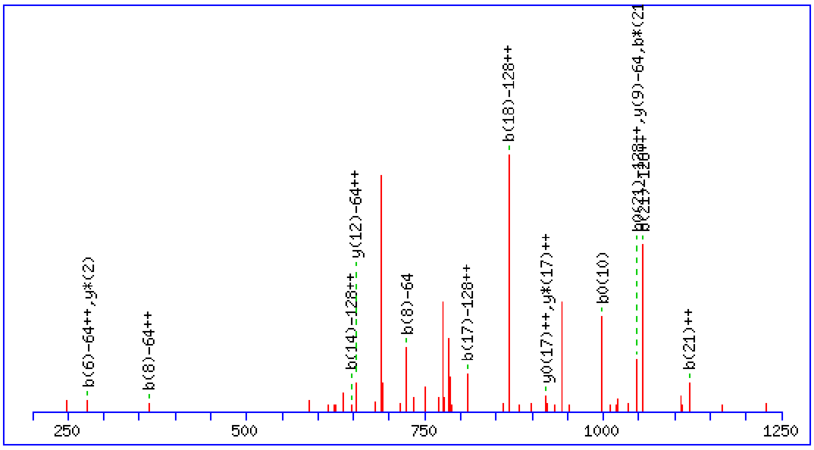
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAQMLSGIDLDSGMRAVDDNFK**
Found in **AT5G42970.1** in **TAIR_Arabidopsis**, Symbols: FUS4, EMB134, COP14, CSN4, FUS8, COP8 | COP8 (CONSTITUTIVE PHOTOMORPHOGENIC 8) | chr5:17254698-17257877 REVERSE

Match to Query 10397: 2385.100464 from(796.040764,3+) index(7217)
Title: Elution from: 63.294 to 63.294 scan no 9257 cid35.00 polarity:+
Data file C7-3_1.mgf

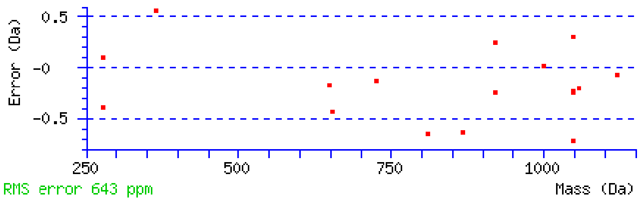
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

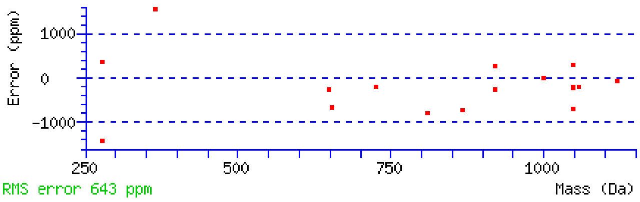


Monoisotopic mass of neutral peptide Mr(calc): 2385.0941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
M14 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 17 **Expect:** 0.046
Matches : 17/414 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**22**
2	143.0815	72.0444					**A**	2187.0677	1094.0375	2170.0411	1085.5242	2169.0571	1085.0322	**21**
3	271.1401	136.0737	254.1135	127.5604			**Q**	2116.0305	1058.5189	2099.0040	1050.0056	2098.0200	1049.5136	**20**
4	354.1772	177.5922	337.1506	169.0790			**M**	1987.9720	994.4896	1970.9454	985.9763	1969.9614	985.4843	**19**
5	467.2613	234.1343	450.2347	225.6210			**L**	1904.9348	952.9711	1887.9083	944.4578	1886.9243	943.9658	**18**
6	554.2933	***277.6503***	537.2667	269.1370	536.2827	268.6450	**S**	1791.8508	896.4290	1774.8242	887.9158	1773.8402	887.4237	**17**
7	611.3148	306.1610	594.2882	297.6477	593.3042	297.1557	**G**	1704.8188	852.9130	1687.7922	844.3997	1686.8082	843.9077	**16**
8	724.3988	***362.7030***	707.3723	354.1898	706.3883	353.6978	**I**	1647.7973	824.4023	1630.7707	815.8890	1629.7867	815.3970	**15**
9	839.4258	420.2165	822.3992	411.7032	821.4152	411.2112	**D**	1534.7132	767.8603	1517.6867	759.3470	1516.7027	758.8550	**14**
10	952.5098	476.7586	935.4833	468.2453	934.4993	467.7533	**L**	1419.6863	710.3468	1402.6597	701.8335	1401.6757	701.3415	**13**
11	1067.5368	534.2720	1050.5102	525.7587	1049.5262	525.2667	**D**	1306.6022	653.8047	1289.5757	645.2915	1288.5917	644.7995	**12**
12	1154.5688	577.7880	1137.5422	569.2748	1136.5582	568.7828	**S**	1191.5753	596.2913	1174.5487	587.7780	1173.5647	587.2860	**11**
13	1211.5903	606.2988	1194.5637	597.7855	1193.5797	597.2935	**G**	1104.5432	552.7753	1087.5167	544.2620	1086.5327	543.7700	**10**
14	1294.6274	***647.8173***	1277.6008	639.3041	1276.6168	638.8120	**M**	1047.5218	524.2645	1030.4952	515.7513	1029.5112	515.2592	**9**
15	1450.7285	725.8679	1433.7019	717.3546	1432.7179	716.8626	**R**	964.4847	482.7460	947.4581	474.2327	946.4741	473.7407	**8**
16	1521.7656	761.3864	1504.7390	752.8732	1503.7550	752.3812	**A**	808.3836	404.6954	791.3570	396.1821	790.3730	395.6901	**7**
17	1620.8340	***810.9206***	1603.8075	802.4074	1602.8234	801.9154	**V**	737.3464	369.1769	720.3199	360.6636	719.3359	360.1716	**6**
18	1735.8610	***868.4341***	1718.8344	859.9208	1717.8504	859.4288	**D**	638.2780	319.6427	621.2515	311.1294	620.2675	310.6374	**5**
19	1850.8879	925.9476	1833.8614	917.4343	1832.8773	916.9423	**D**	523.2511	262.1292	506.2245	253.6159	505.2405	253.1239	**4**
20	1964.9308	982.9691	1947.9043	974.4558	1946.9203	973.9638	**N**	408.2241	204.6157	391.1976	196.1024			**3**
21	2111.9992	***1056.5033***	2094.9727	1047.9900	2093.9887	1047.4980	**F**	294.1812	147.5942	277.1547	139.0810			**2**
22							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT5G42970.1





NCBI **BLAST** search of AAQMLSGIDLDSGMRAVDDNFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.9	2385.0941	0.0064	AAQMLSGIDLDSGMRAVDDNFK
2.5	2385.0981	0.0024	SKMDGEYQDPSIHLYIMAQK
1.9	2385.1006	-0.0001	MDYKVSRSGEIVEGEVEDSEK
1.6	2385.1006	-0.0001	VEFDEEGKVSGVTSEGETAKCK
1.6	2385.1014	-0.0010	ICDDMEESLKTMKAVLWER
0.6	2385.0988	0.0017	MSLSTFSGGSTTACAACKHQRK
0.5	2385.0974	0.0031	MSNSELMAPTNNLAMSTEKIR

Mascot: http://www.matrixscience.com/

AT5G42980.1

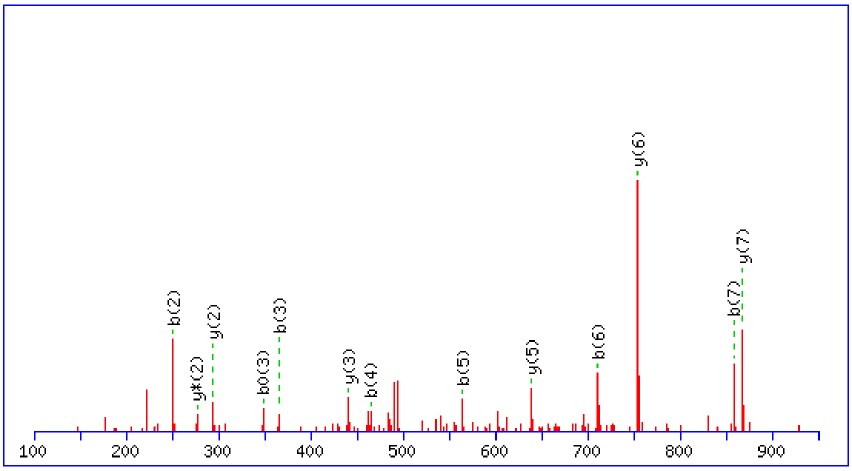
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLDVVFFK**
Found in **AT5G42980.1** in **TAIR_Arabidopsis**, Symbols: ATH3, ATTRXH3, TRXH3, ATTRX3 | ATTRX3 (thioredoxin H-type 3); thiol-disulfide exchange intermediate | chr5:17260000-17260946 FORWARD

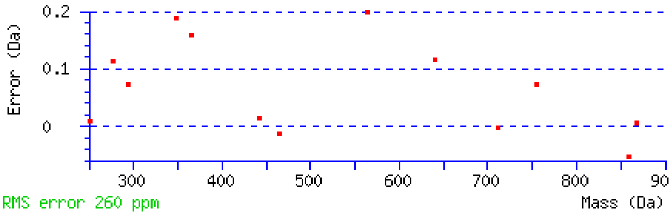
Match to Query 2475: 1003.549202 from(502.781877,2+) index(5727)
Title: Elution from: 51.387 to 51.387 scan no 7311 cid35.00 polarity:+
Data file D6h-1_3.mgf

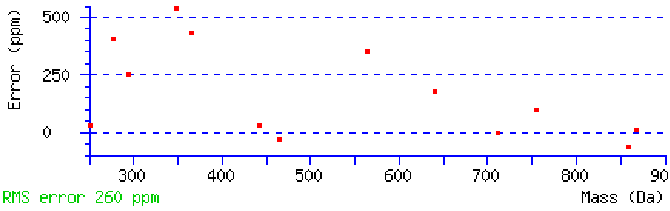
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1003.5491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00055
Matches : 13/56 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367			H							8
2	***251.1503***	126.0788			L	***867.4975***	434.2524	850.4709	425.7391	849.4869	425.2471	7
3	***366.1772***	183.5922	348.1666	174.5870	D	***754.4134***	377.7103	737.3869	369.1971	736.4028	368.7051	6
4	***465.2456***	233.1264	447.2350	224.1212	V	***639.3865***	320.1969	622.3599	311.6836			5
5	***564.3140***	282.6606	546.3035	273.6554	V	540.3180	270.6627	523.2915	262.1494			4
6	***711.3824***	356.1949	693.3719	347.1896	F	***441.2496***	221.1285	424.2231	212.6152			3
7	***858.4509***	429.7291	840.4403	420.7238	F	***294.1812***	147.5942	277.1547	139.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HLDVVFFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.4	1003.5491	0.0001	HLDVVFFK

AT5G42980.1

3.2	1003.5484	0.0008	KKPMTGQAK
3.1	1003.5464	0.0028	HRWLHQK
2.7	1003.5484	0.0008	MNRTIIEK
2.0	1003.5491	0.0001	HLLSKYFP
1.4	1003.5484	0.0008	KAAMADAAKK

Mascot: http://www.matrixscience.com/

AT5G43910.1

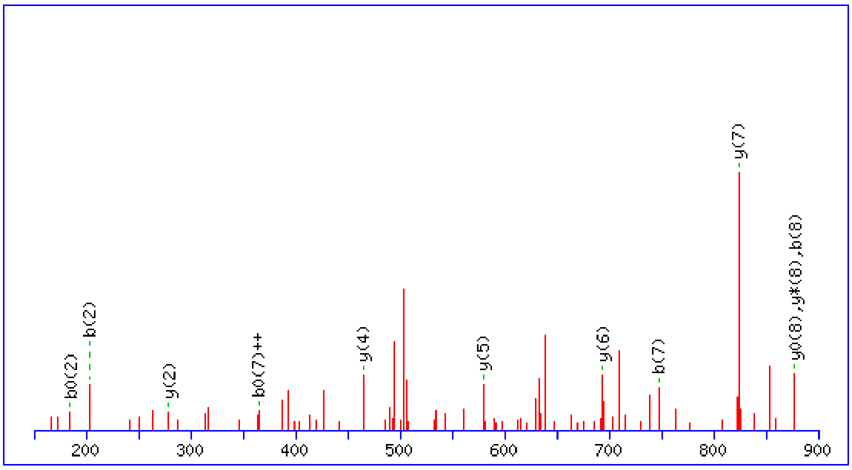
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAELLLAQK**
Found in **AT5G43910.1** in **TAIR_Arabidopsis**, Symbols: | pfkB-type carbohydrate kinase family protein | chr5:17685169-17687312 REVERSE

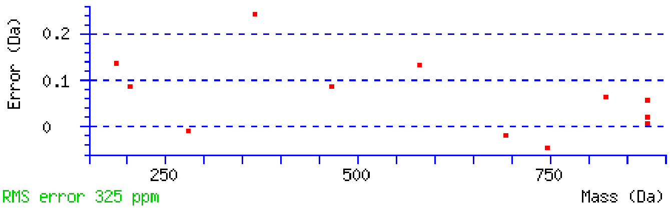
Match to Query 2674: 1024.543738 from(513.279145,2+) index(4026)
Title: Elution from: 38.877 to 38.877 scan no 5086 cid35.00 polarity:+
Data file 0-3_1.mgf

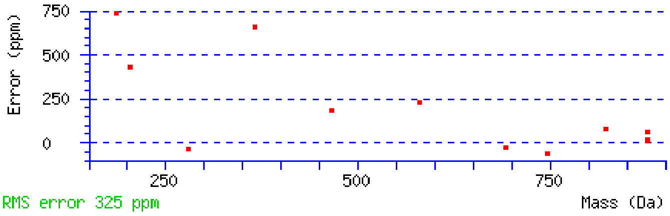
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1024.5431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0065
Matches : 12/70 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							9
2	**203.0811**	102.0442			185.0705	93.0389	A	895.5107	448.2590	877.4872	439.2472	877.5002	439.2537	8
3	333.1207	167.0640			315.1101	158.0587	E	***823.4766***	412.2419	805.4530	403.2301	805.4660	403.2367	7
4	447.2018	224.1045			429.1912	215.0992	L	***693.4370***	347.2221	675.4134	338.2103			6
5	561.2829	281.1451			543.2723	272.1398	L	***579.3559***	290.1816	561.3323	281.1698			5
6	675.3640	338.1856			657.3534	329.1803	L	***465.2748***	233.1410	447.2512	224.1292			4
7	**747.3981**	374.2027			729.3876	365.1974	A	351.1937	176.1005	333.1701	167.0887			3
8	**877.4508**	439.2290	859.4272	430.2172	859.4402	430.2237	Q	***279.1595***	140.0834	261.1359	131.0716			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EAELLLAQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.4	1024.5431	0.0006	EAELLLAQK

AT5G43910.1

12.8	1024.5458	-0.0020	TKKHQIEK
11.5	1024.5431	0.0006	SLPELSQLK
10.9	1024.5431	0.0006	AEETPKVLK
9.3	1024.5458	-0.0020	LSHSVKVGGK
8.9	1024.5431	0.0006	QSIPSIELK
8.1	1024.5431	0.0006	VDVKLESPK
6.0	1024.5431	0.0006	TDLPAIEKK
5.1	1024.5431	0.0007	TVVVGDPSLK
0.6	1024.5431	0.0006	VLGEINELK

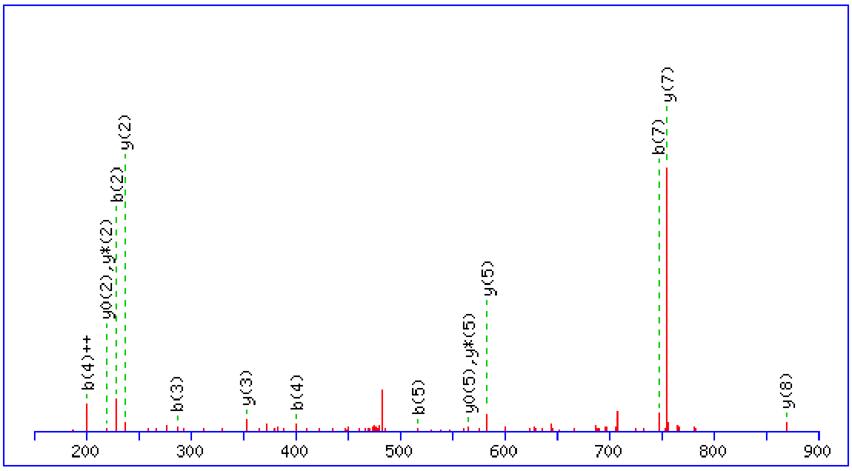
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGIDIDSK**
Found in **AT5G43940.1** in **TAIR_Arabidopsis**, Symbols: ADH2 | ADH2 (ALCOHOL DEHYDROGENASE 2); formaldehyde dehydrogenase (glutathione) | chr5:17701492-17703606 FORWARD

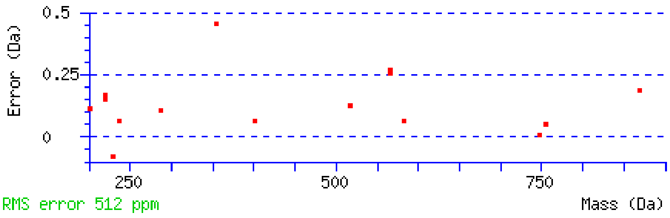
Match to Query 2456: 982.516778 from(492.265665,2+) index(5399)
Title: Elution from: 47.723 to 47.723 scan no 6753 cid35.00 polarity:+
Data file D6h-1_1.mgf

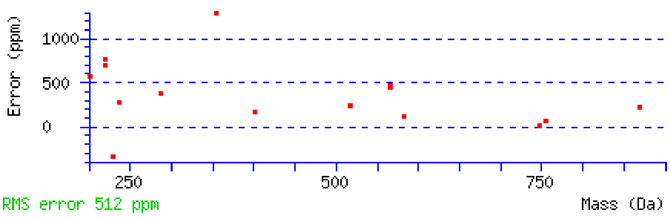
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 982.5195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0041
Matches : 15/70 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478			I							9
2	***229.1695***	115.0884			I	***869.4457***	435.2265	851.4221	426.2147	851.4351	426.2212	8
3	***287.1880***	144.0976			G	***755.3646***	378.1859	737.3410	369.1741	737.3540	369.1807	7
4	***401.2691***	201.1382			I	697.3461	349.1767	679.3225	340.1649	679.3355	340.1714	6
5	***517.2930***	259.1502	499.2825	250.1449	D	***583.2650***	292.1361	565.2414	283.1243	565.2544	283.1309	5
6	631.3741	316.1907	613.3636	307.1854	I	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
7	***747.3981***	374.2027	729.3876	365.1974	D	***353.1599***	177.0836	335.1363	168.0718	335.1493	168.0783	3
8	835.4272	418.2172	817.4166	409.2120	S	***237.1359***	119.0716	219.1124	110.0598	219.1254	110.0663	2
9					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IIGIDIDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G43940.1

31.6	982.5195	-0.0027	IIGIDIDSK
10.4	982.5195	-0.0027	LLEELAASK
4.8	982.5195	-0.0027	ILSVDLEGK
4.8	982.5148	0.0020	LIACGTPLK
4.8	982.5148	0.0020	LIPLMNQK
4.8	982.5195	-0.0027	LLEVDKEK
4.8	982.5195	-0.0027	LLQETIEK
4.8	982.5175	-0.0007	LLRPAPMR
3.9	982.5148	0.0020	LPNAIMAVK

AT5G44130.1

Mascot Search Results

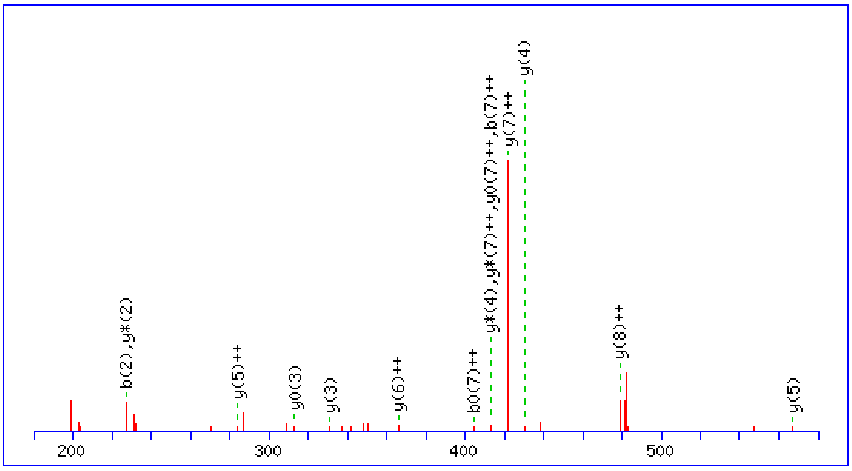
Peptide View

MS/MS Fragmentation of **LILYHVSPK**
Found in **AT5G44130.1** in **TAIR_Arabidopsis**, Symbols: FLA13 | FLA13 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 13 PRECURSOR) | chr5:17778355-17779098 FORWARD

Match to Query 2885: 1068.633267 from(357.218365,3+) index(2793)
Title: Elution from: 27.778 to 27.778 scan no 3471 cid35.00 polarity:+
Data file D6h-3_3.mgf

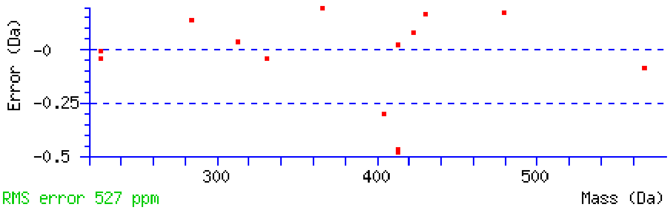
Click mouse within plot area to zoom in by factor of two about that point

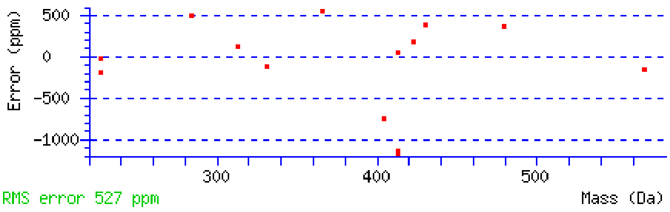
Or, Plot from 180 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1068.6331
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.014
Matches : 15/64 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			**L**							**9**
2	227.1754	114.0913			**I**	956.5564	478.7818	939.5298	470.2686	938.5458	469.7765	**8**
3	340.2595	170.6334			**L**	843.4723	422.2398	826.4458	413.7265	825.4617	413.2345	**7**
4	503.3228	252.1650			**Y**	730.3883	365.6978	713.3617	357.1845	712.3777	356.6925	**6**
5	640.3817	320.6945			**H**	***567.3249***	284.1661	550.2984	275.6528	549.3144	275.1608	**5**
6	739.4501	370.2287			**V**	***430.2660***	215.6366	413.2395	207.1234	412.2554	206.6314	**4**
7	826.4822	413.7447	808.4716	404.7394	**S**	***331.1976***	166.1024	314.1710	157.5892	313.1870	157.0972	**3**
8	923.5349	462.2711	905.5243	453.2658	**P**	244.1656	122.5864	227.1390	114.0731			**2**
9					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LILYHVSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G44130.1

18.6	1068.6331	0.0001	LILYHVSPK

Mascot: http://www.matrixscience.com/

AT5G44340.1

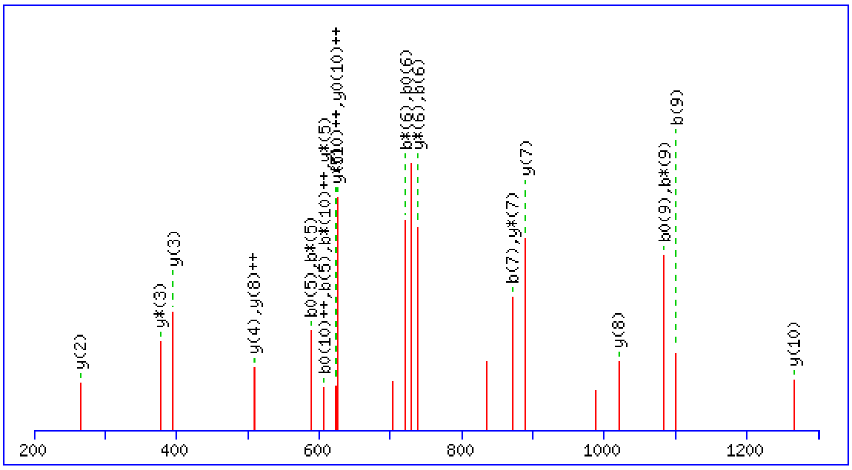
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVDEQMMNIQNK**
Found in **AT5G44340.1** in **TAIR_Arabidopsis**, Symbols: TUB4 | TUB4 (tubulin beta-4 chain) | chr5:17876669-17878221 REVERSE

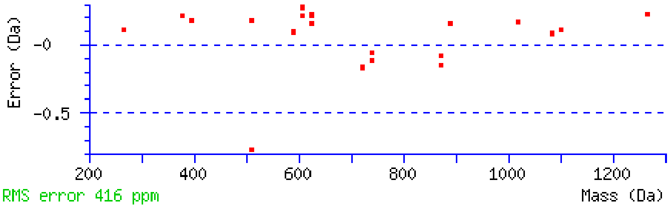
Match to Query 6590: 1494.604474 from(748.309513,2+) index(3692)
Title: Elution from: 34.650 to 34.650 scan no 4541 cid35.00 polarity:+
Data file C7-1_1.mgf

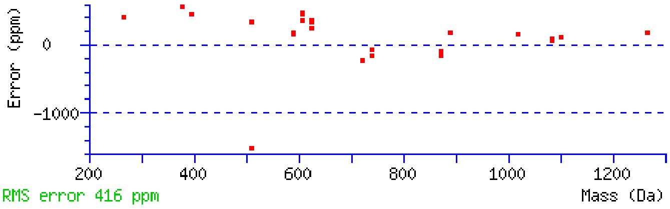
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1494.6037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 1.6e-006
Matches : 26/108 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	**E**							**12**
2	231.1124	116.0598			213.1018	107.0545	**V**	1365.5714	683.2893	1347.5478	674.2775	1347.5608	674.2840	**11**
3	347.1363	174.0718			329.1258	165.0665	**D**	***1265.5059***	633.2566	1247.4823	624.2448	1247.4953	624.2513	**10**
4	477.1760	239.0916			459.1654	230.0863	**E**	1149.4819	575.2446	1131.4583	566.2328	1131.4714	566.2393	**9**
5	**607.2286**	304.1179	589.2050	295.1061	589.2180	295.1127	**Q**	***1019.4423***	510.2248	1001.4187	501.2130			**8**
6	**739.2661**	370.1367	721.2425	361.1249	721.2556	361.1314	**M**	***889.3897***	445.1985	871.3661	436.1867			**7**
7	**871.3036**	436.1555	853.2801	427.1437	853.2931	427.1502	**M**	757.3521	379.1797	739.3285	370.1679			**6**
8	987.3406	494.1740	969.3171	485.1622	969.3301	485.1687	**N**	***625.3146***	313.1609	607.2910	304.1492			**5**
9	**1101.4217**	551.2145	1083.3982	542.2027	1083.4112	542.2092	**I**	***509.2776***	255.1424	491.2540	246.1307			**4**
10	1231.4744	616.2408	1213.4508	607.2290	1213.4638	607.2355	**Q**	***395.1965***	198.1019	377.1729	189.0901			**3**
11	1347.5114	674.2593	1329.4878	665.2475	1329.5008	665.2540	**N**	***265.1439***	133.0756	247.1203	124.0638			**2**
12							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of EVDEQMMNIQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G44340.1

Score	Mr(calc)	Delta	Sequence
63.6	1494.6037	0.0008	EVDEQMMNIQNK

Mascot: http://www.matrixscience.com/

AT5G44700.1

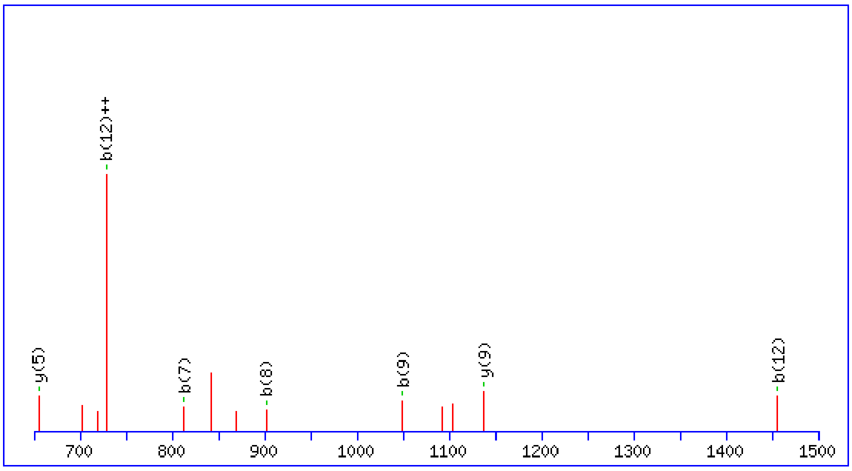
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDLMSNKSFNREVK**
Found in **AT5G44700.1** in **TAIR_Arabidopsis**, Symbols: EDA23, GSO2 | EDA23 (embryo sac development arrest 23); ATP binding / protein serine/threonine kinase | chr5:18050276-18054121 REVERSE

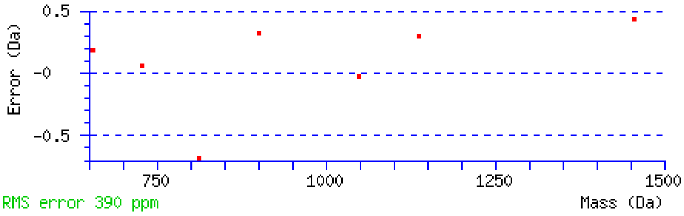
Match to Query 8439: 1702.743514 from(852.379033,2+) index(7985)
Title: Elution from: 70.111 to 70.111 scan no 10371 cid35.00 polarity:+
Data file C7-2_1.mgf

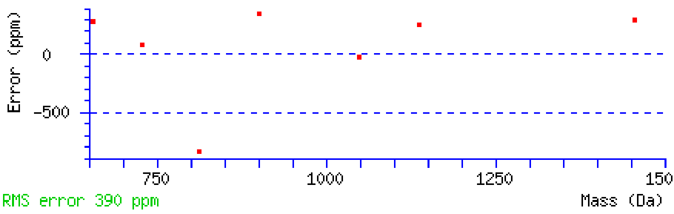
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1702.7471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.03
Matches : 7/142 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							14
2	233.0552	117.0313			215.0447	108.0260	D	1587.7304	794.3688	1569.7068	785.3570	1569.7198	785.3636	13
3	347.1363	174.0718			329.1258	165.0665	L	1471.7064	736.3568	1453.6828	727.3451	1453.6959	727.3516	12
4	479.1739	240.0906			461.1633	231.0853	M	1357.6253	679.3163	1339.6017	670.3045	1339.6148	670.3110	11
5	567.2029	284.1051			549.1923	275.0998	S	1225.5878	613.2975	1207.5642	604.2857	1207.5772	604.2923	10
6	683.2399	342.1236	665.2163	333.1118	665.2293	333.1183	N	1137.5587	569.2830	1119.5352	560.2712	1119.5482	560.2777	9
7	*813.3289*	407.1681	795.3054	398.1563	795.3184	398.1628	K	1021.5217	511.2645	1003.4982	502.2527	1003.5112	502.2592	8
8	*901.3580*	451.1826	883.3344	442.1708	883.3474	442.1774	S	891.4327	446.2200	873.4091	437.2082	873.4221	437.2147	7
9	*1049.4235*	525.2154	1031.3999	516.2036	1031.4129	516.2101	F	803.4036	402.2055	785.3801	393.1937	785.3931	393.2002	6
10	1165.4605	583.2339	1147.4369	574.2221	1147.4499	574.2286	N	655.3382	328.1727	637.3146	319.1609	637.3276	319.1675	5
11	1325.5497	663.2785	1307.5261	654.2667	1307.5391	654.2732	R	539.3012	270.1542	521.2776	261.1424	521.2906	261.1490	4
12	*1455.5893*	728.2983	1437.5657	719.2865	1437.5788	719.2930	E	379.2120	190.1096	361.1884	181.0978	361.2014	181.1043	3
13	1555.6548	778.3310	1537.6312	769.3192	1537.6442	769.3257	V	249.1723	125.0898	231.1487	116.0780			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DDLMSNKSFNREVK

AT5G44700.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	1702.7471	-0.0036	DDLMSNKSFNREVK
22.0	1702.7442	-0.0007	MVPFAGWSMPIQYK
2.8	1702.7393	0.0042	SSASSSSASDLLRREQ
2.8	1702.7401	0.0034	TGSRSDVCIMKGDVR

Mascot: http://www.matrixscience.com/

AT5G44720.1

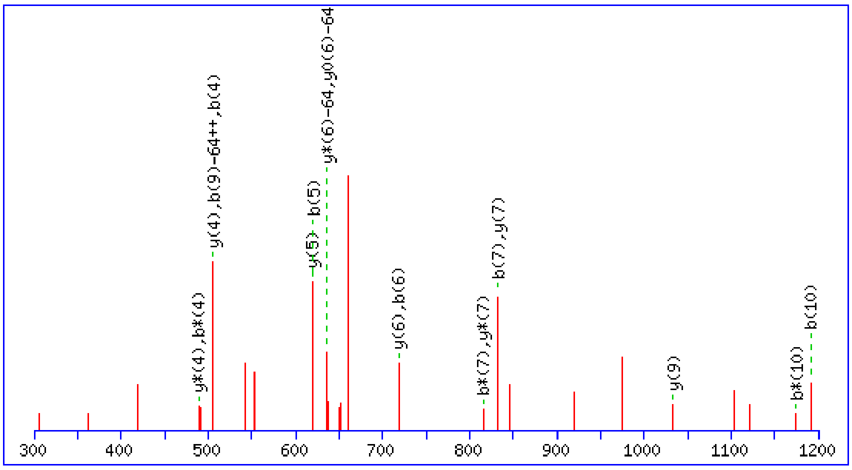
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FRSDNVLMPDK**
Found in **AT5G44720.1** in **TAIR_Arabidopsis**, Symbols: | molybdenum cofactor sulfurase family protein | chr5:18060313-18062502 FORWARD

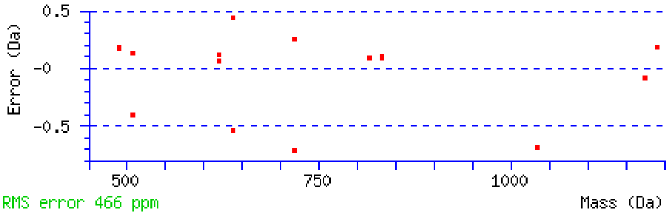
Match to Query 5051: 1336.645502 from(669.330027,2+) index(1720)
Title: Elution from: 21.716 to 21.716 scan no 2258 cid35.00 polarity:+
Data file D6h-3_1.mgf

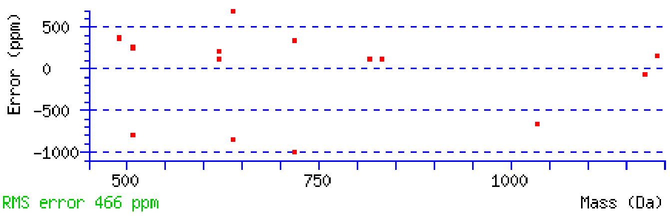
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1336.6445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 **Expect:** 0.0045
Matches : 18/172 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							11
2	304.1768	152.5920	287.1503	144.0788			R	1190.5834	595.7953	1173.5568	587.2821	1172.5728	586.7901	10
3	391.2088	196.1081	374.1823	187.5948	373.1983	187.1028	S	***1034.4823***	517.7448	1017.4557	509.2315	1016.4717	508.7395	9
4	***506.2358***	253.6215	489.2092	245.1082	488.2252	244.6162	D	947.4503	474.2288	930.4237	465.7155	929.4397	465.2235	8
5	***620.2787***	310.6430	603.2522	302.1297	602.2681	301.6377	N	***832.4233***	416.7153	815.3968	408.2020	814.4128	407.7100	7
6	***719.3471***	360.1772	702.3206	351.6639	701.3365	351.1719	V	***718.3804***	359.6938	701.3538	351.1806	700.3698	350.6886	6
7	***832.4312***	416.7192	815.4046	408.2060	814.4206	407.7139	L	***619.3120***	310.1596	602.2854	301.6464	601.3014	301.1543	5
8	979.4666	490.2369	962.4400	481.7237	961.4560	481.2316	M	***506.2279***	253.6176	489.2014	245.1043	488.2173	244.6123	4
9	1076.5193	538.7633	1059.4928	530.2500	1058.5088	529.7580	P	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
10	***1191.5463***	596.2768	1174.5197	587.7635	1173.5357	587.2715	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FRSDNVLMPDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G44720.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.1	1336.6445	0.0010	FRSDNVLMPDK
19.5	1336.6479	-0.0024	SMALAEMVNVTR
5.9	1336.6470	-0.0015	SVASLSQSESGASK
2.0	1336.6445	0.0010	TNCILEAFGNAK
1.7	1336.6486	-0.0031	MFNPVDLPNFK
1.7	1336.6445	0.0010	RIGDDDCFVLK
0.1	1336.6484	-0.0029	YGARGDGRADATK

AT5G45080.1

Mascot Search Results

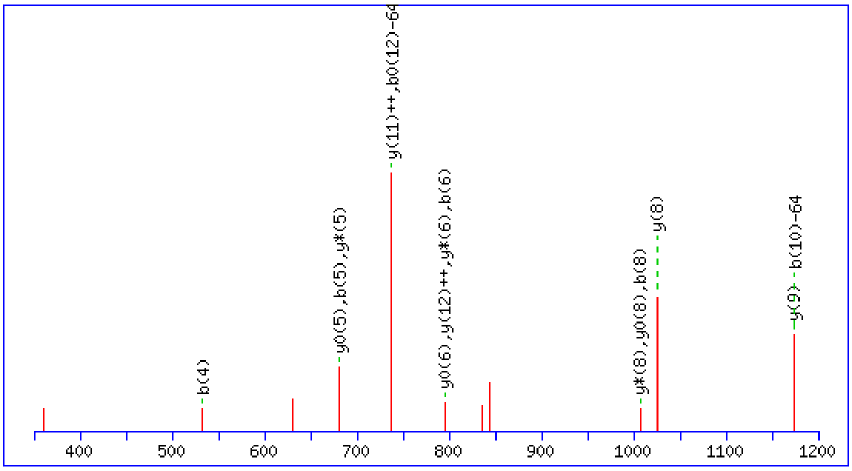
Peptide View

MS/MS Fragmentation of **NNRHMLPITQKWK**
Found in **AT5G45080.1** in **TAIR_Arabidopsis**, Symbols: ATPP2-A6 | ATPP2-A6 (Phloem protein 2-A6); transmembrane receptor | chr5:18208802-18210434 REVERSE

Match to Query 8114: 1704.814370 from(853.414461,2+) index(8014)
Title: Elution from: 70.458 to 70.458 scan no 10487 cid35.00 polarity:+
Data file D12h-1_2.mgf

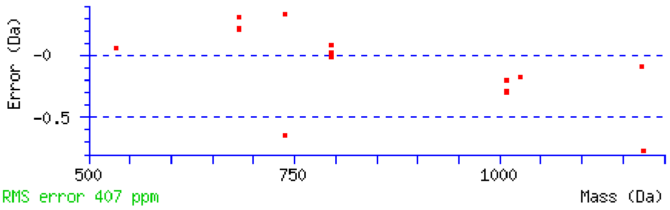
Click mouse within plot area to zoom in by factor of two about that point

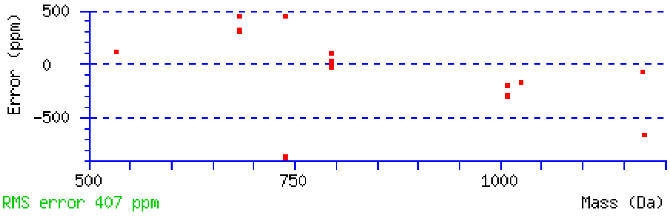
Or, Plot from 350 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1704.8171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 **Expect:** 0.006
Matches : 17/184 fragment ions using 13 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	117.0443	59.0258	99.0207	50.0140			N							13
2	233.0813	117.0443	215.0577	108.0325			N	1589.7873	795.3973	1571.7638	786.3855	1571.7768	786.3920	12
3	393.1705	197.0889	375.1469	188.0771			R	1473.7503	737.3788	1455.7268	728.3670	1455.7398	728.3735	11
4	***533.2205***	267.1139	515.1970	258.1021			H	1313.6611	657.3342	1295.6375	648.3224	1295.6505	648.3289	10
5	***681.2530***	341.1301	663.2294	332.1183			M	**1173.6111**	587.3092	1155.5875	578.2974	1155.6005	578.3039	9
6	***795.3341***	398.1707	777.3105	389.1589			L	**1025.5786**	513.2930	1007.5551	504.2812	1007.5681	504.2877	8
7	893.3839	447.1956	875.3603	438.1838			P	911.4975	456.2524	893.4740	447.2406	893.4870	447.2471	7
8	***1007.4650***	504.2361	989.4414	495.2243			I	813.4477	407.2275	795.4242	398.2157	795.4372	398.2222	6
9	1109.5097	555.2585	1091.4861	546.2467	1091.4991	546.2532	T	699.3666	350.1870	681.3431	341.1752	681.3561	341.1817	5
10	1239.5623	620.2848	1221.5387	611.2730	1221.5518	611.2795	Q	597.3219	299.1646	579.2984	290.1528			4
11	1369.6514	685.3293	1351.6278	676.3175	1351.6408	676.3240	K	467.2693	234.1383	449.2457	225.1265			3
12	1557.7247	779.3660	1539.7012	770.3542	1539.7142	770.3607	W	337.1803	169.0938	319.1567	160.0820			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NNRHMLPITQKWK

AT5G45080.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.3	1704.8171	-0.0027	NNRHMLPITQKWK
3.1	1704.8169	-0.0025	TEDPEIAQTARPKTK
2.5	1704.8121	0.0022	LTGSAKIRAGSYSGGMK
2.2	1704.8191	-0.0048	HDSVDGPSYNLLLKK
1.7	1704.8169	-0.0025	NIQVVDSSNNLKEPK
1.4	1704.8169	-0.0025	DITQLVEIRPESER
1.3	1704.8117	0.0026	LNQTSFSSLVMAYVK
0.6	1704.8121	0.0022	RILDEKHMDLAQAK

Mascot: http://www.matrixscience.com/

AT5G45140.1

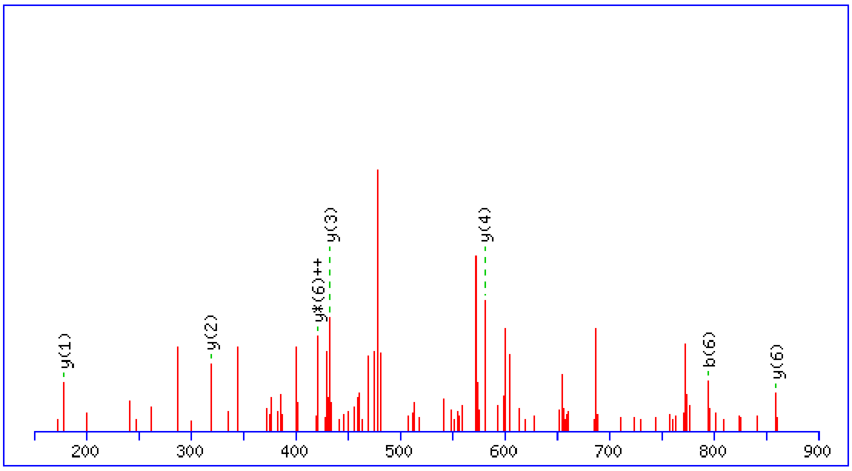
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYLFLHR**
Found in **AT5G45140.1** in **TAIR_Arabidopsis**, Symbols: NRPC2 | NRPC2 (nuclear RNA polymerase C 2); DNA binding / DNA-directed RNA polymerase | chr5:18264643-18274940 REVERSE

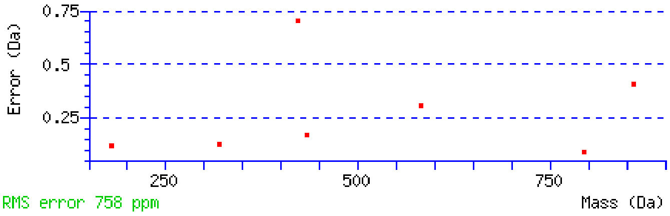
Match to Query 2239: 972.521206 from(487.267879,2+) index(3493)
Title: Elution from: 34.937 to 34.937 scan no 4408 cid35.00 polarity:+
Data file 0-3_1.mgf

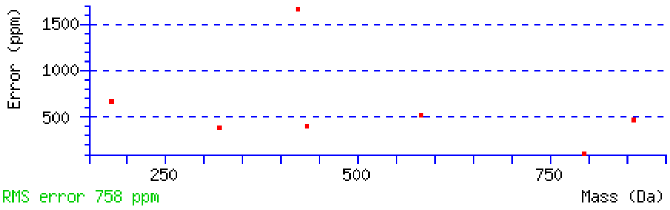
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 972.5189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.027
Matches : 7/36 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	115.0884	58.0478	I					7
2	279.1487	140.0780	Y	***859.4451***	430.2262	841.4215	421.2144	6
3	393.2298	197.1186	L	695.3848	348.1960	677.3612	339.1842	5
4	541.2953	271.1513	F	***581.3037***	291.1555	563.2801	282.1437	4
5	655.3764	328.1918	L	***433.2382***	217.1227	415.2146	208.1109	3
6	795.4264	398.2168	H	***319.1571***	160.0822	301.1335	151.0704	2
7			R	***179.1071***	90.0572	161.0835	81.0454	1





NCBI **BLAST** search of IYLFLHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.0	972.5189	0.0023	IYLFLHR
6.1	972.5201	0.0011	KDALKVMR

AT5G45140.1

Mascot: http://www.matrixscience.com/

AT5G45360.1

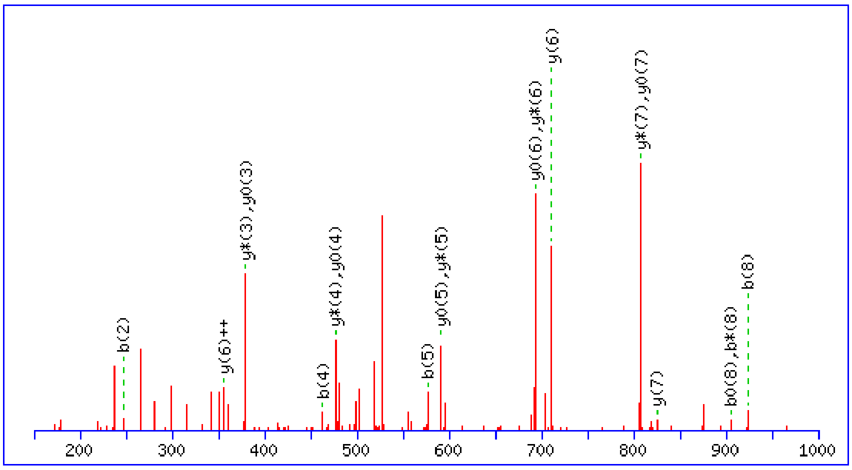
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WGLTLPSRK**
Found in **AT5G45360.1** in **TAIR_Arabidopsis**, Symbols: | F-box family protein | chr5:18402010-18403897 REVERSE

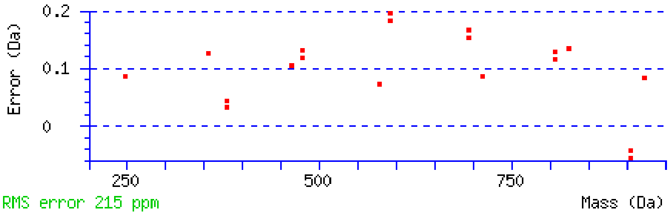
Match to Query 2687: 1070.568342 from(536.291447,2+) index(7136)
Title: Elution from: 64.348 to 64.348 scan no 9419 cid35.00 polarity:+
Data file D1d-2_3.mgf

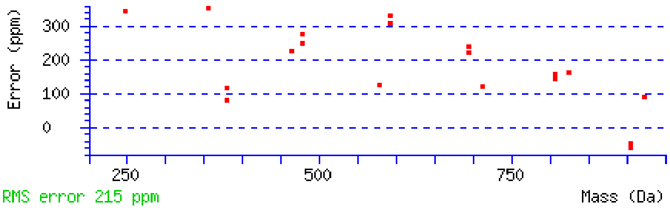
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1070.5665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.043
Matches : 19/72 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	189.0807	95.0440					W							9
2	***247.0992***	124.0532					G	883.5004	442.2538	865.4768	433.2420	865.4898	433.2486	8
3	361.1803	181.0938					L	**825.4819**	413.2446	807.4583	404.2328	807.4713	404.2393	7
4	***463.2250***	232.1161			445.2144	223.1108	T	**711.4008**	356.2040	693.3772	347.1922	693.3902	347.1988	6
5	***577.3061***	289.1567			559.2955	280.1514	L	609.3561	305.1817	591.3325	296.1699	591.3455	296.1764	5
6	675.3559	338.1816			657.3453	329.1763	P	495.2750	248.1411	477.2514	239.1293	477.2644	239.1358	4
7	763.3849	382.1961			745.3744	373.1908	S	397.2252	199.1162	379.2016	190.1044	379.2146	190.1109	3
8	***923.4742***	462.2407	905.4506	453.2289	905.4636	453.2354	R	309.1961	155.1017	291.1725	146.0899			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of WGLTLPSRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	1070.5665	0.0018	WGLTLPSRK

AT5G45360.1

9.9	1070.5672	0.0011	KLTEMTPLK
6.8	1070.5672	0.0011	LMVISEKPK
1.5	1070.5672	0.0011	METNLLLVK
0.9	1070.5699	-0.0015	IMGRDKPIK
0.4	1070.5672	0.0011	NLMLLIDTK

AT5G45390.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **RFAMPNTR**
Found in **AT5G45390.1** in **TAIR_Arabidopsis**, Symbols: NCLPP3, NCLPP4, CLPP4 | CLPP4 (Clp protease proteolytic subunit 4); endopeptidase Clp | chr5:18413578-18414813 FORWARD

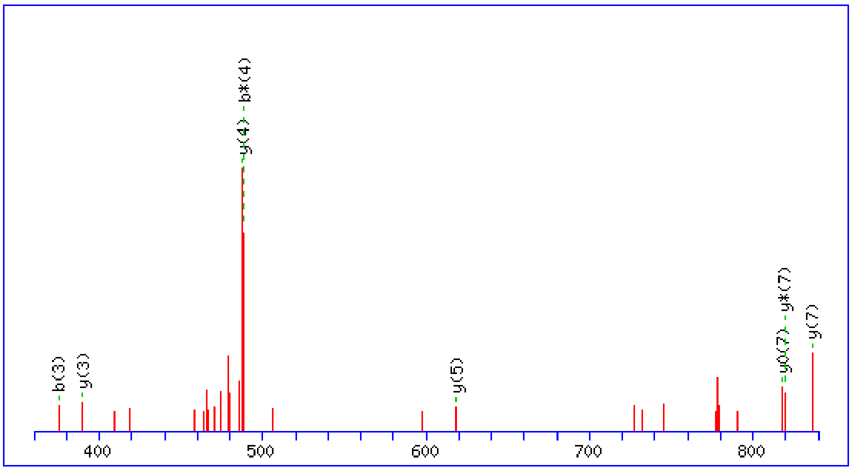
Match to Query 2466: 991.502676 from(496.758614,2+) index(1415)
Title: Elution from: 18.753 to 18.753 scan no 1896 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 360 to 840 Da Full range

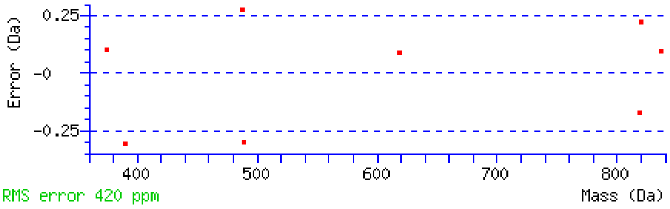
Label all possible matches ○ Label matches used for scoring ●

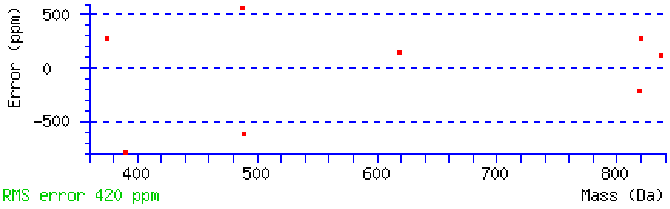
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 991.5022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.025
Matches : 9/70 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			**R**							**8**
2	304.1768	152.5920	287.1503	144.0788			**F**	***836.4083***	418.7078	819.3818	410.1945	818.3978	409.7025	**7**
3	**375.2139**	188.1106	358.1874	179.5973			**A**	689.3399	345.1736	672.3134	336.6603	671.3294	336.1683	**6**
4	506.2544	253.6308	489.2279	245.1176			**M**	***618.3028***	309.6550	601.2763	301.1418	600.2922	300.6498	**5**
5	603.3072	302.1572	586.2806	293.6439			**P**	***487.2623***	244.1348	470.2358	235.6215	469.2518	235.1295	**4**
6	717.3501	359.1787	700.3235	350.6654			**N**	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	**3**
7	**818.3978**	409.7025	801.3712	401.1892	800.3872	400.6972	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
8							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of RFAMPNTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.4	991.5022	0.0005	RFAMPNTR

AT5G45390.1

11.5	991.5008	0.0018	MLVGGSGDIK
10.9	991.5047	-0.0020	SASESRVTR
10.7	991.5055	-0.0028	RGKMPTMR
7.6	991.5021	0.0005	RAMWERK
7.4	991.5008	0.0019	MEVELLSR
6.1	991.5055	-0.0028	MAARGAMLR
5.4	991.5008	0.0018	NVLVTGDMK
2.9	991.5055	-0.0028	RGKMPTMR
2.1	991.5008	0.0019	VMANSLVDK

AT5G45470.1

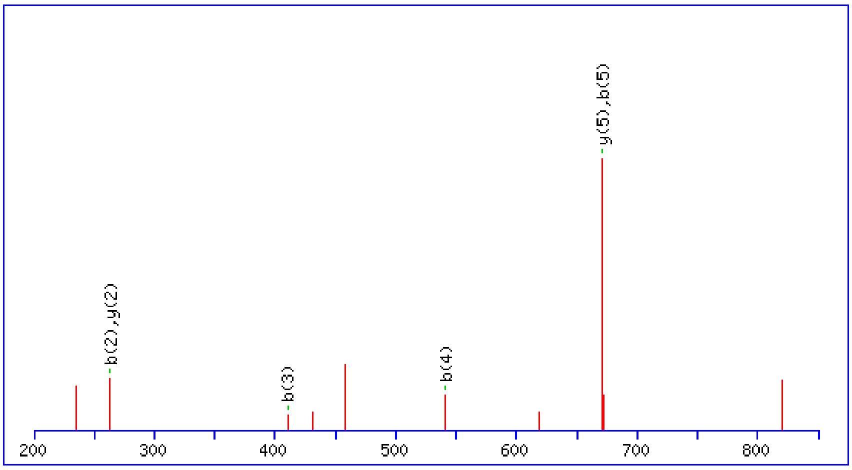
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FIFEELK**
Found in **AT5G45470.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45530.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45540.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45460.1); similar to unnamed protein

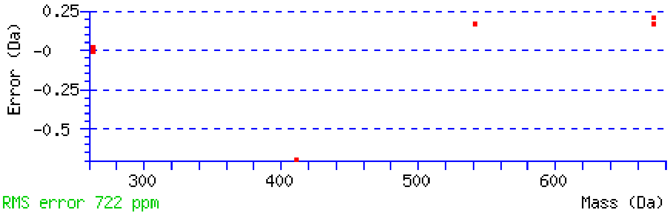
Match to Query 2007: 932.473452 from(467.244002,2+) index(8171)
Title: Elution from: 71.749 to 71.749 scan no 10640 cid35.00 polarity:+
Data file C7-2_1.mgf

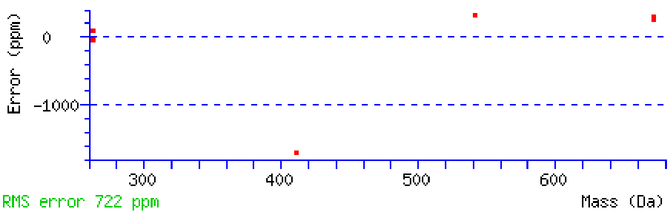
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 932.4719
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.045
Matches : 6/50 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0727	75.0400			F							7
2	***263.1538***	132.0805			I	785.4138	393.2105	767.3902	384.1987	767.4032	384.2052	6
3	***411.2193***	206.1133			F	**671.3327**	336.1700	653.3091	327.1582	653.3221	327.1647	5
4	***541.2589***	271.1331	523.2483	262.1278	E	523.2672	262.1373	505.2436	253.1255	505.2567	253.1320	4
5	***671.2985***	336.1529	653.2880	327.1476	E	393.2276	197.1174	375.2040	188.1056	375.2170	188.1122	3
6	785.3796	393.1935	767.3691	384.1882	L	**263.1880**	132.0976	245.1644	123.0858			2
7					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FIFEELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.7	932.4719	0.0015	FIFEELK

AT5G45470.1

21.5	932.4724	0.0011	LFKDDKR
16.3	932.4724	0.0011	FLKEQTR
12.6	932.4719	0.0015	FLFELEK
12.6	932.4724	0.0011	GSFNQKLK
10.5	932.4746	-0.0012	IFNIYPR
10.5	932.4746	-0.0012	IFVGPFSR
10.5	932.4724	0.0011	IPNHEAIK
10.5	932.4753	-0.0019	LYMELLK
10.4	932.4746	-0.0012	FIQVYPR

Mascot: http://www.matrixscience.com/

AT5G45620.1

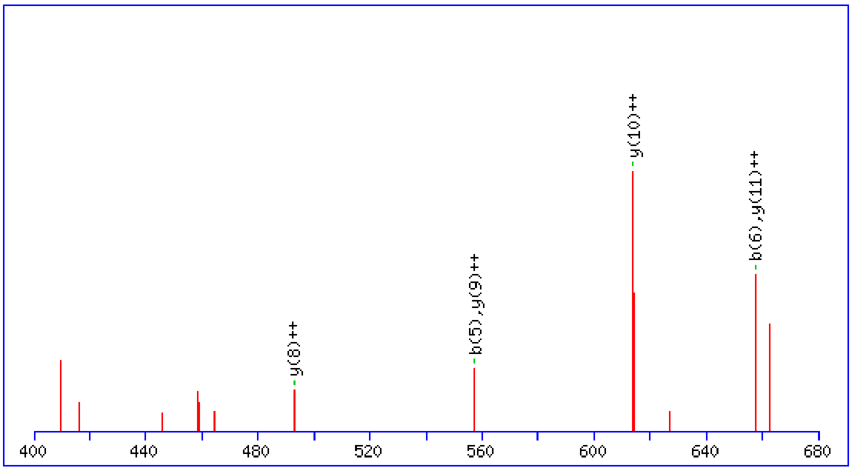
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSIEDVEHLLMK**
Found in **AT5G45620.1** in **TAIR_Arabidopsis**, Symbols: | 26S proteasome regulatory subunit, putative (RPN9) | chr5:18518817-18521095 FORWARD

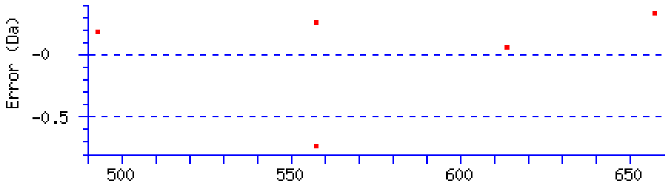
Match to Query 5496: 1425.755727 from(476.259185,3+) index(10719)
Title: Elution from: 103.581 to 103.581 scan no 15423 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 680 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

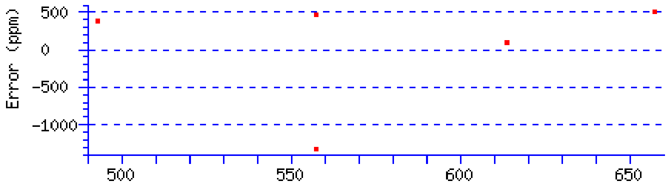


Monoisotopic mass of neutral peptide Mr(calc): 1425.7537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0028
Matches : 6/98 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							12
2	201.1234	101.0653	183.1128	92.0600	S	1313.6770	657.3421	1296.6504	648.8288	1295.6664	648.3368	11
3	314.2074	157.6074	296.1969	148.6021	I	1226.6449	613.8261	1209.6184	605.3128	1208.6344	604.8208	10
4	443.2500	222.1287	425.2395	213.1234	E	1113.5609	557.2841	1096.5343	548.7708	1095.5503	548.2788	9
5	**558.2770**	279.6421	540.2664	270.6368	D	984.5183	492.7628	967.4917	484.2495	966.5077	483.7575	8
6	**657.3454**	329.1763	639.3348	320.1710	V	869.4913	435.2493	852.4648	426.7360	851.4808	426.2440	7
7	786.3880	393.6976	768.3774	384.6923	E	770.4229	385.7151	753.3964	377.2018	752.4124	376.7098	6
8	923.4469	462.2271	905.4363	453.2218	H	641.3803	321.1938	624.3538	312.6805			5
9	1036.5310	518.7691	1018.5204	509.7638	L	504.3214	252.6643	487.2949	244.1511			4
10	1149.6150	575.3111	1131.6044	566.3059	L	391.2374	196.1223	374.2108	187.6090			3
11	1280.6555	640.8314	1262.6449	631.8261	M	278.1533	139.5803	261.1267	131.0670			2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 659 ppm



RMS error 659 ppm

NCBI **BLAST** search of LSIEDVEHLLMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G45620.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.3	1425.7537	0.0020	LSIEDVEHLLMK
5.7	1425.7576	-0.0018	SILSGSYLTSSRR
1.4	1425.7537	0.0020	TLPGEICELPGLK

AT5G45680.1

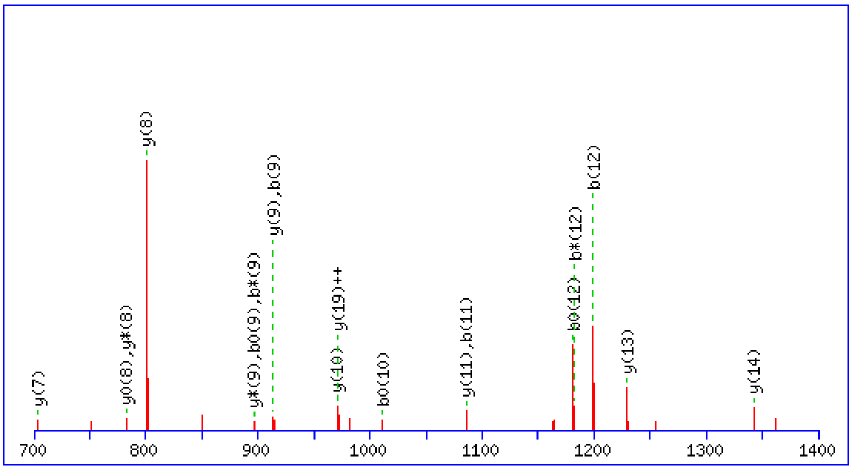
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GWDQGILGSDGIPPMLTGGK**
Found in **AT5G45680.1** in **TAIR_Arabidopsis**, Symbols: | FK506-binding protein 1 (FKBP13) | chr5:18548121-18549355 FORWARD

Match to Query 9397: 1997.985738 from(1000.000145,2+) index(10195)
Title: Elution from: 96.018 to 96.018 scan no 14300 cid35.00 polarity:+
Data file D1d-2_1.mgf

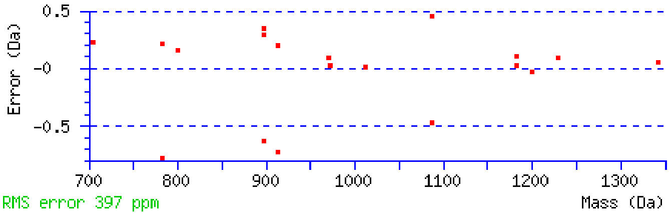
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 700 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

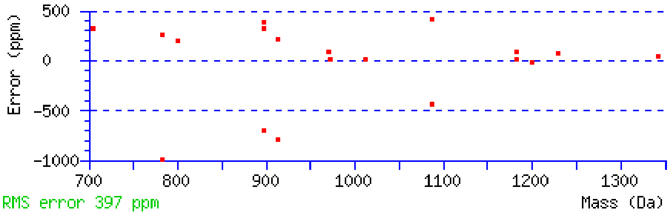


Monoisotopic mass of neutral peptide Mr(calc): 1997.9881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00028
Matches : 19/212 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							20
2	244.1081	122.5577					W	1941.9739	971.4906	1924.9473	962.9773	1923.9633	962.4853	19
3	359.1350	180.0711			341.1244	171.0659	D	1755.8946	878.4509	1738.8680	869.9376	1737.8840	869.4456	18
4	487.1936	244.1004	470.1670	235.5872	469.1830	235.0951	Q	1640.8676	820.9374	1623.8411	812.4242	1622.8571	811.9322	17
5	544.2150	272.6112	527.1885	264.0979	526.2045	263.6059	G	1512.8090	756.9082	1495.7825	748.3949	1494.7985	747.9029	16
6	657.2991	329.1532	640.2726	320.6399	639.2885	320.1479	I	1455.7876	728.3974	1438.7610	719.8842	1437.7770	719.3921	15
7	770.3832	385.6952	753.3566	377.1819	752.3726	376.6899	L	***1342.7035***	671.8554	1325.6770	663.3421	1324.6929	662.8501	14
8	827.4046	414.2060	810.3781	405.6927	809.3941	405.2007	G	***1229.6195***	615.3134	1212.5929	606.8001	1211.6089	606.3081	13
9	**914.4367**	457.7220	897.4101	449.2087	896.4261	448.7167	S	1172.5980	586.8026	1155.5714	578.2894	1154.5874	577.7973	12
10	1029.4636	515.2354	1012.4371	506.7222	1011.4530	506.2302	D	***1085.5660***	543.2866	1068.5394	534.7733	1067.5554	534.2813	11
11	**1086.4851**	543.7462	1069.4585	535.2329	1068.4745	534.7409	G	***970.5390***	485.7731	953.5125	477.2599	952.5285	476.7679	10
12	**1199.5691**	600.2882	1182.5426	591.7749	1181.5586	591.2829	I	***913.5176***	457.2624	896.4910	448.7491	895.5070	448.2571	9
13	1296.6219	648.8146	1279.5953	640.3013	1278.6113	639.8093	P	***800.4335***	400.7204	783.4069	392.2071	782.4229	391.7151	8
14	1393.6747	697.3410	1376.6481	688.8277	1375.6641	688.3357	P	***703.3807***	352.1940	686.3542	343.6807	685.3702	343.1887	7
15	1524.7151	762.8612	1507.6886	754.3479	1506.7046	753.8559	M	606.3280	303.6676	589.3014	295.1543	588.3174	294.6623	6
16	1637.7992	819.4032	1620.7727	810.8900	1619.7886	810.3980	L	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	5
17	1738.8469	869.9271	1721.8203	861.4138	1720.8363	860.9218	T	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	4
18	1795.8683	898.4378	1778.8418	889.9245	1777.8578	889.4325	G	261.1557	131.0815	244.1292	122.5682			3
19	1852.8898	926.9485	1835.8633	918.4353	1834.8792	917.9433	G	204.1343	102.5708	187.1077	94.0575			2
20							K	147.1128	74.0600	130.0863	65.5468			1

AT5G45680.1





NCBI **BLAST** search of GWDQGILGSDGIPPMLTGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.3	1997.9881	-0.0023	GWDQGILGSDGIPPMLTGGK
3.5	1997.9914	-0.0057	LQELGPMTQMQDPPLLR

Mascot: http://www.matrixscience.com/

AT5G45930.1

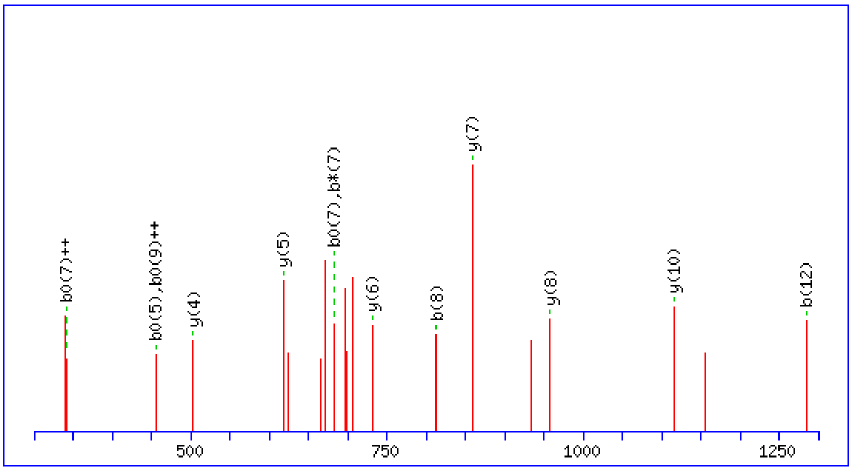
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SNLSAVQIDQDLK**
Found in **AT5G45930.1** in **TAIR_Arabidopsis**, Symbols: CHL I2, CHLI-2, CHLI2 | CHLI2; magnesium chelatase | chr5:18645322-18646792 FORWARD

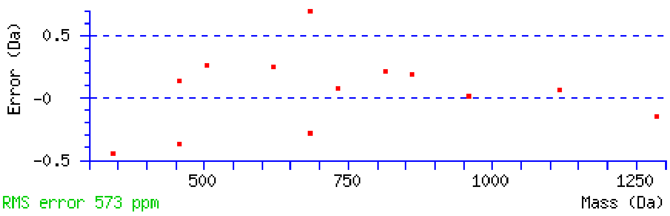
Match to Query 5708: 1429.741504 from(715.878028,2+) index(5135)
Title: Elution from: 45.940 to 45.940 scan no 6422 cid35.00 polarity:+
Data file D12h-1_2.mgf

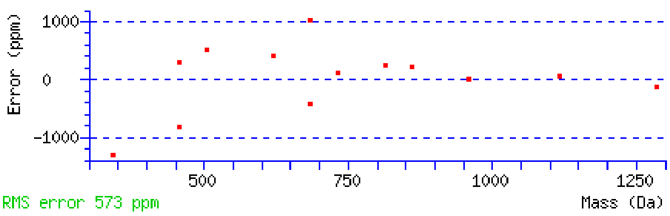
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1429.7413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00014
Matches : 13/138 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	N	1343.7165	672.3619	1326.6900	663.8486	1325.7060	663.3566	12
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	L	1229.6736	615.3404	1212.6470	606.8272	1211.6630	606.3352	11
4	402.1983	201.6028	385.1718	193.0895	384.1878	192.5975	S	***1116.5895***	558.7984	1099.5630	550.2851	1098.5790	549.7931	10
5	473.2354	237.1214	456.2089	228.6081	455.2249	228.1161	A	1029.5575	515.2824	1012.5310	506.7691	1011.5469	506.2771	9
6	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	V	***958.5204***	479.7638	941.4938	471.2506	940.5098	470.7585	8
7	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	Q	***859.4520***	430.2296	842.4254	421.7164	841.4414	421.2243	7
8	**813.4465**	407.2269	796.4199	398.7136	795.4359	398.2216	I	***731.3934***	366.2003	714.3668	357.6871	713.3828	357.1951	6
9	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	D	***618.3093***	309.6583	601.2828	301.1450	600.2988	300.6530	5
10	1056.5320	528.7696	1039.5055	520.2564	1038.5214	519.7644	Q	***503.2824***	252.1448	486.2558	243.6316	485.2718	243.1396	4
11	1171.5590	586.2831	1154.5324	577.7698	1153.5484	577.2778	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
12	**1284.6430**	642.8251	1267.6165	634.3119	1266.6325	633.8199	L	260.1969	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SNLSAVQIDQDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G45930.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.2	1429.7413	0.0002	SNLSAVQIDQDLK

Mascot: http://www.matrixscience.com/

AT5G46110.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLNHGFADAIAK**
Found in **AT5G46110.1** in **TAIR_Arabidopsis**, Symbols: TPT, APE2 | APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT); antiporter/ triose-phosphate transmembrane transporter | chr5:18714833-18717439 FORWARD

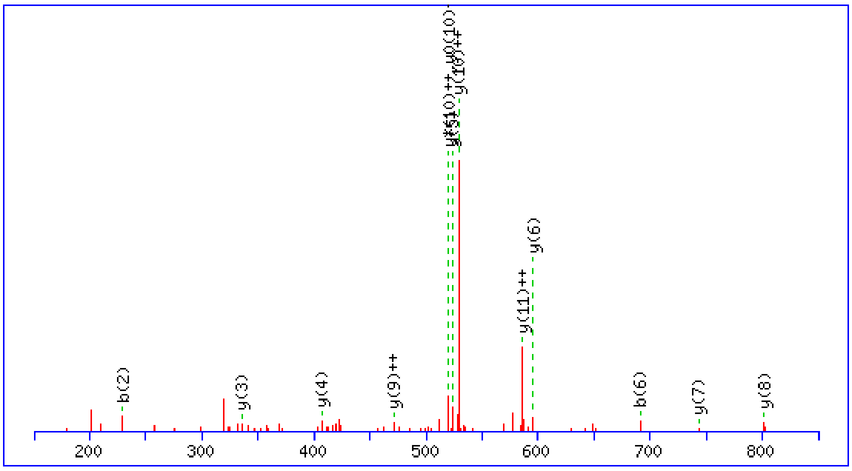
Match to Query 4618: 1284.639819 from(429.220549,3+) index(3764)
Title: Elution from: 36.037 to 36.037 scan no 4728 cid35.00 polarity:+
Data file 0-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 850 Da Full range

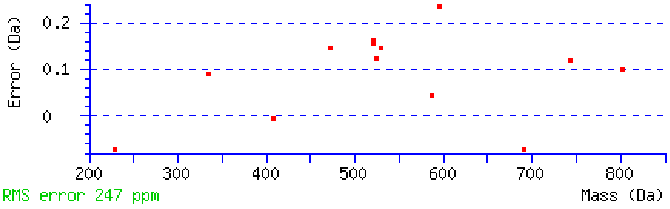
Label all possible matches ○ Label matches used for scoring ●

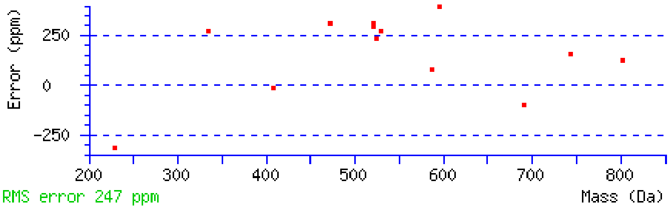
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1284.6403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00011
Matches : 13/106 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478					**L**							**12**
2	**229.1695**	115.0884					**L**	1171.5665	586.2869	1153.5429	577.2751	1153.5559	577.2816	**11**
3	345.2065	173.1069	327.1829	164.0951			**N**	1057.4854	529.2463	1039.4618	520.2345	1039.4748	520.2410	**10**
4	485.2565	243.1319	467.2329	234.1201			**H**	941.4484	471.2278	923.4248	462.2160	923.4378	462.2225	**9**
5	543.2750	272.1411	525.2514	263.1293			**G**	***801.3983***	401.2028	783.3748	392.1910	783.3878	392.1975	**8**
6	**691.3404**	346.1739	673.3169	337.1621			**F**	***743.3798***	372.1936	725.3563	363.1818	725.3693	363.1883	**7**
7	763.3746	382.1909	745.3510	373.1791			**A**	***595.3144***	298.1608	577.2908	289.1490	577.3038	289.1556	**6**
8	879.3986	440.2029	861.3750	431.1911	861.3880	431.1976	**D**	***523.2802***	262.1438	505.2567	253.1320	505.2697	253.1385	**5**
9	951.4327	476.2200	933.4091	467.2082	933.4221	467.2147	**A**	***407.2563***	204.1318	389.2327	195.1200			**4**
10	1065.5138	533.2605	1047.4902	524.2488	1047.5032	524.2553	**I**	***335.2221***	168.1147	317.1985	159.1029			**3**
11	1137.5480	569.2776	1119.5244	560.2658	1119.5374	560.2723	**A**	221.1410	111.0741	203.1174	102.0624			**2**
12							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of LLNHGFADAIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G46110.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.4	1284.6403	-0.0005	LLNHGFADAIAK
2.5	1284.6362	0.0036	YMKLMNTVKK
0.4	1284.6403	-0.0005	AATASLSAFFRK

AT5G46160.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDDNAVVLVDSKDK**
Found in **AT5G46160.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L14 family protein / huellenlos paralog (HLP) | chr5:18728683-18729568 REVERSE

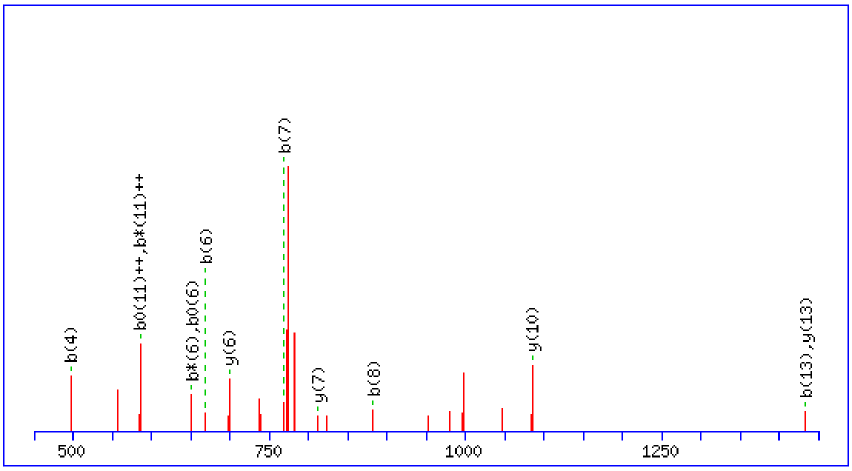
Match to Query 7017: 1580.729462 from(791.372007,2+) index(7215)
Title: Elution from: 66.569 to 66.569 scan no 9505 cid35.00 polarity:+
Data file D12h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 450 to 1450 Da Full range

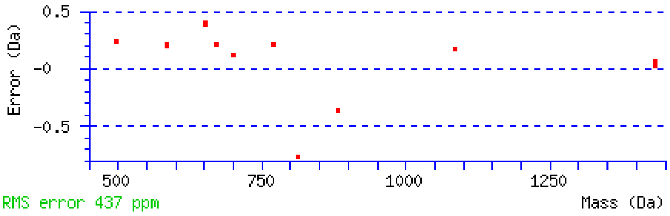
Label all possible matches ○ Label matches used for scoring ●

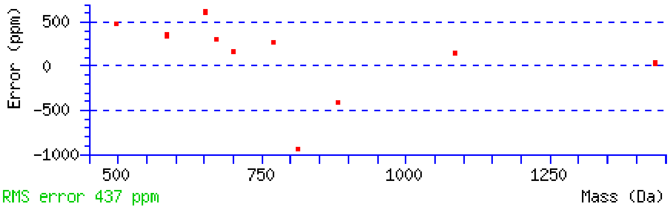
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1580.7276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.028
Matches : 13/146 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							14
2	265.0967	133.0520			247.0861	124.0467	D	**1433.6695**	717.3384	1415.6459	708.3266	1415.6589	708.3331	13
3	381.1207	191.0640			363.1101	182.0587	D	1317.6455	659.3264	1299.6219	650.3146	1299.6349	650.3211	12
4	***497.1577***	249.0825	479.1341	240.0707	479.1471	240.0772	N	1201.6215	601.3144	1183.5979	592.3026	1183.6110	592.3091	11
5	569.1918	285.0996	551.1682	276.0878	551.1813	276.0943	A	**1085.5845**	543.2959	1067.5609	534.2841	1067.5740	534.2906	10
6	***669.2573***	335.1323	651.2337	326.1205	651.2467	326.1270	V	1013.5504	507.2788	995.5268	498.2670	995.5398	498.2735	9
7	***769.3227***	385.1650	751.2991	376.1532	751.3122	376.1597	V	913.4849	457.2461	895.4613	448.2343	895.4744	448.2408	8
8	***883.4038***	442.2056	865.3802	433.1938	865.3933	433.2003	L	**813.4195**	407.2134	795.3959	398.2016	795.4089	398.2081	7
9	983.4693	492.2383	965.4457	483.2265	965.4587	483.2330	V	**699.3384**	350.1728	681.3148	341.1610	681.3278	341.1675	6
10	1099.4933	550.2503	1081.4697	541.2385	1081.4827	541.2450	D	599.2729	300.1401	581.2493	291.1283	581.2624	291.1348	5
11	1187.5223	594.2648	1169.4987	585.2530	1169.5117	585.2595	S	483.2489	242.1281	465.2254	233.1163	465.2384	233.1228	4
12	1317.6113	659.3093	1299.5878	650.2975	1299.6008	650.3040	K	395.2199	198.1136	377.1963	189.1018	377.2093	189.1083	3
13	***1433.6353***	717.3213	1415.6117	708.3095	1415.6248	708.3160	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FDDNAVVLVDSKDK

AT5G46160.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	1580.7276	0.0018	FDDNAVVLVDSKDK
16.6	1580.7281	0.0014	VTGLDGDAEKSANRK
7.7	1580.7280	0.0014	REIQDETDRITGK
4.1	1580.7310	-0.0016	EASASVSKDAEVMLK
2.4	1580.7310	-0.0015	MDELKGAEKVTAEK
2.1	1580.7281	0.0014	QVEEVTVSNTNRGK
1.7	1580.7289	0.0005	MLQHLRTTMLER
1.5	1580.7263	0.0032	MLEVMSNAGQDIKK
0.4	1580.7333	-0.0038	FPSMNSTAIDLLEK
0.4	1580.7281	0.0014	EALSSRRAEADDLK

AT5G46250.1

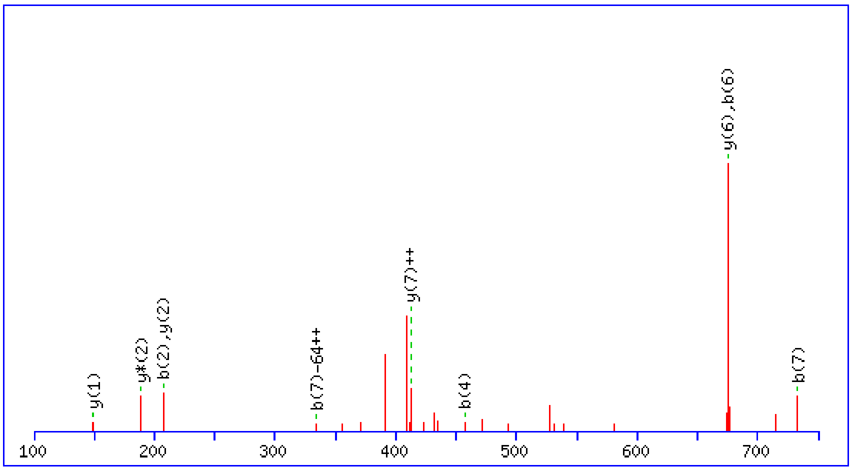
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFTMGRGK**
Found in **AT5G46250.1** in **TAIR_Arabidopsis**, Symbols: | RNA recognition motif (RRM)-containing protein | chr5:18772615-18775283 FORWARD

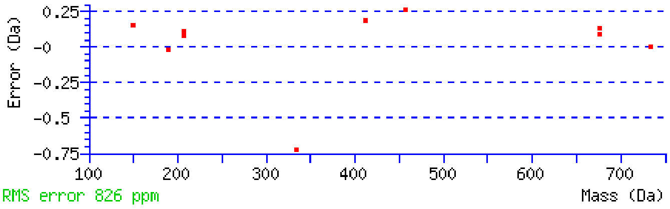
Match to Query 1474: 880.386268 from(441.200410,2+) index(6519)
Title: Elution from: 57.810 to 57.810 scan no 8395 cid35.00 polarity:+
Data file D6h-3_1.mgf

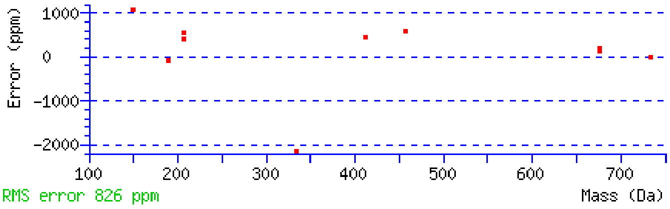
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 880.3869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.009
Matches : 10/96 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	59.0258	30.0165					G							8
2	***207.0912***	104.0492					F	823.3757	412.1915	805.3521	403.1797	805.3652	403.1862	7
3	309.1359	155.0716			291.1254	146.0663	T	**675.3103**	338.1588	657.2867	329.1470	657.2997	329.1535	6
4	***457.1684***	229.0878			439.1578	220.0825	M	573.2656	287.1364	555.2420	278.1246			5
5	515.1869	258.0971			497.1763	249.0918	G	425.2331	213.1202	407.2095	204.1084			4
6	***675.2761***	338.1417	657.2525	329.1299	657.2656	329.1364	R	367.2146	184.1109	349.1910	175.0992			3
7	***733.2946***	367.1509	715.2710	358.1392	715.2841	358.1457	G	**207.1254**	104.0663	189.1018	95.0545			2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GFTMGRGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G46250.1

25.5	880.3869	-0.0006	GFTMGRGK
21.4	880.3865	-0.0002	GMFDFLK
21.2	880.3869	-0.0007	MGAARGYK
14.9	880.3869	-0.0007	MTRNGFK
9.6	880.3869	-0.0007	GFQMRSK
8.6	880.3869	-0.0007	FGKNMTR
8.4	880.3869	-0.0007	QAYMRGK
8.4	880.3843	0.0020	STMGLYGK
8.1	880.3843	0.0020	MFSVASSK
2.4	880.3843	0.0020	TYNSIMK

AT5G46290.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALESANLGGDK**
Found in **AT5G46290.1** in **TAIR_Arabidopsis**, Symbols: KAS I | KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); fatty-acid synthase | chr5:18791666-18793856 REVERSE

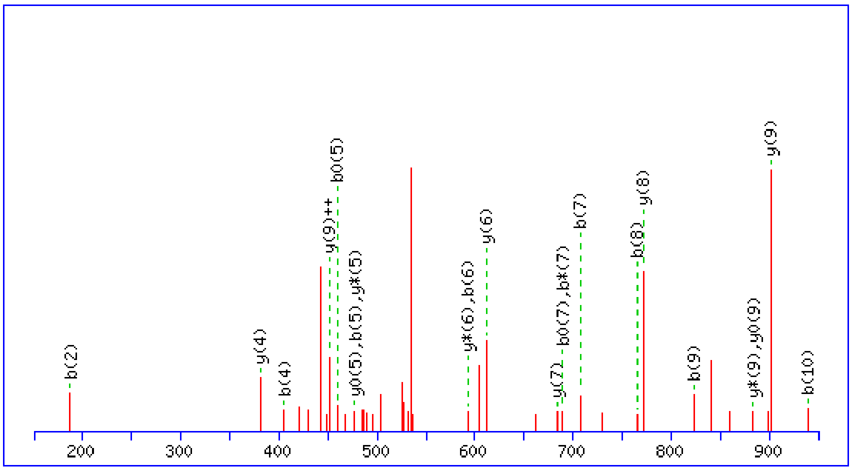
Match to Query 3473: 1086.498716 from(544.256634,2+) index(1336)
Title: Elution from: 18.921 to 18.921 scan no 1836 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

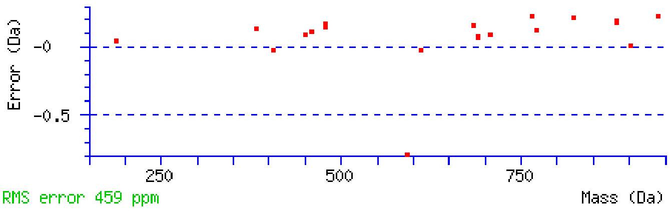
Label all possible matches ○ Label matches used for scoring ●

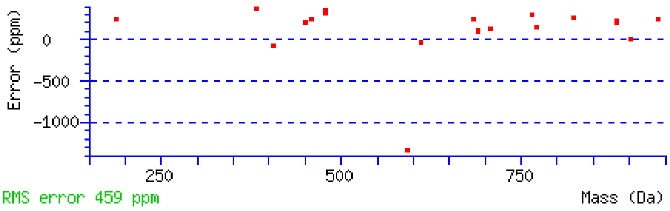
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1086.4968
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.7e-005
Matches : 22/104 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							11
2	***187.1225***	94.0649					L	1015.4699	508.2386	997.4463	499.2268	997.4593	499.2333	10
3	317.1622	159.0847			299.1516	150.0794	E	**901.3888**	451.1980	883.3652	442.1862	883.3782	442.1927	9
4	***405.1912***	203.0992			387.1807	194.0940	S	**771.3492**	386.1782	753.3256	377.1664	753.3386	377.1729	8
5	***477.2254***	239.1163			459.2148	230.1110	A	**683.3201**	342.1637	665.2965	333.1519	665.3095	333.1584	7
6	***593.2624***	297.1348	575.2388	288.1230	575.2518	288.1295	N	**611.2859**	306.1466	593.2624	297.1348	593.2754	297.1413	6
7	***707.3435***	354.1754	689.3199	345.1636	689.3329	345.1701	L	495.2489	248.1281	477.2254	239.1163	477.2384	239.1228	5
8	***765.3620***	383.1846	747.3384	374.1728	747.3514	374.1793	G	**381.1678**	191.0876	363.1443	182.0758	363.1573	182.0823	4
9	***823.3805***	412.1939	805.3569	403.1821	805.3699	403.1886	G	323.1494	162.0783	305.1258	153.0665	305.1388	153.0730	3
10	***939.4044***	470.2059	921.3809	461.1941	921.3939	461.2006	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ALESANLGGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G46290.1

Score	Mr(calc)	Delta	Sequence
52.2	1086.4968	0.0020	ALESANLGGDK
9.7	1086.5012	-0.0025	FYKDFTAGK
9.6	1086.4967	0.0020	EQVNDLQTK
8.8	1086.4967	0.0020	QVGETALNDK
6.0	1086.4967	0.0020	GEEVDGLSIR
5.7	1086.4976	0.0011	EMGHVKMVK
4.6	1086.4967	0.0020	ATEDLVAAER
2.1	1086.4990	-0.0003	VPGIFADNDK
1.0	1086.4967	0.0020	EDDLADRLK
0.9	1086.4990	-0.0003	LAPFGEENAK

AT5G46460.1

MATRIX SCIENCE Mascot Search Results

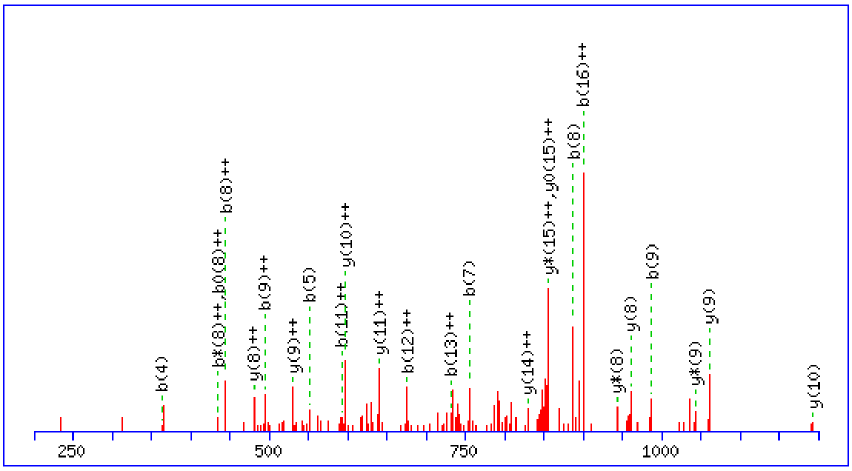
Peptide View

MS/MS Fragmentation of **DTAAWNSMVHGYLQFGK**
Found in **AT5G46460.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:18857532-18859625 FORWARD

Match to Query 9234: 1946.823054 from(649.948294,3+) index(7946)
Title: Elution from: 72.116 to 72.116 scan no 10495 cid35.00 polarity:+
Data file D1d-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

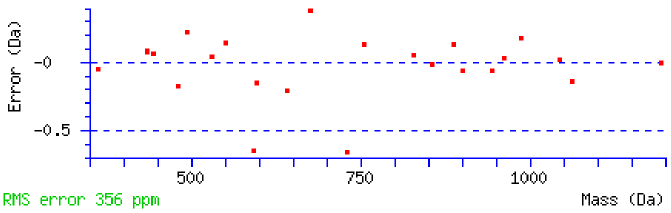
Or, Plot from 200 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

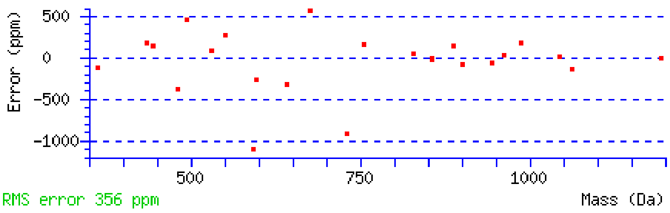


Monoisotopic mass of neutral peptide Mr(calc): 1946.8255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.025
Matches : 25/162 fragment ions using 63 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	**D**							**17**
2	219.0760	110.0416			201.0654	101.0363	**T**	1831.8089	916.4081	1813.7853	907.3963	1813.7983	907.4028	**16**
3	291.1101	146.0587			273.0996	137.0534	**A**	1729.7642	865.3857	1711.7406	856.3739	1711.7536	856.3804	**15**
4	***363.1443***	182.0758			345.1337	173.0705	**A**	1657.7300	829.3686	1639.7064	820.3569	1639.7194	820.3634	**14**
5	***551.2176***	276.1125			533.2071	267.1072	**W**	1585.6959	793.3516	1567.6723	784.3398	1567.6853	784.3463	**13**
6	667.2546	334.1310	649.2311	325.1192	649.2441	325.1257	**N**	1397.6225	699.3149	1379.5989	690.3031	1379.6119	690.3096	**12**
7	***755.2837***	378.1455	737.2601	369.1337	737.2731	369.1402	**S**	1281.5855	641.2964	1263.5619	632.2846	1263.5749	632.2911	**11**
8	***887.3212***	***444.1643***	869.2976	435.1525	869.3107	435.1590	**M**	**1193.5564**	597.2818	1175.5328	588.2701			**10**
9	***987.3867***	***494.1970***	969.3631	485.1852	969.3761	485.1917	**V**	**1061.5189**	531.2631	1043.4953	522.2513			**9**
10	1127.4367	564.2220	1109.4131	555.2102	1109.4261	555.2167	**H**	**961.4534**	481.2304	943.4299	472.2186			**8**
11	1185.4552	***593.2312***	1167.4316	584.2194	1167.4446	584.2260	**G**	821.4034	411.2054	803.3798	402.1936			**7**
12	1349.5156	***675.2614***	1331.4920	666.2496	1331.5050	666.2561	**Y**	763.3849	382.1961	745.3613	373.1843			**6**
13	1463.5967	***732.3020***	1445.5731	723.2902	1445.5861	723.2967	**L**	599.3246	300.1659	581.3010	291.1541			**5**
14	1593.6493	797.3283	1575.6257	788.3165	1575.6387	788.3230	**Q**	485.2435	243.1254	467.2199	234.1136			**4**
15	1741.7148	871.3610	1723.6912	862.3492	1723.7042	862.3557	**F**	355.1908	178.0990	337.1672	169.0873			**3**
16	1799.7333	***900.3703***	1781.7097	891.3585	1781.7227	891.3650	**G**	207.1254	104.0663	189.1018	95.0545			**2**
17							**K**	149.1069	75.0571	131.0833	66.0453			**1**

AT5G46460.1





NCBI **BLAST** search of DTAAWNSMVHGYLQFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.7	1946.8255	-0.0025	DTAAWNSMVHGYLQFGK
8.7	1946.8245	-0.0014	EGNMAAASDLLLDMQRR
6.9	1946.8218	0.0012	AGRSNEVSMILEEMSEK
3.2	1946.8218	0.0013	MSTKEVDEQMINVQNK
3.2	1946.8218	0.0013	MSTKEVDEQMLNVQNK
2.9	1946.8240	-0.0010	LMKSMGWEEGEGLGKDK
2.8	1946.8218	0.0012	ESMIEMIEENNIRASK
2.1	1946.8233	-0.0002	NQTGDFGIAFKETCAHK
0.2	1946.8265	-0.0035	LCKSQDLTESLSDESSK
0.1	1946.8288	-0.0057	SNLFQVGEDDVIMESTK

Mascot: http://www.matrixscience.com/

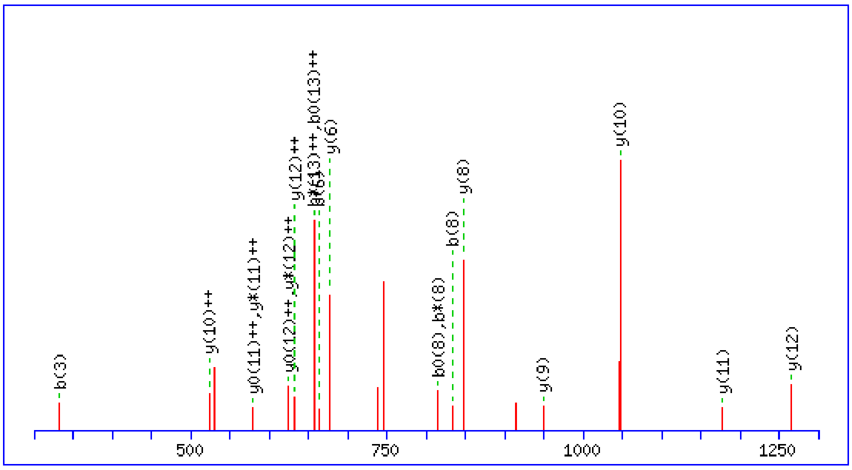
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQSQPTPAPGQLPR**
Found in **AT5G46800.1** in **TAIR_Arabidopsis**, Symbols: BOU | BOU (A BOUT DE SOUFFLE); binding | chr5:19006006-19007037 REVERSE

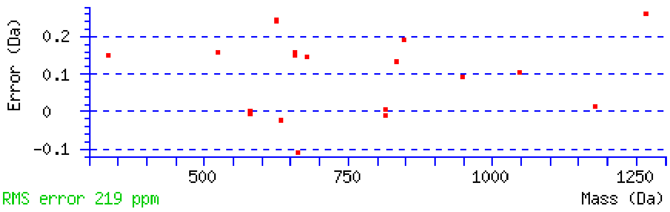
Match to Query 6473: 1508.742386 from(755.378469,2+) index(2650)
Title: Elution from: 26.942 to 26.942 scan no 3295 cid35.00 polarity:+
Data file C7-3_2.mgf

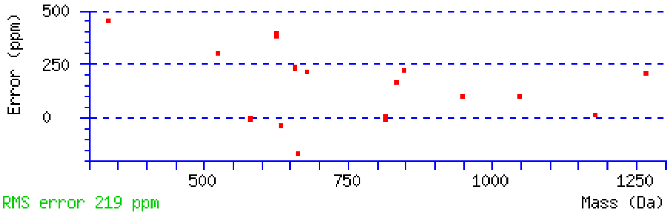
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1508.7456
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00012
Matches : 19/134 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							14
2	245.1410	123.0741	227.1174	114.0624			Q	1395.6718	698.3395	1377.6482	689.3277	1377.6612	689.3342	13
3	**333.1701**	167.0887	315.1465	158.0769	315.1595	158.0834	S	***1265.6191***	633.3132	1247.5955	624.3014	1247.6085	624.3079	12
4	463.2227	232.1150	445.1991	223.1032	445.2122	223.1097	Q	***1177.5900***	589.2987	1159.5665	580.2869	1159.5795	580.2934	11
5	561.2725	281.1399	543.2489	272.1281	543.2620	272.1346	P	***1047.5374***	524.2723	1029.5138	515.2605	1029.5268	515.2671	10
6	**663.3172**	332.1623	645.2937	323.1505	645.3067	323.1570	T	***949.4876***	475.2474	931.4640	466.2356	931.4770	466.2422	9
7	761.3670	381.1872	743.3435	372.1754	743.3565	372.1819	P	***847.4429***	424.2251	829.4193	415.2133			8
8	**833.4012**	417.2042	815.3776	408.1924	815.3906	408.1990	A	749.3931	375.2002	731.3695	366.1884			7
9	931.4510	466.2291	913.4274	457.2173	913.4404	457.2239	P	***677.3589***	339.1831	659.3354	330.1713			6
10	989.4695	495.2384	971.4459	486.2266	971.4589	486.2331	G	579.3091	290.1582	561.2856	281.1464			5
11	1119.5221	560.2647	1101.4986	551.2529	1101.5116	551.2594	Q	521.2906	261.1490	503.2671	252.1372			4
12	1233.6032	617.3053	1215.5797	608.2935	1215.5927	608.3000	L	391.2380	196.1226	373.2144	187.1108			3
13	1331.6530	666.3302	1313.6295	657.3184	1313.6425	657.3249	P	277.1569	139.0821	259.1333	130.0703			2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LQSQPTPAPGQLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G46800.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.1	1508.7456	-0.0032	LQSQPTPAPGQLPR
24.6	1508.7429	-0.0005	EISEIVFTVSNVR
8.6	1508.7429	-0.0005	SELPKDQGYIKSK
4.8	1508.7456	-0.0032	GLRERPPSSYSLK
0.9	1508.7433	-0.0009	ELLRTTEESVRR
0.6	1508.7429	-0.0005	SLKEQLENAFSVK
0.3	1508.7463	-0.0039	LKSTGMKEQDVLK

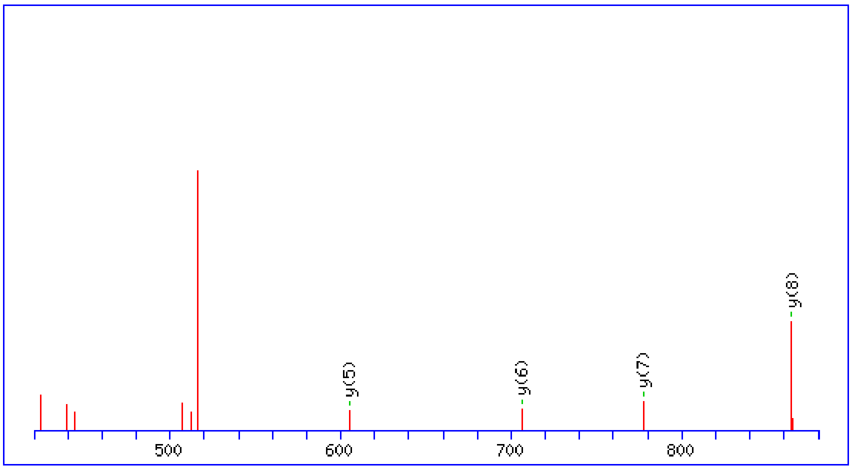
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LASATTDLEK**
Found in **AT5G47030.1** in **TAIR_Arabidopsis**, Symbols: | ATP synthase delta' chain, mitochondrial | chr5:19107611-19109261 FORWARD

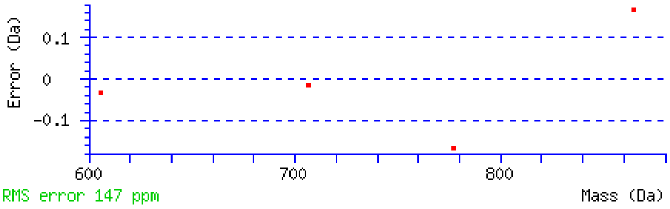
Match to Query 2859: 1047.545090 from(524.779821,2+) index(1139)
Title: Elution from: 15.666 to 15.666 scan no 1531 cid35.00 polarity:+
Data file 0-2_3.mgf

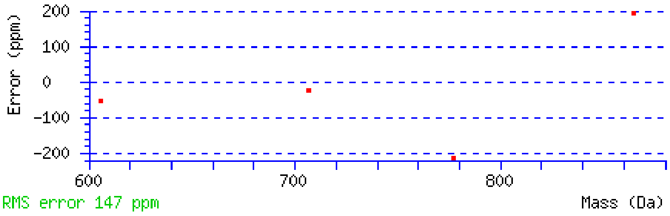
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 420 to 880 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1047.5448
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00057
Matches : 4/84 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							10
2	185.1285	93.0679			A	935.4680	468.2376	918.4415	459.7244	917.4575	459.2324	9
3	272.1605	136.5839	254.1499	127.5786	S	***864.4309***	432.7191	847.4044	424.2058	846.4203	423.7138	8
4	343.1976	172.1024	325.1870	163.0972	A	***777.3989***	389.2031	760.3723	380.6898	759.3883	380.1978	7
5	444.2453	222.6263	426.2347	213.6210	T	***706.3618***	353.6845	689.3352	345.1712	688.3512	344.6792	6
6	545.2930	273.1501	527.2824	264.1448	T	***605.3141***	303.1607	588.2875	294.6474	587.3035	294.1554	5
7	660.3199	330.6636	642.3093	321.6583	D	504.2664	252.6368	487.2399	244.1236	486.2558	243.6316	4
8	773.4040	387.2056	755.3934	378.2003	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	902.4466	451.7269	884.4360	442.7216	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LASATTDLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G47030.1

38.9	1047.5448	0.0003	LASATTDLEK
10.0	1047.5461	-0.0011	RDDGGLFLR
3.5	1047.5461	-0.0011	GDEFGVLRR

AT5G47160.1

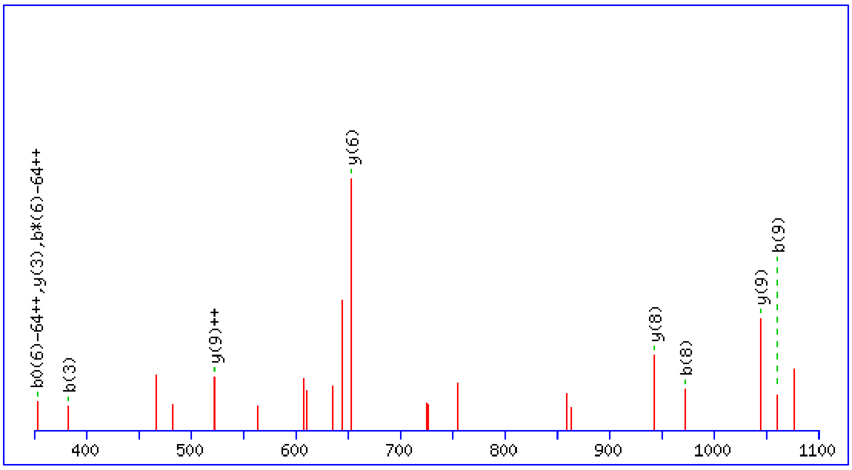
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MMTQRISPSNK**
Found in **AT5G47160.1** in **TAIR_Arabidopsis**, Symbols: | YDG/SRA domain-containing protein | chr5:19173958-19175205 FORWARD

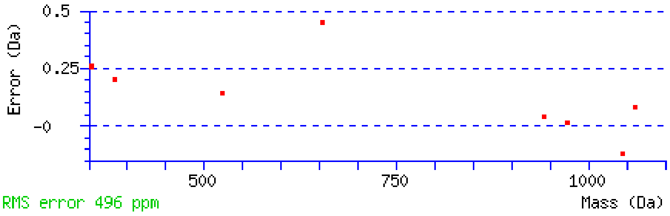
Match to Query 4810: 1324.582996 from(663.298774,2+) index(3626)
Title: Elution from: 35.068 to 35.068 scan no 4550 cid35.00 polarity:+
Data file D6h-1_3.mgf

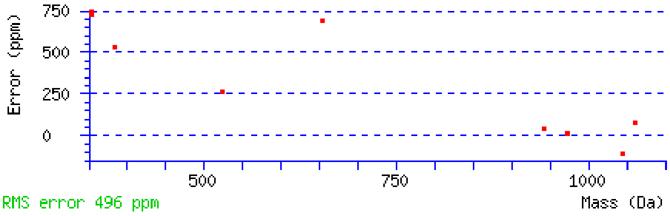
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1324.5822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.036
Matches : 10/160 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	133.0448	67.0260					M							11
2	281.0772	141.0423					M	1193.5519	597.2796	1175.5284	588.2678	1175.5414	588.2743	10
3	***383.1219***	192.0646			365.1114	183.0593	T	***1045.5195***	523.2634	1027.4959	514.2516	1027.5089	514.2581	9
4	513.1746	257.0909	495.1510	248.0791	495.1640	248.0857	Q	***943.4748***	472.2410	925.4512	463.2292	925.4642	463.2358	8
5	673.2638	337.1356	655.2403	328.1238	655.2533	328.1303	R	813.4221	407.2147	795.3986	398.2029	795.4116	398.2094	7
6	787.3449	394.1761	769.3214	385.1643	769.3344	385.1708	I	***653.3329***	327.1701	635.3093	318.1583	635.3223	318.1648	6
7	875.3740	438.1906	857.3504	429.1788	857.3634	429.1854	S	539.2518	270.1295	521.2282	261.1177	521.2412	261.1243	5
8	***973.4238***	487.2155	955.4002	478.2037	955.4132	478.2103	P	451.2227	226.1150	433.1991	217.1032	433.2122	217.1097	4
9	***1061.4529***	531.2301	1043.4293	522.2183	1043.4423	522.2248	S	***353.1729***	177.0901	335.1493	168.0783	335.1624	168.0848	3
10	1177.4899	589.2486	1159.4663	580.2368	1159.4793	580.2433	N	265.1439	133.0756	247.1203	124.0638			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MMTQRISPSNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G47160.1

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
23.9	1324.5822	0.0008	MMTQRISPSNK	Oxidation M2 50.00%
23.9	1324.5822	0.0008	MMTQRISPSNK	Oxidation M1 50.00%
5.4	1324.5813	0.0017	SVSSAASGNSINSK	
3.7	1324.5835	-0.0005	ADFKEQVSETR	
2.8	1324.5858	-0.0028	FISDPDARDFK	
2.4	1324.5835	-0.0005	NYTQEERLEK	
1.9	1324.5865	-0.0035	FLEDLMSSEVK	
1.7	1324.5813	0.0017	TGSGGSGGSGSKLEK	
1.5	1324.5869	-0.0039	ETCTSVNGKSVK	
1.5	1324.5862	-0.0032	WLAETRSSNSR	

AT5G47190.1

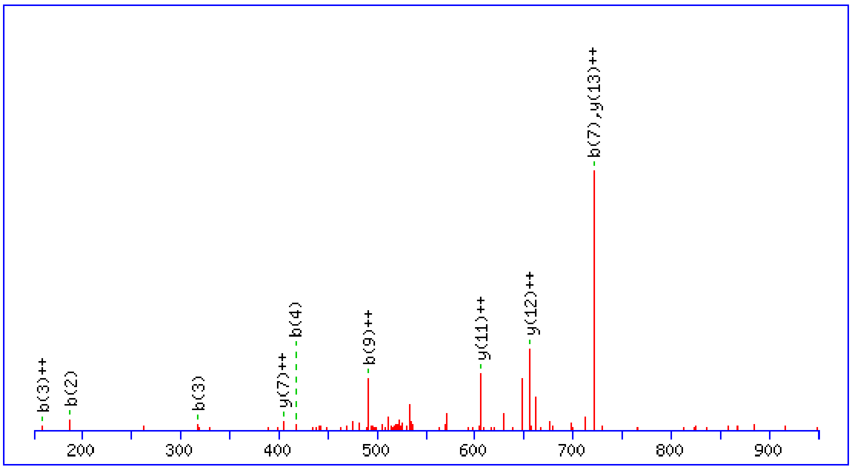
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIEVAETVRPVPGLR**
Found in **AT5G47190.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L19 family protein | chr5:19181659-19183291 REVERSE

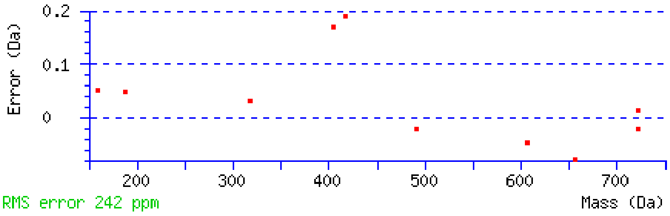
Match to Query 7436: 1626.857841 from(543.293223,3+) index(5094)
Title: Elution from: 45.648 to 45.648 scan no 6372 cid35.00 polarity:+
Data file D12h-1_2.mgf

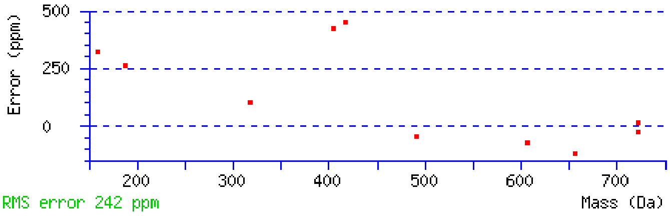
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1626.8580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.0088
Matches : 10/132 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							15
2	***187.1225***	94.0649					I	1555.8311	778.4192	1537.8075	769.4074	1537.8205	769.4139	14
3	***317.1622***	**159.0847**			299.1516	150.0794	E	1441.7500	721.3786	1423.7264	712.3668	1423.7394	712.3734	13
4	***417.2276***	209.1174			399.2170	200.1122	V	1311.7104	656.3588	1293.6868	647.3470	1293.6998	647.3535	12
5	489.2618	245.1345			471.2512	236.1292	A	1211.6449	606.3261	1193.6213	597.3143	1193.6344	597.3208	11
6	619.3014	310.1543			601.2908	301.1490	E	1139.6108	570.3090	1121.5872	561.2972	1121.6002	561.3037	10
7	***721.3461***	361.1767			703.3355	352.1714	T	1009.5711	505.2892	991.5476	496.2774	991.5606	496.2839	9
8	821.4115	411.2094			803.4010	402.2041	V	907.5264	454.2669	889.5029	445.2551			8
9	981.5008	**491.2540**	963.4772	482.2422	963.4902	482.2488	R	807.4610	404.2341	789.4374	395.2223			7
10	1079.5506	540.2789	1061.5270	531.2671	1061.5400	531.2737	P	647.3717	324.1895	629.3482	315.1777			6
11	1179.6160	590.3117	1161.5925	581.2999	1161.6055	581.3064	V	549.3219	275.1646	531.2984	266.1528			5
12	1277.6658	639.3366	1259.6423	630.3248	1259.6553	630.3313	P	449.2565	225.1319	431.2329	216.1201			4
13	1335.6843	668.3458	1317.6608	659.3340	1317.6738	659.3405	G	351.2067	176.1070	333.1831	167.0952			3
14	1449.7654	725.3864	1431.7419	716.3746	1431.7549	716.3811	L	293.1882	147.0977	275.1646	138.0859			2
15							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of AIEVAETVRPVPGLR

AT5G47190.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.1	1626.8580	-0.0001	AIEVAETVRPVPGLR
3.5	1626.8602	-0.0024	LAFGPQNLLHSVIAK

AT5G47210.1

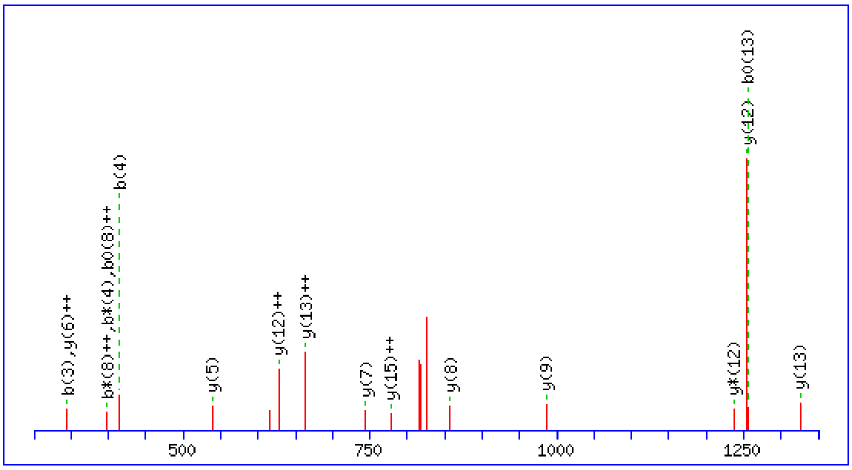
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNDAPGNENGFSGGYR**
Found in **AT5G47210.1** in **TAIR_Arabidopsis**, Symbols: | nuclear RNA-binding protein, putative | chr5:19186449-19188239 REVERSE

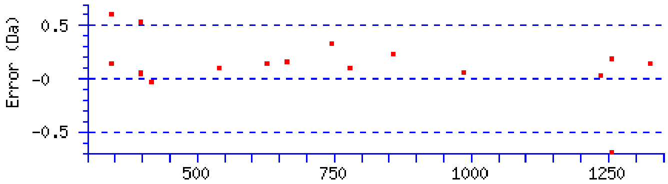
Match to Query 7836: 1667.692474 from(834.853513,2+) index(2071)
Title: Elution from: 24.718 to 24.718 scan no 2697 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

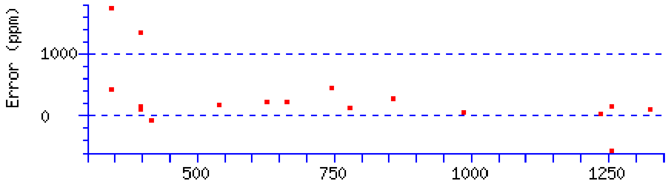


Monoisotopic mass of neutral peptide Mr(calc): 1667.6924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.5e-006
Matches : 17/168 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							16
2	229.0931	115.0502	212.0666	106.5369			N	1554.6568	777.8320	1537.6302	769.3188	1536.6462	768.8267	15
3	**344.1201**	172.5637	327.0935	164.0504	326.1095	163.5584	D	1440.6138	720.8106	1423.5873	712.2973	1422.6033	711.8053	14
4	**415.1572**	208.0822	398.1306	199.5690	397.1466	199.0769	A	***1325.5869***	663.2971	1308.5604	654.7838	1307.5763	654.2918	13
5	512.2100	256.6086	495.1834	248.0953	494.1994	247.6033	P	***1254.5498***	627.7785	1237.5232	619.2653	1236.5392	618.7733	12
6	569.2314	285.1193	552.2049	276.6061	551.2209	276.1141	G	1157.4970	579.2522	1140.4705	570.7389	1139.4865	570.2469	11
7	683.2743	342.1408	666.2478	333.6275	665.2638	333.1355	N	1100.4756	550.7414	1083.4490	542.2281	1082.4650	541.7361	10
8	812.3169	406.6621	795.2904	398.1488	794.3064	397.6568	E	***986.4326***	493.7200	969.4061	485.2067	968.4221	484.7147	9
9	926.3599	463.6836	909.3333	455.1703	908.3493	454.6783	N	***857.3900***	429.1987	840.3635	420.6854	839.3795	420.1934	8
10	983.3813	492.1943	966.3548	483.6810	965.3708	483.1890	G	***743.3471***	372.1772	726.3206	363.6639	725.3365	363.1719	7
11	1130.4497	565.7285	1113.4232	557.2152	1112.4392	556.7232	F	686.3257	343.6665	669.2991	335.1532	668.3151	334.6612	6
12	1217.4818	609.2445	1200.4552	600.7312	1199.4712	600.2392	S	***539.2572***	270.1323	522.2307	261.6190	521.2467	261.1270	5
13	1274.5032	637.7553	1257.4767	629.2420	1256.4927	628.7500	G	452.2252	226.6162	435.1987	218.1030			4
14	1331.5247	666.2660	1314.4981	657.7527	1313.5141	657.2607	G	395.2037	198.1055	378.1772	189.5922			3
15	1494.5880	747.7977	1477.5615	739.2844	1476.5775	738.7924	Y	338.1823	169.5948	321.1557	161.0815			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 586 ppm



RMS error 586 ppm

AT5G47210.1

NCBI **BLAST** search of NNDAPGNENGFSGGYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.3	1667.6924	0.0001	NNDAPGNENGFSGGYR
1.1	1667.6911	0.0014	DVSIADDNQYEDER

Mascot: http://www.matrixscience.com/

AT5G47690.1

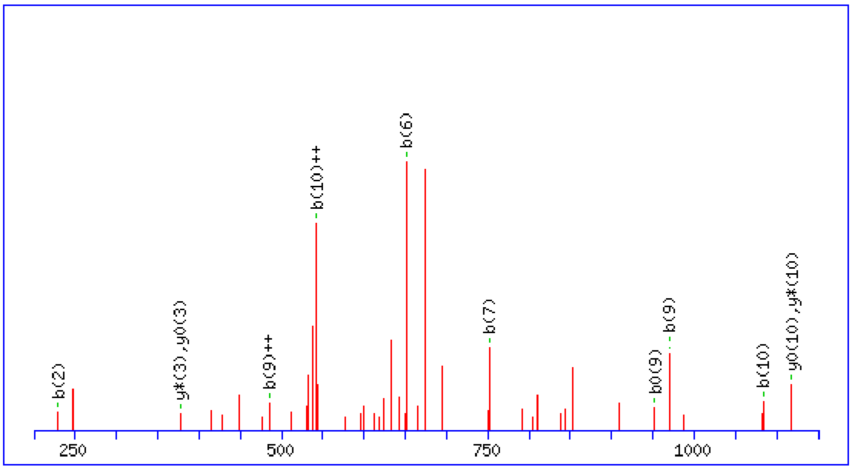
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLVASCVSEITR**
Found in **AT5G47690.1** in **TAIR_Arabidopsis**, Symbols: | binding | chr5:19335125-19344240 FORWARD

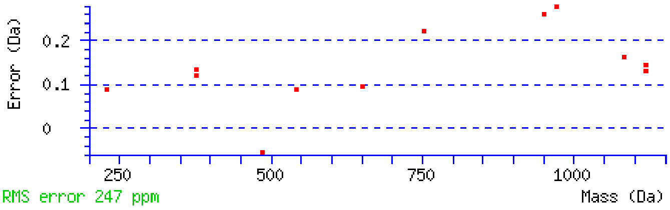
Match to Query 5140: 1362.676146 from(682.345349,2+) index(4625)
Title: Elution from: 43.078 to 43.078 scan no 5866 cid35.00 polarity:+
Data file 0-1_2.mgf

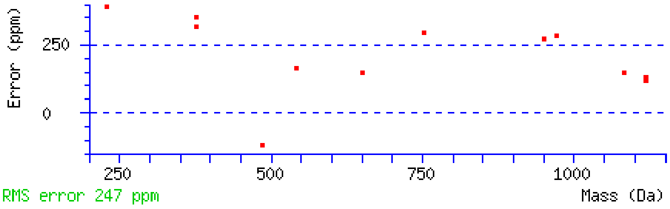
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1362.6753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.036
Matches : 12/100 fragment ions using 18 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0884	58.0478			L							12
2	***229.1695***	115.0884			L	1249.6015	625.3044	1231.5779	616.2926	1231.5910	616.2991	11
3	329.2349	165.1211			V	1135.5204	568.2638	1117.4968	559.2521	1117.5099	559.2586	10
4	401.2691	201.1382			A	1035.4550	518.2311	1017.4314	509.2193	1017.4444	509.2258	9
5	489.2981	245.1527	471.2876	236.1474	S	963.4208	482.2141	945.3972	473.2023	945.4103	473.2088	8
6	***651.3229***	326.1651	633.3123	317.1598	C	875.3918	438.1995	857.3682	429.1877	857.3812	429.1942	7
7	***751.3883***	376.1978	733.3777	367.1925	V	713.3670	357.1872	695.3435	348.1754	695.3565	348.1819	6
8	839.4174	420.2123	821.4068	411.2070	S	613.3016	307.1544	595.2780	298.1426	595.2910	298.1492	5
9	***969.4570***	**485.2321**	951.4464	476.2269	E	525.2725	263.1399	507.2489	254.1281	507.2620	254.1346	4
10	***1083.5381***	**542.2727**	1065.5275	533.2674	I	395.2329	198.1201	377.2093	189.1083	377.2223	189.1148	3
11	1185.5828	593.2950	1167.5722	584.2898	T	281.1518	141.0795	263.1282	132.0677	263.1412	132.0743	2
12					R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LLVASCVSEITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G47690.1

Score	Mr(calc)	Delta	Sequence
24.3	1362.6753	0.0008	LLVASCVSEITR
5.9	1362.6742	0.0020	IFVFTTNHIEK
3.3	1362.6724	0.0038	TAALQRAEEKAR
2.4	1362.6780	-0.0019	KNKLVVDNQMR
0.8	1362.6773	-0.0012	ARFKLSHAQQR

AT5G47790.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKTGSEAGVAKR**
Found in **AT5G47790.1** in **TAIR_Arabidopsis**, Symbols: | forkhead-associated domain-containing protein / FHA domain-containing protein | chr5:19368622-19369805 FORWARD

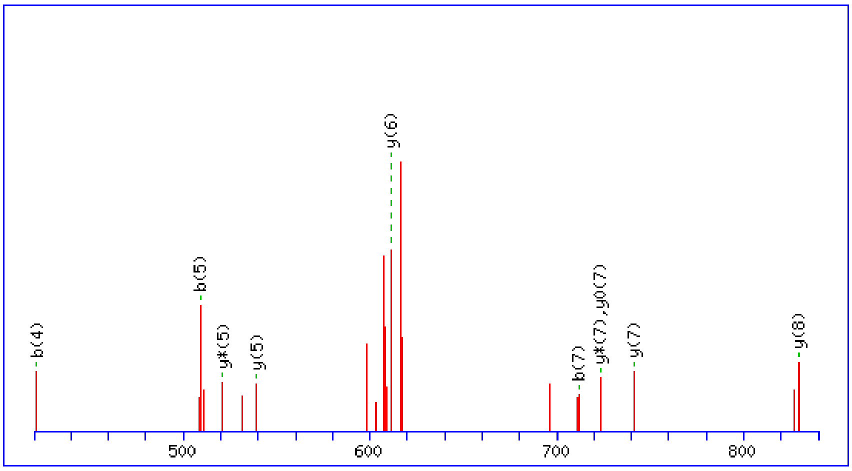
Match to Query 4213: 1248.604544 from(625.309548,2+) index(4095)
Title: Elution from: 37.451 to 37.451 scan no 5132 cid35.00 polarity:+
Data file D6h-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 420 to 840 Da Full range

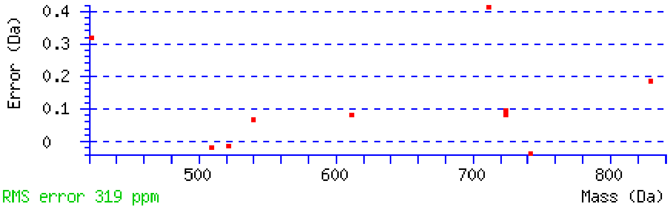
Label all possible matches ○ Label matches used for scoring ●

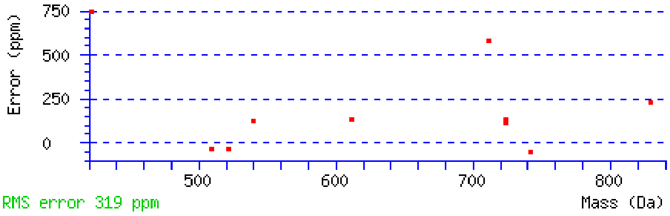
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1248.6016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.038
Matches : 10/118 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	**E**							**12**
2	261.1359	131.0716	243.1124	122.0598	243.1254	122.0663	**K**	1119.5693	560.2883	1101.5457	551.2765	1101.5587	551.2830	**11**
3	363.1806	182.0940	345.1571	173.0822	345.1701	173.0887	**T**	989.4803	495.2438	971.4567	486.2320	971.4697	486.2385	**10**
4	**421.1991**	211.1032	403.1756	202.0914	403.1886	202.0979	**G**	887.4356	444.2214	869.4120	435.2096	869.4250	435.2161	**9**
5	**509.2282**	255.1177	491.2046	246.1060	491.2176	246.1125	**S**	***829.4171***	415.2122	811.3935	406.2004	811.4065	406.2069	**8**
6	639.2678	320.1376	621.2443	311.1258	621.2573	311.1323	**E**	***741.3880***	371.1976	723.3644	362.1858	723.3774	362.1924	**7**
7	**711.3020**	356.1546	693.2784	347.1428	693.2914	347.1493	**A**	***611.3484***	306.1778	593.3248	297.1660			**6**
8	769.3205	385.1639	751.2969	376.1521	751.3099	376.1586	**G**	***539.3142***	270.1607	521.2906	261.1490			**5**
9	869.3859	435.1966	851.3624	426.1848	851.3754	426.1913	**V**	481.2957	241.1515	463.2721	232.1397			**4**
10	941.4201	471.2137	923.3965	462.2019	923.4095	462.2084	**A**	381.2303	191.1188	363.2067	182.1070			**3**
11	1071.5091	536.2582	1053.4855	527.2464	1053.4986	527.2529	**K**	309.1961	155.1017	291.1725	146.0899			**2**
12							**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of EKTGSEAGVAKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G47790.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.6	1248.6016	0.0029	EKTGSEAGVAKR
17.9	1248.6039	0.0007	KFNDVVNEIR
13.9	1248.6073	-0.0027	VMKKAQDEIR
10.2	1248.6073	-0.0027	KMVEEGQKLR
10.2	1248.6039	0.0007	NTTTWQNLKK
7.3	1248.6073	-0.0027	NLSSMVLLSNR
6.5	1248.6012	0.0033	EFIDATGGSVLK
5.8	1248.6039	0.0006	SLQSWKESLR
5.6	1248.6016	0.0029	SDTISAVIDRR
3.8	1248.6012	0.0033	LQDFVLSSEAK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAPIYTQPR**
Found in **AT5G48300.1** in **TAIR_Arabidopsis**, Symbols: APS1, ADG1 | ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE SMALL SUBUNIT 1); glucose-1-phosphate adenylyltransferase | chr5:19587552-19589783 FORWARD

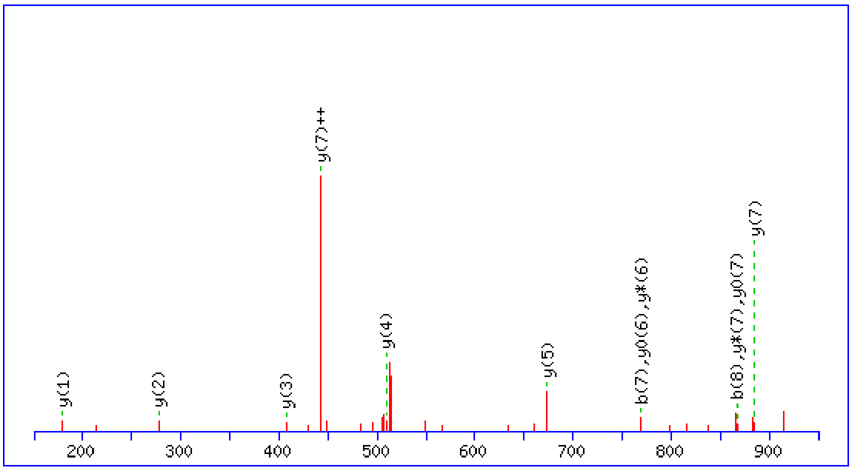
Match to Query 2876: 1044.500904 from(523.257728,2+) index(1120)
Title: Elution from: 18.871 to 18.871 scan no 1648 cid35.00 polarity:+
Data file D6h-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 950 Da Full range

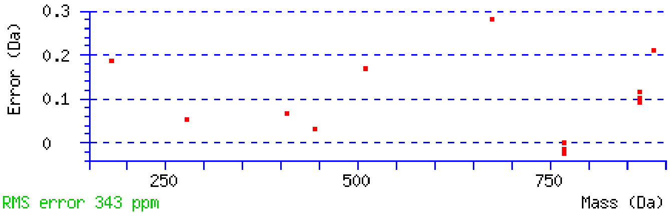
Label all possible matches ○ Label matches used for scoring ●

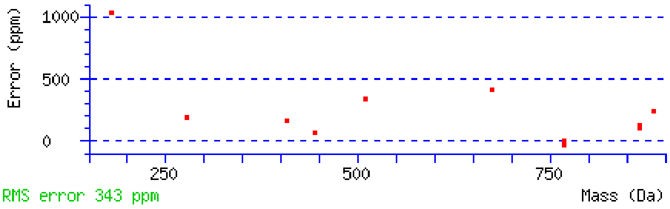
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1044.5015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0049
Matches : 13/78 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	89.0363	45.0218			71.0258	36.0165	S							9
2	161.0705	81.0389			143.0599	72.0336	A	957.4797	479.2435	939.4561	470.2317	939.4691	470.2382	8
3	259.1203	130.0638			241.1097	121.0585	P	***885.4455***	443.2264	867.4219	434.2146	867.4349	434.2211	7
4	373.2014	187.1043			355.1908	178.0990	I	787.3957	394.2015	769.3721	385.1897	769.3851	385.1962	6
5	537.2618	269.1345			519.2512	260.1292	Y	***673.3146***	337.1609	655.2910	328.1492	655.3040	328.1557	5
6	639.3065	320.1569			621.2959	311.1516	T	***509.2543***	255.1308	491.2307	246.1190	491.2437	246.1255	4
7	**769.3591**	385.1832	751.3355	376.1714	751.3485	376.1779	Q	***407.2095***	204.1084	389.1860	195.0966			3
8	**867.4089**	434.2081	849.3853	425.1963	849.3983	425.2028	P	***277.1569***	139.0821	259.1333	130.0703			2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of SAPIYTQPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G48300.1

34.4	1044.5015	-0.0005	SAPIYTQPR
18.7	1044.5019	-0.0010	RDQQIVNR
14.9	1044.4992	0.0017	QVGVASISDR
12.3	1044.4992	0.0017	EGSGIAVKDR
9.5	1044.4992	0.0017	GAVSDINLSR
9.5	1044.5014	-0.0005	QVEKPFER
9.4	1044.5037	-0.0028	KYAYIYGR
9.4	1044.4992	0.0017	AGATGSITTPR
9.3	1044.4992	0.0017	RTDEELLR
8.1	1044.4992	0.0017	KNDGDLTLR

AT5G48480.1

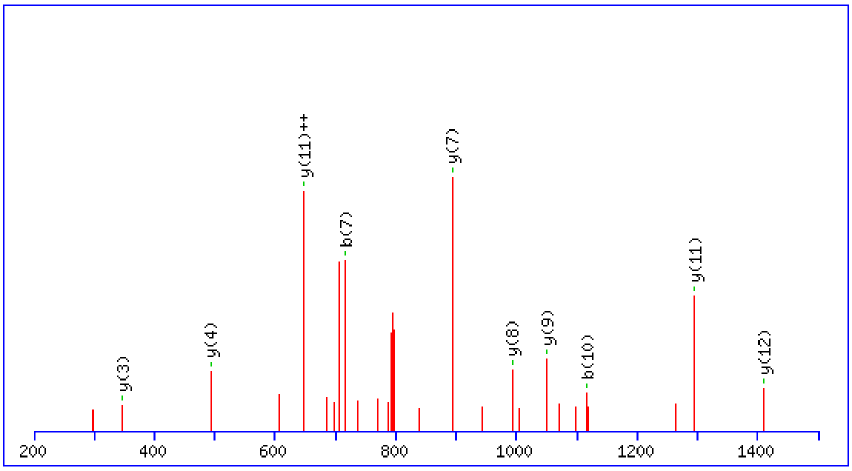
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTDPFGVTWIFAEK**
Found in **AT5G48480.1** in **TAIR_Arabidopsis**, Symbols: | Identical to Uncharacterized protein At5g48480 [Arabidopsis Thaliana] (GB:Q9LV66); similar to unknown [Populus trichocarpa] (GB:ABK95611.1); contains domain SSF54593 (SSF54593) | chr5:19662040-19662884 FORWARD

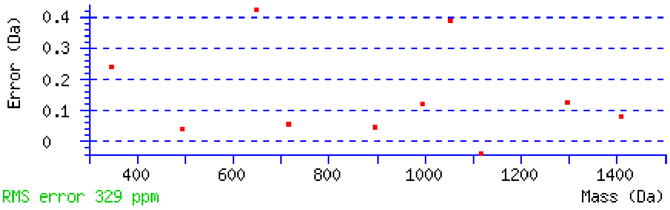
Match to Query 7663: 1608.818102 from(805.416327,2+) index(10979)
Title: Elution from: 104.945 to 104.945 scan no 15537 cid35.00 polarity:+
Data file D12h-1_1.mgf

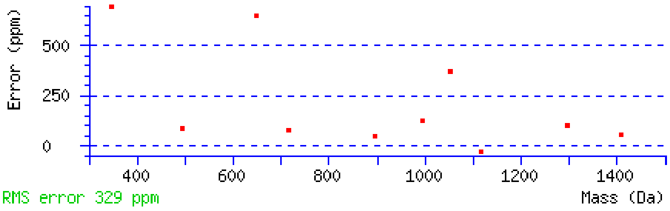
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1608.8188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 2.3e-006
Matches : 10/126 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							14
2	201.1234	101.0653	183.1128	92.0600	T	1510.7577	755.8825	1493.7311	747.3692	1492.7471	746.8772	13
3	316.1503	158.5788	298.1397	149.5735	D	***1409.7100***	705.3586	1392.6834	696.8454	1391.6994	696.3533	12
4	413.2031	207.1052	395.1925	198.0999	P	***1294.6830***	647.8452	1277.6565	639.3319	1276.6725	638.8399	11
5	560.2715	280.6394	542.2609	271.6341	F	1197.6303	599.3188	1180.6037	590.8055	1179.6197	590.3135	10
6	617.2930	309.1501	599.2824	300.1448	G	***1050.5619***	525.7846	1033.5353	517.2713	1032.5513	516.7793	9
7	**716.3614**	358.6843	698.3508	349.6790	V	***993.5404***	497.2738	976.5138	488.7606	975.5298	488.2686	8
8	817.4090	409.2082	799.3985	400.2029	T	***894.4720***	447.7396	877.4454	439.2264	876.4614	438.7343	7
9	1003.4884	502.2478	985.4778	493.2425	W	793.4243	397.2158	776.3978	388.7025	775.4137	388.2105	6
10	**1116.5724**	558.7899	1098.5619	549.7846	I	607.3450	304.1761	590.3184	295.6629	589.3344	295.1708	5
11	1263.6408	632.3241	1245.6303	623.3188	F	***494.2609***	247.6341	477.2344	239.1208	476.2504	238.6288	4
12	1334.6780	667.8426	1316.6674	658.8373	A	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
13	1463.7205	732.3639	1445.7100	723.3586	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
14					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VTDPFGVTWIFAEK

AT5G48480.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.6	1608.8188	-0.0007	VTDPFGVTWIFAEK

AT5G48850.1

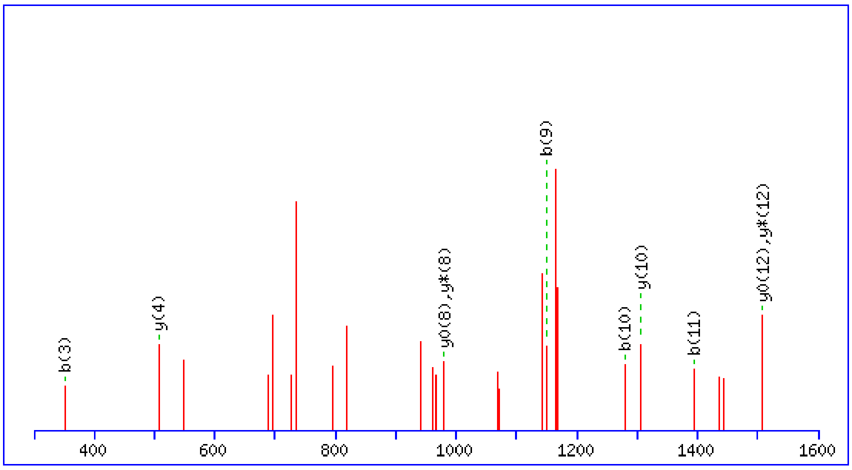
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCGRMEEQVELLK**
Found in **AT5G48850.1** in **TAIR_Arabidopsis**, Symbols: | male sterility MS5 family protein | chr5:19822802-19824925 REVERSE

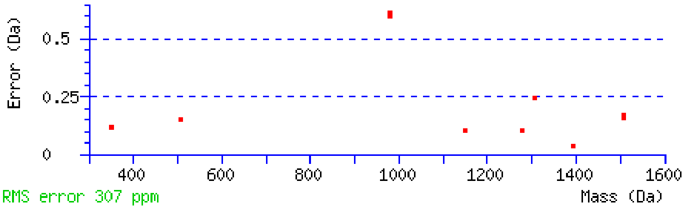
Match to Query 8070: 1654.751240 from(828.382896,2+) index(11012)
Title: Elution from: 105.603 to 105.603 scan no 15610 cid35.00 polarity:+
Data file D12h-1_1.mgf

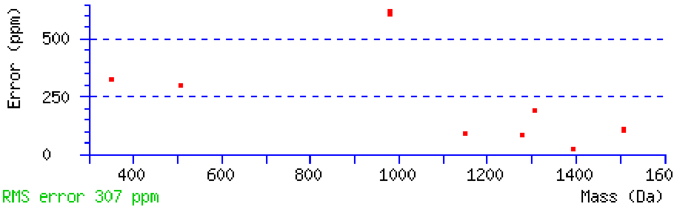
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1654.7527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.049
Matches : 11/198 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							13
2	293.1210	147.0642	275.0974	138.0524			C	1525.6710	763.3391	1507.6474	754.3273	1507.6604	754.3338	12
3	***351.1395***	176.0734	333.1159	167.0616			G	1363.6462	682.3268	1345.6227	673.3150	1345.6357	673.3215	11
4	511.2288	256.1180	493.2052	247.1062			R	**1305.6277**	653.3175	1287.6042	644.3057	1287.6172	644.3122	10
5	659.2612	330.1342	641.2376	321.1225			M	1145.5385	573.2729	1127.5149	564.2611	1127.5279	564.2676	9
6	789.3008	395.1541	771.2773	386.1423	771.2903	386.1488	E	997.5061	499.2567	979.4825	490.2449	979.4955	490.2514	8
7	919.3405	460.1739	901.3169	451.1621	901.3299	451.1686	E	867.4664	434.2369	849.4428	425.2251	849.4559	425.2316	7
8	1049.3931	525.2002	1031.3695	516.1884	1031.3826	516.1949	Q	737.4268	369.2170	719.4032	360.2052	719.4162	360.2118	6
9	***1149.4586***	575.2329	1131.4350	566.2211	1131.4480	566.2276	V	607.3741	304.1907	589.3506	295.1789	589.3636	295.1854	5
10	***1279.4982***	640.2527	1261.4746	631.2409	1261.4876	631.2475	E	**507.3087**	254.1580	489.2851	245.1462	489.2981	245.1527	4
11	***1393.5793***	697.2933	1375.5557	688.2815	1375.5687	688.2880	L	377.2691	189.1382	359.2455	180.1264			3
12	***1507.6604***	754.3338	1489.6368	745.3220	1489.6498	745.3286	L	263.1880	132.0976	245.1644	123.0858			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KCGRMEEQVELLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G48850.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.4	1654.7527	-0.0015	KCGRMEEQVELLK
11.9	1654.7554	-0.0041	MAQQVLGCTSRPIR
4.3	1654.7493	0.0019	CGLRLVYASDEPQK
3.5	1654.7515	-0.0003	MEAGDFVGAHKFVTK
3.4	1654.7467	0.0046	DAYPNVMEDLKSLK
3.1	1654.7527	-0.0015	KNQENVVMMKPSSK
2.9	1654.7527	-0.0015	KNQENVVMMKPSSK
0.8	1654.7467	0.0046	VSDALEIFEEMLSR
0.8	1654.7467	0.0046	MADIAILVAEEYER
0.1	1654.7467	0.0046	DATEEMINLAIGFAK

AT5G49910.1

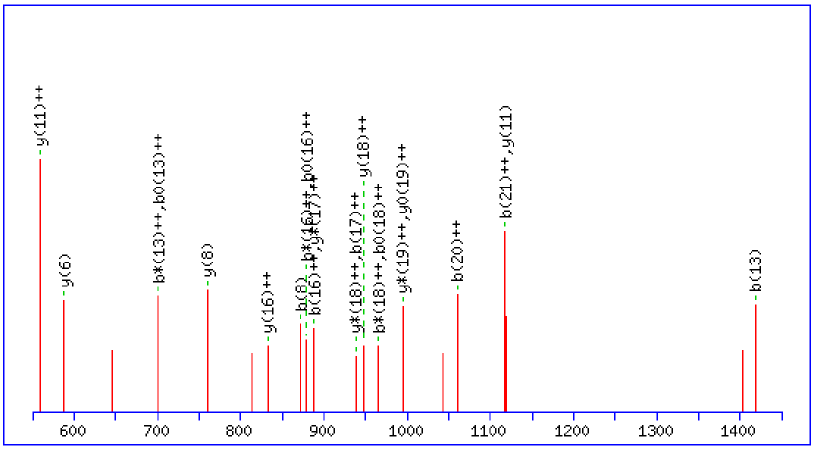
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IELSSLTQTNMSLPFITATADGPK**
Found in **AT5G49910.1** in **TAIR_Arabidopsis**, Symbols: HSC70-7, cpHSC70-2 | cpHSC70-2 (HEAT SHOCK PROTEIN 70-7); ATP binding / unfolded protein binding | chr5:20320696-20323521 FORWARD

Match to Query 10423: 2534.289738 from(845.770522,3+) index(10433)
Title: Elution from: 100.294 to 100.294 scan no 14727 cid35.00 polarity:+
Data file D6h-2_2.mgf

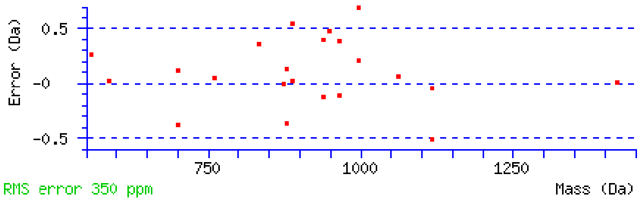
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

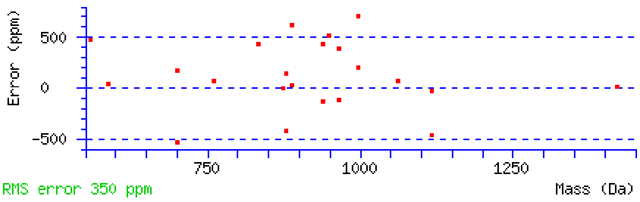


Monoisotopic mass of neutral peptide Mr(calc): 2534.2938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0037
Matches : 22/254 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**I**							**24**
2	243.1339	122.0706			225.1234	113.0653	**E**	2422.2170	1211.6121	2405.1905	1203.0989	2404.2065	1202.6069	**23**
3	356.2180	178.6126			338.2074	169.6074	**L**	2293.1744	1147.0909	2276.1479	1138.5776	2275.1639	1138.0856	**22**
4	443.2500	222.1287			425.2395	213.1234	**S**	2180.0904	1090.5488	2163.0638	1082.0355	2162.0798	1081.5435	**21**
5	530.2821	265.6447			512.2715	256.6394	**S**	2093.0583	1047.0328	2076.0318	1038.5195	2075.0478	1038.0275	**20**
6	643.3661	322.1867			625.3556	313.1814	**L**	2006.0263	1003.5168	1988.9998	995.0035	1988.0157	994.5115	**19**
7	744.4138	372.7105			726.4032	363.7053	**T**	1892.9422	946.9748	1875.9157	938.4615	1874.9317	937.9695	**18**
8	**872.4724**	436.7398	855.4458	428.2266	854.4618	427.7345	**Q**	1791.8946	896.4509	1774.8680	887.9376	1773.8840	887.4456	**17**
9	973.5201	487.2637	956.4935	478.7504	955.5095	478.2584	**T**	1663.8360	832.4216	1646.8094	823.9084	1645.8254	823.4163	**16**
10	1087.5630	544.2851	1070.5364	535.7719	1069.5524	535.2798	**N**	1562.7883	781.8978	1545.7618	773.3845	1544.7777	772.8925	**15**
11	1218.6035	609.8054	1201.5769	601.2921	1200.5929	600.8001	**M**	1448.7454	724.8763	1431.7188	716.3631	1430.7348	715.8710	**14**
12	1305.6355	653.3214	1288.6089	644.8081	1287.6249	644.3161	**S**	1317.7049	659.3561	1300.6783	650.8428	1299.6943	650.3508	**13**
13	**1418.7196**	709.8634	1401.6930	701.3501	1400.7090	700.8581	**L**	1230.6729	615.8401	1213.6463	607.3268	1212.6623	606.8348	**12**
14	1515.7723	758.3898	1498.7458	749.8765	1497.7618	749.3845	**P**	***1117.5888***	559.2980	1100.5623	550.7848	1099.5782	550.2928	**11**
15	1662.8407	831.9240	1645.8142	823.4107	1644.8302	822.9187	**F**	1020.5360	510.7717	1003.5095	502.2584	1002.5255	501.7664	**10**
16	1775.9248	***888.4660***	1758.8983	879.9528	1757.9142	879.4608	**I**	873.4676	437.2375	856.4411	428.7242	855.4571	428.2322	**9**
17	1876.9725	***938.9899***	1859.9459	930.4766	1858.9619	929.9846	**T**	***760.3836***	380.6954	743.3570	372.1821	742.3730	371.6901	**8**
18	1948.0096	974.5084	1930.9830	965.9952	1929.9990	965.5032	**A**	659.3359	330.1716	642.3093	321.6583	641.3253	321.1663	**7**
19	2049.0573	1025.0323	2032.0307	1016.5190	2031.0467	1016.0270	**T**	***588.2988***	294.6530	571.2722	286.1397	570.2882	285.6477	**6**
20	2120.0944	***1060.5508***	2103.0678	1052.0376	2102.0838	1051.5455	**A**	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	**5**
21	2235.1213	***1118.0643***	2218.0948	1109.5510	2217.1108	1109.0590	**D**	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	**4**
22	2292.1428	1146.5750	2275.1162	1138.0618	2274.1322	1137.5698	**G**	301.1870	151.0972	284.1605	142.5839			**3**
23	2389.1956	1195.1014	2372.1690	1186.5881	2371.1850	1186.0961	**P**	244.1656	122.5864	227.1390	114.0731			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**

AT5G49910.1





NCBI **BLAST** search of IELSSLTQTNMSLPFITATADGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.1	2534.2938	-0.0041	IELSSLTQTNMSLPFITATADGPK
3.9	2534.2832	0.0065	TDASGVSMLKEHLMRTSSGLVTSK

AT5G50250.1

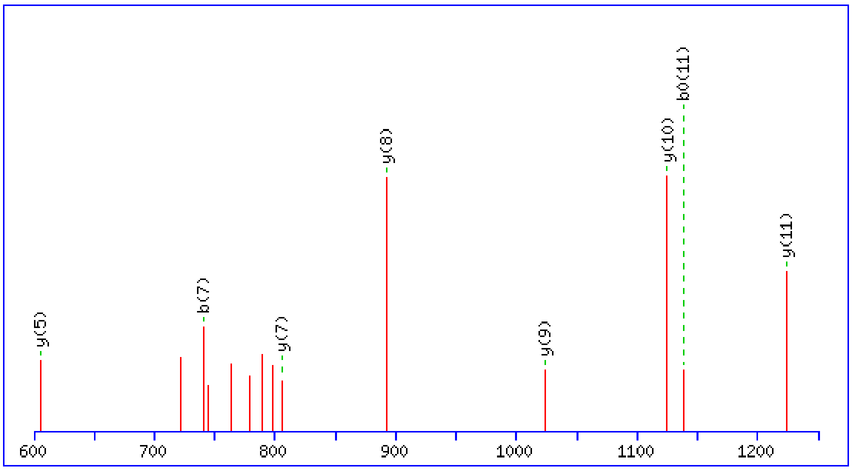
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGFVTMSTVEEAEK**
Found in **AT5G50250.1** in **TAIR_Arabidopsis**, Symbols: | 31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative | chr5:20469903-20471191 REVERSE

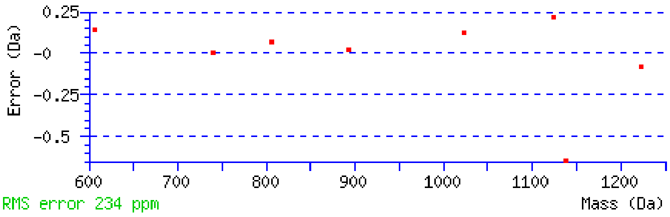
Match to Query 7284: 1630.755194 from(816.384873,2+) index(7761)
Title: Elution from: 68.858 to 68.858 scan no 10228 cid35.00 polarity:+
Data file D12h-3_2.mgf

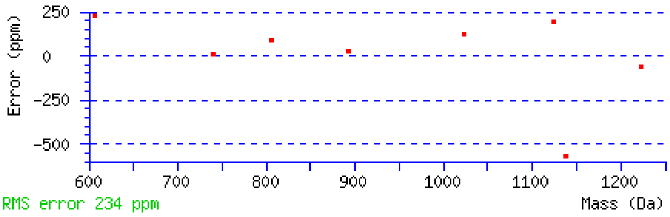
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1630.7549
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 9e-005
Matches : 8/128 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							15
2	205.0972	103.0522			F	1574.7407	787.8740	1557.7141	779.3607	1556.7301	778.8687	14
3	262.1186	131.5629			G	1427.6723	714.3398	1410.6457	705.8265	1409.6617	705.3345	13
4	409.1870	205.0972			F	1370.6508	685.8290	1353.6243	677.3158	1352.6402	676.8238	12
5	508.2554	254.6314			V	***1223.5824***	612.2948	1206.5558	603.7816	1205.5718	603.2896	11
6	609.3031	305.1552	591.2926	296.1499	T	***1124.5140***	562.7606	1107.4874	554.2474	1106.5034	553.7553	10
7	740.3436	370.6754	722.3330	361.6702	M	***1023.4663***	512.2368	1006.4398	503.7235	1005.4557	503.2315	9
8	827.3756	414.1915	809.3651	405.1862	S	***892.4258***	446.7165	875.3993	438.2033	874.4153	437.7113	8
9	928.4233	464.7153	910.4128	455.7100	T	***805.3938***	403.2005	788.3672	394.6873	787.3832	394.1953	7
10	1027.4917	514.2495	1009.4812	505.2442	V	704.3461	352.6767	687.3196	344.1634	686.3355	343.6714	6
11	1156.5343	578.7708	1138.5238	569.7655	E	***605.2777***	303.1425	588.2511	294.6292	587.2671	294.1372	5
12	1285.5769	643.2921	1267.5664	634.2868	E	476.2351	238.6212	459.2086	230.1079	458.2245	229.6159	4
13	1356.6140	678.8107	1338.6035	669.8054	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
14	1485.6566	743.3320	1467.6461	734.3267	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15					K	147.1128	74.0600	130.0863	65.5468			1





AT5G50250.1

NCBI **BLAST** search of GFGFVTMSTVEEAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.9	1630.7549	0.0003	GFGFVTMSTVEEAEK

Mascot: http://www.matrixscience.com/

AT5G50280.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEALVIQTEMEKK**
Found in **AT5G50280.1** in **TAIR_Arabidopsis**, Symbols: EMB1006 | EMB1006 (EMBRYO DEFECTIVE 1006) | chr5:20476464-20478730 FORWARD

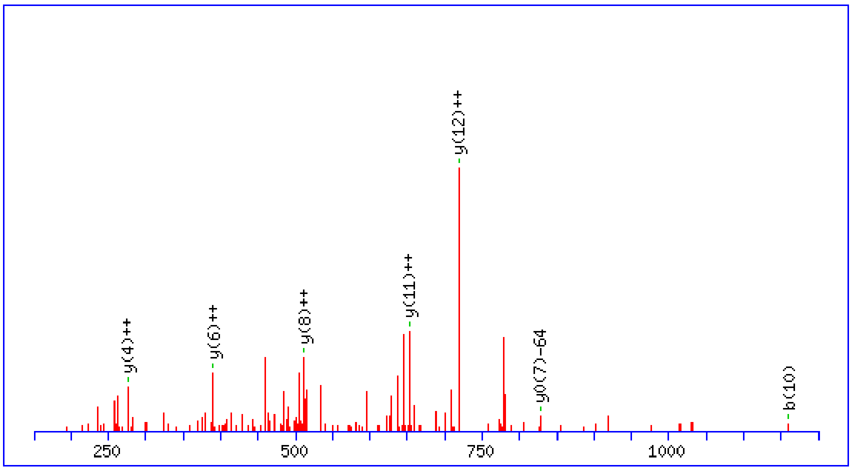
Match to Query 6941: 1562.785605 from(521.935811,3+) index(2346)
Title: Elution from: 24.924 to 24.924 scan no 2942 cid35.00 polarity:+
Data file C7-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1200 Da Full range

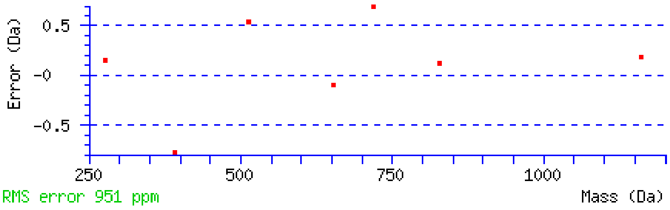
Label all possible matches ○ Label matches used for scoring ●

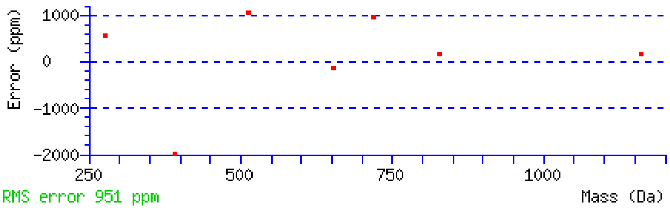
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1562.7861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.013
Matches : 7/200 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	259.0925	130.0499			241.0819	121.0446	E	1434.7509	717.8791	1417.7243	709.3658	1416.7403	708.8738	12
3	330.1296	165.5684			312.1190	156.5631	A	1305.7083	653.3578	1288.6817	644.8445	1287.6977	644.3525	11
4	443.2136	222.1105			425.2031	213.1052	L	1234.6712	617.8392	1217.6446	609.3259	1216.6606	608.8339	10
5	542.2821	271.6447			524.2715	262.6394	V	1121.5871	561.2972	1104.5605	552.7839	1103.5765	552.2919	9
6	655.3661	328.1867			637.3556	319.1814	I	1022.5187	511.7630	1005.4921	503.2497	1004.5081	502.7577	8
7	783.4247	392.2160	766.3981	383.7027	765.4141	383.2107	Q	909.4346	455.2209	892.4081	446.7077	891.4240	446.2157	7
8	884.4724	442.7398	867.4458	434.2266	866.4618	433.7345	T	781.3760	391.1917	764.3495	382.6784	763.3655	382.1864	6
9	1013.5150	507.2611	996.4884	498.7478	995.5044	498.2558	E	680.3284	340.6678	663.3018	332.1545	662.3178	331.6625	5
10	1160.5504	580.7788	1143.5238	572.2655	1142.5398	571.7735	M	551.2858	276.1465	534.2592	267.6332	533.2752	267.1412	4
11	1289.5930	645.3001	1272.5664	636.7868	1271.5824	636.2948	E	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	3
12	1417.6879	709.3476	1400.6614	700.8343	1399.6774	700.3423	K	275.2078	138.1075	258.1812	129.5942			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EEALVIQTEMEKK

AT5G50280.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.7	1562.7861	-0.0005	EEALVIQTEMEKK
24.5	1562.7861	-0.0005	KMDLTAEELKEEK
3.5	1562.7837	0.0019	TYSMMINGFVKLK
3.4	1562.7828	0.0028	EESPLETLFITER
0.2	1562.7875	-0.0019	QSGVRASVPCFDLK

AT5G50330.2

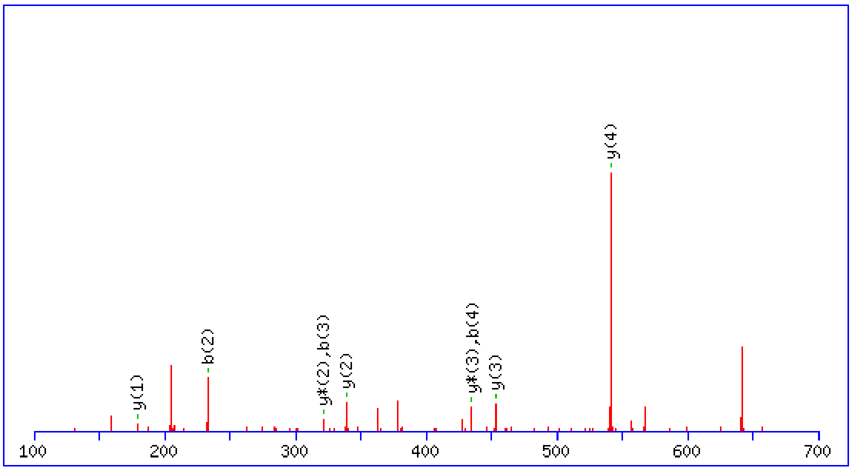
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RASLRR**
Found in **AT5G50330.2** in **TAIR_Arabidopsis**, Symbols: | ATP binding / electron carrier/ heme binding / iron ion binding / protein kinase | chr5:20502632-20505789 REVERSE

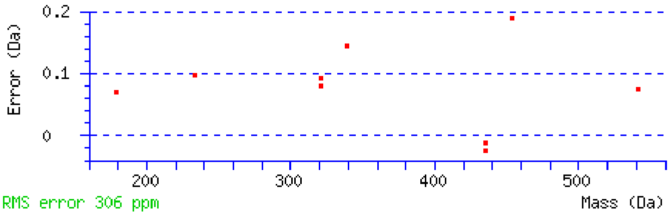
Match to Query 968: 772.423464 from(387.219008,2+) index(4463)
Title: Elution from: 40.407 to 40.407 scan no 5555 cid35.00 polarity:+
Data file D1d-3_1.mgf

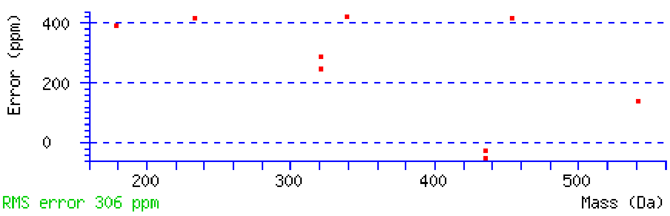
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 772.4226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.034
Matches : 9/50 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							6
2	**233.1307**	117.0690	215.1071	108.0572			A	613.3407	307.1740	595.3171	298.1622	595.3301	298.1687	5
3	**321.1597**	161.0835	303.1362	152.0717	303.1492	152.0782	S	***541.3065***	271.1569	523.2829	262.1451	523.2959	262.1516	4
4	**435.2408**	218.1241	417.2173	209.1123	417.2303	209.1188	L	***453.2774***	227.1424	435.2539	218.1306			3
5	595.3301	298.1687	577.3065	289.1569	577.3195	289.1634	R	***339.1963***	170.1018	321.1728	161.0900			2
6							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RASLRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.2	772.4226	0.0008	RASLRR
17.4	772.4251	-0.0017	MVLYLK
14.6	772.4222	0.0013	RAIFAGK

AT5G50330.2

9.8	772.4256	-0.0021	ARKMIK
9.7	772.4256	-0.0021	MVTRKK
7.7	772.4226	0.0008	RAIRSR
7.5	772.4256	-0.0021	KTKMVR
7.3	772.4256	-0.0021	TKVMKR
7.2	772.4256	-0.0021	MKKSIR
6.5	772.4226	0.0009	ARRVTR

AT5G50850.1

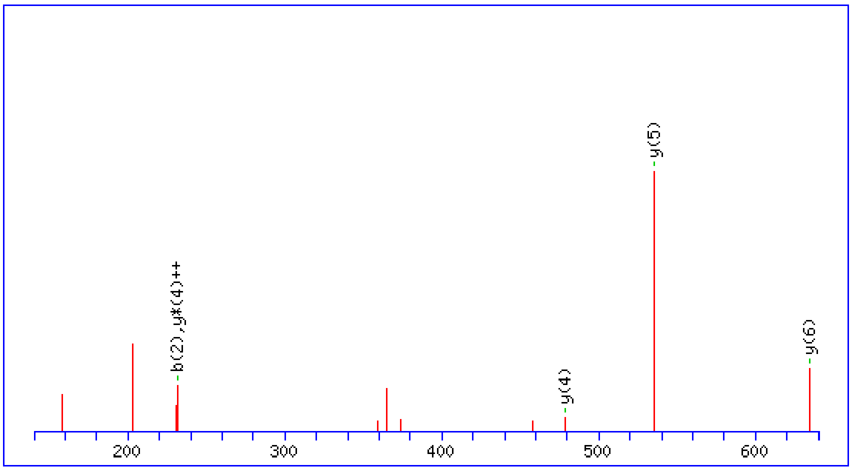
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVGFALK**
Found in **AT5G50850.1** in **TAIR_Arabidopsis**, Symbols: MAB1 | MAB1 (MACCI-BOU); pyruvate dehydrogenase (acetyl-transferring) | chr5:20706897-20710202 FORWARD

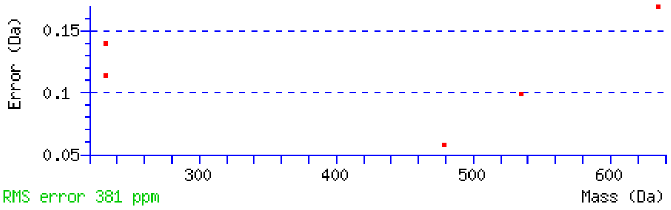
Match to Query 839: 764.425268 from(383.219910,2+) index(4528)
Title: Elution from: 42.125 to 42.125 scan no 5683 cid35.00 polarity:+
Data file D12h-3_1.mgf

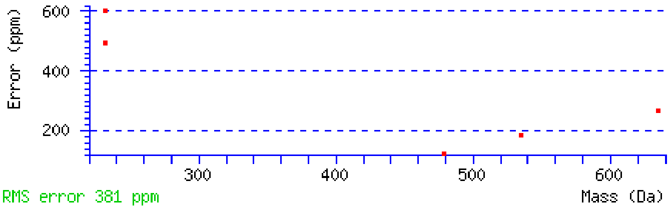
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 640 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 764.4255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.018
Matches : 5/36 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	132.0478	66.5275	M					7
2	231.1162	116.0617	V	***634.3923***	317.6998	617.3657	309.1865	6
3	288.1376	144.5725	G	***535.3239***	268.1656	518.2973	259.6523	5
4	435.2061	218.1067	F	***478.3024***	239.6548	461.2758	231.1416	4
5	506.2432	253.6252	A	331.2340	166.1206	314.2074	157.6074	3
6	619.3272	310.1673	L	260.1969	130.6021	243.1703	122.0888	2
7			K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of MVGFALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.9	764.4255	-0.0002	MVGFALK

AT5G50920.1

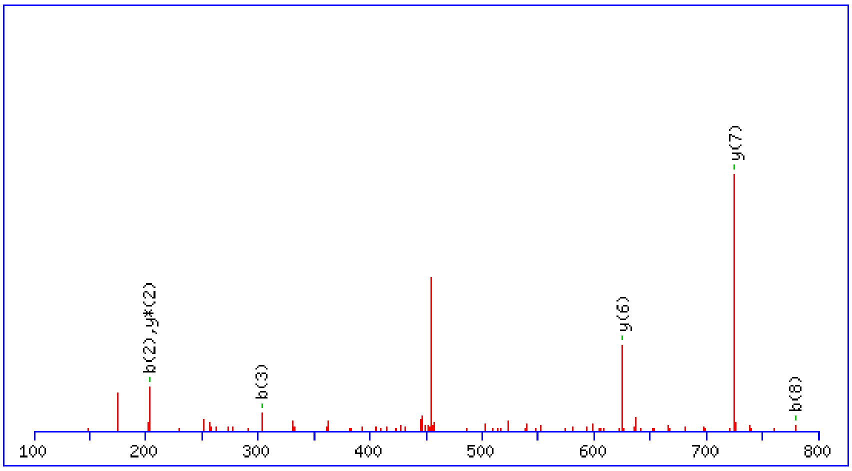
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEVSAIQAK**
Found in **AT5G50920.1** in **TAIR_Arabidopsis**, Symbols: ATHSP93-V, HSP93-V, CLPC, DCA1, CLPC1 | CLPC (HEAT SHOCK PROTEIN 93-V); ATP binding / ATPase | chr5:20732936-20737026 REVERSE

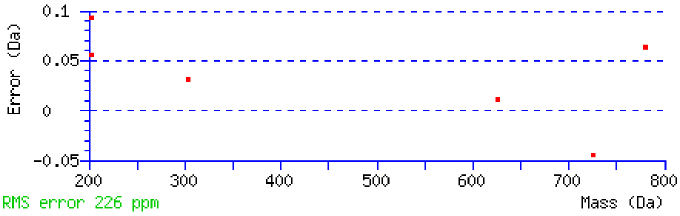
Match to Query 1761: 926.471328 from(464.242940,2+) index(3005)
Title: Elution from: 29.908 to 29.908 scan no 3734 cid35.00 polarity:+
Data file D6h-2_3.mgf

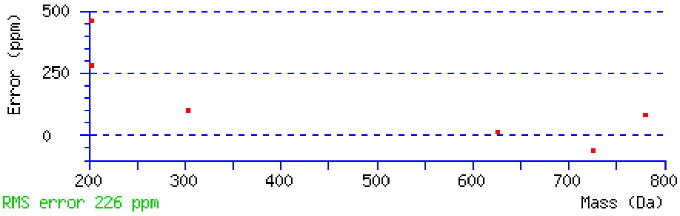
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 926.4699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.023
Matches : 6/72 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							9
2	***203.0811***	102.0442			185.0705	93.0389	E	855.4431	428.2252	837.4195	419.2134	837.4325	419.2199	8
3	***303.1465***	152.0769			285.1359	143.0716	V	**725.4034**	363.2054	707.3798	354.1936	707.3929	354.2001	7
4	391.1756	196.0914			373.1650	187.0861	S	**625.3380**	313.1726	607.3144	304.1608	607.3274	304.1673	6
5	463.2097	232.1085			445.1991	223.1032	A	537.3089	269.1581	519.2853	260.1463			5
6	577.2908	289.1490			559.2802	280.1438	I	465.2748	233.1410	447.2512	224.1292			4
7	707.3435	354.1754	689.3199	345.1636	689.3329	345.1701	Q	351.1937	176.1005	333.1701	167.0887			3
8	***779.3776***	390.1924	761.3540	381.1807	761.3670	381.1872	A	221.1410	111.0741	203.1174	102.0624			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AEVSAIQAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G50920.1

27.8	926.4699	0.0014	AEVSAIQAK
21.0	926.4722	-0.0008	FLQGLDPK
18.0	926.4699	0.0014	NATIEQLK
18.0	926.4699	0.0014	NATLQEIK
17.5	926.4699	0.0014	QAEAEKLK
15.8	926.4699	0.0014	AEVEIISR
15.8	926.4699	0.0014	ISVEEALR
15.8	926.4699	0.0014	SLVDDVLR
15.8	926.4699	0.0014	VTVIEAER
15.2	926.4726	-0.0013	KAKHSTNK

Mascot Search Results

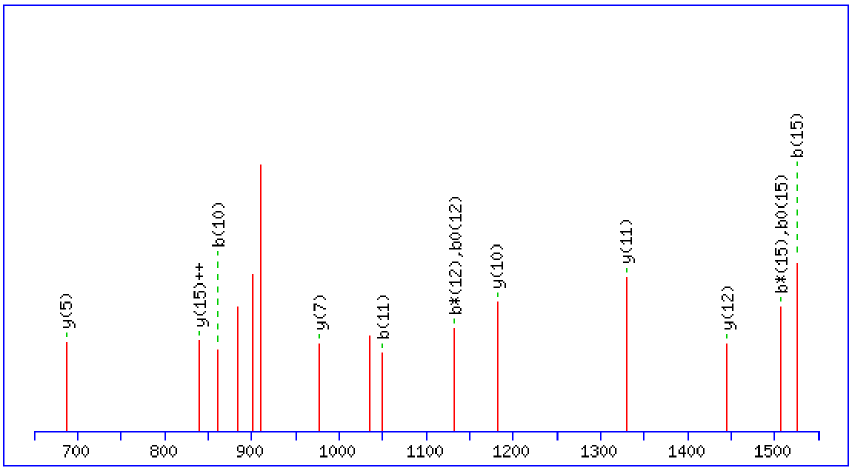
Peptide View

MS/MS Fragmentation of **SAAASNFGSGWTWLAYK**
Found in **AT5G51100.1** in **TAIR_Arabidopsis**, Symbols: FSD2 | FSD2 (FE SUPEROXIDE DISMUTASE 2); iron superoxide dismutase | chr5:20790583-20792861 REVERSE

Match to Query 8574: 1836.799740 from(919.407146,2+) index(9107)
Title: Elution from: 82.452 to 82.452 scan no 12463 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

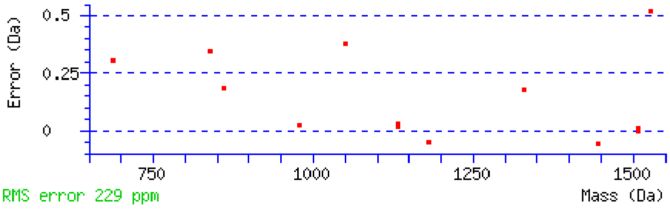
Or, Plot from 650 to 1550 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

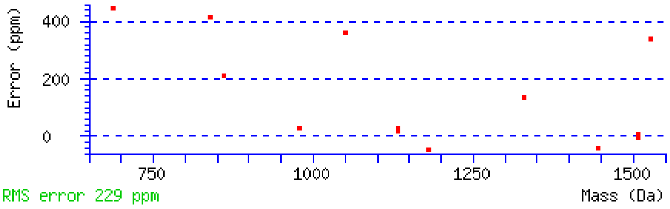


Monoisotopic mass of neutral peptide Mr(calc): 1836.7958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0017
Matches : 13/172 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							17
2	161.0705	81.0389			143.0599	72.0336	A	1749.7740	875.3906	1731.7504	866.3788	1731.7634	866.3853	16
3	233.1046	117.0560			215.0941	108.0507	A	1677.7398	839.3736	1659.7162	830.3618	1659.7293	830.3683	15
4	305.1388	153.0730			287.1282	144.0677	A	1605.7057	803.3565	1587.6821	794.3447	1587.6951	794.3512	14
5	393.1678	197.0876			375.1573	188.0823	S	1533.6715	767.3394	1515.6480	758.3276	1515.6610	758.3341	13
6	509.2048	255.1061	491.1813	246.0943	491.1943	246.1008	N	***1445.6425***	723.3249	1427.6189	714.3131	1427.6319	714.3196	12
7	657.2703	329.1388	639.2467	320.1270	639.2597	320.1335	F	***1329.6055***	665.3064	1311.5819	656.2946	1311.5949	656.3011	11
8	715.2888	358.1480	697.2652	349.1362	697.2782	349.1428	G	***1181.5400***	591.2737	1163.5164	582.2619	1163.5295	582.2684	10
9	803.3179	402.1626	785.2943	393.1508	785.3073	393.1573	S	1123.5215	562.2644	1105.4979	553.2526	1105.5110	553.2591	9
10	***861.3364***	431.1718	843.3128	422.1600	843.3258	422.1665	G	1035.4925	518.2499	1017.4689	509.2381	1017.4819	509.2446	8
11	***1049.4097***	525.2085	1031.3862	516.1967	1031.3992	516.2032	W	***977.4740***	489.2406	959.4504	480.2288	959.4634	480.2353	7
12	1151.4545	576.2309	1133.4309	567.2191	1133.4439	567.2256	T	789.4006	395.2039	771.3770	386.1921	771.3900	386.1986	6
13	1339.5278	670.2676	1321.5043	661.2558	1321.5173	661.2623	W	***687.3559***	344.1816	669.3323	335.1698			5
14	1453.6089	727.3081	1435.5853	718.2963	1435.5984	718.3028	L	499.2825	250.1449	481.2589	241.1331			4
15	***1525.6431***	763.3252	1507.6195	754.3134	1507.6325	754.3199	A	385.2014	193.1043	367.1778	184.0925			3
16	1689.7034	845.3554	1671.6799	836.3436	1671.6929	836.3501	Y	313.1672	157.0873	295.1437	148.0755			2
17							K	149.1069	75.0571	131.0833	66.0453			1

AT5G51100.1





NCBI **BLAST** search of SAAASNFGSGWTWLAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.6	1836.7958	0.0040	SAAASNFGSGWTWLAYK
9.4	1836.8000	-0.0003	HHSQTVSMVIGGNNRR
0.7	1836.8021	-0.0023	TFTAARLDSSSGVNGSSR
0.3	1836.7994	0.0003	EQKSEADPNVQSNELK
0.1	1836.7998	-0.0001	AEMLFDEMVKKGFDK
0.1	1836.7998	-0.0001	FEMMDKLLYDGVAQK

Mascot: http://www.matrixscience.com/

AT5G51110.1

Mascot Search Results

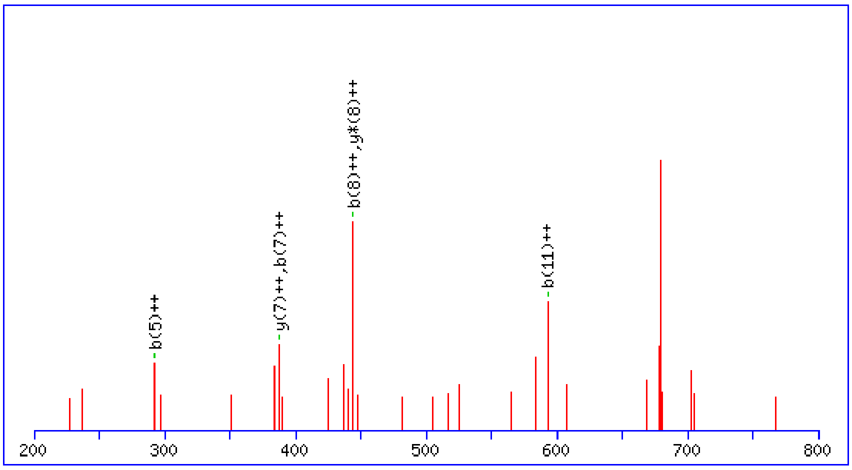
Peptide View

MS/MS Fragmentation of **IDDIKTSDLSPR**
Found in **AT5G51110.1** in **TAIR_Arabidopsis**, Symbols: | similar to dehydratase family [Arabidopsis thaliana] (TAIR:AT1G29810.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62291.1); contains InterPro domain Transcriptional coactivator/pterin dehydratase (InterPro:IPR001533) |

Match to Query 5093: 1358.700804 from(453.907544,3+) index(3429)
Title: Elution from: 33.783 to 33.783 scan no 4288 cid35.00 polarity:+
Data file D6h-1_2.mgf

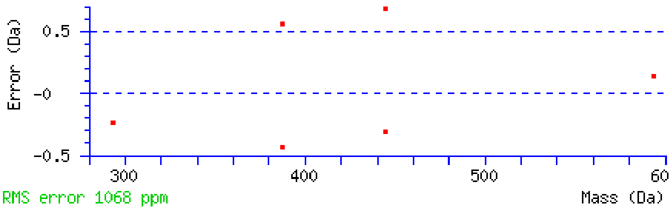
Click mouse within plot area to zoom in by factor of two about that point

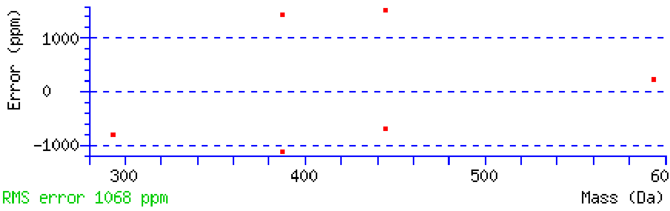
Or, Plot from 200 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1358.7041
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.023
Matches : 6/118 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							12
2	229.1183	115.0628			211.1077	106.0575	D	1246.6274	623.8173	1229.6008	615.3040	1228.6168	614.8120	11
3	344.1452	172.5763			326.1347	163.5710	D	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	10
4	457.2293	229.1183			439.2187	220.1130	I	1016.5735	508.7904	999.5469	500.2771	998.5629	499.7851	9
5	585.3243	***293.1658***	568.2977	284.6525	567.3137	284.1605	K	903.4894	452.2483	886.4629	443.7351	885.4789	443.2431	8
6	686.3719	343.6896	669.3454	335.1763	668.3614	334.6843	T	775.3945	388.2009	758.3679	379.6876	757.3839	379.1956	7
7	773.4040	***387.2056***	756.3774	378.6923	755.3934	378.2003	S	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	6
8	888.4309	***444.7191***	871.4044	436.2058	870.4203	435.7138	D	587.3148	294.1610	570.2882	285.6477	569.3042	285.1557	5
9	1001.5150	501.2611	984.4884	492.7478	983.5044	492.2558	L	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
10	1088.5470	544.7771	1071.5204	536.2639	1070.5364	535.7719	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
11	1185.5998	***593.3035***	1168.5732	584.7902	1167.5892	584.2982	P	272.1717	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IDDIKTSDLSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G51110.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	1358.7041	-0.0033	IDDIKTSDLSPR
12.2	1358.6976	0.0032	VDACSKINSIPR
10.7	1358.7017	-0.0009	HVVFGQVIEGMK
7.6	1358.7041	-0.0033	SAAKETAKVDDPK
0.1	1358.7015	-0.0007	GSGRVRGSEEVAR

AT5G51270.1

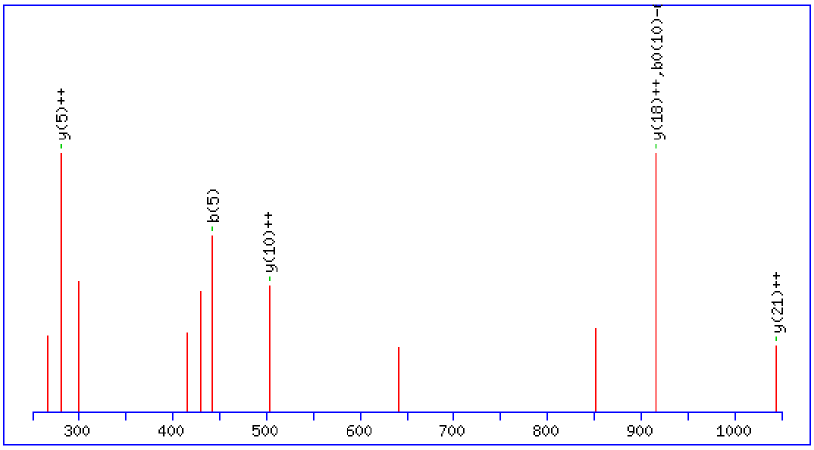
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADLAAPSEPMTVALAISGSIKSK**
Found in **AT5G51270.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr5:20852363-20855488 REVERSE

Match to Query 9981: 2272.198761 from(758.406863,3+) index(10912)
Title: Elution from: 123.733 to 123.733 scan no 16311 cid35.00 polarity:+
Data file D1d-3_2.mgf

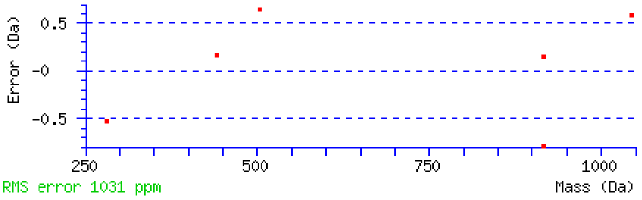
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

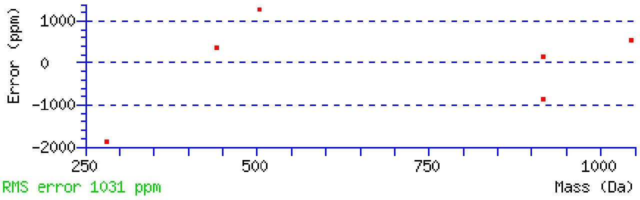


Monoisotopic mass of neutral peptide Mr(calc): 2272.1984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.029
Matches : 6/330 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							23
2	187.0713	94.0393			169.0608	85.0340	D	2202.1686	1101.5879	2185.1421	1093.0747	2184.1580	1092.5827	22
3	300.1554	150.5813			282.1448	141.5761	L	2087.1417	1044.0745	2070.1151	1035.5612	2069.1311	1035.0692	21
4	371.1925	186.0999			353.1819	177.0946	A	1974.0576	987.5324	1957.0311	979.0192	1956.0470	978.5272	20
5	442.2296	221.6185			424.2191	212.6132	A	1903.0205	952.0139	1885.9939	943.5006	1885.0099	943.0086	19
6	539.2824	270.1448			521.2718	261.1396	P	1831.9834	916.4953	1814.9568	907.9821	1813.9728	907.4900	18
7	626.3144	313.6608			608.3039	304.6556	S	1734.9306	867.9689	1717.9041	859.4557	1716.9200	858.9637	17
8	755.3570	378.1821			737.3464	369.1769	E	1647.8986	824.4529	1630.8720	815.9397	1629.8880	815.4476	16
9	852.4098	426.7085			834.3992	417.7032	P	1518.8560	759.9316	1501.8294	751.4184	1500.8454	750.9264	15
10	999.4452	500.2262			981.4346	491.2209	M	1421.8032	711.4053	1404.7767	702.8920	1403.7927	702.4000	14
11	1100.4929	550.7501			1082.4823	541.7448	T	1274.7678	637.8876	1257.7413	629.3743	1256.7573	628.8823	13
12	1199.5613	600.2843			1181.5507	591.2790	V	1173.7201	587.3637	1156.6936	578.8504	1155.7096	578.3584	12
13	1270.5984	635.8028			1252.5878	626.7975	A	1074.6517	537.8295	1057.6252	529.3162	1056.6412	528.8242	11
14	1383.6824	692.3449			1365.6719	683.3396	L	1003.6146	502.3109	986.5881	493.7977	985.6041	493.3057	10
15	1454.7196	727.8634			1436.7090	718.8581	A	890.5306	445.7689	873.5040	437.2556	872.5200	436.7636	9
16	1567.8036	784.4054			1549.7931	775.4002	I	819.4934	410.2504	802.4669	401.7371	801.4829	401.2451	8
17	1654.8357	827.9215			1636.8251	818.9162	S	706.4094	353.7083	689.3828	345.1951	688.3988	344.7030	7
18	1711.8571	856.4322			1693.8465	847.4269	G	619.3774	310.1923	602.3508	301.6790	601.3668	301.1870	6
19	1798.8891	899.9482			1780.8786	890.9429	S	562.3559	281.6816	545.3293	273.1683	544.3453	272.6763	5
20	1911.9732	956.4902			1893.9626	947.4850	I	475.3239	238.1656	458.2973	229.6523	457.3133	229.1603	4
21	2040.0682	1020.5377	2023.0416	1012.0244	2022.0576	1011.5324	K	362.2398	181.6235	345.2132	173.1103	344.2292	172.6183	3
22	2127.1002	1064.0537	2110.0736	1055.5405	2109.0896	1055.0485	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
23							K	147.1128	74.0600	130.0863	65.5468			1

AT5G51270.1





NCBI **BLAST** search of ADLAAPSEPMTVALAISGSIKSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.2	2272.1984	0.0004	ADLAAPSEPMTVALAISGSIKSK
7.0	2272.1951	0.0037	ALGVKPSPDQFETLIDKADTK
2.2	2272.1984	0.0003	ALQELVLSGCSKLESVPTDVK
0.3	2272.2038	-0.0051	LFEVAHDQSRTCPVIIFLK
0.2	2272.1998	-0.0010	VLLDHSVENLMEALNGLHLR

Mascot: http://www.matrixscience.com/

AT5G51500.1

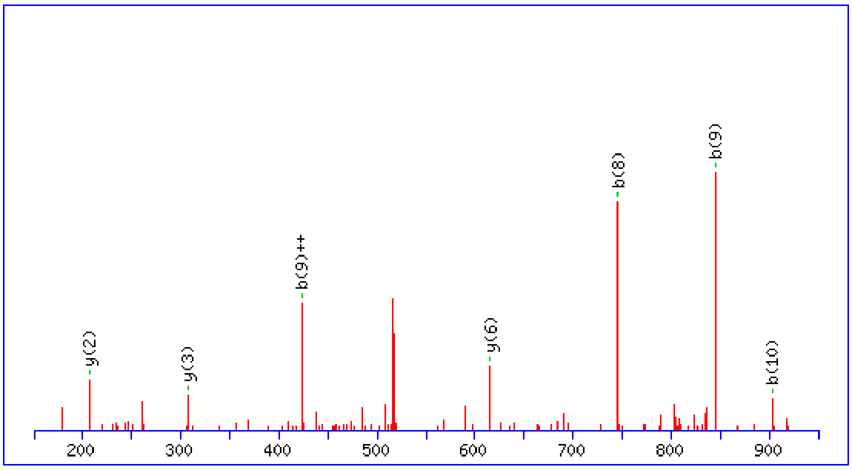
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASDASAFSVGK**
Found in **AT5G51500.1** in **TAIR_Arabidopsis**, Symbols: | pectinesterase family protein | chr5:20935155-20937064 REVERSE

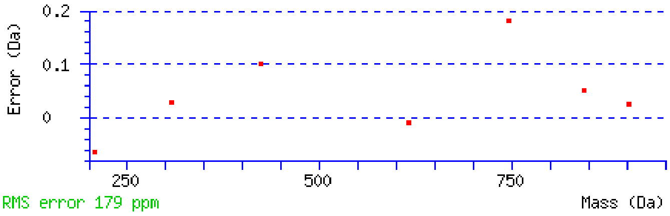
Match to Query 2952: 1050.461228 from(526.237890,2+) index(4156)
Title: Elution from: 38.462 to 38.462 scan no 5154 cid35.00 polarity:+
Data file D12h-1_2.mgf

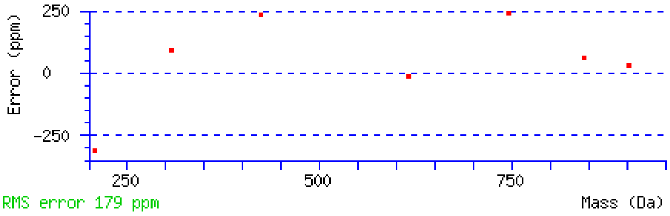
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1050.4626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.0091
Matches : 7/92 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244			A							11
2	161.0705	81.0389	143.0599	72.0336	S	979.4357	490.2215	961.4122	481.2097	961.4252	481.2162	10
3	277.0945	139.0509	259.0839	130.0456	D	891.4067	446.2070	873.3831	437.1952	873.3961	437.2017	9
4	349.1286	175.0679	331.1180	166.0627	A	775.3827	388.1950	757.3591	379.1832	757.3721	379.1897	8
5	437.1577	219.0825	419.1471	210.0772	S	703.3485	352.1779	685.3250	343.1661	685.3380	343.1726	7
6	509.1918	255.0996	491.1813	246.0943	A	***615.3195***	308.1634	597.2959	299.1516	597.3089	299.1581	6
7	657.2573	329.1323	639.2467	320.1270	F	543.2853	272.1463	525.2617	263.1345	525.2748	263.1410	5
8	***745.2863***	373.1468	727.2758	364.1415	S	395.2199	198.1136	377.1963	189.1018	377.2093	189.1083	4
9	***845.3518***	423.1795	827.3412	414.1742	V	***307.1908***	154.0990	289.1672	145.0873			3
10	***903.3703***	452.1888	885.3597	443.1835	G	***207.1254***	104.0663	189.1018	95.0545			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ASDASAFSVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G51500.1

Score	Mr(calc)	Delta	Sequence
27.9	1050.4626	-0.0014	ASDASAFSVGK
11.6	1050.4612	0.0000	MSGCLGKTGK
2.8	1050.4635	-0.0022	MVQVMFPR
2.3	1050.4604	0.0008	AASSSSSSQVK
2.0	1050.4583	0.0029	DNARMSRGK
2.0	1050.4583	0.0029	NNKGTCRGK
2.0	1050.4626	-0.0014	NSVDGYISGK
2.0	1050.4626	-0.0014	SDATVTFNGK
1.0	1050.4612	0.0000	TGTVVVMCR
0.8	1050.4632	-0.0020	MNFHRRR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAEIPDIDLSQVGVTK**
Found in **AT5G51820.1** in **TAIR_Arabidopsis**, Symbols: ATPGMP, PGM1, STF1, PGM | PGM (PHOSPHOGLUCOMUTASE) | chr5:21080757-21085159 REVERSE

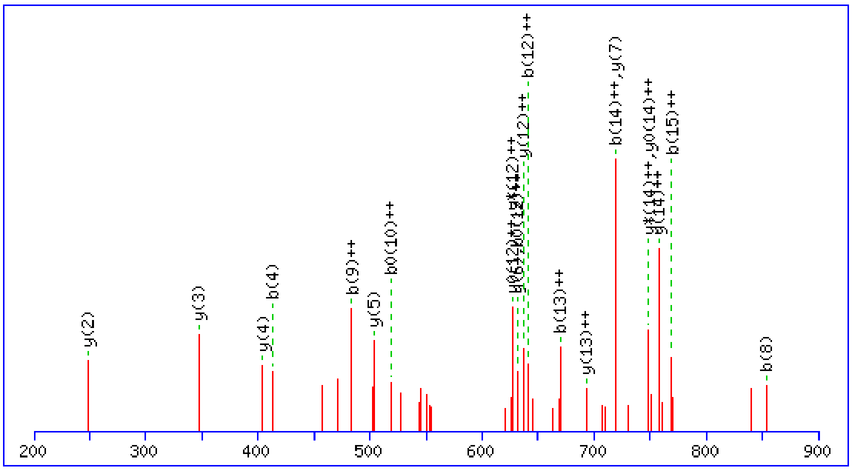
Match to Query 7454: 1682.909568 from(561.977132,3+) index(7895)
Title: Elution from: 70.742 to 70.742 scan no 10465 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

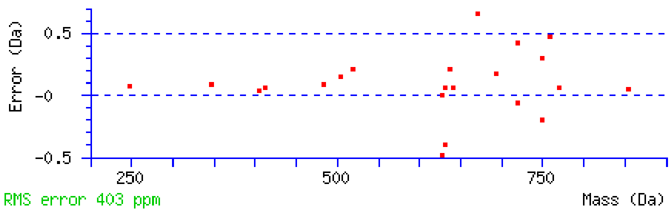
Show Y-axis ☐

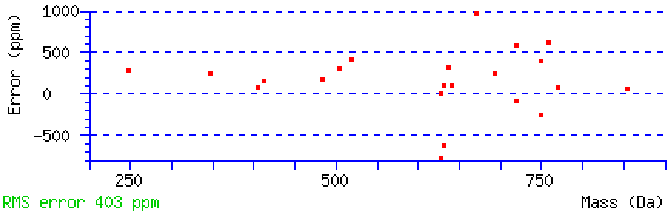


Monoisotopic mass of neutral peptide Mr(calc): 1682.9091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 1e-005
Matches : 22/154 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							16
2	171.1128	86.0600					A	1584.8479	792.9276	1567.8214	784.4143	1566.8374	783.9223	15
3	300.1554	150.5813			282.1448	141.5761	E	1513.8108	757.4090	1496.7843	748.8958	1495.8003	748.4038	14
4	**413.2395**	207.1234			395.2289	198.1181	I	1384.7682	692.8877	1367.7417	684.3745	1366.7577	683.8825	13
5	510.2922	255.6498			492.2817	246.6445	P	1271.6842	636.3457	1254.6576	627.8324	1253.6736	627.3404	12
6	625.3192	313.1632			607.3086	304.1579	D	1174.6314	587.8193	1157.6048	579.3061	1156.6208	578.8141	11
7	738.4032	369.7053			720.3927	360.7000	I	1059.6045	530.3059	1042.5779	521.7926	1041.5939	521.3006	10
8	**853.4302**	427.2187			835.4196	418.2134	D	946.5204	473.7638	929.4938	465.2506	928.5098	464.7585	9
9	966.5142	***483.7608***			948.5037	474.7555	L	831.4934	416.2504	814.4669	407.7371	813.4829	407.2451	8
10	1053.5463	527.2768			1035.5357	518.2715	S	***718.4094***	359.7083	701.3828	351.1951	700.3988	350.7030	7
11	1181.6048	591.3061	1164.5783	582.7928	1163.5943	582.3008	Q	***631.3774***	316.1923	614.3508	307.6790	613.3668	307.1870	6
12	1280.6733	***640.8403***	1263.6467	632.3270	1262.6627	631.8350	V	***503.3188***	252.1630	486.2922	243.6498	485.3082	243.1577	5
13	1337.6947	***669.3510***	1320.6682	660.8377	1319.6842	660.3457	G	***404.2504***	202.6288	387.2238	194.1155	386.2398	193.6235	4
14	1436.7631	***718.8852***	1419.7366	710.3719	1418.7526	709.8799	V	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
15	1537.8108	***769.4090***	1520.7843	760.8958	1519.8003	760.4038	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
16							K	147.1128	74.0600	130.0863	65.5468			1

AT5G51820.1





NCBI **BLAST** search of VAEIPDIDLSQVGVTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.1	1682.9091	0.0005	VAEIPDIDLSQVGVTK
10.6	1682.9099	-0.0004	VMISEVPTMAIHLVK
4.3	1682.9099	-0.0004	VMISEVPTMAIHLVK
2.7	1682.9065	0.0030	MVIPLWKANLEEPK
2.3	1682.9079	0.0017	WNNHKIMVKWLSK
0.2	1682.9138	-0.0042	SEHVMVLGKGNKGISK

Mascot: http://www.matrixscience.com/

AT5G52290.1

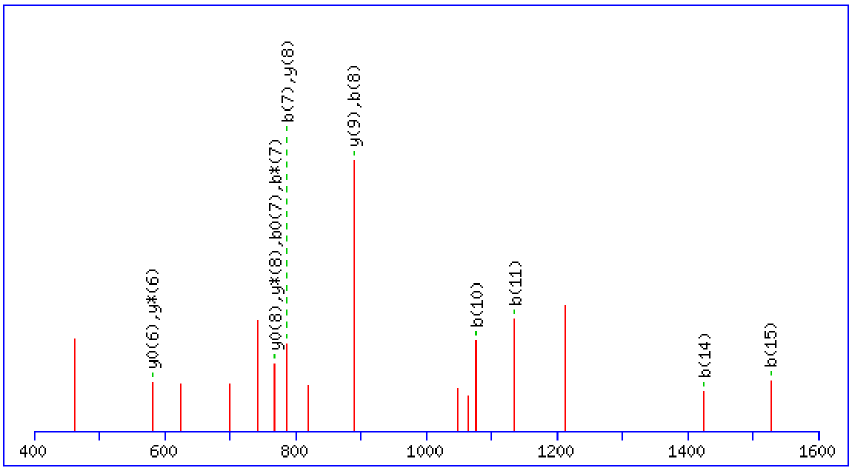
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKQSLSYTANGTGQTK**
Found in **AT5G52290.1** in **TAIR_Arabidopsis**, Symbols: | similar to unnamed protein product [Vitis vinifera] (GB:CAO17244.1) | chr5:21247579-21253780 REVERSE

Match to Query 7558: 1674.766322 from(838.390437,2+) index(10358)
Title: Elution from: 104.358 to 104.358 scan no 15195 cid35.00 polarity:+
Data file D6h-2_3.mgf

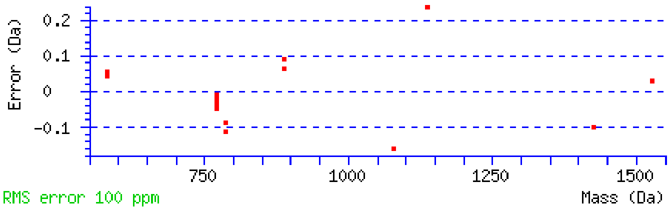
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

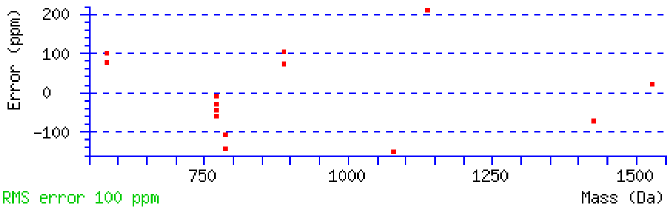


Monoisotopic mass of neutral peptide Mr(calc): 1674.7699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0023
Matches : 14/170 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							16
2	203.1305	102.0689	185.1069	93.0571			K	1603.7431	802.3752	1585.7195	793.3634	1585.7325	793.3699	15
3	333.1831	167.0952	315.1595	158.0834			Q	1473.6540	737.3307	1455.6305	728.3189	1455.6435	728.3254	14
4	421.2122	211.1097	403.1886	202.0979	403.2016	202.1044	S	1343.6014	672.3043	1325.5778	663.2925	1325.5908	663.2991	13
5	535.2933	268.1503	517.2697	259.1385	517.2827	259.1450	L	1255.5723	628.2898	1237.5487	619.2780	1237.5618	619.2845	12
6	623.3223	312.1648	605.2987	303.1530	605.3118	303.1595	S	1141.4912	571.2493	1123.4676	562.2375	1123.4807	562.2440	11
7	***787.3827***	394.1950	769.3591	385.1832	769.3721	385.1897	Y	1053.4622	527.2347	1035.4386	518.2229	1035.4516	518.2294	10
8	***889.4274***	445.2173	871.4038	436.2055	871.4168	436.2121	T	**889.4018**	445.2045	871.3782	436.1927	871.3912	436.1993	9
9	961.4616	481.2344	943.4380	472.2226	943.4510	472.2291	A	**787.3571**	394.1822	769.3335	385.1704	769.3465	385.1769	8
10	***1077.4986***	539.2529	1059.4750	530.2411	1059.4880	530.2476	N	715.3229	358.1651	697.2994	349.1533	697.3124	349.1598	7
11	***1135.5171***	568.2622	1117.4935	559.2504	1117.5065	559.2569	G	599.2859	300.1466	581.2624	291.1348	581.2754	291.1413	6
12	1237.5618	619.2845	1219.5382	610.2727	1219.5512	610.2792	T	541.2674	271.1374	523.2439	262.1256	523.2569	262.1321	5
13	1295.5803	648.2938	1277.5567	639.2820	1277.5697	639.2885	G	439.2227	220.1150	421.1991	211.1032	421.2122	211.1097	4
14	***1425.6329***	713.3201	1407.6093	704.3083	1407.6223	704.3148	Q	381.2042	191.1058	363.1806	182.0940	363.1937	182.1005	3
15	***1527.6776***	764.3424	1509.6540	755.3307	1509.6671	755.3372	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT5G52290.1





NCBI **BLAST** search of AKQSLSYTANGTGQTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.2	1674.7699	-0.0036	AKQSLSYTANGTGQTK
4.5	1674.7652	0.0011	YGLSNGESGGMLGKRK
3.2	1674.7686	-0.0023	KRSTICMSLQQSSK
2.5	1674.7614	0.0050	FEGDIGFNTIEFLR
2.0	1674.7634	0.0029	KMLNVETFCIVMR
1.6	1674.7681	-0.0018	IDKEFMSQMAKVAK
1.4	1674.7652	0.0011	DSRFLREVEMLSR
0.1	1674.7708	-0.0045	RSSMSVEAFPMRLK

Mascot: http://www.matrixscience.com/

AT5G52310.1

Mascot Search Results

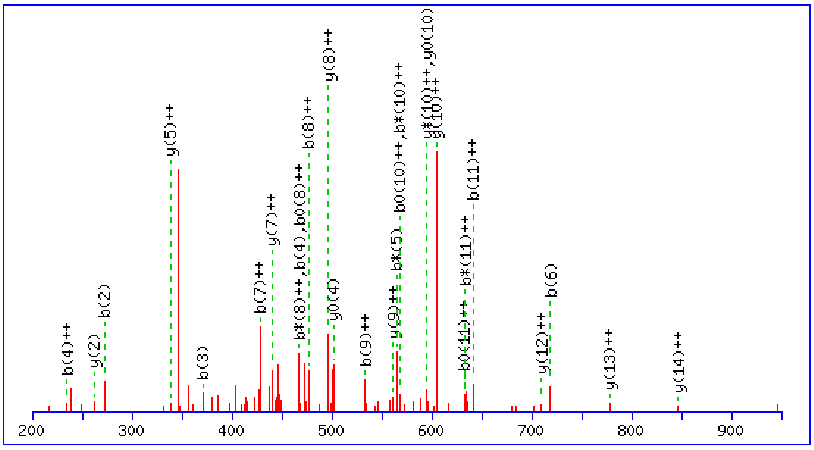
Peptide View

MS/MS Fragmentation of **RDVPIHHPLSELSDREESR**
Found in **AT5G52310.1** in **TAIR_Arabidopsis**, Symbols: LTI78, RD29A, LTI140, COR78 | COR78 (COLD REGULATED 78) | chr5:21258155-21260552 FORWARD

Match to Query 10561: 2271.134985 from(455.234273,5+) index(2621)
Title: Elution from: 27.399 to 27.399 scan no 3277 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

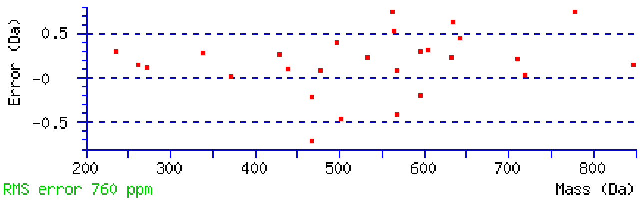
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

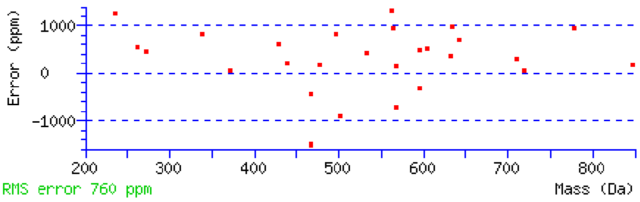


Monoisotopic mass of neutral peptide Mr(calc): 2271.1356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.002
Matches : 28/212 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			**R**							**19**
2	***272.1353***	136.5713	255.1088	128.0580	254.1248	127.5660	**D**	2116.0418	1058.5245	2099.0152	1050.0112	2098.0312	1049.5192	**18**
3	***371.2037***	186.1055	354.1772	177.5922	353.1932	177.1002	**V**	2001.0148	1001.0111	1983.9883	992.4978	1983.0043	992.0058	**17**
4	***468.2565***	***234.6319***	451.2300	226.1186	450.2459	225.6266	**P**	1901.9464	951.4768	1884.9199	942.9636	1883.9358	942.4716	**16**
5	581.3406	291.1739	564.3140	282.6606	563.3300	282.1686	**I**	1804.8936	902.9505	1787.8671	894.4372	1786.8831	893.9452	**15**
6	***718.3995***	359.7034	701.3729	351.1901	700.3889	350.6981	**H**	1691.8096	846.4084	1674.7830	837.8952	1673.7990	837.4031	**14**
7	855.4584	**428.2328**	838.4318	419.7196	837.4478	419.2276	**H**	1554.7507	777.8790	1537.7241	769.3657	1536.7401	768.8737	**13**
8	952.5112	**476.7592**	935.4846	468.2459	934.5006	467.7539	**P**	1417.6918	709.3495	1400.6652	700.8362	1399.6812	700.3442	**12**
9	1065.5952	**533.3012**	1048.5687	524.7880	1047.5847	524.2960	**L**	1320.6390	660.8231	1303.6124	652.3099	1302.6284	651.8179	**11**
10	1152.6273	576.8173	1135.6007	568.3040	1134.6167	567.8120	**S**	1207.5549	604.2811	1190.5284	595.7678	1189.5444	595.2758	**10**
11	1281.6698	**641.3386**	1264.6433	632.8253	1263.6593	632.3333	**E**	1120.5229	560.7651	1103.4964	552.2518	1102.5123	551.7598	**9**
12	1394.7539	697.8806	1377.7274	689.3673	1376.7433	688.8753	**L**	991.4803	496.2438	974.4538	487.7305	973.4697	487.2385	**8**
13	1481.7859	741.3966	1464.7594	732.8833	1463.7754	732.3913	**S**	878.3962	439.7018	861.3697	431.1885	860.3857	430.6965	**7**
14	1596.8129	798.9101	1579.7863	790.3968	1578.8023	789.9048	**D**	791.3642	396.1857	774.3377	387.6725	773.3537	387.1805	**6**
15	1752.9140	876.9606	1735.8874	868.4474	1734.9034	867.9554	**R**	676.3373	338.6723	659.3107	330.1590	658.3267	329.6670	**5**
16	1881.9566	941.4819	1864.9300	932.9687	1863.9460	932.4766	**E**	520.2362	260.6217	503.2096	252.1084	502.2256	251.6164	**4**
17	2010.9992	1006.0032	1993.9726	997.4900	1992.9886	996.9979	**E**	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	**3**
18	2098.0312	1049.5192	2081.0047	1041.0060	2080.0206	1040.5140	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**

AT5G52310.1





NCBI **BLAST** search of RDVPIHHPLSELSDREESR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.9	2271.1356	-0.0006	RDVPIHHPLSELSDREESR
3.7	2271.1358	-0.0008	MTHDDVYLSFLPLAHILDR
1.8	2271.1391	-0.0042	IDLGNGKSFSGMGISMFSPKAK
0.3	2271.1405	-0.0055	RRITFFANSLFMNMPSAPR

Mascot: http://www.matrixscience.com/

AT5G52470.1

Mascot Search Results

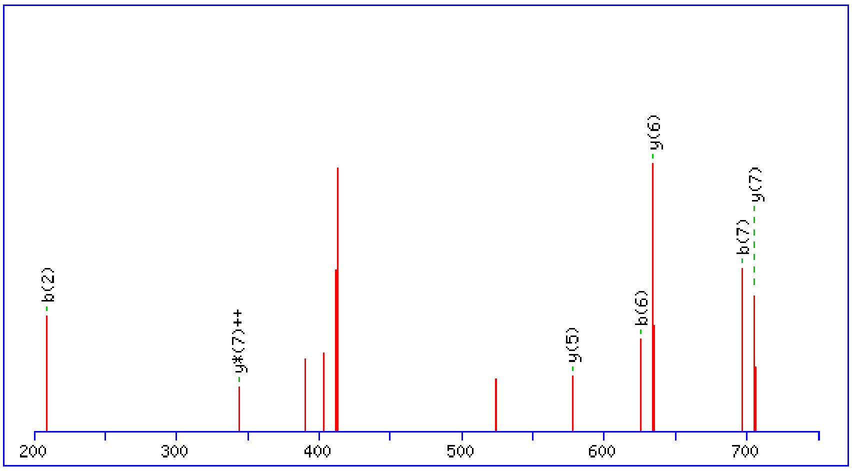
Peptide View

MS/MS Fragmentation of **HAGVFIAK**
Found in **AT5G52470.1** in **TAIR_Arabidopsis**, Symbols: FBR1, ATFIB1, ATFBR1, SKIP7, FIB1 | FIB1 (FIBRILLARIN 1) | chr5:21311516-21313735 FORWARD

Match to Query 1400: 841.481128 from(421.747840,2+) index(844)
Title: Elution from: 14.885 to 14.885 scan no 1248 cid35.00 polarity:+
Data file D12h-1_1.mgf

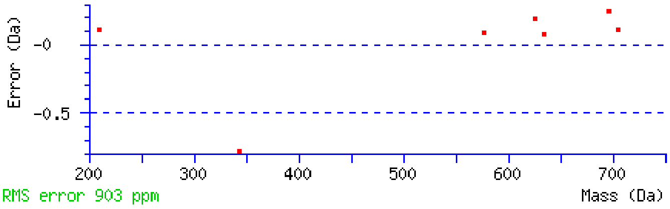
Click mouse within plot area to zoom in by factor of two about that point

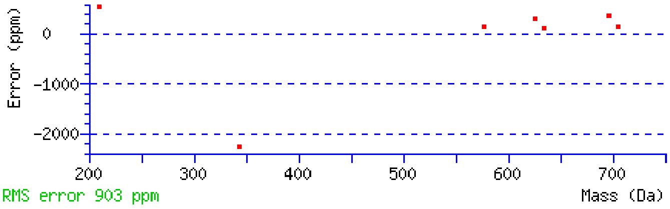
Or, Plot from 200 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 841.4810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0028
Matches : 7/42 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	138.0662	69.5367	**H**					**8**
2	***209.1033***	105.0553	**A**	***705.4294***	353.2183	688.4028	344.7051	**7**
3	266.1248	133.5660	**G**	***634.3923***	317.6998	617.3657	309.1865	**6**
4	365.1932	183.1002	**V**	***577.3708***	289.1890	560.3443	280.6758	**5**
5	512.2616	256.6344	**F**	478.3024	239.6548	461.2758	231.1416	**4**
6	***625.3457***	313.1765	**I**	331.2340	166.1206	314.2074	157.6074	**3**
7	***696.3828***	348.6950	**A**	218.1499	109.5786	201.1234	101.0653	**2**
8			**K**	147.1128	74.0600	130.0863	65.5468	**1**





NCBI **BLAST** search of HAGVFIAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.8	841.4810	0.0001	HAGVFIAK

AT5G52470.1

2.3	841.4810	0.0001	HQGFLIK
1.6	841.4810	0.0001	IFAGHLGK
1.6	841.4810	0.0001	QFLHGLK
1.5	841.4810	0.0001	YTFKRK
1.0	841.4810	0.0001	FALHVGAK

AT5G52530.1

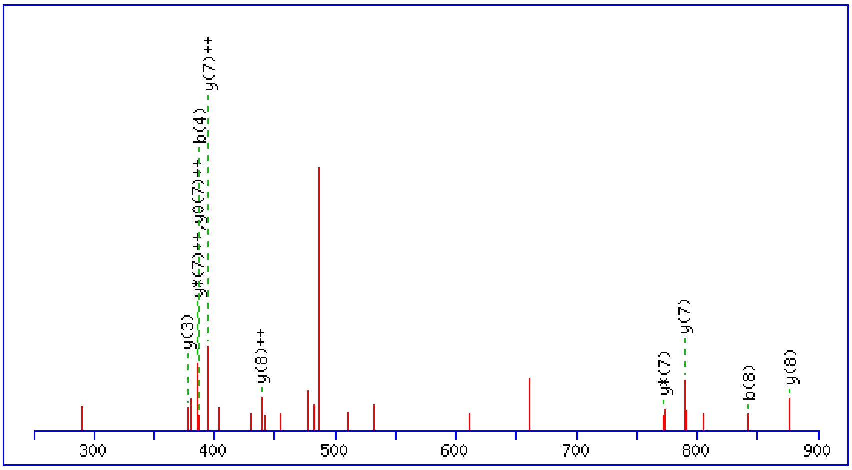
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSADEPTEK**
Found in **AT5G52530.1** in **TAIR_Arabidopsis**, Symbols: | dentin sialophosphoprotein-related | chr5:21335441-21338108 FORWARD

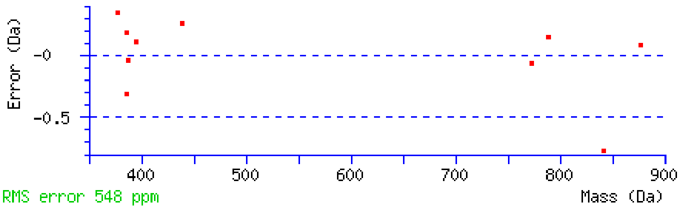
Match to Query 2261: 988.469174 from(495.241863,2+) index(738)
Title: Elution from: 12.561 to 12.561 scan no 1050 cid35.00 polarity:+
Data file D12h-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

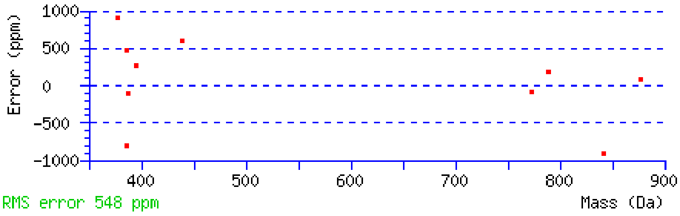


```
Monoisotopic mass of neutral peptide Mr(calc): 988.4713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17  Expect: 0.038
Matches : 10/76 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							9
2	201.1234	101.0653	183.1128	92.0600	S	***876.3945***	438.7009	859.3680	430.1876	858.3840	429.6956	8
3	272.1605	136.5839	254.1499	127.5786	A	***789.3625***	395.1849	772.3359	386.6716	771.3519	386.1796	7
4	***387.1874***	194.0974	369.1769	185.0921	D	718.3254	359.6663	701.2988	351.1531	700.3148	350.6610	6
5	516.2300	258.6186	498.2195	249.6134	E	603.2984	302.1529	586.2719	293.6396	585.2879	293.1476	5
6	613.2828	307.1450	595.2722	298.1397	P	474.2558	237.6316	457.2293	229.1183	456.2453	228.6263	4
7	714.3305	357.6689	696.3199	348.6636	T	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	3
8	***843.3731***	422.1902	825.3625	413.1849	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 548 ppm



RMS error 548 ppm

NCBI **BLAST** search of LSADEPTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.3	988.4713	-0.0021	LSADEPTEK

AT5G52530.1

10.1	988.4686	0.0006	ISDDNRNR
5.7	988.4688	0.0004	MFNISYAK
1.7	988.4713	-0.0021	EAELAEEAK
0.5	988.4713	-0.0021	ETLEDPSAK
0.0	988.4686	0.0006	SPASDGSRGR

AT5G52560.1

Mascot Search Results

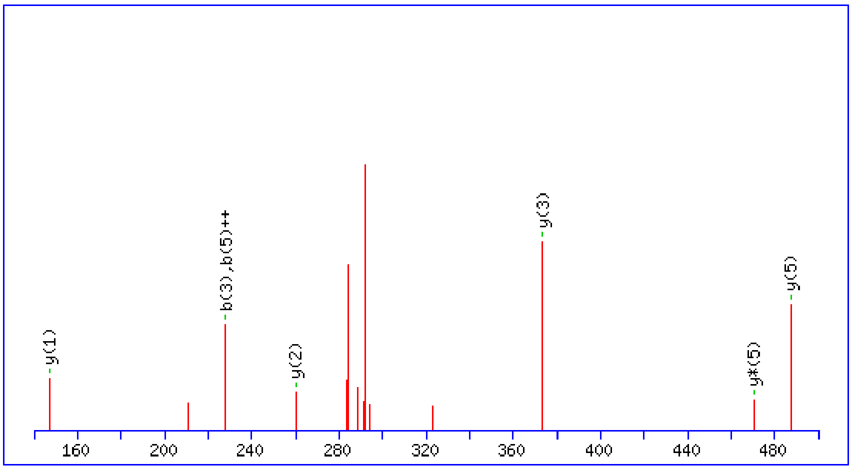
Peptide View

MS/MS Fragmentation of **LGGLIK**
Found in **AT5G52560.1** in **TAIR_Arabidopsis**, Symbols: ATUSP | ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR PYROPHOSPHORYLASE); UTP-monosaccharide-1-phosphate uridylyltransferase/ UTP:arabinose-1-phosphate uridylyltransferase/ UTP:galactose-1-phosphate uridylyltransferase/ UTP:glucose-1-phosphate uri

Match to Query 515: 599.400848 from(300.707700,2+) index(2560)
Title: Elution from: 26.025 to 26.025 scan no 3167 cid35.00 polarity:+
Data file D1d-3_2.mgf

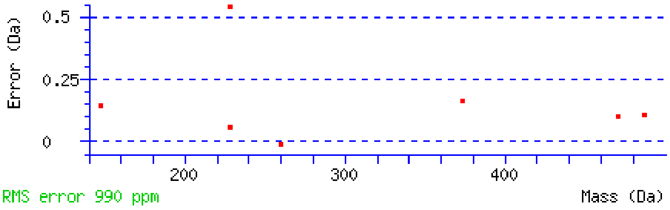
Click mouse within plot area to zoom in by factor of two about that point

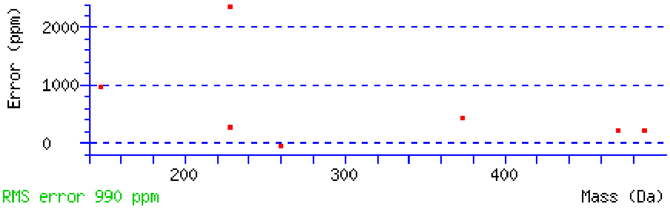
Or, Plot from 140 to 500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 599.4006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.011
Matches : 7/30 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.0913	57.5493	L					6
2	171.1128	86.0600	G	***487.3239***	244.1656	470.2973	235.6523	5
3	228.1343	114.5708	G	430.3024	215.6548	413.2758	207.1416	4
4	341.2183	171.1128	L	***373.2809***	187.1441	356.2544	178.6308	3
5	454.3024	227.6548	I	***260.1969***	130.6021	243.1703	122.0888	2
6			K	***147.1128***	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of LGGLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.1	599.4006	0.0002	IGGILK
29.1	599.4006	0.0002	IINIK

AT5G52560.1

29.1	599.4006	0.0002	IINLK
29.1	599.4006	0.0002	ILNIK
29.1	599.4006	0.0002	ILNLK
29.1	599.4006	0.0002	INILK
29.1	599.4006	0.0002	INLLK
29.1	599.4006	0.0002	LGGLIK
29.1	599.4006	0.0002	LGGLLK
29.1	599.4006	0.0002	LINIK

AT5G52650.1

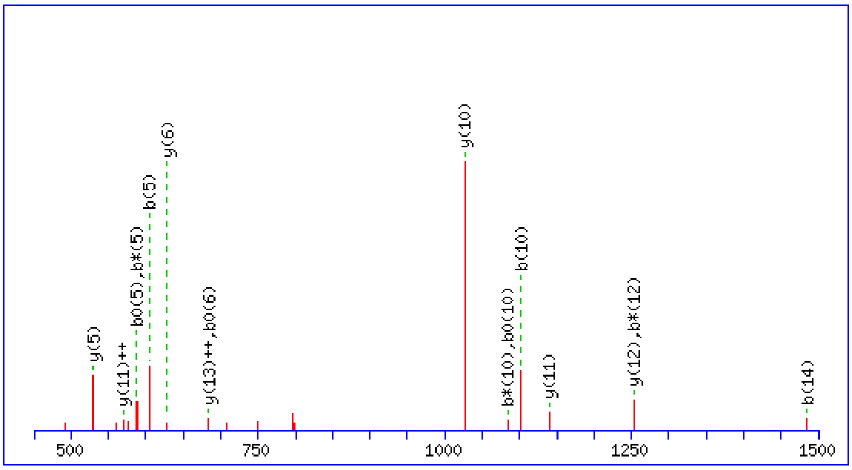
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYLNLPSDVVPATLK**
Found in **AT5G52650.1** in **TAIR_Arabidopsis**, Symbols: | 40S ribosomal protein S10 (RPS10C) | chr5:21373007-21374229 REVERSE

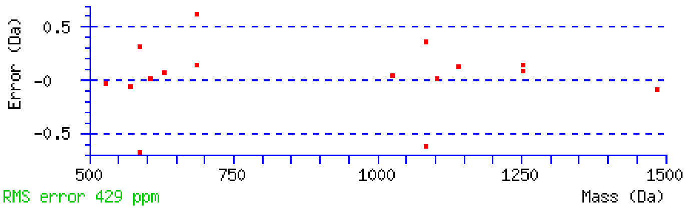
Match to Query 7340: 1629.895110 from(815.954831,2+) index(8367)
Title: Elution from: 74.540 to 74.540 scan no 11161 cid35.00 polarity:+
Data file 0-1_3.mgf

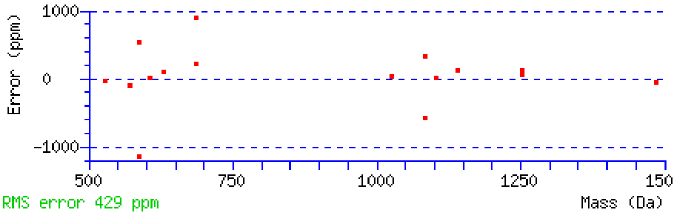
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1629.8978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00035
Matches : 16/158 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							15
2	265.1183	133.0628			247.1077	124.0575	Y	1529.8574	765.4323	1512.8308	756.9190	1511.8468	756.4270	14
3	378.2023	189.6048			360.1918	180.5995	L	1366.7940	683.9007	1349.7675	675.3874	1348.7835	674.8954	13
4	492.2453	246.6263	475.2187	238.1130	474.2347	237.6210	N	***1253.7100***	627.3586	1236.6834	618.8454	1235.6994	618.3533	12
5	**605.3293**	303.1683	588.3028	294.6550	587.3188	294.1630	L	***1139.6671***	570.3372	1122.6405	561.8239	1121.6565	561.3319	11
6	702.3821	351.6947	685.3556	343.1814	684.3715	342.6894	P	***1026.5830***	513.7951	1009.5564	505.2819	1008.5724	504.7898	10
7	789.4141	395.2107	772.3876	386.6974	771.4036	386.2054	S	929.5302	465.2687	912.5037	456.7555	911.5197	456.2635	9
8	904.4411	452.7242	887.4145	444.2109	886.4305	443.7189	D	842.4982	421.7527	825.4716	413.2395	824.4876	412.7475	8
9	1003.5095	502.2584	986.4829	493.7451	985.4989	493.2531	V	727.4713	364.2393	710.4447	355.7260	709.4607	355.2340	7
10	**1102.5779**	551.7926	1085.5514	543.2793	1084.5673	542.7873	V	***628.4028***	314.7051	611.3763	306.1918	610.3923	305.6998	6
11	1199.6307	600.3190	1182.6041	591.8057	1181.6201	591.3137	P	***529.3344***	265.1709	512.3079	256.6576	511.3239	256.1656	5
12	1270.6678	635.8375	1253.6412	627.3243	1252.6572	626.8322	A	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
13	1371.7155	686.3614	1354.6889	677.8481	1353.7049	677.3561	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
14	**1484.7995**	742.9034	1467.7730	734.3901	1466.7890	733.8981	L	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TYLNLPSDVVPATLK

AT5G52650.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.3	1629.8978	-0.0027	TYLNLPSDVVPATLK
4.8	1629.8978	-0.0027	LGTDQLFIAVDPLTK

AT5G52840.1

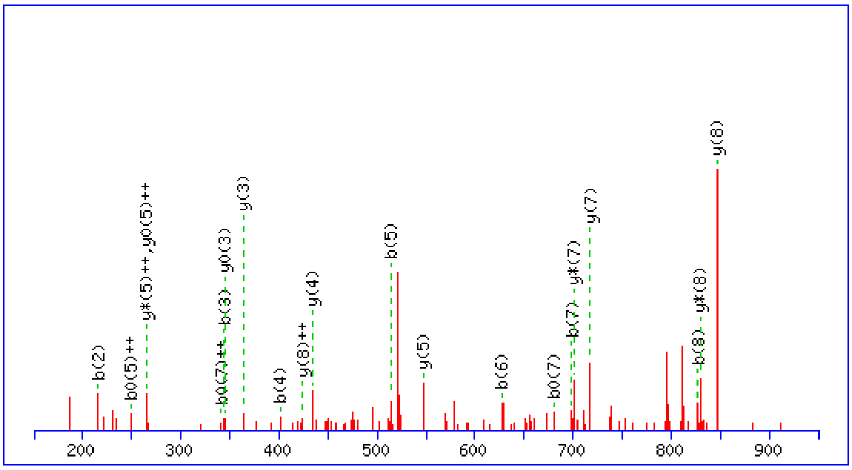
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEGLIAESK**
Found in **AT5G52840.1** in **TAIR_Arabidopsis**, Symbols: | NADH-ubiquinone oxidoreductase-related | chr5:21430944-21432020 FORWARD

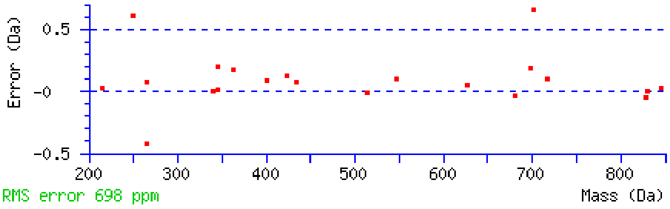
Match to Query 3030: 1059.579562 from(530.797057,2+) index(4946)
Title: Elution from: 44.469 to 44.469 scan no 6200 cid35.00 polarity:+
Data file 0-1_3.mgf

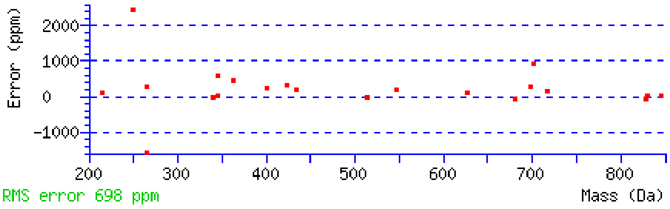
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1059.5812
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00016
Matches : 21/88 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	***215.1390***	108.0731	197.1285	99.0679	L	959.5408	480.2740	942.5142	471.7608	941.5302	471.2687	9
3	***344.1816***	172.5944	326.1710	163.5892	E	**846.4567**	423.7320	829.4302	415.2187	828.4462	414.7267	8
4	***401.2031***	201.1052	383.1925	192.0999	G	**717.4141**	359.2107	700.3876	350.6974	699.4036	350.2054	7
5	***514.2871***	257.6472	496.2766	248.6419	L	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
6	***627.3712***	314.1892	609.3606	305.1840	I	**547.3086**	274.1579	530.2821	265.6447	529.2980	265.1527	5
7	***698.4083***	349.7078	680.3978	340.7025	A	**434.2245**	217.6159	417.1980	209.1026	416.2140	208.6106	4
8	***827.4509***	414.2291	809.4403	405.2238	E	**363.1874**	182.0974	346.1609	173.5841	345.1769	173.0921	3
9	914.4829	457.7451	896.4724	448.7398	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TLEGLIAESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G52840.1

45.0	1059.5812	-0.0016	TLEGLIAESK
1.6	1059.5812	-0.0016	LTEASVALEK

Mascot: http://www.matrixscience.com/

AT5G53000.1

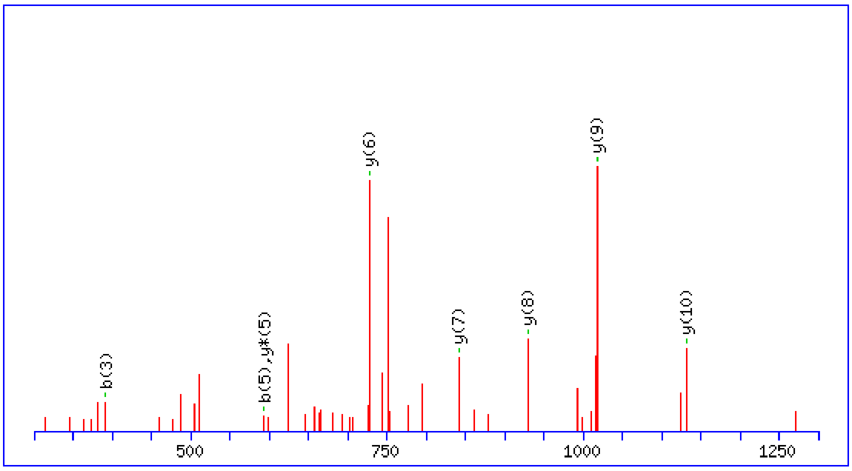
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAWLSSINLAICK**
Found in **AT5G53000.1** in **TAIR_Arabidopsis**, Symbols: TAP46 | TAP46 (2A PHOSPHATASE ASSOCIATED PROTEIN OF 46 KD) | chr5:21502880-21505095 REVERSE

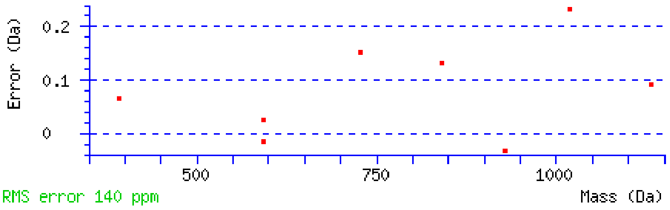
Match to Query 6224: 1520.722786 from(761.368669,2+) index(5711)
Title: Elution from: 50.800 to 50.800 scan no 7293 cid35.00 polarity:+
Data file D6h-2_3.mgf

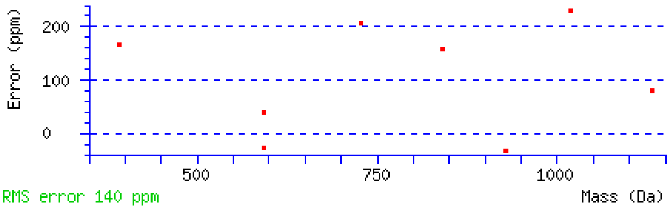
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1520.7252
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0038
Matches : 8/116 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271			113.0363	57.0218	E							13
2	203.0811	102.0442			185.0705	93.0389	A	1391.6928	696.3500	1373.6692	687.3382	1373.6822	687.3448	12
3	**391.1544**	196.0809			373.1439	187.0756	W	1319.6586	660.3330	1301.6351	651.3212	1301.6481	651.3277	11
4	505.2355	253.1214			487.2250	244.1161	L	***1131.5853***	566.2963	1113.5617	557.2845	1113.5747	557.2910	10
5	**593.2646**	297.1359			575.2540	288.1307	S	***1017.5042***	509.2557	999.4806	500.2439	999.4936	500.2504	9
6	681.2937	341.1505			663.2831	332.1452	S	***929.4751***	465.2412	911.4515	456.2294	911.4645	456.2359	8
7	795.3748	398.1910			777.3642	389.1857	I	***841.4460***	421.2267	823.4225	412.2149			7
8	911.4118	456.2095	893.3882	447.1977	893.4012	447.2042	N	***727.3649***	364.1861	709.3414	355.1743			6
9	1025.4929	513.2501	1007.4693	504.2383	1007.4823	504.2448	L	611.3279	306.1676	593.3044	297.1558			5
10	1097.5270	549.2671	1079.5034	540.2553	1079.5164	540.2619	A	497.2468	249.1271	479.2233	240.1153			4
11	1211.6081	606.3077	1193.5845	597.2959	1193.5975	597.3024	I	425.2127	213.1100	407.1891	204.0982			3
12	1373.6328	687.3200	1355.6092	678.3083	1355.6223	678.3148	C	311.1316	156.0694	293.1080	147.0576			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of EAWLSSINLAICK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G53000.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.1	1520.7252	-0.0024	EAWLSSINLAICK
19.9	1520.7195	0.0032	EEKLPPGSYEKAR
19.3	1520.7240	-0.0012	FTHLSPVWYDLK
8.3	1520.7195	0.0033	RPDLNSTTLFDPK
6.6	1520.7218	0.0010	YAEAFLPQLSHTK
4.6	1520.7222	0.0006	DGPTYLSHKKGAAR
4.1	1520.7256	-0.0028	CSIRETHLTKQK
1.0	1520.7222	0.0006	AVGAAGGYRLSPEPR

AT5G53400.1

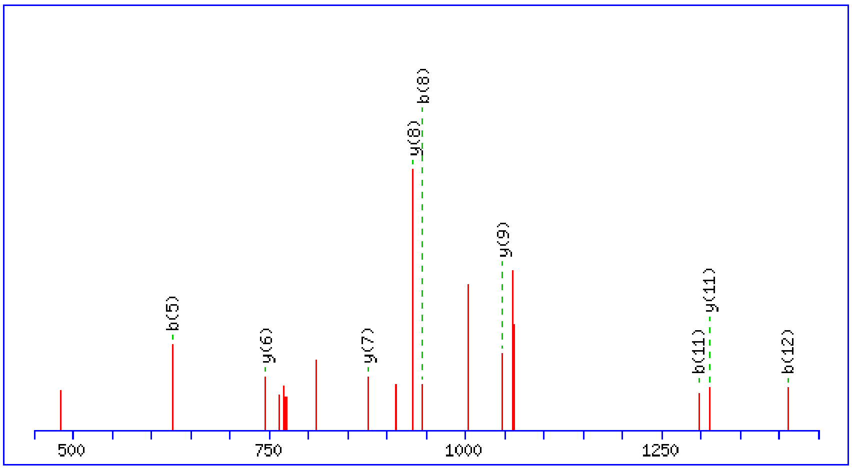
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFDFLGEQSDFLK**
Found in **AT5G53400.1** in **TAIR_Arabidopsis**, Symbols: | nuclear movement family protein | chr5:21678814-21680609 FORWARD

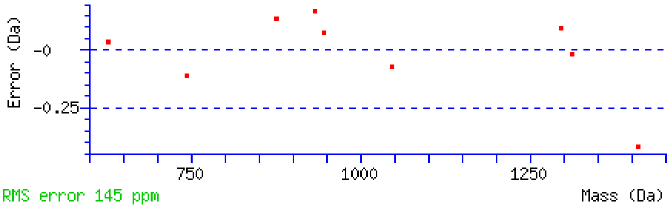
Match to Query 6814: 1558.712074 from(780.363313,2+) index(9999)
Title: Elution from: 93.420 to 93.420 scan no 14023 cid35.00 polarity:+
Data file 0-1_2.mgf

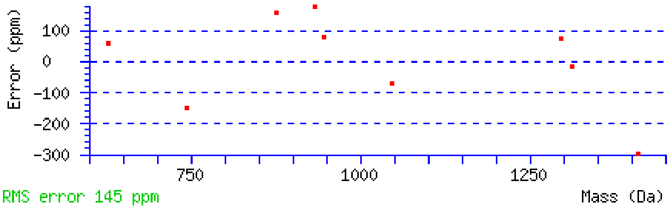
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1558.7113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0044
Matches : 9/120 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							13
2	249.1382	125.0727					F	1459.6532	730.3302	1441.6296	721.3185	1441.6426	721.3250	12
3	365.1622	183.0847			347.1516	174.0794	D	***1311.5878***	656.2975	1293.5642	647.2857	1293.5772	647.2922	11
4	513.2276	257.1174			495.2170	248.1122	F	1195.5638	598.2855	1177.5402	589.2737	1177.5532	589.2802	10
5	***627.3087***	314.1580			609.2981	305.1527	L	***1047.4983***	524.2528	1029.4748	515.2410	1029.4878	515.2475	9
6	685.3272	343.1672			667.3166	334.1620	G	***933.4172***	467.2123	915.3937	458.2005	915.4067	458.2070	8
7	815.3668	408.1871			797.3563	399.1818	E	***875.3987***	438.2030	857.3752	429.1912	857.3882	429.1977	7
8	***945.4195***	473.2134	927.3959	464.2016	927.4089	464.2081	Q	***745.3591***	373.1832	727.3355	364.1714	727.3485	364.1779	6
9	1033.4485	517.2279	1015.4250	508.2161	1015.4380	508.2226	S	615.3065	308.1569	597.2829	299.1451	597.2959	299.1516	5
10	1149.4725	575.2399	1131.4489	566.2281	1131.4619	566.2346	D	527.2774	264.1423	509.2538	255.1305	509.2668	255.1371	4
11	***1297.5380***	649.2726	1279.5144	640.2608	1279.5274	640.2673	F	411.2534	206.1303	393.2298	197.1186			3
12	***1411.6191***	706.3132	1393.5955	697.3014	1393.6085	697.3079	L	263.1880	132.0976	245.1644	123.0858			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of VFDFLGEQSDFLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G53400.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1558.7113	0.0007	VFDFLGEQSDFLK
22.1	1558.7148	-0.0027	MTLFTQEPSFSIK
7.4	1558.7152	-0.0031	SGKCDASVKLQYGK
3.2	1558.7096	0.0025	HRKEAEEGVEEVK
2.2	1558.7078	0.0043	KKGADMEFLSAAMK
0.4	1558.7159	-0.0038	TTTLSALTMSMNLK
0.4	1558.7118	0.0003	YELGRTLGEGNFGK
0.3	1558.7168	-0.0047	RRYSPPYYSPPR
0.1	1558.7104	0.0016	MARNLYDEMLRK
0.1	1558.7114	0.0007	IYIEGYAWSVSEK

Mascot Search Results

Peptide View

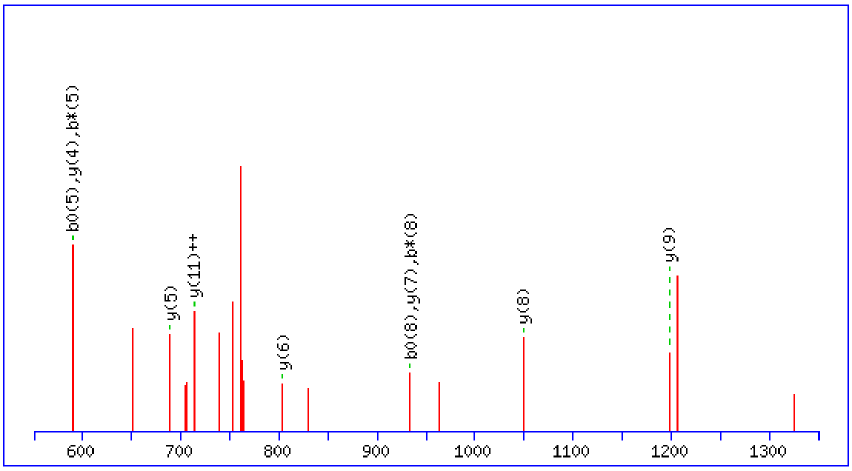
MS/MS Fragmentation of **IPEFNELVYQNR**
Found in **AT5G53460.1** in **TAIR_Arabidopsis**, Symbols: GLT1 | GLT1 (NADH-dependent glutamate synthase 1 gene) | chr5:21717744-21726855 FORWARD

Match to Query 6648: 1538.712282 from(770.363417,2+) index(7173)
Title: Elution from: 64.260 to 64.260 scan no 9393 cid35.00 polarity:+
Data file 0-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

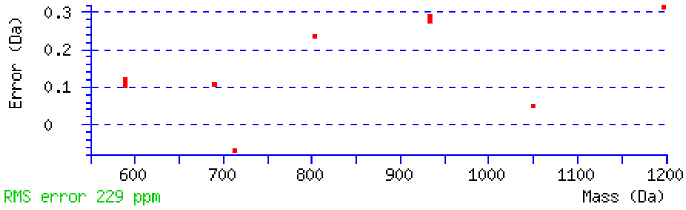
Or, Plot from 550 to 1350 Da Full range

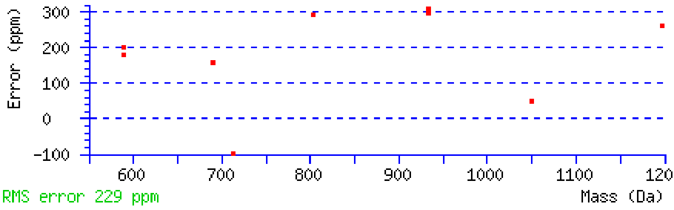
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1538.7090
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0039
Matches : 11/108 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					I							12
2	213.1382	107.0727					P	1425.6351	713.3212	1407.6116	704.3094	1407.6246	704.3159	11
3	343.1778	172.0925			325.1672	163.0873	E	1327.5854	664.2963	1309.5618	655.2845	1309.5748	655.2910	10
4	491.2433	246.1253			473.2327	237.1200	F	***1197.5457***	599.2765	1179.5221	590.2647	1179.5352	590.2712	9
5	607.2802	304.1438	589.2567	295.1320	589.2697	295.1385	N	***1049.4803***	525.2438	1031.4567	516.2320	1031.4697	516.2385	8
6	737.3199	369.1636	719.2963	360.1518	719.3093	360.1583	E	***933.4433***	467.2253	915.4197	458.2135	915.4327	458.2200	7
7	851.4010	426.2041	833.3774	417.1923	833.3904	417.1988	L	***803.4036***	402.2055	785.3801	393.1937			6
8	951.4664	476.2369	933.4428	467.2251	933.4559	467.2316	V	***689.3225***	345.1649	671.2990	336.1531			5
9	1115.5268	558.2670	1097.5032	549.2552	1097.5162	549.2617	Y	***589.2571***	295.1322	571.2335	286.1204			4
10	1245.5794	623.2934	1227.5559	614.2816	1227.5689	614.2881	Q	425.1967	213.1020	407.1732	204.0902			3
11	1361.6164	681.3119	1343.5928	672.3001	1343.6059	672.3066	N	295.1441	148.0757	277.1205	139.0639			2
12							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of IPEFNELVYQNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G53460.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.6	1538.7090	0.0033	IPEFNELVYQNR
12.4	1538.7097	0.0026	ILMEDEKFVSEGK
6.7	1538.7101	0.0022	INMLELEKSSSNR
5.4	1538.7101	0.0022	AATQLTASPVTMSAR

AT5G53480.1

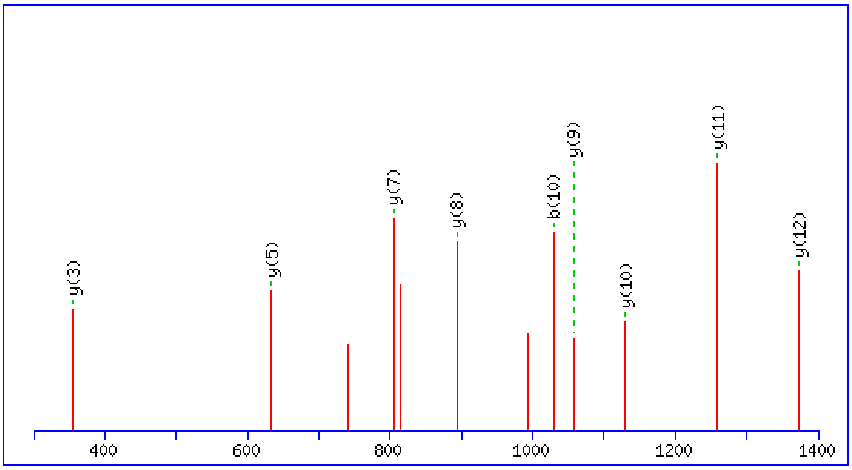
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGILEAYSGIFQGFK**
Found in **AT5G53480.1** in **TAIR_Arabidopsis**, Symbols: | importin beta-2, putative | chr5:21731242-21733935 FORWARD

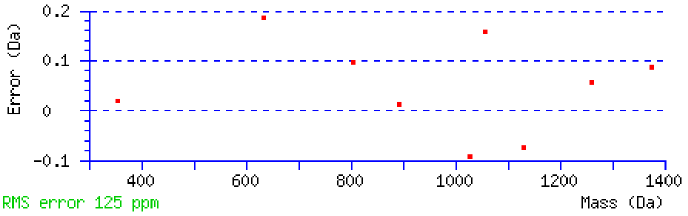
Match to Query 7298: 1660.783728 from(831.399140,2+) index(10099)
Title: Elution from: 99.688 to 99.688 scan no 14670 cid35.00 polarity:+
Data file D1d-2_2.mgf

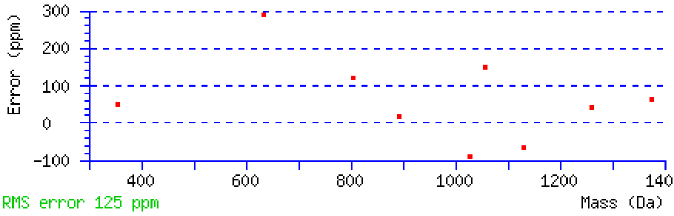
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 1400 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1660.7821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 2.8e-006
Matches : 9/146 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0443	59.0258	99.0207	50.0140			N							15
2	175.0628	88.0350	157.0392	79.0232			G	1545.7524	773.3798	1527.7288	764.3681	1527.7419	764.3746	14
3	289.1439	145.0756	271.1203	136.0638			I	1487.7339	744.3706	1469.7103	735.3588	1469.7234	735.3653	13
4	403.2250	202.1161	385.2014	193.1043			L	***1373.6528***	687.3300	1355.6292	678.3183	1355.6423	678.3248	12
5	533.2646	267.1359	515.2410	258.1241	515.2540	258.1307	E	***1259.5717***	630.2895	1241.5481	621.2777	1241.5612	621.2842	11
6	605.2987	303.1530	587.2752	294.1412	587.2882	294.1477	A	***1129.5321***	565.2697	1111.5085	556.2579	1111.5215	556.2644	10
7	769.3591	385.1832	751.3355	376.1714	751.3485	376.1779	Y	***1057.4979***	529.2526	1039.4744	520.2408	1039.4874	520.2473	9
8	857.3882	429.1977	839.3646	420.1859	839.3776	420.1924	S	***893.4376***	447.2224	875.4140	438.2106	875.4270	438.2171	8
9	915.4067	458.2070	897.3831	449.1952	897.3961	449.2017	G	***805.4085***	403.2079	787.3849	394.1961			7
10	1029.4878	515.2475	1011.4642	506.2357	1011.4772	506.2422	I	747.3900	374.1986	729.3664	365.1869			6
11	1177.5532	589.2802	1159.5296	580.2685	1159.5427	580.2750	F	***633.3089***	317.1581	615.2853	308.1463			5
12	1307.6059	654.3066	1289.5823	645.2948	1289.5953	645.3013	Q	485.2435	243.1254	467.2199	234.1136			4
13	1365.6244	683.3158	1347.6008	674.3040	1347.6138	674.3105	G	***355.1908***	178.0990	337.1672	169.0873			3
14	1513.6898	757.3485	1495.6662	748.3368	1495.6793	748.3433	F	297.1723	149.0898	279.1487	140.0780			2
15							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of NGILEAYSGIFQGFK

AT5G53480.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.0	1660.7821	0.0016	NGILEAYSGIFQGFK
8.6	1660.7855	-0.0018	LLDKGASYFVMDLR
2.9	1660.7828	0.0009	ETELKLMSYFLEK
1.1	1660.7803	0.0034	TNHKDLKAQLDNGGK

AT5G53490.1

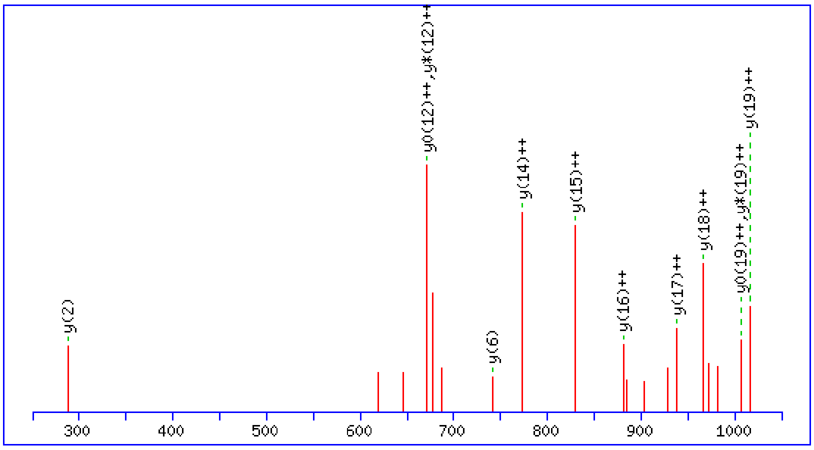
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFVGNTIGQANGVYDKPLDLR**
Found in **AT5G53490.1** in **TAIR_Arabidopsis**, Symbols: | thylakoid lumenal 17.4 kDa protein, chloroplast | chr5:21740714-21741847 REVERSE

Match to Query 9970: 2247.164028 from(750.061952,3+) index(6778)
Title: Elution from: 59.721 to 59.721 scan no 8767 cid35.00 polarity:+
Data file D6h-3_2.mgf

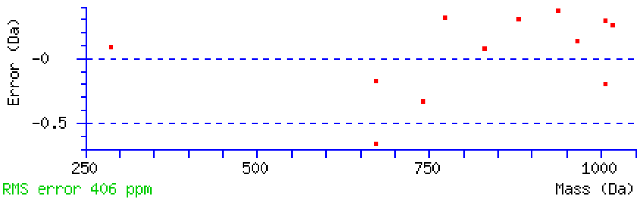
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

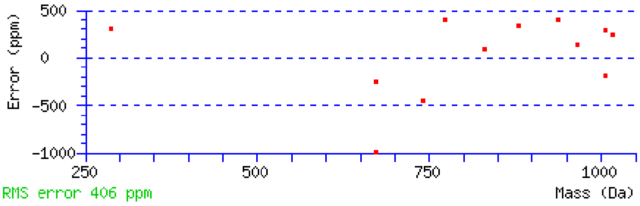


Monoisotopic mass of neutral peptide Mr(calc): 2247.1648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 4.9e-005
Matches : 12/218 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							21
2	219.1128	110.0600					F	2177.1349	1089.0711	2160.1084	1080.5578	2159.1244	1080.0658	20
3	318.1812	159.5942					V	2030.0665	1015.5369	2013.0400	1007.0236	2012.0560	1006.5316	19
4	375.2027	188.1050					G	1930.9981	966.0027	1913.9716	957.4894	1912.9876	956.9974	18
5	489.2456	245.1264	472.2191	236.6132			N	1873.9767	937.4920	1856.9501	928.9787	1855.9661	928.4867	17
6	590.2933	295.6503	573.2667	287.1370	572.2827	286.6450	T	1759.9337	880.4705	1742.9072	871.9572	1741.9232	871.4652	16
7	703.3774	352.1923	686.3508	343.6790	685.3668	343.1870	I	1658.8860	829.9467	1641.8595	821.4334	1640.8755	820.9414	15
8	760.3988	380.7030	743.3723	372.1898	742.3883	371.6978	G	1545.8020	773.4046	1528.7754	764.8914	1527.7914	764.3993	14
9	888.4574	444.7323	871.4308	436.2191	870.4468	435.7271	Q	1488.7805	744.8939	1471.7540	736.3806	1470.7700	735.8886	13
10	959.4945	480.2509	942.4680	471.7376	941.4839	471.2456	A	1360.7219	680.8646	1343.6954	672.3513	1342.7114	671.8593	12
11	1073.5374	537.2724	1056.5109	528.7591	1055.5269	528.2671	N	1289.6848	645.3461	1272.6583	636.8328	1271.6743	636.3408	11
12	1130.5589	565.7831	1113.5324	557.2698	1112.5483	556.7778	G	1175.6419	588.3246	1158.6154	579.8113	1157.6313	579.3193	10
13	1229.6273	615.3173	1212.6008	606.8040	1211.6167	606.3120	V	1118.6204	559.8139	1101.5939	551.3006	1100.6099	550.8086	9
14	1392.6906	696.8490	1375.6641	688.3357	1374.6801	687.8437	Y	1019.5520	510.2796	1002.5255	501.7664	1001.5415	501.2744	8
15	1507.7176	754.3624	1490.6910	745.8492	1489.7070	745.3571	D	856.4887	428.7480	839.4621	420.2347	838.4781	419.7427	7
16	1635.8125	818.4099	1618.7860	809.8966	1617.8020	809.4046	K	**741.4617**	371.2345	724.4352	362.7212	723.4512	362.2292	6
17	1732.8653	866.9363	1715.8388	858.4230	1714.8547	857.9310	P	613.3668	307.1870	596.3402	298.6738	595.3562	298.1817	5
18	1845.9494	923.4783	1828.9228	914.9651	1827.9388	914.4730	L	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
19	1960.9763	980.9918	1943.9498	972.4785	1942.9658	971.9865	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
20	2074.0604	1037.5338	2057.0338	1029.0206	2056.0498	1028.5285	L	**288.2030**	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1

AT5G53490.1





NCBI **BLAST** search of AFVGNTIGQANGVYDKPLDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.6	2247.1648	-0.0008	AFVGNTIGQANGVYDKPLDLR
2.6	2247.1582	0.0058	RLKHINLSSSPEISGCFFR
1.4	2247.1607	0.0033	NDHLLSVDNAKIEQGTPAGIR
1.1	2247.1643	-0.0002	IMLYSPVPMSPLESLASSAVR
0.6	2247.1603	0.0037	AAVLGANDGLVSTASLMMGVGAVK

Mascot: http://www.matrixscience.com/

AT5G53560.1

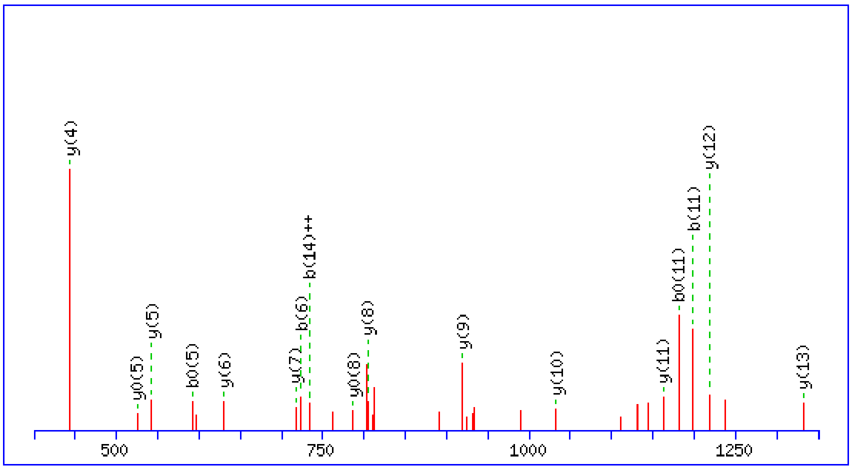
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFIGEIDSSSVPATR**
Found in **AT5G53560.1** in **TAIR_Arabidopsis**, Symbols: B5 #2, ATB5-A | ATB5-A (Cytochrome b5 A) | chr5:21776854-21777579 FORWARD

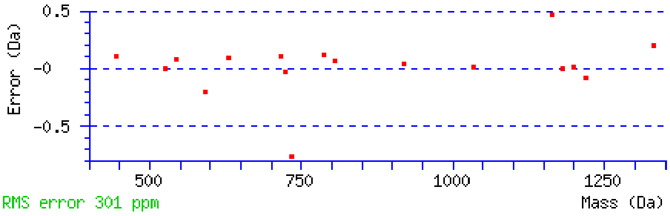
Match to Query 7261: 1640.803422 from(821.408987,2+) index(6198)
Title: Elution from: 55.236 to 55.236 scan no 7931 cid35.00 polarity:+
Data file C7-1_3.mgf

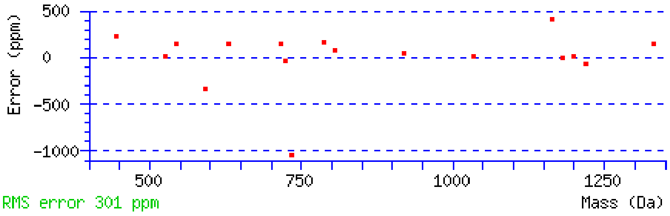
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1640.8046
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 2.9e-008
Matches : 17/130 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389			Y							15
2	311.1390	156.0731			F	1478.7485	739.8779	1461.7220	731.3646	1460.7380	730.8726	14
3	424.2231	212.6152			I	***1331.6801***	666.3437	1314.6536	657.8304	1313.6696	657.3384	13
4	481.2445	241.1259			G	***1218.5961***	609.8017	1201.5695	601.2884	1200.5855	600.7964	12
5	610.2871	305.6472	592.2766	296.6419	E	***1161.5746***	581.2909	1144.5481	572.7777	1143.5640	572.2857	11
6	**723.3712**	362.1892	705.3606	353.1840	I	***1032.5320***	516.7696	1015.5055	508.2564	1014.5214	507.7644	10
7	838.3981	419.7027	820.3876	410.6974	D	***919.4480***	460.2276	902.4214	451.7143	901.4374	451.2223	9
8	925.4302	463.2187	907.4196	454.2134	S	***804.4210***	402.7141	787.3945	394.2009	786.4104	393.7089	8
9	1012.4622	506.7347	994.4516	497.7295	S	***717.3890***	359.1981	700.3624	350.6849	699.3784	350.1928	7
10	1099.4942	550.2508	1081.4837	541.2455	S	***630.3570***	315.6821	613.3304	307.1688	612.3464	306.6768	6
11	**1198.5626**	599.7850	1180.5521	590.7797	V	***543.3249***	272.1661	526.2984	263.6528	525.3144	263.1608	5
12	1295.6154	648.3113	1277.6048	639.3061	P	***444.2565***	222.6319	427.2300	214.1186	426.2459	213.6266	4
13	1366.6525	683.8299	1348.6420	674.8246	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
14	1467.7002	734.3537	1449.6896	725.3485	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
15					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YFIGEIDSSSVPATR

AT5G53560.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
80.5	1640.8046	-0.0012	YFIGEIDSSSVPATR
0.3	1640.8015	0.0020	TITNGGFVEIKRCM

AT5G53890.1

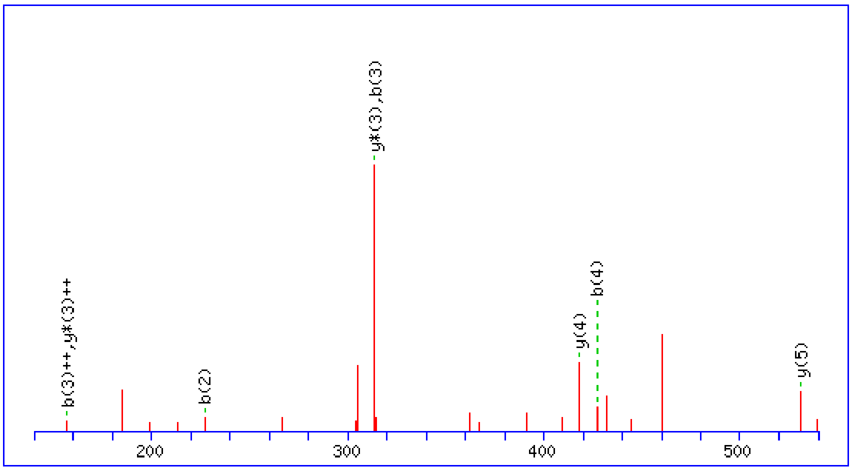
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILSLAK**
Found in **AT5G53890.1** in **TAIR_Arabidopsis**, Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr5:21894461-21897571 FORWARD

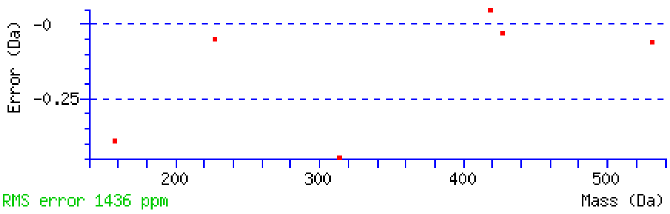
Match to Query 444: 643.426814 from(322.720683,2+) index(691)
Title: Elution from: 15.743 to 15.743 scan no 1123 cid35.00 polarity:+
Data file D1d-1-2.mgf

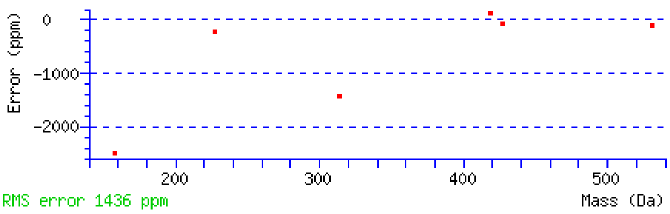
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 540 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 643.4268
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.032
Matches : 8/40 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							6
2	***227.1754***	114.0913			L	***531.3501***	266.1787	514.3235	257.6654	513.3395	257.1734	5
3	***314.2074***	157.6074	296.1969	148.6021	S	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	4
4	***427.2915***	214.1494	409.2809	205.1441	L	331.2340	166.1206	314.2074	157.6074			3
5	498.3286	249.6679	480.3180	240.6627	A	218.1499	109.5786	201.1234	101.0653			2
6					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ILSLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	643.4268	-0.0000	IISLAK
22.1	643.4268	-0.0000	ILSLAK
20.2	643.4268	-0.0000	LLLSAK

AT5G53890.1

18.5	643.4268	-0.0000	LLIGTK
13.6	643.4268	-0.0000	LLTVAK
13.4	643.4268	-0.0000	IISAIK
13.4	643.4268	-0.0000	IISALK
13.4	643.4268	-0.0000	LISALK
13.4	643.4268	-0.0000	LLSAIK
12.2	643.4268	-0.0000	LLGLTK

AT5G54160.1

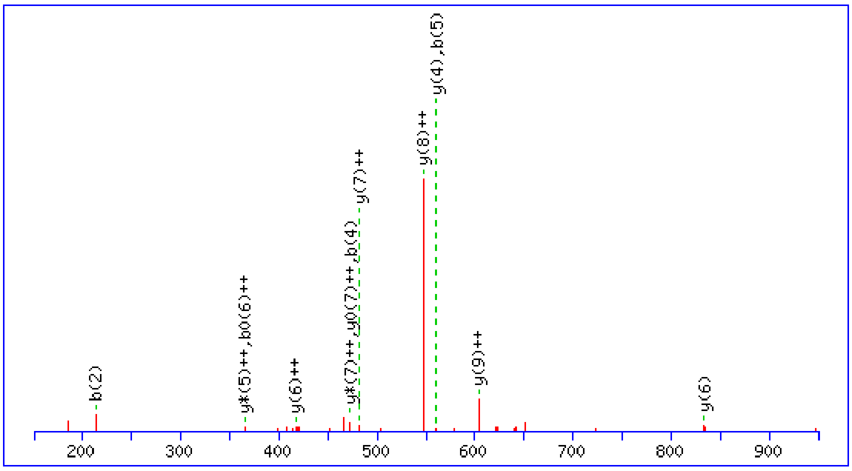
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLMESWYHLK**
Found in **AT5G54160.1** in **TAIR_Arabidopsis**, Symbols: OMT1, ATOMT1 | ATOMT1 (O-METHYLTRANSFERASE 1) | chr5:21999301-22001393 FORWARD

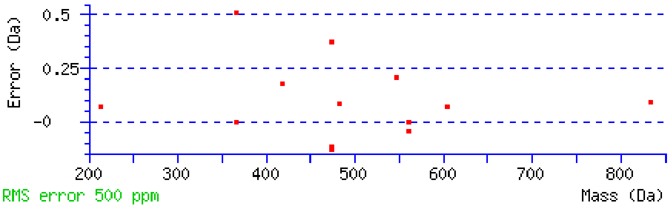
Match to Query 4608: 1304.658111 from(435.893313,3+) index(6141)
Title: Elution from: 56.579 to 56.579 scan no 7938 cid35.00 polarity:+
Data file D1d-2_1.mgf

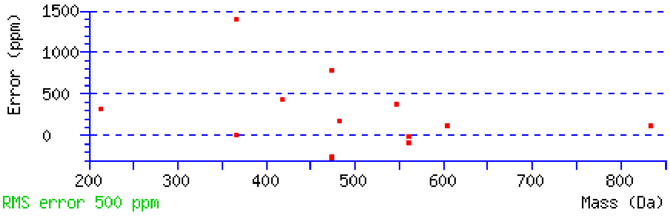
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1304.6587
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.048
Matches : 13/74 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							10
2	***213.1598***	107.0835			L	1206.5976	603.8024	1189.5710	595.2892	1188.5870	594.7972	9
3	344.2002	172.6038			M	1093.5135	547.2604	1076.4870	538.7471	1075.5030	538.2551	8
4	***473.2428***	237.1251	455.2323	228.1198	E	962.4730	481.7402	945.4465	473.2269	944.4625	472.7349	7
5	***560.2749***	280.6411	542.2643	271.6358	S	**833.4304**	417.2189	816.4039	408.7056	815.4199	408.2136	6
6	746.3542	373.6807	728.3436	364.6754	W	746.3984	373.7028	729.3719	365.1896			5
7	909.4175	455.2124	891.4069	446.2071	Y	**560.3191**	280.6632	543.2926	272.1499			4
8	1046.4764	523.7418	1028.4658	514.7366	H	397.2558	199.1315	380.2292	190.6183			3
9	1159.5605	580.2839	1141.5499	571.2786	L	260.1969	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VLMESWYHLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G54160.1

Score	Mr(calc)	Delta	Sequence
21.3	1304.6587	-0.0006	VLMESWYHLK
4.8	1304.6612	-0.0031	VIEDDAFLLDR
4.3	1304.6585	-0.0004	NPTDPKNNHLR
3.1	1304.6572	0.0009	SNSILVSGESGAGK
1.7	1304.6581	0.0001	EGMVMTEKPKR

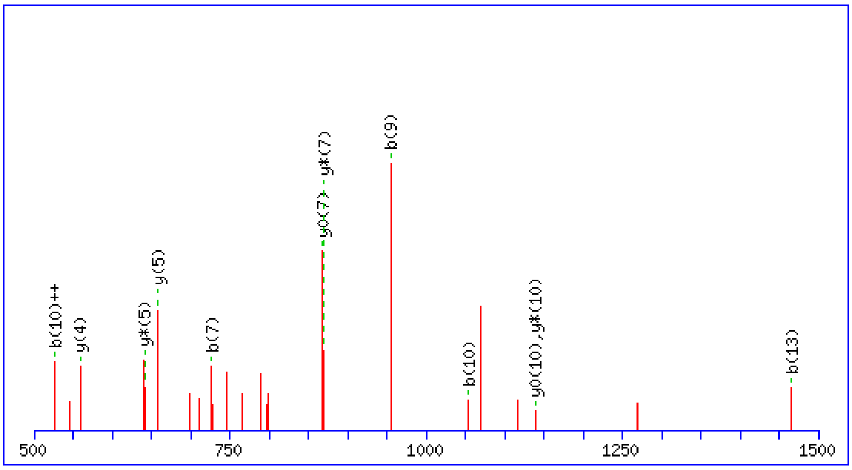
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TRVVDGVDLVHKFK**
Found in **AT5G54200.1** in **TAIR_Arabidopsis**, Symbols: | WD-40 repeat family protein | chr5:22010791-22014302 REVERSE

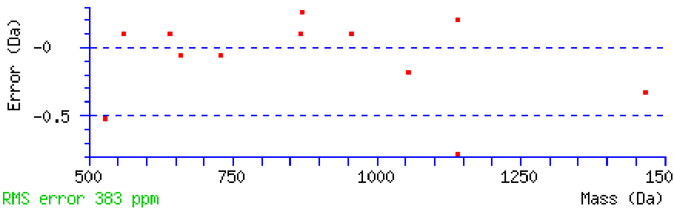
Match to Query 6695: 1611.907836 from(806.961194,2+) index(8823)
Title: Elution from: 82.227 to 82.227 scan no 12164 cid35.00 polarity:+
Data file D1d-1_3.mgf

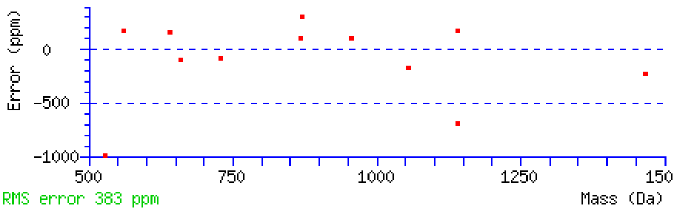
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1611.9097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 0.038
Matches : 12/142 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	258.1561	129.5817	241.1295	121.0684	240.1455	120.5764	R	1511.8693	756.4383	1494.8427	747.9250	1493.8587	747.4330	13
3	357.2245	179.1159	340.1979	170.6026	339.2139	170.1106	V	1355.7682	678.3877	1338.7416	669.8744	1337.7576	669.3824	12
4	456.2929	228.6501	439.2663	220.1368	438.2823	219.6448	V	1256.6997	628.8535	1239.6732	620.3402	1238.6892	619.8482	11
5	571.3198	286.1636	554.2933	277.6503	553.3093	277.1583	D	1157.6313	579.3193	1140.6048	570.8060	1139.6208	570.3140	10
6	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	G	1042.6044	521.8058	1025.5778	513.2926	1024.5938	512.8006	9
7	***727.4097***	364.2085	710.3832	355.6952	709.3992	355.2032	V	985.5829	493.2951	968.5564	484.7818	967.5724	484.2898	8
8	842.4367	421.7220	825.4101	413.2087	824.4261	412.7167	D	886.5145	443.7609	869.4880	435.2476	868.5039	434.7556	7
9	***955.5207***	478.2640	938.4942	469.7507	937.5102	469.2587	L	771.4876	386.2474	754.4610	377.7341			6
10	***1054.5891***	527.7982	1037.5626	519.2849	1036.5786	518.7929	V	**658.4035**	329.7054	641.3770	321.1921			5
11	1191.6480	596.3277	1174.6215	587.8144	1173.6375	587.3224	H	**559.3351**	280.1712	542.3085	271.6579			4
12	1319.7430	660.3751	1302.7165	651.8619	1301.7324	651.3699	K	422.2762	211.6417	405.2496	203.1285			3
13	***1466.8114***	733.9094	1449.7849	725.3961	1448.8009	724.9041	F	294.1812	147.5942	277.1547	139.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TRVVDGVDLVHKFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G54200.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.4	1611.9097	-0.0019	TRVVDGVDLVHKFK
10.7	1611.9056	0.0022	KTLAEANNLRLQNK
9.3	1611.9097	-0.0018	FREPLGVRVSVEPK
9.1	1611.9083	-0.0005	EEVDKVLAALDGLIK

Mascot: http://www.matrixscience.com/

AT5G54270.1

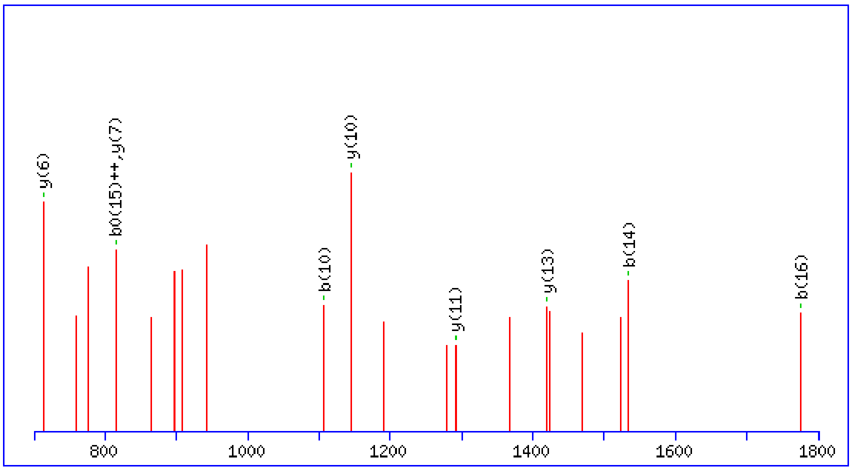
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WAMLGAFGCITPEVLQK**
Found in **AT5G54270.1** in **TAIR_Arabidopsis**, Symbols: LHCB3*1, LHCB3 | LHCB3 (LIGHT-HARVESTING CHLOROPHYLL BINDING PROTEIN 3) | chr5:22055650-22056609 FORWARD

Match to Query 9191: 1919.965140 from(960.989846,2+) index(10625)
Title: Elution from: 103.078 to 103.078 scan no 15251 cid35.00 polarity:+
Data file D12h-2_1.mgf

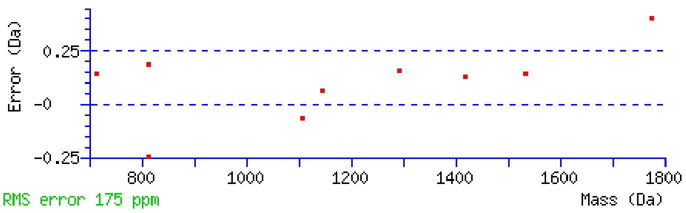
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 700 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

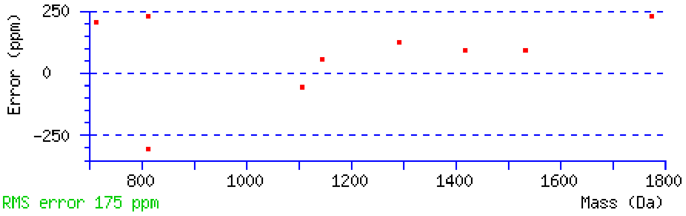


Monoisotopic mass of neutral peptide Mr(calc): 1919.9638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00033
Matches : 9/134 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							17
2	258.1237	129.5655					A	1734.8917	867.9495	1717.8652	859.4362	1716.8812	858.9442	16
3	389.1642	195.0857					M	1663.8546	832.4309	1646.8281	823.9177	1645.8440	823.4257	15
4	502.2483	251.6278					L	1532.8141	766.9107	1515.7876	758.3974	1514.8036	757.9054	14
5	559.2697	280.1385					G	***1419.7301***	710.3687	1402.7035	701.8554	1401.7195	701.3634	13
6	630.3068	315.6571					A	1362.7086	681.8579	1345.6821	673.3447	1344.6980	672.8527	12
7	777.3752	389.1913					F	***1291.6715***	646.3394	1274.6449	637.8261	1273.6609	637.3341	11
8	834.3967	417.7020					G	***1144.6031***	572.8052	1127.5765	564.2919	1126.5925	563.7999	10
9	994.4274	497.7173					C	1087.5816	544.2944	1070.5551	535.7812	1069.5710	535.2892	9
10	***1107.5114***	554.2593					I	927.5510	464.2791	910.5244	455.7658	909.5404	455.2738	8
11	1208.5591	604.7832			1190.5485	595.7779	T	***814.4669***	407.7371	797.4403	399.2238	796.4563	398.7318	7
12	1305.6119	653.3096			1287.6013	644.3043	P	***713.4192***	357.2132	696.3927	348.7000	695.4087	348.2080	6
13	1434.6545	717.8309			1416.6439	708.8256	E	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
14	***1533.7229***	767.3651			1515.7123	758.3598	V	487.3239	244.1656	470.2973	235.6523			4
15	1646.8069	823.9071			1628.7964	814.9018	L	388.2554	194.6314	371.2289	186.1181			3
16	***1774.8655***	887.9364	1757.8390	879.4231	1756.8549	878.9311	Q	275.1714	138.0893	258.1448	129.5761			2
17							K	147.1128	74.0600	130.0863	65.5468			1

AT5G54270.1





NCBI **BLAST** search of WAMLGAFGCITPEVLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.6	1919.9638	0.0014	WAMLGAFGCITPEVLQK
6.1	1919.9622	0.0029	SVDRVEQSNELLKEMK
1.9	1919.9662	-0.0011	TLMELLNQLDGFDNLGK
1.5	1919.9701	-0.0050	AASQAWDATTATTRTIQK
1.4	1919.9604	0.0047	FHVMFVFALVTDDHVK
1.3	1919.9622	0.0029	RKTGEMLDNTEADVVVK
0.3	1919.9661	-0.0009	NGGVLTGSASRGSKSASAGEK

Mascot: http://www.matrixscience.com/

AT5G54400.1

MATRIX SCIENCE

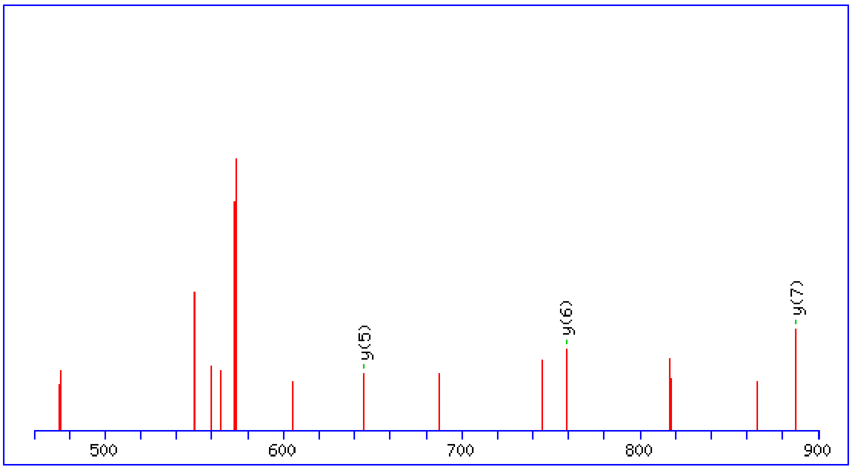
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEEIRVSKR**
Found in **AT5G54400.1** in **TAIR_Arabidopsis**, Symbols: | methyltransferase | chr5:22107906-22109224 FORWARD

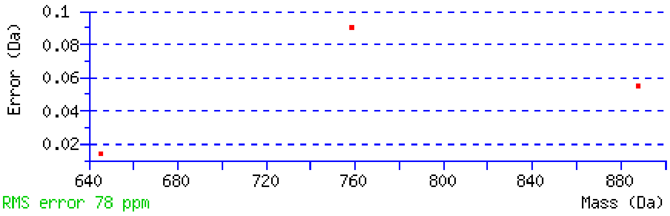
Match to Query 4083: 1162.613214 from(582.313883,2+) index(3367)
Title: Elution from: 33.466 to 33.466 scan no 4195 cid35.00 polarity:+
Data file D12h-3_1.mgf

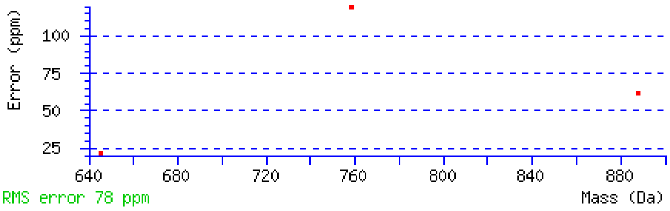
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 460 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1162.6128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.032
Matches : 3/120 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							9
2	277.0853	139.0463			259.0747	130.0410	E	1016.5847	508.7960	999.5582	500.2827	998.5742	499.7907	8
3	406.1279	203.5676			388.1173	194.5623	E	*887.5421*	444.2747	870.5156	435.7614	869.5316	435.2694	7
4	519.2119	260.1096			501.2014	251.1043	I	*758.4995*	379.7534	741.4730	371.2401	740.4890	370.7481	6
5	675.3130	338.1602	658.2865	329.6469	657.3025	329.1549	R	*645.4155*	323.2114	628.3889	314.6981	627.4049	314.2061	5
6	774.3815	387.6944	757.3549	379.1811	756.3709	378.6891	V	489.3144	245.1608	472.2878	236.6475	471.3038	236.1555	4
7	861.4135	431.2104	844.3869	422.6971	843.4029	422.2051	S	390.2459	195.6266	373.2194	187.1133	372.2354	186.6213	3
8	989.5084	495.2579	972.4819	486.7446	971.4979	486.2526	K	303.2139	152.1106	286.1874	143.5973			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MEEIRVSKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G54400.1

19.7	1162.6128	0.0004	MEEIRVSKR
1.9	1162.6128	0.0004	ACSSASIARLK

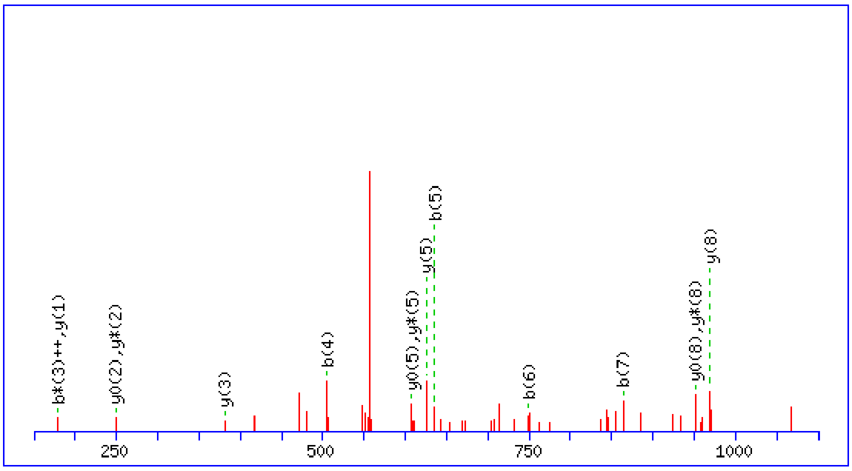
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RVLEEILSR**
Found in **AT5G54510.1** in **TAIR_Arabidopsis**, Symbols: GH3.6, DFL1 | DFL1/GH3.6 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase | chr5:22148547-22150790 REVERSE

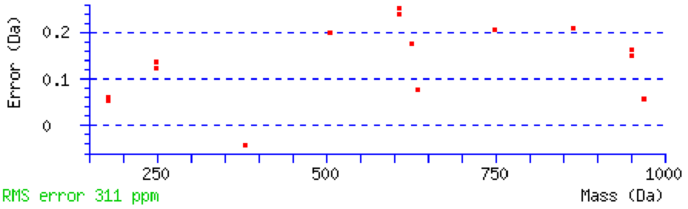
Match to Query 3201: 1128.603952 from(565.309252,2+) index(3111)
Title: Elution from: 34.018 to 34.018 scan no 3993 cid35.00 polarity:+
Data file D1d-1_1.mgf

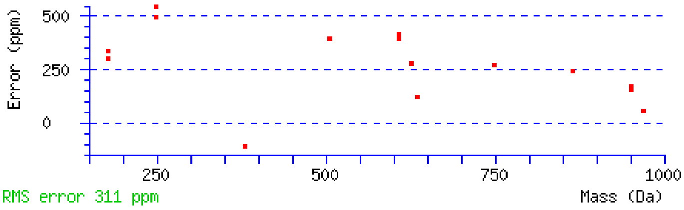
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1128.6061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0047
Matches : 16/88 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							9
2	261.1620	131.0846	243.1384	122.0728			V	***969.5242***	485.2657	951.5006	476.2539	951.5136	476.2604	8
3	375.2431	188.1252	357.2195	179.1134			L	869.4587	435.2330	851.4351	426.2212	851.4481	426.2277	7
4	***505.2827***	253.1450	487.2591	244.1332	487.2721	244.1397	E	755.3776	378.1924	737.3540	369.1807	737.3670	369.1872	6
5	***635.3223***	318.1648	617.2987	309.1530	617.3118	309.1595	E	***625.3380***	313.1726	607.3144	304.1608	607.3274	304.1673	5
6	***749.4034***	375.2054	731.3798	366.1936	731.3929	366.2001	I	495.2984	248.1528	477.2748	239.1410	477.2878	239.1475	4
7	***863.4845***	432.2459	845.4609	423.2341	845.4740	423.2406	L	***381.2173***	191.1123	363.1937	182.1005	363.2067	182.1070	3
8	***951.5136***	476.2604	933.4900	467.2486	933.5030	467.2552	S	267.1362	134.0717	249.1126	125.0599	249.1256	125.0664	2
9							R	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RVLEEILSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G54510.1

31.1	1128.6061	-0.0022	RVLEEILSR
9.1	1128.6061	-0.0022	KKLENEVVR
8.5	1128.6061	-0.0022	LAQSVKELAR
7.7	1128.6061	-0.0022	LRVLEESLR
5.8	1128.6036	0.0003	VFLMAHLKR
5.7	1128.6061	-0.0022	GEIPTKKVSR
2.4	1128.6061	-0.0022	DRLISLIER
1.5	1128.6061	-0.0022	LLKEQEAKR
1.1	1128.6061	-0.0022	AVNVLSVGSIR
0.8	1128.6061	-0.0022	ASQGLKLEIR

AT5G54580.1

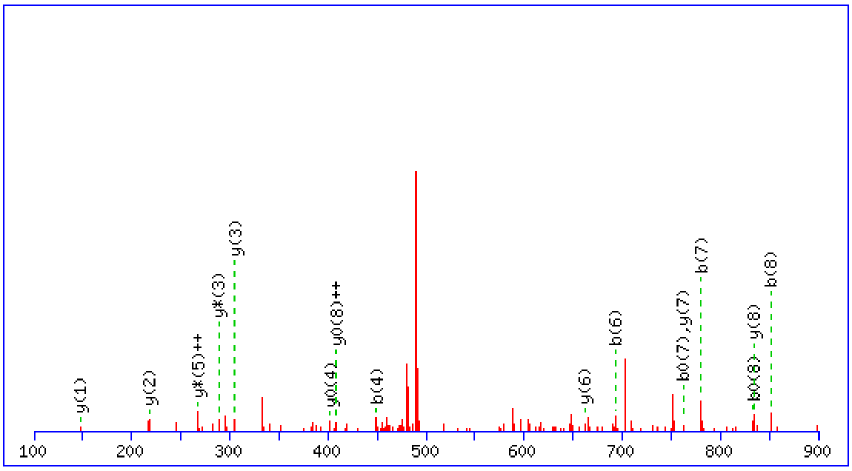
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YATLEDSAK**
Found in **AT5G54580.1** in **TAIR_Arabidopsis**, Symbols: | RNA recognition motif (RRM)-containing protein | chr5:22188558-22189882 FORWARD

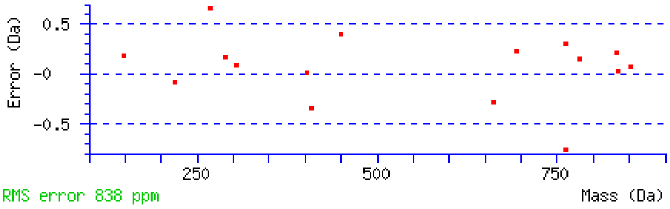
Match to Query 2158: 996.478538 from(499.246545,2+) index(3588)
Title: Elution from: 37.359 to 37.359 scan no 4610 cid35.00 polarity:+
Data file D12h-2_1.mgf

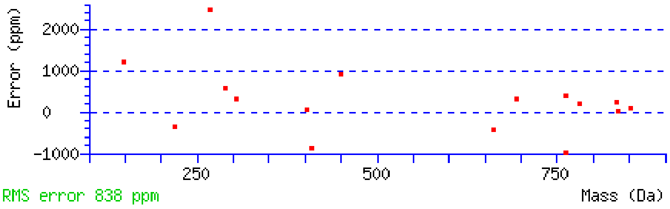
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 996.4764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.019
Matches : 16/72 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			**Y**							**9**
2	235.1077	118.0575			**A**	***834.4203***	417.7138	817.3938	409.2005	816.4098	408.7085	**8**
3	336.1554	168.5813	318.1448	159.5761	**T**	***763.3832***	382.1953	746.3567	373.6820	745.3727	373.1900	**7**
4	**449.2395**	225.1234	431.2289	216.1181	**L**	***662.3355***	331.6714	645.3090	323.1581	644.3250	322.6661	**6**
5	578.2821	289.6447	560.2715	280.6394	**E**	549.2515	275.1294	532.2249	266.6161	531.2409	266.1241	**5**
6	**693.3090**	347.1581	675.2984	338.1529	**D**	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	**4**
7	**780.3410**	390.6742	762.3305	381.6689	**S**	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
8	**851.3781**	426.1927	833.3676	417.1874	**A**	***218.1499***	109.5786	201.1234	101.0653			**2**
9					**K**	***147.1128***	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of YATLEDSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G54580.1

20.8	996.4764	0.0022	YATLEDSAK
8.6	996.4811	-0.0026	GSSCGFRVK
4.8	996.4811	-0.0025	RMREDFK
1.7	996.4811	-0.0025	SHHKETMK
0.2	996.4763	0.0022	LAEESSYAK

AT5G54600.1

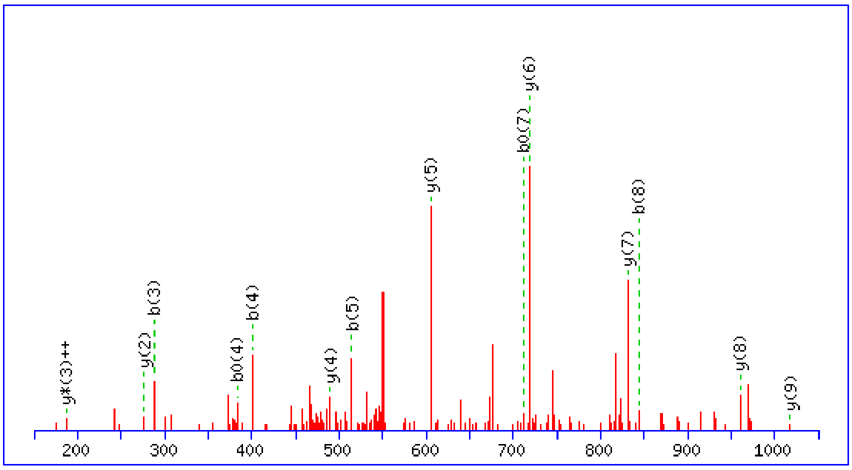
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGELIDTIEK**
Found in **AT5G54600.1** in **TAIR_Arabidopsis**, Symbols: | 50S ribosomal protein L24, chloroplast (CL24) | chr5:22200272-22201629 FORWARD

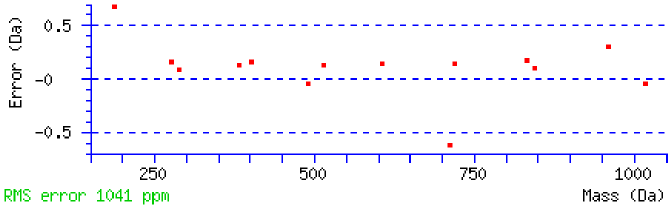
Match to Query 3594: 1117.583920 from(559.799236,2+) index(4740)
Title: Elution from: 42.531 to 42.531 scan no 5900 cid35.00 polarity:+
Data file C7-1_1.mgf

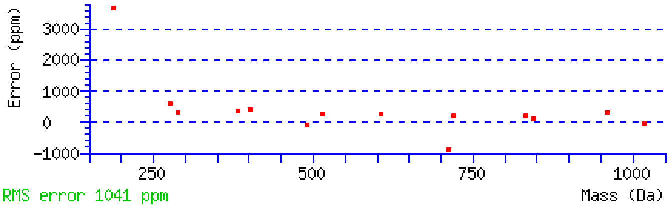
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1117.5867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0015
Matches : 14/88 fragment ions using 40 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	159.0764	80.0418	141.0659	71.0366	G	***1017.5463***	509.2768	1000.5197	500.7635	999.5357	500.2715	9
3	**288.1190**	144.5631	270.1084	135.5579	E	***960.5248***	480.7660	943.4983	472.2528	942.5142	471.7608	8
4	**401.2031**	201.1052	383.1925	192.0999	L	***831.4822***	416.2447	814.4557	407.7315	813.4716	407.2395	7
5	**514.2871**	257.6472	496.2766	248.6419	I	***718.3981***	359.7027	701.3716	351.1894	700.3876	350.6974	6
6	629.3141	315.1607	611.3035	306.1554	D	***605.3141***	303.1607	588.2875	294.6474	587.3035	294.1554	5
7	730.3618	365.6845	712.3512	356.6792	T	***490.2871***	245.6472	473.2606	237.1339	472.2766	236.6419	4
8	**843.4458**	422.2266	825.4353	413.2213	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	972.4884	486.7478	954.4779	477.7426	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
10					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TGELIDTIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G54600.1

32.4	1117.5867	-0.0027	TGELIDTIEK
2.7	1117.5840	-0.0000	ATKSGGANGSIR
2.3	1117.5840	-0.0001	SAVSGEGRVTR

AT5G54690.1

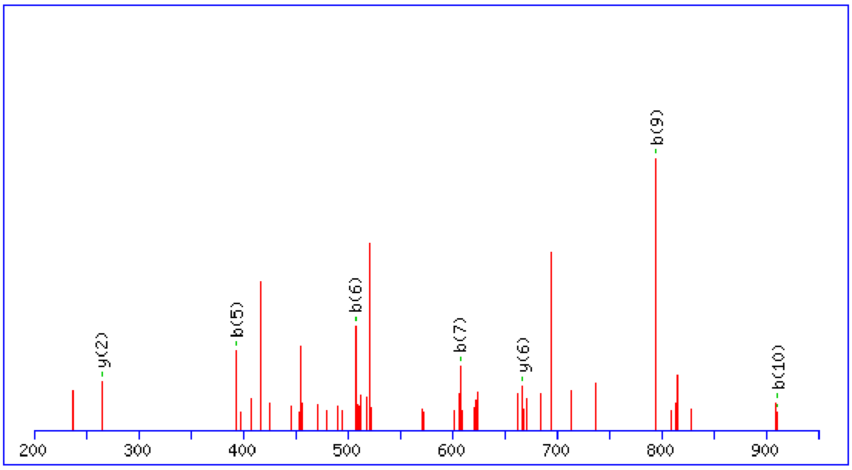
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGSSVIVANNK**
Found in **AT5G54690.1** in **TAIR_Arabidopsis**, Symbols: GAUT12, LGT6, IRX8 | GAUT12/IRX8/LGT6 (GALACTURONOSYLTRANSFERASE 12); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr5:22236661-22238995 REVERS

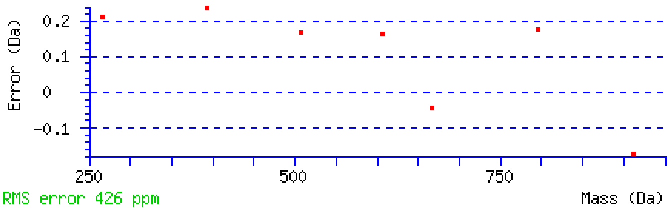
Match to Query 3179: 1058.516292 from(530.265422,2+) index(5177)
Title: Elution from: 46.668 to 46.668 scan no 6479 cid35.00 polarity:+
Data file C7-2_1.mgf

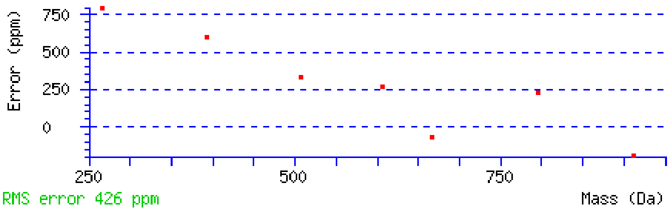
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1058.5149
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.019
Matches : 7/86 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	59.0258	30.0165					**G**							**11**
2	117.0443	59.0258					**G**	1001.5036	501.2555	983.4801	492.2437	983.4931	492.2502	**10**
3	205.0733	103.0403			187.0628	94.0350	**S**	943.4851	472.2462	925.4616	463.2344	925.4746	463.2409	**9**
4	293.1024	147.0548			275.0918	138.0496	**S**	855.4561	428.2317	837.4325	419.2199	837.4455	419.2264	**8**
5	***393.1678***	197.0876			375.1573	188.0823	**V**	767.4270	384.2171	749.4034	375.2054			**7**
6	***507.2489***	254.1281			489.2384	245.1228	**I**	**667.3616**	334.1844	649.3380	325.1726			**6**
7	***607.3144***	304.1608			589.3038	295.1556	**V**	553.2805	277.1439	535.2569	268.1321			**5**
8	679.3485	340.1779			661.3380	331.1726	**A**	453.2150	227.1111	435.1914	218.0994			**4**
9	***795.3855***	398.1964	777.3620	389.1846	777.3750	389.1911	**N**	381.1809	191.0941	363.1573	182.0823			**3**
10	***911.4225***	456.2149	893.3990	447.2031	893.4120	447.2096	**N**	**265.1439**	133.0756	247.1203	124.0638			**2**
11							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of GGSSVIVANNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G54690.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.0	1058.5149	0.0014	GGSSVIVANNK
23.3	1058.5171	-0.0008	VYGLDINPR
12.7	1058.5171	-0.0008	YDGLVIPGGR
10.4	1058.5178	-0.0015	IMEIASLEK
7.4	1058.5148	0.0014	ELEVQGRSK
7.3	1058.5149	0.0014	LENSLARDK
6.2	1058.5149	0.0014	KDKENLNGK
4.0	1058.5149	0.0014	ANRDSIIEK
3.5	1058.5171	-0.0008	FGLGDKPANK
1.9	1058.5149	0.0014	ELSRNGIEK

AT5G54770.1

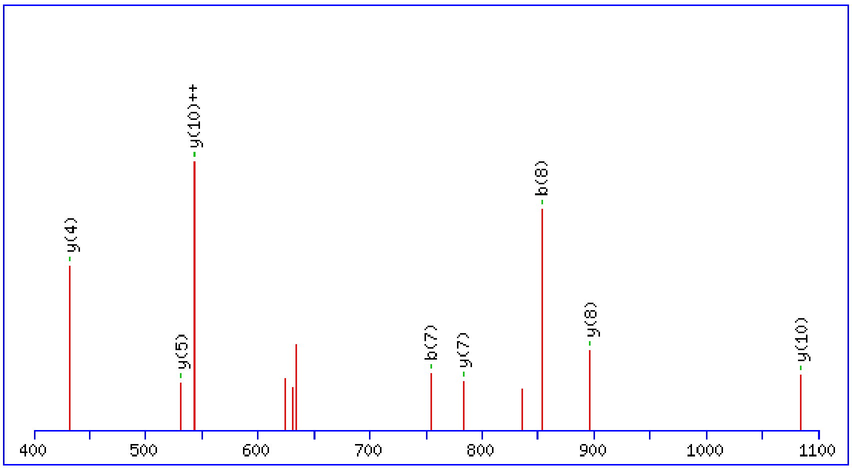
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIGMIDHVPGMK**
Found in **AT5G54770.1** in **TAIR_Arabidopsis**, Symbols: TZ, THI1 | THI1 (THIAZOLE REQUIRING) | chr5:22263860-22265117 FORWARD

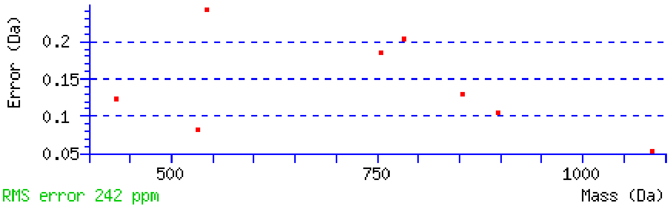
Match to Query 5018: 1283.636322 from(642.825437,2+) index(5510)
Title: Elution from: 48.608 to 48.608 scan no 6904 cid35.00 polarity:+
Data file D6h-1_1.mgf

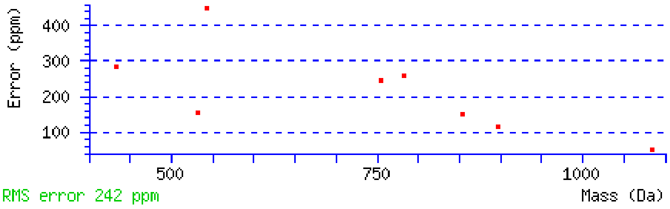
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1283.6366
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.0001
Matches : 8/98 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	**S**							**12**
2	201.1234	101.0653	183.1128	92.0600	**I**	1197.6119	599.3096	1180.5853	590.7963	1179.6013	590.3043	**11**
3	258.1448	129.5761	240.1343	120.5708	**G**	***1084.5278***	542.7675	1067.5013	534.2543	1066.5172	533.7623	**10**
4	389.1853	195.0963	371.1748	186.0910	**M**	1027.5063	514.2568	1010.4798	505.7435	1009.4958	505.2515	**9**
5	502.2694	251.6383	484.2588	242.6330	**I**	***896.4659***	448.7366	879.4393	440.2233	878.4553	439.7313	**8**
6	617.2963	309.1518	599.2858	300.1465	**D**	***783.3818***	392.1945	766.3552	383.6813	765.3712	383.1892	**7**
7	**754.3552**	377.6813	736.3447	368.6760	**H**	668.3548	334.6811	651.3283	326.1678			**6**
8	**853.4236**	427.2155	835.4131	418.2102	**V**	***531.2959***	266.1516	514.2694	257.6383			**5**
9	950.4764	475.7418	932.4658	466.7366	**P**	***432.2275***	216.6174	415.2010	208.1041			**4**
10	1007.4979	504.2526	989.4873	495.2473	**G**	335.1748	168.0910	318.1482	159.5777			**3**
11	1138.5384	569.7728	1120.5278	560.7675	**M**	278.1533	139.5803	261.1267	131.0670			**2**
12					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SIGMIDHVPGMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G54770.1

Score	Mr(calc)	Delta	Sequence
45.5	1283.6366	-0.0003	SIGMIDHVPGMK
0.5	1283.6357	0.0006	NSFTSNSTSVLK

AT5G54810.1

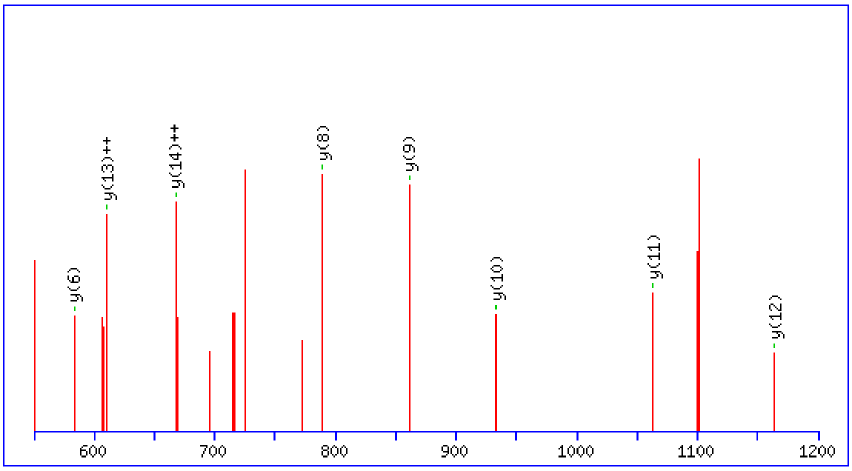
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MIGVEAAGFGLDSGK**
Found in **AT5G54810.1** in **TAIR_Arabidopsis**, Symbols: TRPB, TRP2, TSB1 | TSB1 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT) | chr5:22282031-22283964 REVERSE

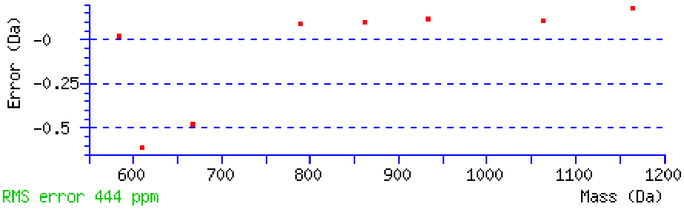
Match to Query 5996: 1466.664412 from(734.339482,2+) index(7135)
Title: Elution from: 63.932 to 63.932 scan no 9339 cid35.00 polarity:+
Data file 0-1_2.mgf

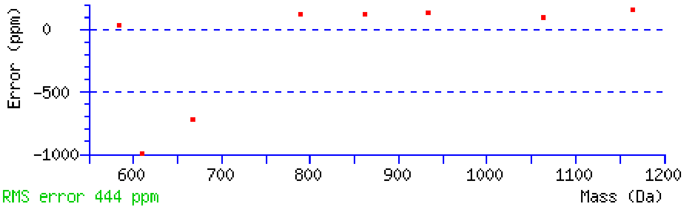
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1466.6651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0012
Matches : 8/128 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260			M							15
2	247.1259	124.0666			I	1335.6349	668.3211	1317.6113	659.3093	1317.6244	659.3158	14
3	305.1444	153.0758			G	1221.5538	611.2806	1203.5302	602.2688	1203.5433	602.2753	13
4	405.2098	203.1086			V	***1163.5353***	582.2713	1145.5118	573.2595	1145.5248	573.2660	12
5	535.2495	268.1284	517.2389	259.1231	E	***1063.4699***	532.2386	1045.4463	523.2268	1045.4593	523.2333	11
6	607.2836	304.1454	589.2731	295.1402	A	***933.4303***	467.2188	915.4067	458.2070	915.4197	458.2135	10
7	679.3178	340.1625	661.3072	331.1572	A	***861.3961***	431.2017	843.3725	422.1899	843.3855	422.1964	9
8	737.3363	369.1718	719.3257	360.1665	G	***789.3620***	395.1846	771.3384	386.1728	771.3514	386.1793	8
9	885.4017	443.2045	867.3912	434.1992	F	731.3435	366.1754	713.3199	357.1636	713.3329	357.1701	7
10	943.4202	472.2137	925.4097	463.2085	G	***583.2780***	292.1426	565.2544	283.1309	565.2674	283.1374	6
11	1057.5013	529.2543	1039.4907	520.2490	L	525.2595	263.1334	507.2359	254.1216	507.2489	254.1281	5
12	1173.5253	587.2663	1155.5147	578.2610	D	411.1784	206.0928	393.1548	197.0811	393.1678	197.0876	4
13	1261.5544	631.2808	1243.5438	622.2755	S	295.1544	148.0809	277.1309	139.0691	277.1439	139.0756	3
14	1319.5729	660.2901	1301.5623	651.2848	G	207.1254	104.0663	189.1018	95.0545			2
15					K	149.1069	75.0571	131.0833	66.0453			1





AT5G54810.1

NCBI **BLAST** search of MIGVEAAGFGLDSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.9	1466.6651	-0.0007	MIGVEAAGFGLDSGK
2.4	1466.6656	-0.0012	GQASAKDGVVVNMR
0.9	1466.6671	-0.0027	YHKAVHRTYDR
0.5	1466.6685	-0.0041	MGLSNMDVEALKK

AT5G54900.1

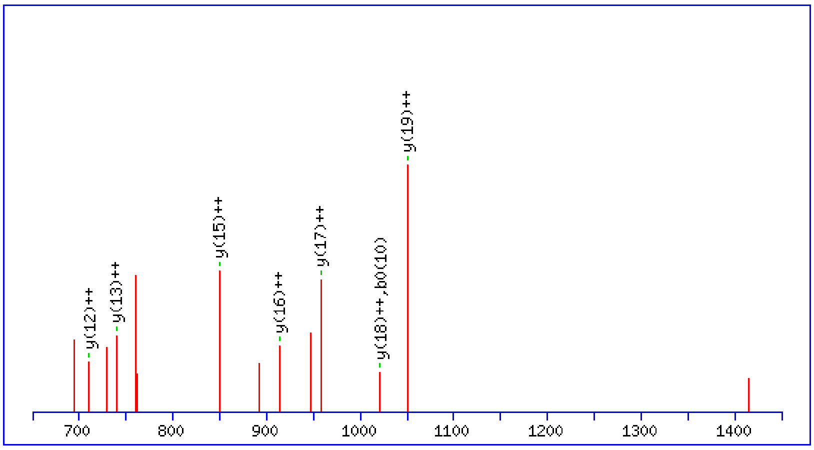
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTGQSEGYGFIEFVSHSVAER**
Found in **AT5G54900.1** in **TAIR_Arabidopsis**, Symbols: ATRBP45A | ATRBP45A (RNA-BINDING PROTEIN 45A); RNA binding | chr5:22312638-22315352 FORWARD

Match to Query 10164: 2312.101698 from(771.707842,3+) index(9724)
Title: Elution from: 88.019 to 88.019 scan no 13341 cid35.00 polarity:+
Data file D6h-3_2.mgf

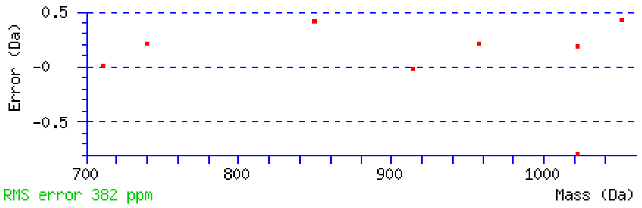
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 650 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

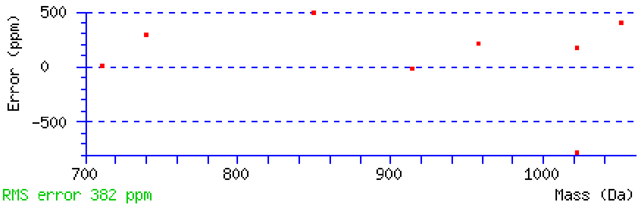


Monoisotopic mass of neutral peptide Mr(calc): 2312.1073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00079
Matches : 8/230 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							21
2	215.1390	108.0731			197.1285	99.0679	T	2200.0305	1100.5189	2183.0040	1092.0056	2182.0200	1091.5136	20
3	272.1605	136.5839			254.1499	127.5786	G	2098.9829	1049.9951	2081.9563	1041.4818	2080.9723	1040.9898	19
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	Q	2041.9614	1021.4843	2024.9348	1012.9711	2023.9508	1012.4791	18
5	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	S	1913.9028	957.4550	1896.8763	948.9418	1895.8923	948.4498	17
6	616.2937	308.6505	599.2671	300.1372	598.2831	299.6452	E	1826.8708	913.9390	1809.8442	905.4258	1808.8602	904.9338	16
7	673.3151	337.1612	656.2886	328.6479	655.3046	328.1559	G	1697.8282	849.4177	1680.8016	840.9045	1679.8176	840.4125	15
8	836.3785	418.6929	819.3519	410.1796	818.3679	409.6876	Y	1640.8067	820.9070	1623.7802	812.3937	1622.7962	811.9017	14
9	893.3999	447.2036	876.3734	438.6903	875.3894	438.1983	G	1477.7434	739.3753	1460.7169	730.8621	1459.7328	730.3701	13
10	1040.4684	520.7378	1023.4418	512.2245	1022.4578	511.7325	F	1420.7219	710.8646	1403.6954	702.3513	1402.7114	701.8593	12
11	1153.5524	577.2798	1136.5259	568.7666	1135.5419	568.2746	I	1273.6535	637.3304	1256.6270	628.8171	1255.6430	628.3251	11
12	1282.5950	641.8011	1265.5685	633.2879	1264.5844	632.7959	E	1160.5695	580.7884	1143.5429	572.2751	1142.5589	571.7831	10
13	1429.6634	715.3354	1412.6369	706.8221	1411.6529	706.3301	F	1031.5269	516.2671	1014.5003	507.7538	1013.5163	507.2618	9
14	1528.7318	764.8696	1511.7053	756.3563	1510.7213	755.8643	V	884.4585	442.7329	867.4319	434.2196	866.4479	433.7276	8
15	1615.7639	808.3856	1598.7373	799.8723	1597.7533	799.3803	S	785.3900	393.1987	768.3635	384.6854	767.3795	384.1934	7
16	1752.8228	876.9150	1735.7962	868.4018	1734.8122	867.9097	H	698.3580	349.6826	681.3315	341.1694	680.3474	340.6774	6
17	1839.8548	920.4310	1822.8283	911.9178	1821.8442	911.4258	S	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
18	1938.9232	969.9652	1921.8967	961.4520	1920.9127	960.9600	V	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
19	2009.9603	1005.4838	1992.9338	996.9705	1991.9498	996.4785	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
20	2139.0029	1070.0051	2121.9764	1061.4918	2120.9924	1060.9998	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
21							R	175.1190	88.0631	158.0924	79.5498			1

AT5G54900.1





NCBI **BLAST** search of LTGQSEGYGFIEFVSHSVAER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.8	2312.1073	-0.0056	LTGQSEGYGFIEFVSHSVAER
5.2	2312.1075	-0.0058	MICRAMVQDSVQGIPSVYAR
3.2	2312.1002	0.0015	DRQVDKMNSQIFTLGCTQR
2.9	2312.0995	0.0022	VKEWGQEVFLTAEATSGMGEK
2.4	2312.0954	0.0063	ADLHEKREVPTEDGMELAEK

AT5G55070.1

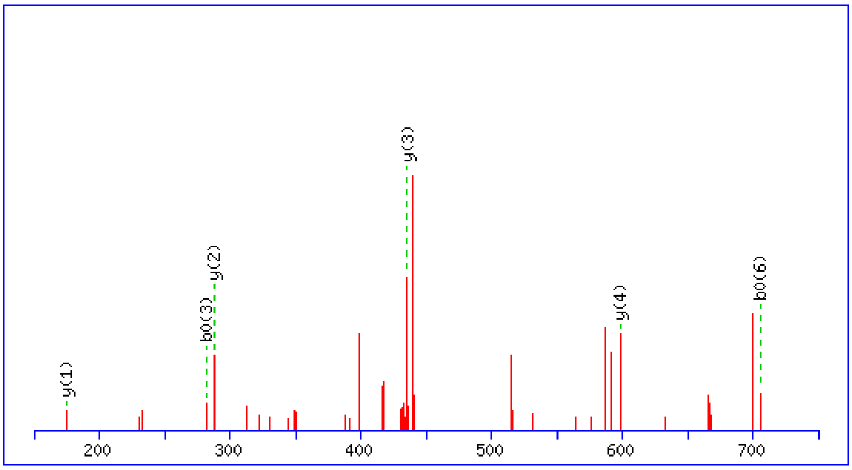
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAVYFLR**
Found in **AT5G55070.1** in **TAIR_Arabidopsis**, Symbols: | 2-oxoacid dehydrogenase family protein | chr5:22364863-22367635 FORWARD

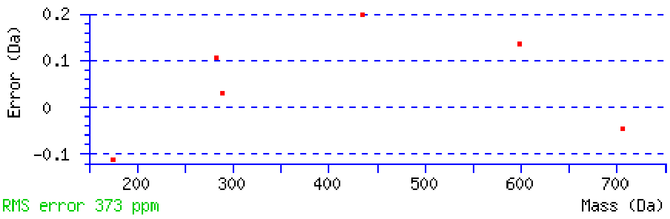
Match to Query 1666: 896.473890 from(449.244221,2+) index(5068)
Title: Elution from: 45.595 to 45.595 scan no 6324 cid35.00 polarity:+
Data file C7-3_1.mgf

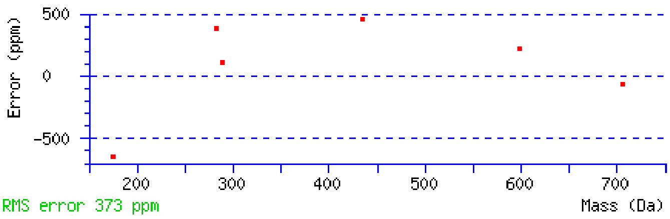
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 896.4756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.049
Matches : 6/48 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.0499	65.5286	112.0393	56.5233	E					7
2	201.0870	101.0471	183.0764	92.0418	A	768.4403	384.7238	751.4137	376.2105	6
3	300.1554	150.5813	282.1448	141.5761	V	697.4032	349.2052	680.3766	340.6920	5
4	463.2187	232.1130	445.2082	223.1077	Y	***598.3348***	299.6710	581.3082	291.1577	4
5	610.2871	305.6472	592.2766	296.6419	F	***435.2714***	218.1394	418.2449	209.6261	3
6	723.3712	362.1892	705.3606	353.1840	L	***288.2030***	144.6051	271.1765	136.0919	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1





NCBI **BLAST** search of EAVYFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.5	896.4756	-0.0017	EAVYFLR
5.3	896.4756	-0.0017	YIADLFR
5.2	896.4716	0.0023	LTHEELR

AT5G55070.1

4.5	896.4756	-0.0017	TVYVYPR

AT5G55160.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQDGNEVFFR**
Found in **AT5G55160.1** in **TAIR_Arabidopsis**, Symbols: SUMO 2, SUMO2, SUM2 | SUM2 (SMALL UBIQUITIN-LIKE MODIFIER 2) | chr5:22400973-22401998 REVERSE

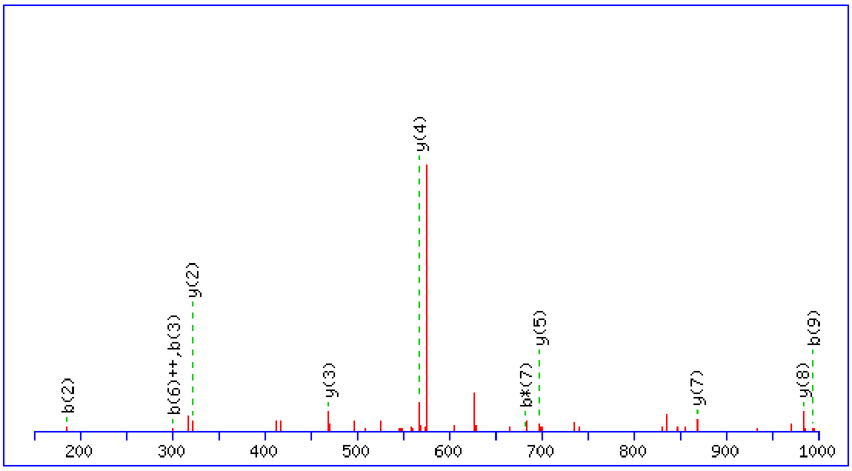
Match to Query 3369: 1167.532406 from(584.773479,2+) index(3497)
Title: Elution from: 35.786 to 35.786 scan no 4485 cid35.00 polarity:+
Data file D1d-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

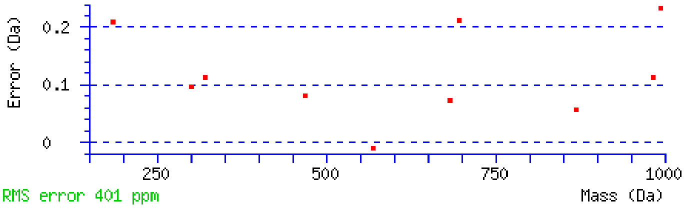
Label all possible matches ○ Label matches used for scoring ●

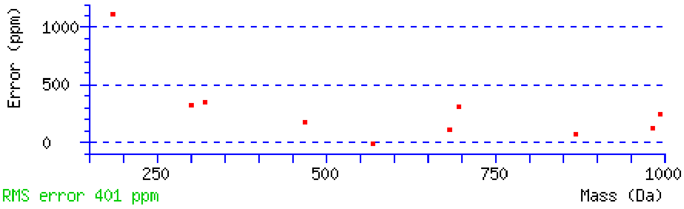
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1167.5309
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.00085
Matches : 11/94 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	**186.0873**	93.5473	169.0608	85.0340			Q	1111.5167	556.2620	1094.4902	547.7487	1093.5061	547.2567	9
3	**301.1143**	151.0608	284.0877	142.5475	283.1037	142.0555	D	***983.4581***	492.2327	966.4316	483.7194	965.4476	483.2274	8
4	358.1357	179.5715	341.1092	171.0582	340.1252	170.5662	G	***868.4312***	434.7192	851.4046	426.2060	850.4206	425.7139	7
5	472.1787	236.5930	455.1521	228.0797	454.1681	227.5877	N	811.4097	406.2085	794.3832	397.6952	793.3991	397.2032	6
6	601.2212	301.1143	584.1947	292.6010	583.2107	292.1090	E	***697.3668***	349.1870	680.3402	340.6738	679.3562	340.1817	5
7	700.2897	350.6485	683.2631	342.1352	682.2791	341.6432	V	***568.3242***	284.6657	551.2976	276.1525			4
8	847.3581	424.1827	830.3315	415.6694	829.3475	415.1774	F	***469.2558***	235.1315	452.2292	226.6183			3
9	**994.4265**	497.7169	977.3999	489.2036	976.4159	488.7116	F	***322.1874***	161.5973	305.1608	153.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GQDGNEVFFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G55160.1

Score	Mr(calc)	Delta	Sequence
33.9	1167.5309	0.0015	GQDGNEVFFR

Mascot: http://www.matrixscience.com/

AT5G55220.1

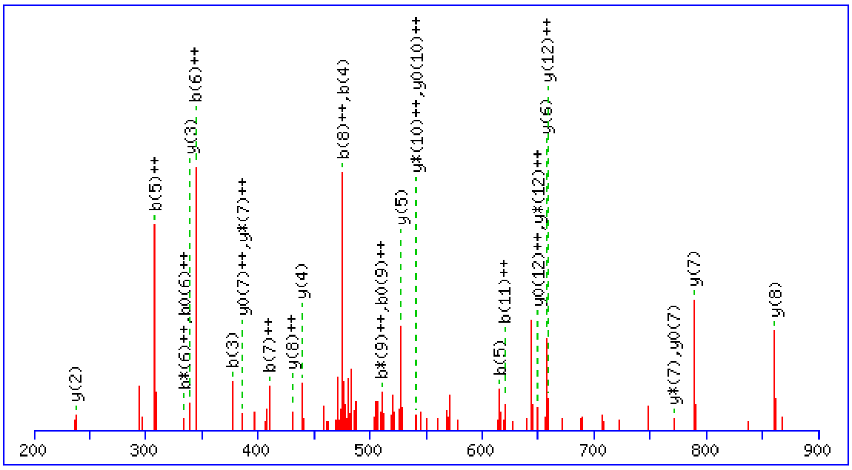
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RTLPHAMESVTGR**
Found in **AT5G55220.1** in **TAIR_Arabidopsis**, Symbols: | trigger factor type chaperone family protein | chr5:22414903-22417904 FORWARD

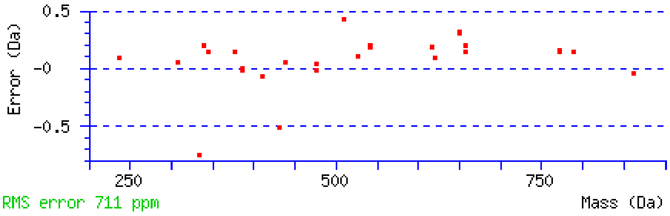
Match to Query 6154: 1474.683447 from(492.568425,3+) index(1682)
Title: Elution from: 21.464 to 21.464 scan no 2215 cid35.00 polarity:+
Data file D6h-3_1.mgf

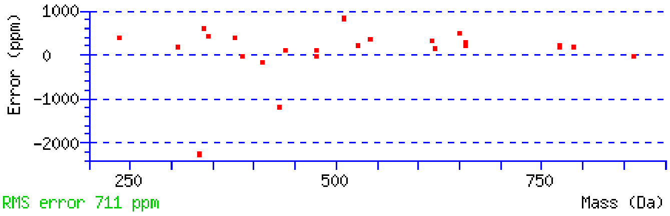
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1474.6837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0048
Matches : 30/138 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							13
2	263.1412	132.0743	245.1177	123.0625	245.1307	123.0690	T	1315.6017	658.3045	1297.5782	649.2927	1297.5912	649.2992	12
3	**377.2223**	189.1148	359.1988	180.1030	359.2118	180.1095	L	1213.5570	607.2822	1195.5334	598.2704	1195.5465	598.2769	11
4	**475.2721**	238.1397	457.2486	229.1279	457.2616	229.1344	P	1099.4759	550.2416	1081.4523	541.2298	1081.4654	541.2363	10
5	**615.3222**	**308.1647**	597.2986	299.1529	597.3116	299.1594	H	1001.4261	501.2167	983.4025	492.2049	983.4156	492.2114	9
6	687.3563	**344.1818**	669.3327	335.1700	669.3457	335.1765	A	**861.3761**	431.1917	843.3525	422.1799	843.3655	422.1864	8
7	819.3938	**410.2006**	801.3702	401.1888	801.3833	401.1953	M	**789.3420**	395.1746	771.3184	386.1628	771.3314	386.1693	7
8	949.4335	**475.2204**	931.4099	466.2086	931.4229	466.2151	E	**657.3044**	329.1559	639.2809	320.1441	639.2939	320.1506	6
9	1037.4625	519.2349	1019.4389	510.2231	1019.4519	510.2296	S	**527.2648**	264.1360	509.2412	255.1243	509.2543	255.1308	5
10	1137.5280	569.2676	1119.5044	560.2558	1119.5174	560.2623	V	**439.2358**	220.1215	421.2122	211.1097	421.2252	211.1162	4
11	1239.5727	**620.2900**	1221.5491	611.2782	1221.5621	611.2847	T	**339.1703**	170.0888	321.1467	161.0770	321.1597	161.0835	3
12	1297.5912	**649.2992**	1279.5676	640.2874	1279.5806	640.2939	G	**237.1256**	119.0664	219.1020	110.0546			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RTLPHAMESVTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G55220.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1474.6837	-0.0003	RTLPHAMESVTGR
15.4	1474.6810	0.0024	EIVQHAMTSAAATK

Mascot: http://www.matrixscience.com/

AT5G55730.1

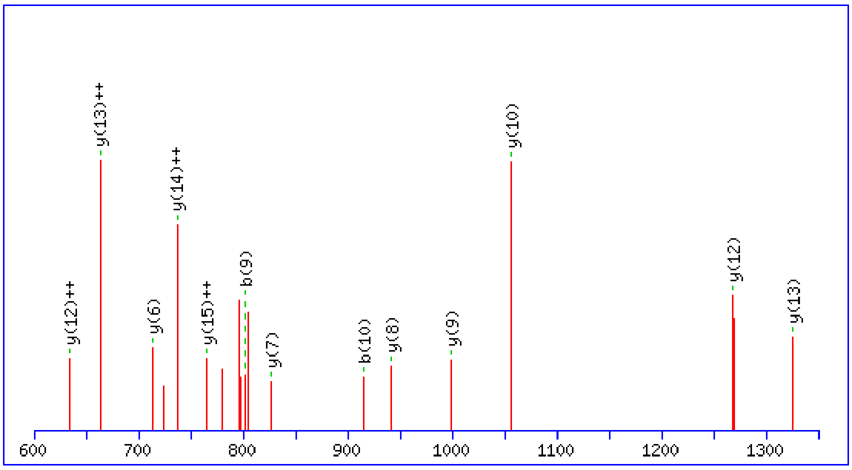
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGFGPDGGDLSSFFVK**
Found in **AT5G55730.1** in **TAIR_Arabidopsis**, Symbols: FLA1 | FLA1 | chr5:22575601-22577618 REVERSE

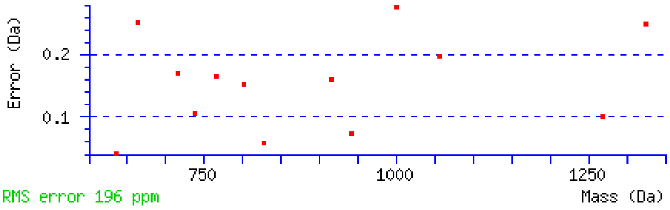
Match to Query 7524: 1627.786748 from(814.900650,2+) index(10091)
Title: Elution from: 94.017 to 94.017 scan no 14022 cid35.00 polarity:+
Data file D6h-2_1.mgf

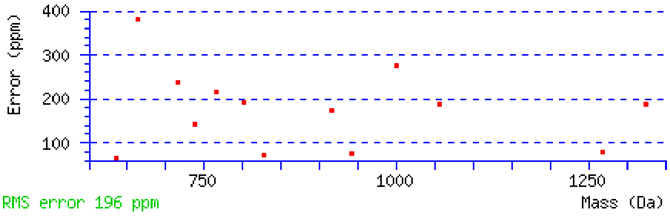
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1627.7883
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 4.3e-006
Matches : 13/132 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			**V**							**16**
2	157.0972	79.0522			**G**	1529.7271	765.3672	1512.7005	756.8539	1511.7165	756.3619	**15**
3	304.1656	152.5864			**F**	1472.7056	736.8564	1455.6791	728.3432	1454.6951	727.8512	**14**
4	361.1870	181.0972			**G**	***1325.6372***	663.3222	1308.6107	654.8090	1307.6266	654.3170	**13**
5	458.2398	229.6235			**P**	***1268.6157***	634.8115	1251.5892	626.2982	1250.6052	625.8062	**12**
6	573.2667	287.1370	555.2562	278.1317	**D**	1171.5630	586.2851	1154.5364	577.7719	1153.5524	577.2798	**11**
7	630.2882	315.6477	612.2776	306.6425	**G**	***1056.5360***	528.7717	1039.5095	520.2584	1038.5255	519.7664	**10**
8	687.3097	344.1585	669.2991	335.1532	**G**	***999.5146***	500.2609	982.4880	491.7477	981.5040	491.2556	**9**
9	**802.3366**	401.6719	784.3260	392.6667	**D**	***942.4931***	471.7502	925.4666	463.2369	924.4825	462.7449	**8**
10	**915.4207**	458.2140	897.4101	449.2087	**L**	***827.4662***	414.2367	810.4396	405.7234	809.4556	405.2314	**7**
11	1002.4527	501.7300	984.4421	492.7247	**S**	***714.3821***	357.6947	697.3556	349.1814	696.3715	348.6894	**6**
12	1089.4847	545.2460	1071.4742	536.2407	**S**	627.3501	314.1787	610.3235	305.6654	609.3395	305.1734	**5**
13	1236.5531	618.7802	1218.5426	609.7749	**F**	540.3180	270.6627	523.2915	262.1494			**4**
14	1383.6216	692.3144	1365.6110	683.3091	**F**	393.2496	197.1285	376.2231	188.6152			**3**
15	1482.6900	741.8486	1464.6794	732.8433	**V**	246.1812	123.5942	229.1547	115.0810			**2**
16					**K**	147.1128	74.0600	130.0863	65.5468			**1**





AT5G55730.1

NCBI **BLAST** search of VGFGPDGGDLSSFFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.4	1627.7883	-0.0015	VGFGPDGGDLSSFFVK
2.5	1627.7842	0.0025	YAAFDDASASGTVVVR

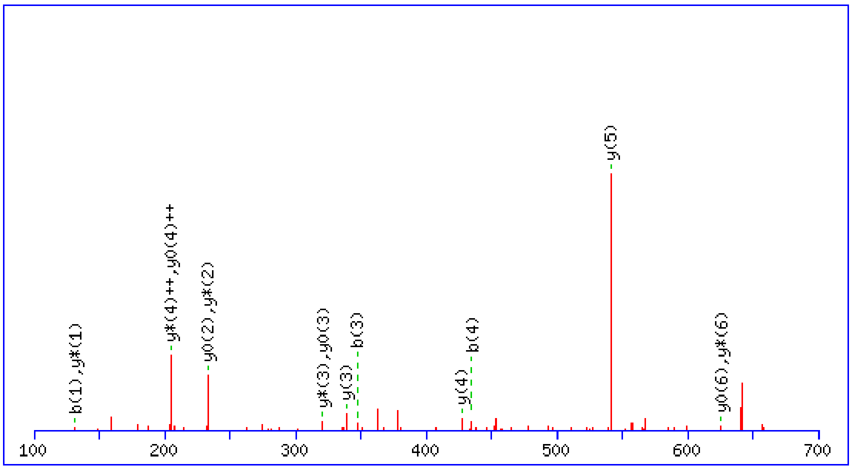
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KTISSTK**
Found in **AT5G55950.1** in **TAIR_Arabidopsis**, Symbols: | transporter-related | chr5:22675637-22677479 REVERSE

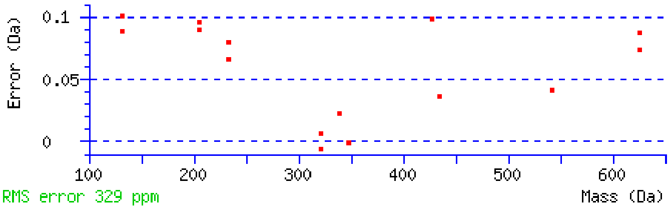
Match to Query 923: 772.419094 from(387.216823,2+) index(4279)
Title: Elution from: 39.780 to 39.780 scan no 5341 cid35.00 polarity:+
Data file C7-3_1.mgf

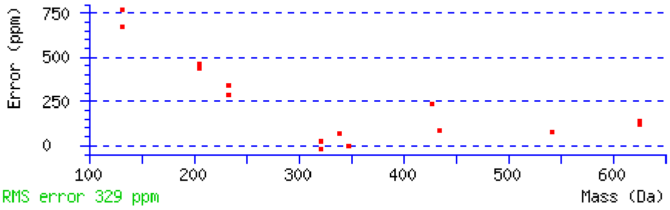
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 772.4173
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.038
Matches : 17/68 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	***131.0963***	66.0518	113.0727	57.0400			K							7
2	***233.1410***	117.0741	215.1174	108.0624	215.1305	108.0689	T	643.3355	322.1714	625.3119	313.1596	625.3250	313.1661	6
3	***347.2221***	174.1147	329.1985	165.1029	329.2116	165.1094	I	**541.2908**	271.1490	523.2672	262.1373	523.2802	262.1438	5
4	***435.2512***	218.1292	417.2276	209.1174	417.2406	209.1239	S	**427.2097**	214.1085	409.1861	205.0967	409.1991	205.1032	4
5	523.2802	262.1438	505.2567	253.1320	505.2697	253.1385	S	**339.1806**	170.0940	321.1571	161.0822	321.1701	161.0887	3
6	***625.3250***	313.1661	607.3014	304.1543	607.3144	304.1608	T	251.1516	126.0794	233.1280	117.0676	233.1410	117.0741	2
7							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KTISSTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.6	772.4173	0.0018	KTISSTK
12.1	772.4182	0.0009	MVMKKK
10.3	772.4173	0.0018	TKSTLSK

AT5G55950.1

9.5	772.4195	-0.0004	TKEFLK
9.3	772.4195	-0.0004	TSFILGK
5.9	772.4199	-0.0008	QTKRTK
5.7	772.4200	-0.0009	ARASTKK
5.2	772.4195	-0.0004	SLAAYIK
5.1	772.4173	0.0018	KTTLSSK
3.8	772.4195	-0.0004	FTEKIK

AT5G56000.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDGQPELFIHIIPDK**
Found in **AT5G56000.1** in **TAIR_Arabidopsis**, Symbols: | heat shock protein 81-4 (HSP81-4) | chr5:22694828-22697293 REVERSE

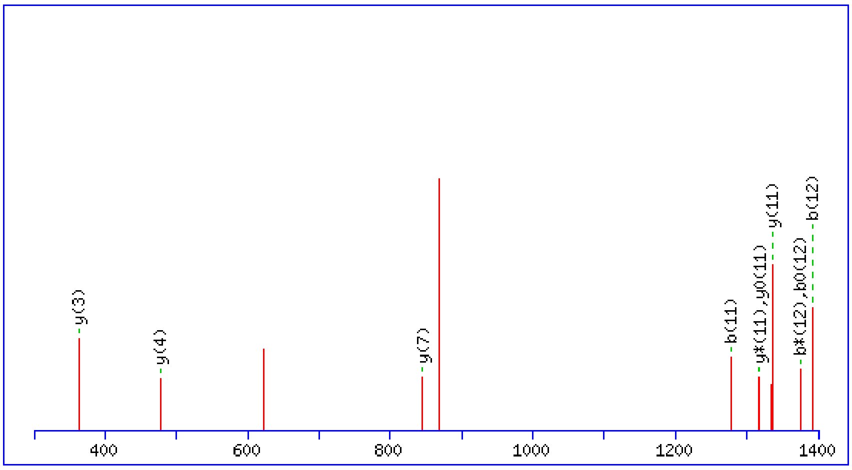
Match to Query 7886: 1752.875976 from(877.445264,2+) index(8245)
Title: Elution from: 77.573 to 77.573 scan no 11203 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1400 Da Full range

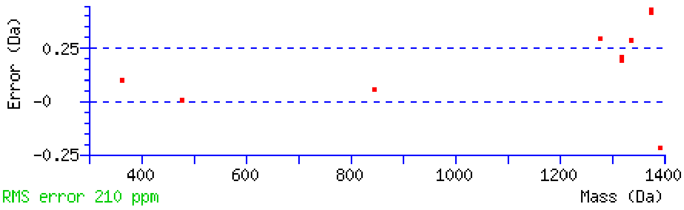
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

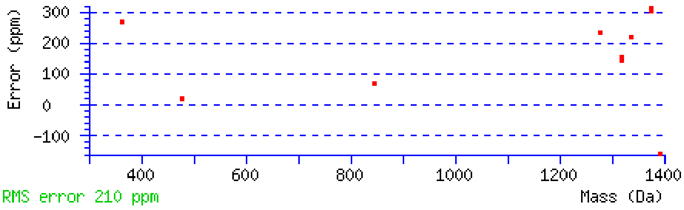


Monoisotopic mass of neutral peptide Mr(calc): 1752.8789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0086
Matches : 10/158 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					L							15
2	231.1124	116.0598			213.1018	107.0545	D	1639.8051	820.4062	1621.7815	811.3944	1621.7945	811.4009	14
3	289.1309	145.0691			271.1203	136.0638	G	1523.7811	762.3942	1505.7575	753.3824	1505.7705	753.3889	13
4	419.1835	210.0954	401.1599	201.0836	401.1729	201.0901	Q	1465.7626	733.3849	1447.7390	724.3731	1447.7520	724.3796	12
5	517.2333	259.1203	499.2097	250.1085	499.2227	250.1150	P	***1335.7099***	668.3586	1317.6864	659.3468	1317.6994	659.3533	11
6	647.2729	324.1401	629.2493	315.1283	629.2624	315.1348	E	1237.6601	619.3337	1219.6366	610.3219	1219.6496	610.3284	10
7	761.3540	381.1807	743.3304	372.1689	743.3435	372.1754	L	1107.6205	554.3139	1089.5969	545.3021	1089.6099	545.3086	9
8	909.4195	455.2134	891.3959	446.2016	891.4089	446.2081	F	993.5394	497.2733	975.5158	488.2616	975.5288	488.2681	8
9	1023.5006	512.2539	1005.4770	503.2421	1005.4900	503.2486	I	***845.4740***	423.2406	827.4504	414.2288	827.4634	414.2353	7
10	1163.5506	582.2789	1145.5270	573.2671	1145.5400	573.2737	H	731.3929	366.2001	713.3693	357.1883	713.3823	357.1948	6
11	**1277.6317**	639.3195	1259.6081	630.3077	1259.6211	630.3142	I	591.3428	296.1751	573.3193	287.1633	573.3323	287.1698	5
12	**1391.7128**	696.3600	1373.6892	687.3482	1373.7022	687.3547	I	***477.2617***	239.1345	459.2382	230.1227	459.2512	230.1292	4
13	1489.7626	745.3849	1471.7390	736.3731	1471.7520	736.3796	P	***363.1807***	182.0940	345.1571	173.0822	345.1701	173.0887	3
14	1605.7866	803.3969	1587.7630	794.3851	1587.7760	794.3916	D	265.1309	133.0691	247.1073	124.0573	247.1203	124.0638	2
15							K	149.1069	75.0571	131.0833	66.0453			1



RMS error 210 ppm



RMS error 210 ppm

NCBI **BLAST** search of LDGQPELFIHIIPDK

AT5G56000.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	1752.8789	-0.0029	LDGQPELFIHIIPDK
10.6	1752.8712	0.0047	RQAQPPPPPPPPPPTR
2.3	1752.8739	0.0021	HHVPPRRSWGASLVK
1.2	1752.8753	0.0007	NMKLRMEAEIAGLLK

AT5G56010.1

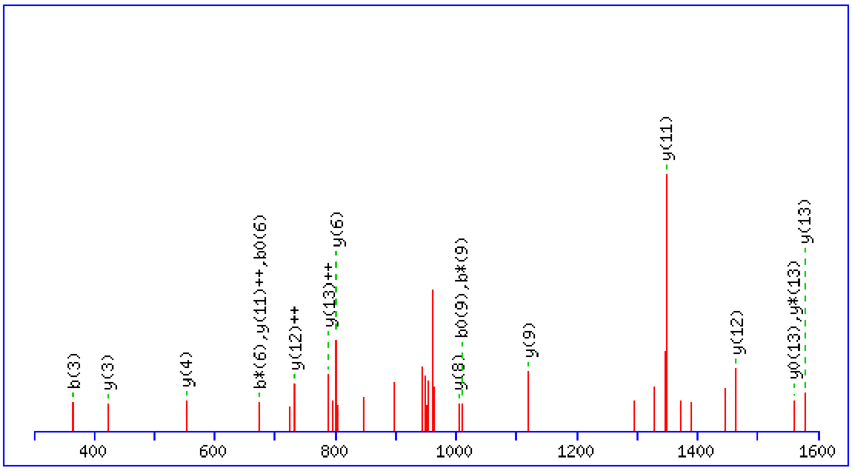
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMEINPENSIMDELRK**
Found in **AT5G56010.1** in **TAIR_Arabidopsis**, Symbols: HSP81-3 | HSP81-3 (Heat shock protein 81-3); ATP binding | chr5:22698636-22701137 FORWARD

Match to Query 9061: 1940.851116 from(971.432834,2+) index(7753)
Title: Elution from: 68.378 to 68.378 scan no 10159 cid35.00 polarity:+
Data file 0-3_2.mgf

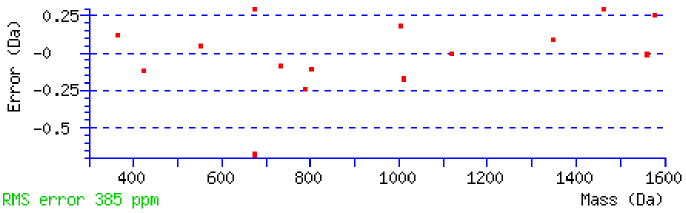
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

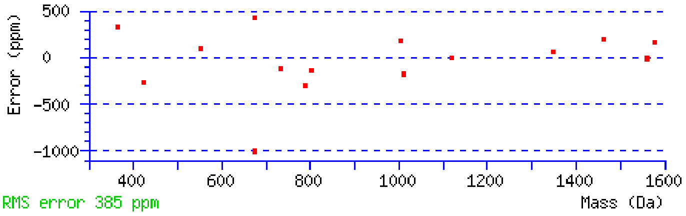


Monoisotopic mass of neutral peptide Mr(calc): 1940.8476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 5.3e-006
Matches : 18/166 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							16
2	235.0895	118.0484			217.0789	109.0431	M	1839.8102	920.4087	1821.7866	911.3969	1821.7996	911.4034	15
3	365.1291	183.0682			347.1186	174.0629	E	1707.7727	854.3900	1689.7491	845.3782	1689.7621	845.3847	14
4	479.2102	240.1088			461.1997	231.1035	I	***1577.7330***	789.3702	1559.7094	780.3584	1559.7225	780.3649	13
5	595.2472	298.1273	577.2236	289.1155	577.2367	289.1220	N	***1463.6519***	732.3296	1445.6283	723.3178	1445.6414	723.3243	12
6	693.2970	347.1522	675.2734	338.1404	675.2865	338.1469	P	***1347.6149***	674.3111	1329.5914	665.2993	1329.6044	665.3058	11
7	823.3367	412.1720	805.3131	403.1602	805.3261	403.1667	E	1249.5651	625.2862	1231.5416	616.2744	1231.5546	616.2809	10
8	939.3737	470.1905	921.3501	461.1787	921.3631	461.1852	N	***1119.5255***	560.2664	1101.5019	551.2546	1101.5149	551.2611	9
9	1027.4027	514.2050	1009.3791	505.1932	1009.3922	505.1997	S	***1003.4885***	502.2479	985.4649	493.2361	985.4779	493.2426	8
10	1141.4838	571.2455	1123.4602	562.2338	1123.4733	562.2403	I	915.4594	458.2334	897.4359	449.2216	897.4489	449.2281	7
11	1273.5213	637.2643	1255.4978	628.2525	1255.5108	628.2590	M	***801.3784***	401.1928	783.3548	392.1810	783.3678	392.1875	6
12	1389.5453	695.2763	1371.5217	686.2645	1371.5348	686.2710	D	669.3408	335.1741	651.3172	326.1623	651.3303	326.1688	5
13	1519.5849	760.2961	1501.5614	751.2843	1501.5744	751.2908	E	***553.3169***	277.1621	535.2933	268.1503	535.3063	268.1568	4
14	1633.6660	817.3367	1615.6425	808.3249	1615.6555	808.3314	L	***423.2772***	212.1423	405.2536	203.1305			3
15	1793.7553	897.3813	1775.7317	888.3695	1775.7447	888.3760	R	309.1961	155.1017	291.1725	146.0899			2
16							K	149.1069	75.0571	131.0833	66.0453			1

AT5G56010.1





NCBI **BLAST** search of TMEINPENSIMDELRK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.1	1940.8476	0.0035	TMEINPENSIMDELRK
0.5	1940.8512	-0.0001	DEEGKNFWAEIEIVDK
0.5	1940.8550	-0.0039	DVMIENIDNILDRGER
0.4	1940.8476	0.0035	KTMEINPENSIMDELR
0.1	1940.8565	-0.0054	LFTWGDGDKNRLGHGDK

Mascot: http://www.matrixscience.com/

AT5G56030.1

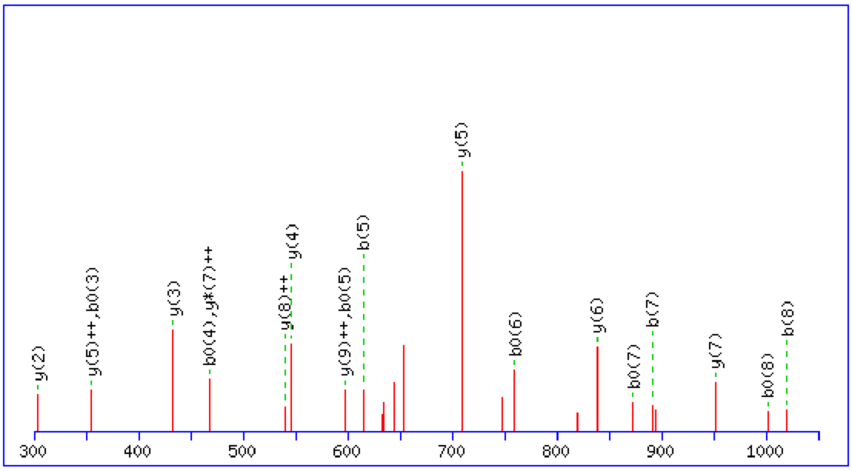
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDQLEYLEER**
Found in **AT5G56030.1** in **TAIR_Arabidopsis**, Symbols: ERD8, HSP81-2 | HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding | chr5:22704149-22706659 FORWARD

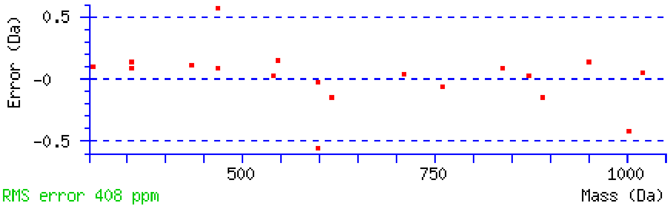
Match to Query 4672: 1322.595942 from(662.305247,2+) index(4950)
Title: Elution from: 44.090 to 44.090 scan no 6218 cid35.00 polarity:+
Data file 0-3_3.mgf

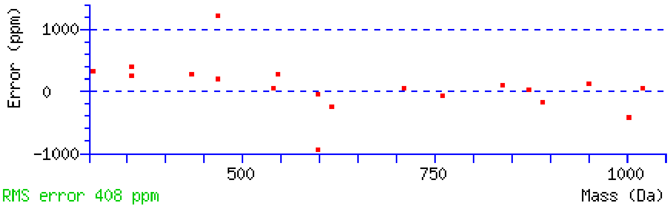
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1322.5990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 4.4e-006
Matches : 19/102 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	245.0768	123.0420			227.0662	114.0368	D	1194.5637	597.7855	1177.5372	589.2722	1176.5531	588.7802	9
3	373.1354	187.0713	356.1088	178.5581	355.1248	178.0661	Q	1079.5368	540.2720	1062.5102	531.7587	1061.5262	531.2667	8
4	486.2195	243.6134	469.1929	235.1001	468.2089	234.6081	L	***951.4782***	476.2427	934.4516	467.7295	933.4676	467.2374	7
5	**615.2620**	308.1347	598.2355	299.6214	597.2515	299.1294	E	***838.3941***	419.7007	821.3676	411.1874	820.3836	410.6954	6
6	778.3254	389.6663	761.2988	381.1531	760.3148	380.6610	Y	***709.3515***	355.1794	692.3250	346.6661	691.3410	346.1741	5
7	**891.4094**	446.2084	874.3829	437.6951	873.3989	437.2031	L	***546.2882***	273.6477	529.2617	265.1345	528.2776	264.6425	4
8	**1020.4520**	510.7297	1003.4255	502.2164	1002.4415	501.7244	E	***433.2041***	217.1057	416.1776	208.5924	415.1936	208.1004	3
9	1149.4946	575.2510	1132.4681	566.7377	1131.4841	566.2457	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EDQLEYLEER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G56030.1

Score	Mr(calc)	Delta	Sequence
58.4	1322.5990	-0.0030	EDQLEYLEER
1.8	1322.5925	0.0034	SPSSFTPCLDGR

AT5G56090.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSTVASISSESK**
Found in **AT5G56090.1** in **TAIR_Arabidopsis**, Symbols: COX15 | COX15 (CYTOCHROME C OXIDASE 15) | chr5:22731860-22733831 FORWARD

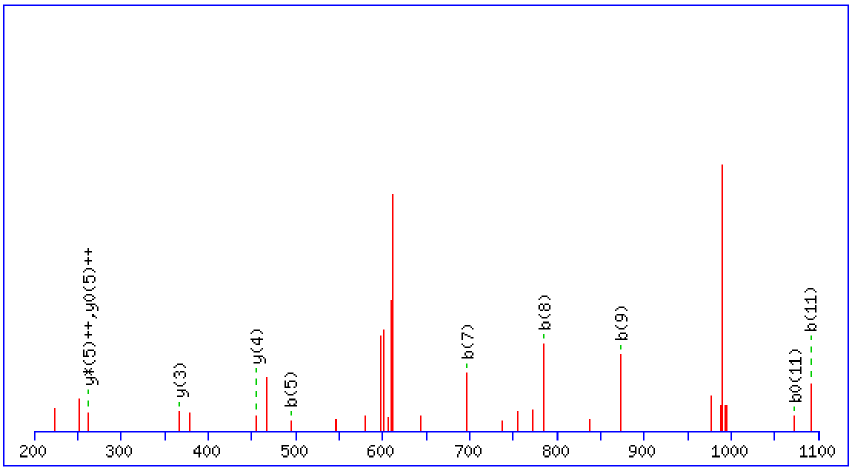
Match to Query 4144: 1238.548258 from(620.281405,2+) index(2068)
Title: Elution from: 23.570 to 23.570 scan no 2644 cid35.00 polarity:+
Data file C7-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1100 Da Full range

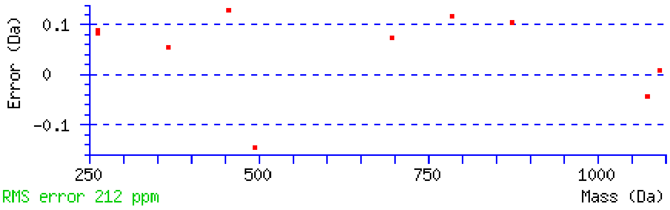
Label all possible matches ○ Label matches used for scoring ●

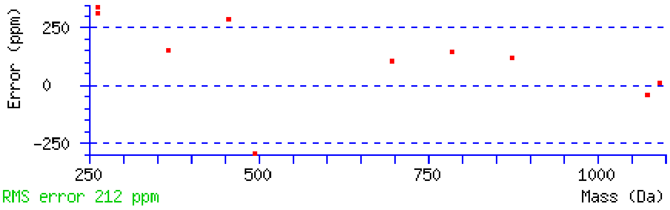
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1238.5475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.022
Matches : 10/106 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260			M							12
2	221.0739	111.0406	203.0633	102.0353	S	1107.5172	554.2623	1089.4936	545.2505	1089.5067	545.2570	11
3	323.1186	162.0629	305.1080	153.0576	T	1019.4882	510.2477	1001.4646	501.2359	1001.4776	501.2424	10
4	423.1840	212.0956	405.1735	203.0904	V	917.4435	459.2254	899.4199	450.2136	899.4329	450.2201	9
5	***495.2182***	248.1127	477.2076	239.1074	A	817.3780	409.1926	799.3544	400.1808	799.3674	400.1874	8
6	583.2472	292.1273	565.2367	283.1220	S	745.3439	373.1756	727.3203	364.1638	727.3333	364.1703	7
7	***697.3283***	349.1678	679.3178	340.1625	I	657.3148	329.1610	639.2912	320.1492	639.3042	320.1558	6
8	***785.3574***	393.1823	767.3468	384.1771	S	543.2337	272.1205	525.2101	263.1087	525.2231	263.1152	5
9	***873.3865***	437.1969	855.3759	428.1916	S	**455.2046**	228.1060	437.1810	219.0942	437.1941	219.1007	4
10	1003.4261	502.2167	985.4155	493.2114	E	**367.1756**	184.0914	349.1520	175.0796	349.1650	175.0861	3
11	***1091.4551***	546.2312	1073.4446	537.2259	S	237.1359	119.0716	219.1124	110.0598	219.1254	110.0663	2
12					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of MSTVASISSESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G56090.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.5	1238.5475	0.0008	MSTVASISSESK
20.1	1238.5501	-0.0019	SEMVDRKASGK
17.6	1238.5454	0.0028	CSKCGQKNLK
13.3	1238.5497	-0.0014	LYSVCTVEEK
12.4	1238.5475	0.0008	MESSISQTLSK
10.8	1238.5501	-0.0019	ETSRKCSVEK
9.0	1238.5468	0.0015	DDSRFNQTLK
8.7	1238.5502	-0.0019	KMKGSQNAESK
7.4	1238.5501	-0.0019	MVGSNTVTATSR
4.0	1238.5454	0.0028	QLMINCRSGK

AT5G56330.1

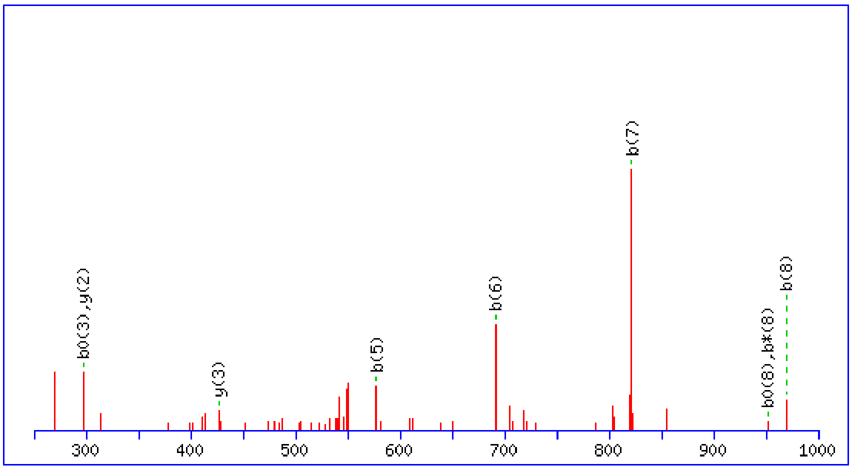
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHDIMLKFK**
Found in **AT5G56330.1** in **TAIR_Arabidopsis**, Symbols: | carbonic anhydrase family protein | chr5:22830994-22833388 FORWARD

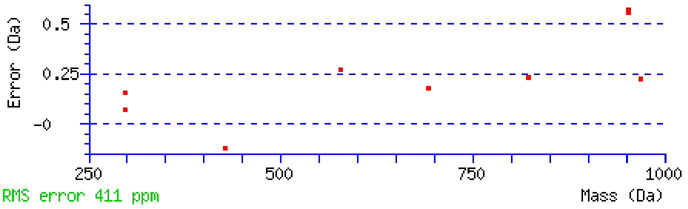
Match to Query 3746: 1116.541718 from(559.278135,2+) index(7815)
Title: Elution from: 68.193 to 68.193 scan no 10171 cid35.00 polarity:+
Data file D6h-1_1.mgf

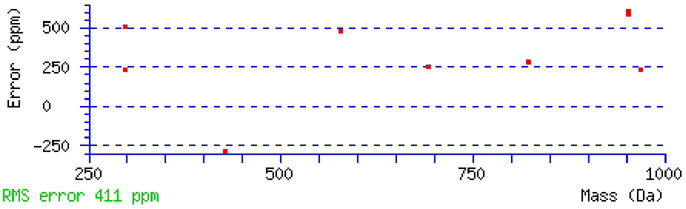
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1116.5412
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 **Expect:** 0.002
Matches : 9/108 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	59.0258	30.0165					G							9
2	199.0758	100.0415					H	1059.5300	530.2686	1041.5064	521.2568	1041.5194	521.2633	8
3	315.0998	158.0535			297.0892	149.0482	D	919.4800	460.2436	901.4564	451.2318	901.4694	451.2383	7
4	429.1809	215.0941			411.1703	206.0888	I	803.4560	402.2316	785.4324	393.2198			6
5	***577.2133***	289.1103			559.2027	280.1050	M	689.3749	345.1911	671.3513	336.1793			5
6	***691.2944***	346.1508			673.2838	337.1456	L	541.3425	271.1749	523.3189	262.1631			4
7	***821.3834***	411.1954	803.3599	402.1836	803.3729	402.1901	K	**427.2614**	214.1343	409.2378	205.1225			3
8	***969.4489***	485.2281	951.4253	476.2163	951.4383	476.2228	F	**297.1723**	149.0898	279.1487	140.0780			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of GHDIMLKFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G56330.1

36.7	1116.5412	0.0005	GHDIMLKFK
13.0	1116.5412	0.0005	MKVTHVDFK
9.3	1116.5401	0.0017	FFWIHLDK
4.8	1116.5390	0.0027	MIASPKQGAGK
3.8	1116.5419	-0.0002	LVMLLDMEK
2.5	1116.5390	0.0027	NANLVAAGVMK
1.8	1116.5437	-0.0020	GEGLSGTVKEK
0.8	1116.5419	-0.0002	VDEMMLLIK
0.8	1116.5419	-0.0002	VDEMMLLIK
0.1	1116.5437	-0.0020	SNGTEKDLIK

AT5G56600.1

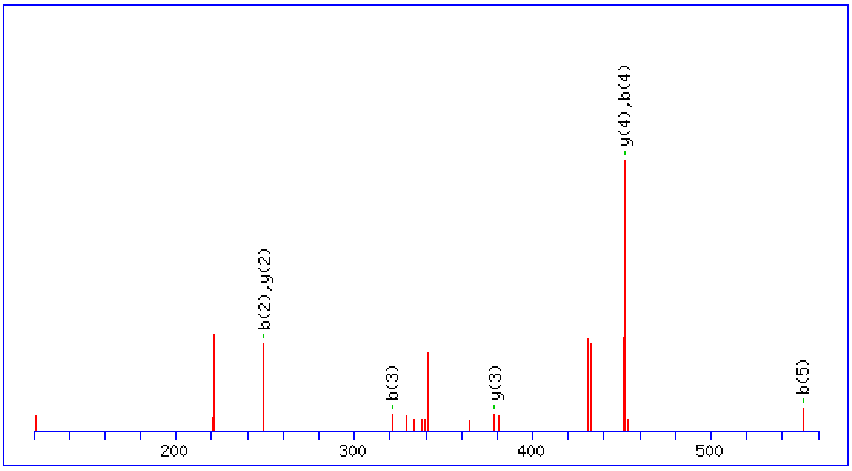
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SRAKVK**
Found in **AT5G56600.1** in **TAIR_Arabidopsis**, Symbols: PFN3, PRF3 | PFN3/PRF3 (PROFILIN 3); actin binding | chr5:22927108-22928047 REVERSE

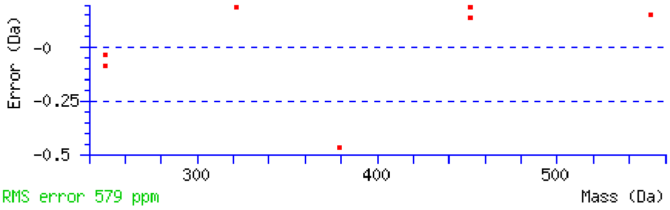
Match to Query 638: 698.405542 from(350.210047,2+) index(2704)
Title: Elution from: 28.003 to 28.003 scan no 3393 cid35.00 polarity:+
Data file 0-1_3.mgf

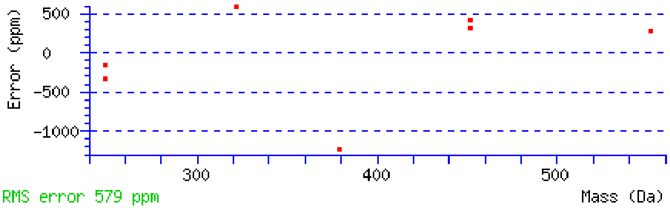
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 560 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 698.4065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0098
Matches : 7/48 fragment ions using 11 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	89.0363	45.0218			71.0258	36.0165	S					6
2	***249.1256***	125.0664	231.1020	116.0546	231.1150	116.0612	R	611.3848	306.1960	593.3612	297.1842	5
3	***321.1597***	161.0835	303.1362	152.0717	303.1492	152.0782	A	**451.2955**	226.1514	433.2719	217.1396	4
4	***451.2488***	226.1280	433.2252	217.1162	433.2382	217.1227	K	**379.2614**	190.1343	361.2378	181.1225	3
5	***551.3142***	276.1607	533.2906	267.1490	533.3037	267.1555	V	**249.1723**	125.0898	231.1487	116.0780	2
6							K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of SRAKVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.2	698.4065	-0.0010	SRAKVK
23.7	698.4061	-0.0006	FVSLVK
22.6	698.4065	-0.0010	SRVKAK

AT5G56600.1

19.1	698.4065	-0.0010	GTRKVK
19.1	698.4065	-0.0010	RSKLGK
14.7	698.4061	-0.0006	FVIVSK
8.6	698.4061	-0.0006	LAVYVK
8.6	698.4061	-0.0006	LVSFVK
8.6	698.4065	-0.0010	RKGTVK
8.6	698.4065	-0.0010	RKTGVK

AT5G56680.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAITAAVAELK**
Found in **AT5G56680.1** in **TAIR_Arabidopsis**, Symbols: EMB2755, SYNC1 | SYNC1 (EMBRYO DEFECTIVE 2755); ATP binding / aminoacyl-tRNA ligase/ asparagine-tRNA ligase/ aspartate-tRNA ligase/ nucleic acid binding / nucleotide binding | chr5:22953871-22956067 FORWARD

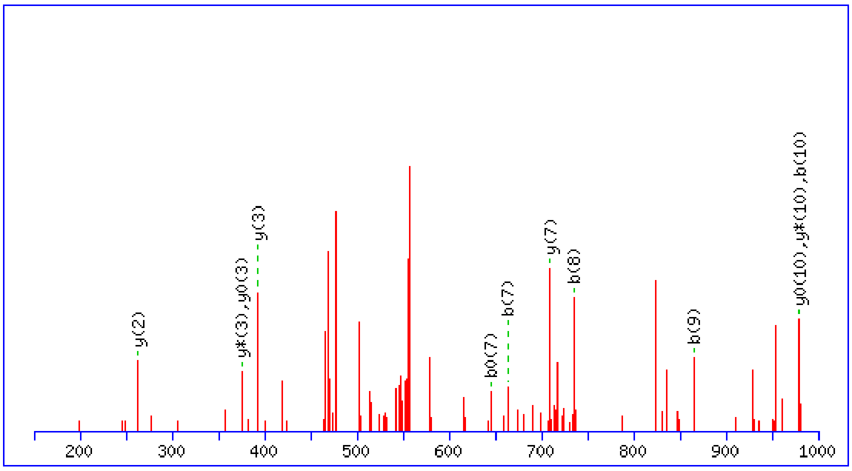
Match to Query 3602: 1126.587110 from(564.300831,2+) index(4331)
Title: Elution from: 40.437 to 40.437 scan no 5473 cid35.00 polarity:+
Data file D6h-3_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

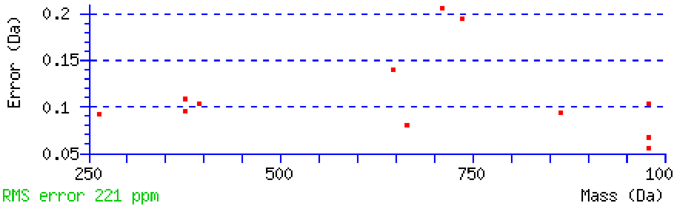
Label all possible matches ○ Label matches used for scoring ●

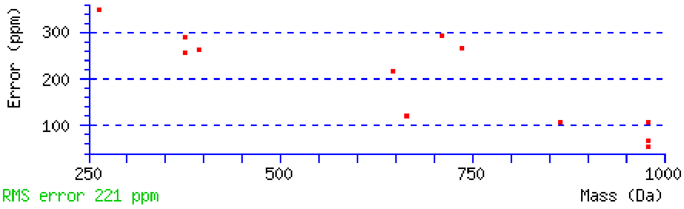
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1126.5878
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.04
Matches : 12/96 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0469	66.0271	113.0363	57.0218	**E**							**11**
2	203.0811	102.0442	185.0705	93.0389	**A**	997.5555	499.2814	979.5319	490.2696	979.5449	490.2761	**10**
3	317.1622	159.0847	299.1516	150.0794	**I**	925.5213	463.2643	907.4977	454.2525	907.5107	454.2590	**9**
4	419.2069	210.1071	401.1963	201.1018	**T**	811.4402	406.2237	793.4166	397.2120	793.4296	397.2185	**8**
5	491.2410	246.1241	473.2304	237.1189	**A**	***709.3955***	355.2014	691.3719	346.1896	691.3849	346.1961	**7**
6	563.2752	282.1412	545.2646	273.1359	**A**	637.3613	319.1843	619.3378	310.1725	619.3508	310.1790	**6**
7	***663.3406***	332.1739	645.3300	323.1687	**V**	565.3272	283.1672	547.3036	274.1554	547.3166	274.1620	**5**
8	***735.3748***	368.1910	717.3642	359.1857	**A**	465.2618	233.1345	447.2382	224.1227	447.2512	224.1292	**4**
9	***865.4144***	433.2108	847.4038	424.2055	**E**	***393.2276***	197.1174	375.2040	188.1056	375.2170	188.1122	**3**
10	***979.4955***	490.2514	961.4849	481.2461	**L**	***263.1880***	132.0976	245.1644	123.0858			**2**
11					**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of EAITAAVAELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G56680.1

Score	Mr(calc)	Delta	Sequence
21.2	1126.5878	-0.0007	EAITAAVAELK
20.3	1126.5905	-0.0034	DRNSLLLPGK
19.3	1126.5878	-0.0007	ELASAAAIELK
12.5	1126.5905	-0.0034	ELTPQRQLK
8.2	1126.5900	-0.0029	FLIQPEIEK
7.0	1126.5878	-0.0007	AELSNIVEIK
3.8	1126.5878	-0.0007	LEKQLEDLK

AT5G56790.1

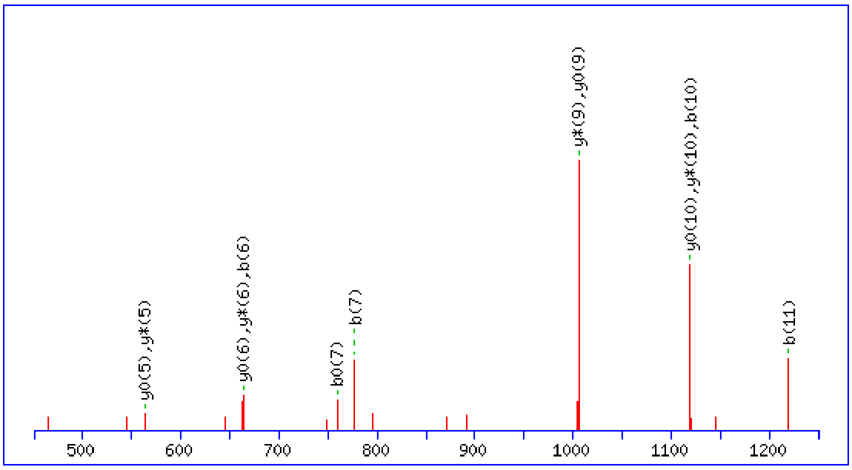
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALLWTLTHVVQPGDR**
Found in **AT5G56790.1** in **TAIR_Arabidopsis**, Symbols: | protein kinase family protein | chr5:22985836-22988617 FORWARD

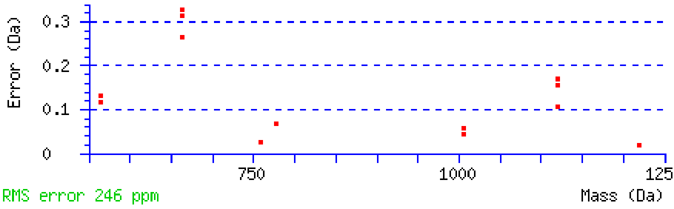
Match to Query 8726: 1798.901948 from(900.458250,2+) index(10202)
Title: Elution from: 94.308 to 94.308 scan no 14281 cid35.00 polarity:+
Data file D6h-3_1.mgf

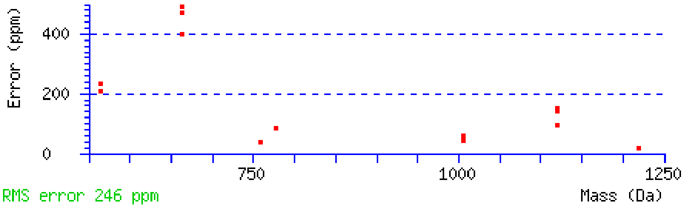
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1798.9000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.035
Matches : 13/146 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	73.0414	37.0244					A							16
2	145.0756	73.0414					A	1727.8732	864.4402	1709.8496	855.4284	1709.8626	855.4349	15
3	259.1567	130.0820					L	1655.8390	828.4232	1637.8155	819.4114	1637.8285	819.4179	14
4	373.2378	187.1225					L	1541.7579	771.3826	1523.7344	762.3708	1523.7474	762.3773	13
5	561.3112	281.1592					W	1427.6768	714.3421	1409.6533	705.3303	1409.6663	705.3368	12
6	***663.3559***	332.1816			645.3453	323.1763	T	1239.6035	620.3054	1221.5799	611.2936	1221.5929	611.3001	11
7	*777.4370*	389.2221			759.4264	380.2168	L	1137.5587	569.2830	1119.5352	560.2712	1119.5482	560.2777	10
8	879.4817	440.2445			861.4711	431.2392	T	1023.4776	512.2425	1005.4541	503.2307	1005.4671	503.2372	9
9	1019.5317	510.2695			1001.5211	501.2642	H	921.4329	461.2201	903.4093	452.2083	903.4224	452.2148	8
10	***1119.5971***	560.3022			1101.5866	551.2969	V	781.3829	391.1951	763.3593	382.1833	763.3723	382.1898	7
11	***1219.6626***	610.3349			1201.6520	601.3297	V	681.3175	341.1624	663.2939	332.1506	663.3069	332.1571	6
12	1349.7152	675.3613	1331.6917	666.3495	1331.7047	666.3560	Q	581.2520	291.1296	563.2284	282.1179	563.2414	282.1244	5
13	1447.7650	724.3862	1429.7415	715.3744	1429.7545	715.3809	P	451.1994	226.1033	433.1758	217.0915	433.1888	217.0980	4
14	1505.7835	753.3954	1487.7600	744.3836	1487.7730	744.3901	G	353.1496	177.0784	335.1260	168.0666	335.1390	168.0731	3
15	1621.8075	811.4074	1603.7839	802.3956	1603.7970	802.4021	D	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	2
16							R	179.1071	90.0572	161.0835	81.0454			1





AT5G56790.1

NCBI **BLAST** search of AALLWTLTHVVQPGDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.9	1798.9000	0.0019	AALLWTLTHVVQPGDR
7.2	1798.9012	0.0007	MSSEIRRNIITKPSK
3.9	1798.9056	-0.0037	SWGRLALVIVTACFGK
1.4	1798.9068	-0.0049	NRKLATVLSIMLCNK

AT5G57290.1

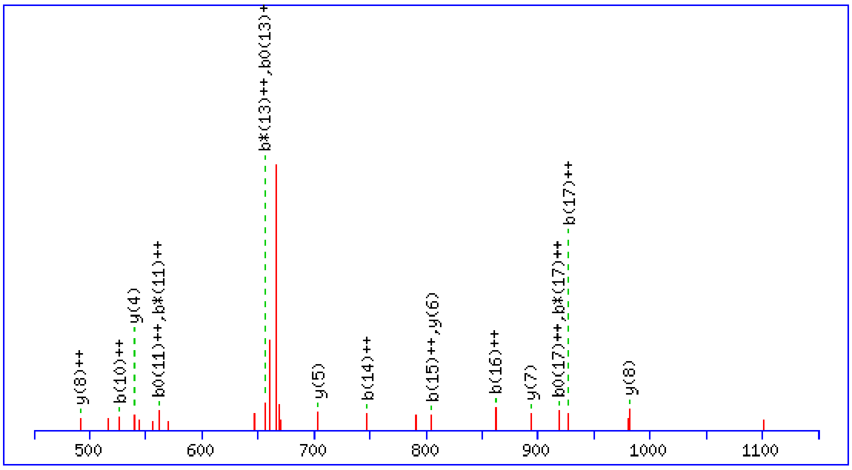
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHEGDLEASASSTYDLQR**
Found in **AT5G57290.1** in **TAIR_Arabidopsis**, Symbols: | 60S acidic ribosomal protein P3 (RPP3B) | chr5:23224275-23225061 REVERSE

Match to Query 9543: 2030.821191 from(677.947673,3+) index(3219)
Title: Elution from: 34.488 to 34.488 scan no 4112 cid35.00 polarity:+
Data file D12h-2_1.mgf

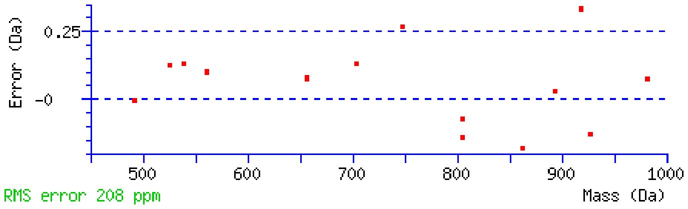
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

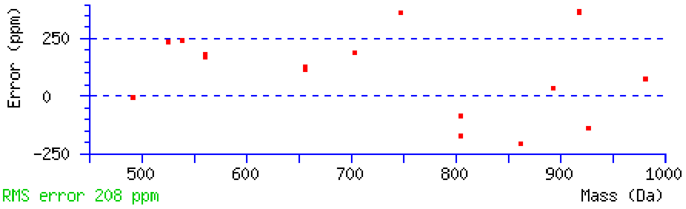


Monoisotopic mass of neutral peptide Mr(calc): 2030.8236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.0062
Matches : 17/194 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							18
2	271.1099	136.0586	253.0864	127.0468			H	1901.7782	951.3928	1883.7546	942.3810	1883.7677	942.3875	17
3	401.1496	201.0784	383.1260	192.0666	383.1390	192.0731	E	1761.7282	881.3677	1743.7046	872.3560	1743.7176	872.3625	16
4	459.1681	230.0877	441.1445	221.0759	441.1575	221.0824	G	1631.6886	816.3479	1613.6650	807.3361	1613.6780	807.3426	15
5	575.1920	288.0997	557.1685	279.0879	557.1815	279.0944	D	1573.6701	787.3387	1555.6465	778.3269	1555.6595	778.3334	14
6	689.2731	345.1402	671.2496	336.1284	671.2626	336.1349	L	1457.6461	729.3267	1439.6225	720.3149	1439.6355	720.3214	13
7	819.3128	410.1600	801.2892	401.1482	801.3022	401.1547	E	1343.5650	672.2861	1325.5414	663.2743	1325.5544	663.2809	12
8	891.3469	446.1771	873.3233	437.1653	873.3364	437.1718	A	1213.5254	607.2663	1195.5018	598.2545	1195.5148	598.2610	11
9	979.3760	490.1916	961.3524	481.1798	961.3654	481.1863	S	1141.4912	571.2493	1123.4676	562.2375	1123.4807	562.2440	10
10	1051.4101	***526.2087***	1033.3865	517.1969	1033.3996	517.2034	A	1053.4622	527.2347	1035.4386	518.2229	1035.4516	518.2294	9
11	1139.4392	570.2232	1121.4156	561.2114	1121.4286	561.2180	S	***981.4280***	491.2176	963.4044	482.2059	963.4175	482.2124	8
12	1227.4683	614.2378	1209.4447	605.2260	1209.4577	605.2325	S	***893.3990***	447.2031	875.3754	438.1913	875.3884	438.1978	7
13	1329.5130	665.2601	1311.4894	656.2483	1311.5024	656.2548	T	***805.3699***	403.1886	787.3463	394.1768	787.3593	394.1833	6
14	1493.5733	***747.2903***	1475.5498	738.2785	1475.5628	738.2850	Y	***703.3252***	352.1662	685.3016	343.1544	685.3146	343.1609	5
15	1609.5973	***805.3023***	1591.5737	796.2905	1591.5867	796.2970	D	***539.2648***	270.1360	521.2412	261.1243	521.2543	261.1308	4
16	1723.6784	***862.3428***	1705.6548	853.3311	1705.6678	853.3376	L	423.2408	212.1241	405.2173	203.1123			3
17	1853.7311	***927.3692***	1835.7075	918.3574	1835.7205	918.3639	Q	309.1597	155.0835	291.1362	146.0717			2
18							R	179.1071	90.0572	161.0835	81.0454			1

AT5G57290.1





NCBI **BLAST** search of QHEGDLEASASSTYDLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.0	2030.8236	-0.0024	QHEGDLEASASSTYDLQR
2.8	2030.8226	-0.0015	DVFMFKTMCKECLER

Mascot: http://www.matrixscience.com/

AT5G57420.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **RFHQDNSTTQQPR**
Found in **AT5G57420.1** in **TAIR_Arabidopsis**, Symbols: IAA33 | IAA33 (indoleacetic acid-induced protein 33); transcription factor | chr5:23287250-23288185 FORWARD

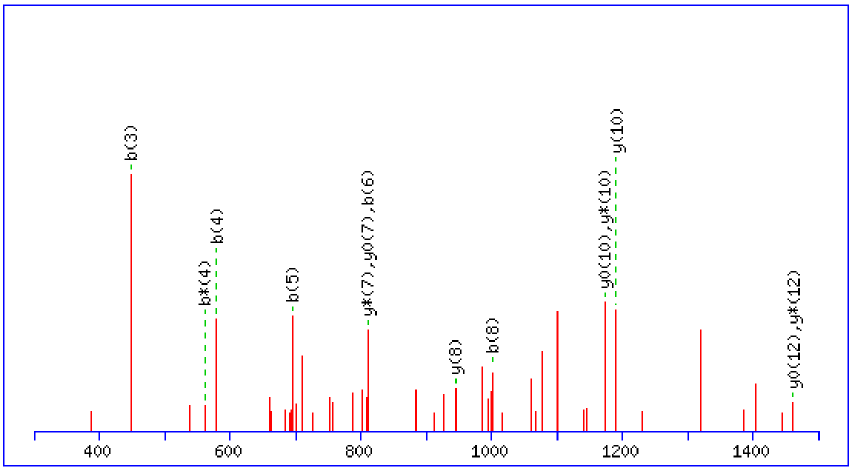
Match to Query 7211: 1638.693756 from(820.354154,2+) index(6627)
Title: Elution from: 58.787 to 58.787 scan no 8612 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1500 Da Full range

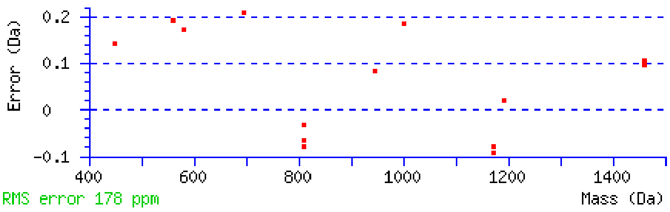
Label all possible matches ○ Label matches used for scoring ●

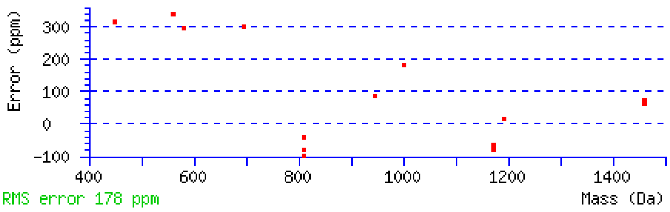
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1638.6917
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0079
Matches : 15/128 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							13
2	309.1620	155.0846	291.1384	146.0728			F	1479.6098	740.3085	1461.5862	731.2967	1461.5992	731.3032	12
3	***449.2120***	225.1096	431.1884	216.0978			H	1331.5443	666.2758	1313.5207	657.2640	1313.5337	657.2705	11
4	***579.2646***	290.1360	561.2411	281.1242			Q	**1191.4943**	596.2508	1173.4707	587.2390	1173.4837	587.2455	10
5	***695.2886***	348.1479	677.2650	339.1362	677.2781	339.1427	D	1061.4416	531.2245	1043.4181	522.2127	1043.4311	522.2192	9
6	***811.3256***	406.1664	793.3020	397.1547	793.3151	397.1612	N	**945.4177**	473.2125	927.3941	464.2007	927.4071	464.2072	8
7	899.3547	450.1810	881.3311	441.1692	881.3441	441.1757	S	829.3807	415.1940	811.3571	406.1822	811.3701	406.1887	7
8	***1001.3994***	501.2033	983.3758	492.1915	983.3888	492.1981	T	741.3516	371.1794	723.3280	362.1677	723.3410	362.1742	6
9	1103.4441	552.2257	1085.4205	543.2139	1085.4335	543.2204	T	639.3069	320.1571	621.2833	311.1453	621.2963	311.1518	5
10	1233.4968	617.2520	1215.4732	608.2402	1215.4862	608.2467	Q	537.2622	269.1347	519.2386	260.1229			4
11	1363.5494	682.2783	1345.5258	673.2665	1345.5388	673.2731	Q	407.2095	204.1084	389.1860	195.0966			3
12	***1461.5992***	731.3032	1443.5756	722.2914	1443.5886	722.2980	P	277.1569	139.0821	259.1333	130.0703			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of RFHQDNSTTQQPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G57420.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.0	1638.6917	0.0020	RFHQDNSTTQQPR
5.0	1638.6920	0.0018	VLTCSDFEHEVASK
1.0	1638.6969	-0.0031	LMNFTWEEKHER
1.0	1638.6924	0.0013	VDNNDPNAMKTLNR

AT5G57655.2

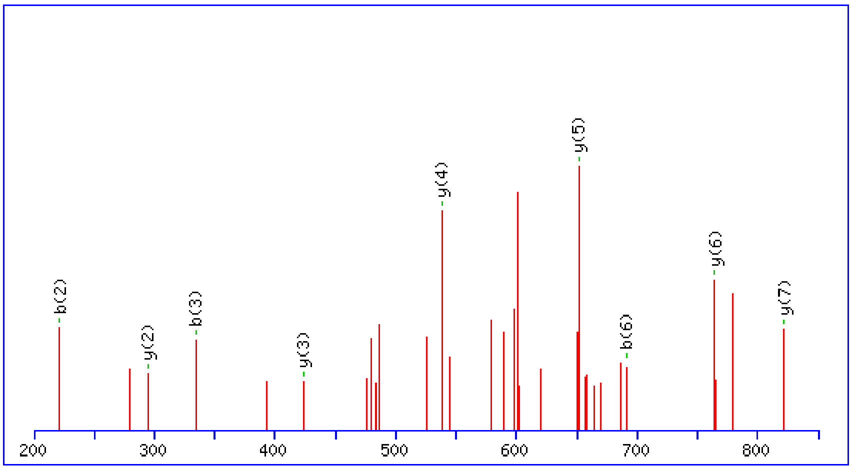
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGLIDEFK**
Found in **AT5G57655.2** in **TAIR_Arabidopsis**, Symbols: | xylose isomerase family protein | chr5:23364256-23367031 FORWARD

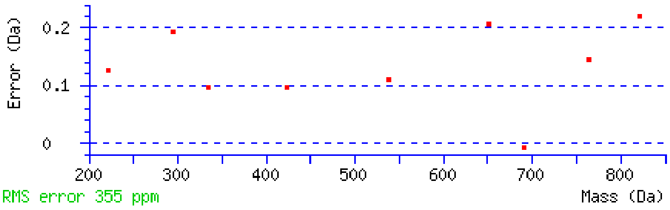
Match to Query 2296: 983.495896 from(492.755224,2+) index(6672)
Title: Elution from: 59.051 to 59.051 scan no 8618 cid35.00 polarity:+
Data file D12h-3_2.mgf

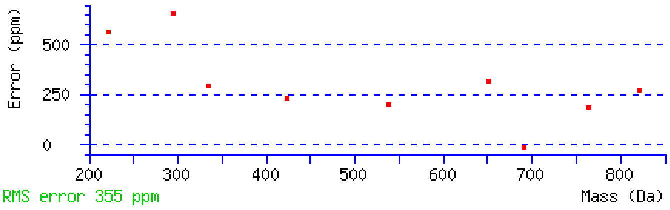
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 983.4964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0011
Matches : 9/58 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							8
2	**221.0921**	111.0497			G	*821.4403*	411.2238	804.4138	402.7105	803.4298	402.2185	7
3	**334.1761**	167.5917			L	*764.4189*	382.7131	747.3923	374.1998	746.4083	373.7078	6
4	447.2602	224.1337			I	*651.3348*	326.1710	634.3083	317.6578	633.3243	317.1658	5
5	562.2871	281.6472	544.2766	272.6419	D	*538.2508*	269.6290	521.2242	261.1157	520.2402	260.6237	4
6	**691.3297**	346.1685	673.3192	337.1632	E	*423.2238*	212.1155	406.1973	203.6023	405.2132	203.1103	3
7	838.3981	419.7027	820.3876	410.6974	F	*294.1812*	147.5942	277.1547	139.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YGLIDEFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.0	983.4964	-0.0005	YGLIDEFK

AT5G57655.2

Mascot: http://www.matrixscience.com/

AT5G57960.1

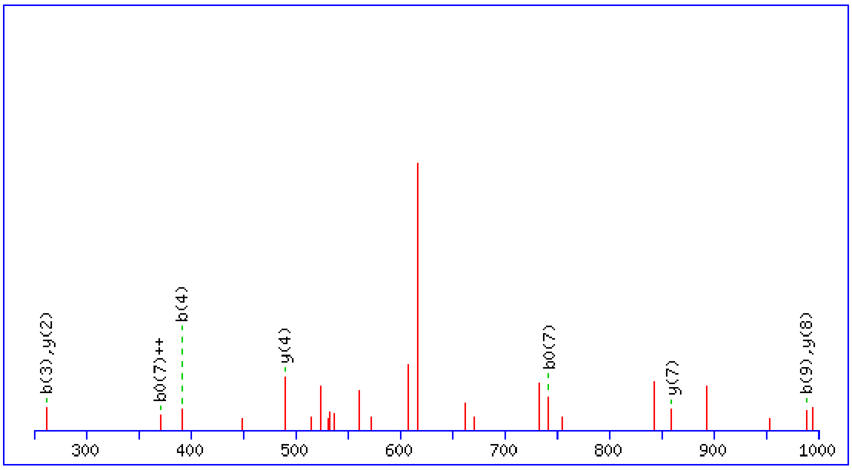
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GMGEKQIEVDK**
Found in **AT5G57960.1** in **TAIR_Arabidopsis**, Symbols: | GTP-binding family protein | chr5:23480359-23483707 REVERSE

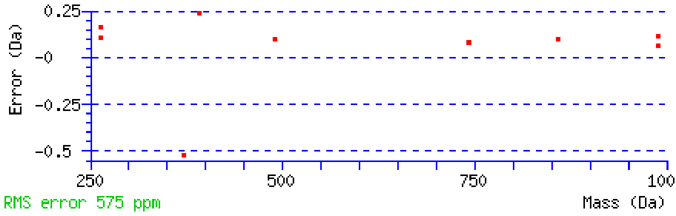
Match to Query 4451: 1248.601298 from(625.307925,2+) index(1355)
Title: Elution from: 19.227 to 19.227 scan no 1859 cid35.00 polarity:+
Data file D12h-1_2.mgf

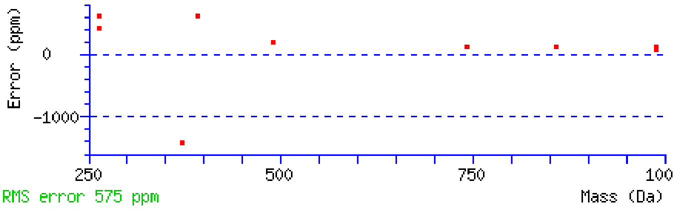
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1248.6020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.041
Matches : 9/154 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							11
2	205.0641	103.0357					M	1192.5878	596.7975	1175.5613	588.2843	1174.5773	587.7923	10
3	**262.0856**	131.5464					G	1045.5524	523.2798	1028.5259	514.7666	1027.5419	514.2746	9
4	**391.1282**	196.0677			373.1176	187.0625	E	***988.5310***	494.7691	971.5044	486.2558	970.5204	485.7638	8
5	519.2232	260.1152	502.1966	251.6019	501.2126	251.1099	K	***859.4884***	430.2478	842.4618	421.7345	841.4778	421.2425	7
6	647.2817	324.1445	630.2552	315.6312	629.2712	315.1392	Q	731.3934	366.2003	714.3668	357.6871	713.3828	357.1951	6
7	760.3658	380.6865	743.3393	372.1733	742.3552	371.6813	I	603.3348	302.1710	586.3083	293.6578	585.3243	293.1658	5
8	889.4084	445.2078	872.3818	436.6946	871.3978	436.2026	E	***490.2508***	245.6290	473.2242	237.1157	472.2402	236.6237	4
9	**988.4768**	494.7420	971.4503	486.2288	970.4662	485.7368	V	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
10	1103.5038	552.2555	1086.4772	543.7422	1085.4932	543.2502	D	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GMGEKQIEVDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G57960.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.6	1248.6020	-0.0007	GMGEKQIEVDK
3.4	1248.6000	0.0013	FNRSAWPDTR
2.4	1248.6033	-0.0020	AFQEMGARAPR
2.4	1248.6020	-0.0007	ENIVASASSPMK
1.6	1248.6020	-0.0007	EELESMRLDK
1.3	1248.6020	-0.0007	KIMQADEDVGK
0.5	1248.6020	-0.0007	LLMQDENDKK
0.2	1248.6019	-0.0006	EEEEAKQMKK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QMAKLLDPK**
Found in **AT5G58003.1** in **TAIR_Arabidopsis**, Symbols: CPL4 | CPL4 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 4); phosphoprotein phosphatase | chr5:23497292-23499150 FORWARD

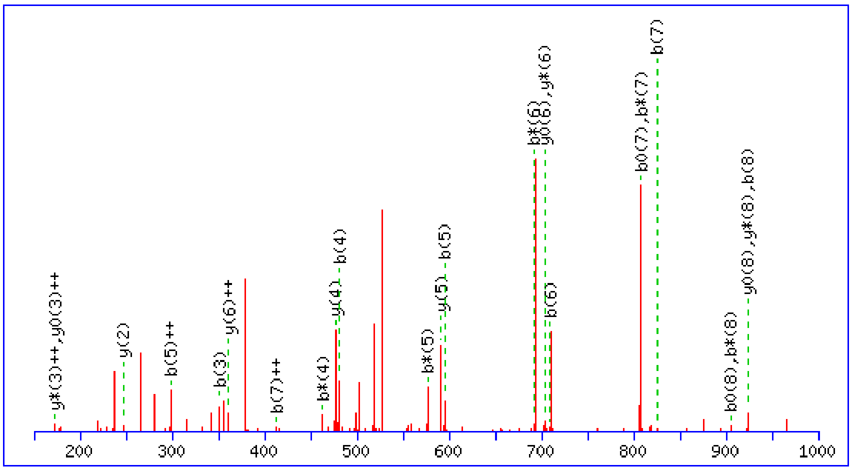
Match to Query 3008: 1070.545996 from(536.280274,2+) index(7288)
Title: Elution from: 64.805 to 64.805 scan no 9597 cid35.00 polarity:+
Data file D6h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

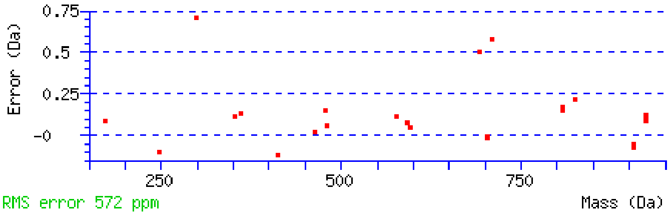
Label all possible matches ○ Label matches used for scoring ●

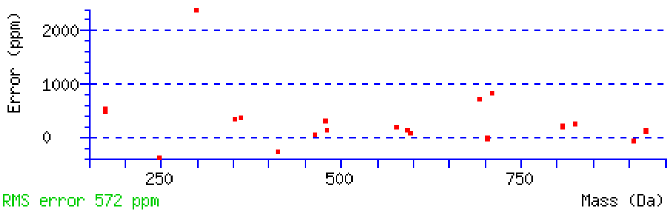
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1070.5438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.013
Matches : 25/118 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							9
2	279.0924	140.0498	261.0688	131.0380			M	941.4985	471.2529	923.4749	462.2411	923.4879	462.2476	8
3	***351.1265***	176.0669	333.1029	167.0551			A	793.4660	397.2367	775.4424	388.2249	775.4555	388.2314	7
4	***481.2155***	241.1114	463.1920	232.0996			K	721.4319	361.2196	703.4083	352.2078	703.4213	352.2143	6
5	***595.2966***	298.1520	577.2731	289.1402			L	**591.3428**	296.1751	573.3193	287.1633	573.3323	287.1698	5
6	***709.3777***	355.1925	691.3542	346.1807			L	**477.2618**	239.1345	459.2382	230.1227	459.2512	230.1292	4
7	***825.4017***	413.2045	807.3781	404.1927	807.3912	404.1992	D	363.1807	182.0940	345.1571	173.0822	345.1701	173.0887	3
8	***923.4515***	462.2294	905.4279	453.2176	905.4410	453.2241	P	**247.1567**	124.0820	229.1331	115.0702			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QMAKLLDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G58003.1

Score	Mr(calc)	Delta	Sequence
26.6	1070.5438	0.0022	QMAKLLDPK
23.0	1070.5486	-0.0026	DKLDTLVEK
20.0	1070.5486	-0.0026	LLDTKDLDK
13.9	1070.5461	-0.0001	FMSSHLLIL
11.7	1070.5487	-0.0027	KWHMTVKK
11.0	1070.5438	0.0022	EKALKDPMK
10.8	1070.5486	-0.0026	IELETITNK
9.1	1070.5438	0.0022	MAASPLVVQK
8.6	1070.5486	-0.0026	EKVIDSELK
7.8	1070.5486	-0.0026	KLSEDLDLK

AT5G58070.1

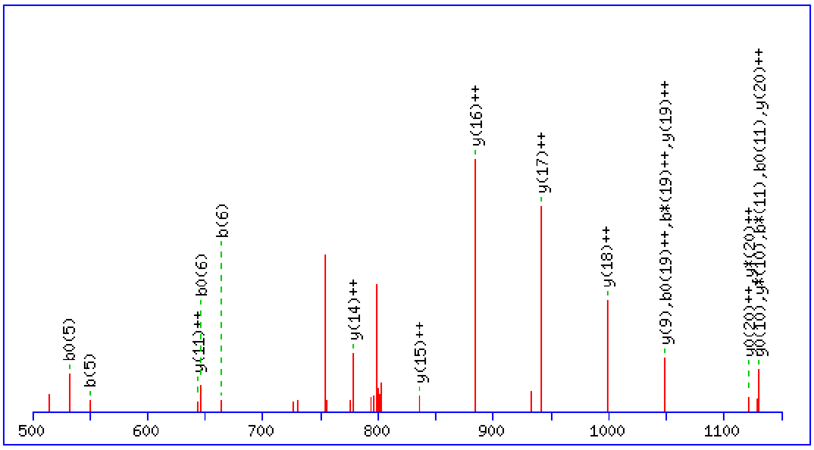
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATYTLNPDGTIHVLNETWSNGK**
Found in **AT5G58070.1** in **TAIR_Arabidopsis**, Symbols: | lipocalin, putative | chr5:23517738-23518382 REVERSE

Match to Query 10186: 2430.174612 from(811.065480,3+) index(7958)
Title: Elution from: 70.942 to 70.942 scan no 10528 cid35.00 polarity:+
Data file D6h-1_3.mgf

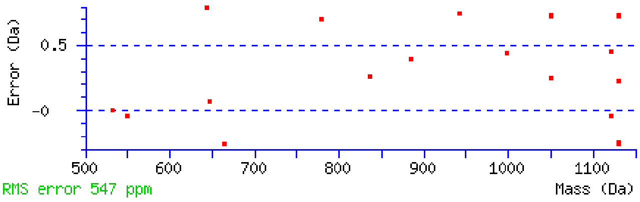
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

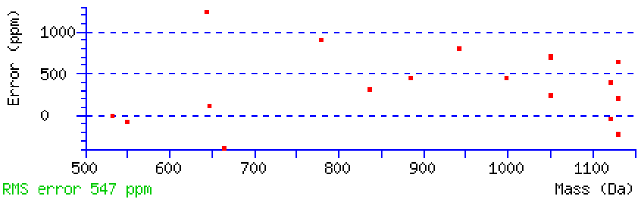


Monoisotopic mass of neutral peptide Mr(calc): 2430.1815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 4.9e-006
Matches : 21/234 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							22
2	173.0921	87.0497			155.0815	78.0444	T	2360.1517	1180.5795	2343.1252	1172.0662	2342.1412	1171.5742	21
3	336.1554	168.5813			318.1448	159.5761	Y	2259.1040	1130.0557	2242.0775	1121.5424	2241.0935	1121.0504	20
4	437.2031	219.1052			419.1925	210.0999	T	2096.0407	1048.5240	2079.0142	1040.0107	2078.0301	1039.5187	19
5	**550.2871**	275.6472			532.2766	266.6419	L	1994.9930	998.0002	1977.9665	989.4869	1976.9825	988.9949	18
6	**664.3301**	332.6687	647.3035	324.1554	646.3195	323.6634	N	1881.9090	941.4581	1864.8824	932.9448	1863.8984	932.4528	17
7	761.3828	381.1951	744.3563	372.6818	743.3723	372.1898	P	1767.8660	884.4367	1750.8395	875.9234	1749.8555	875.4314	16
8	876.4098	438.7085	859.3832	430.1953	858.3992	429.7032	D	1670.8133	835.9103	1653.7867	827.3970	1652.8027	826.9050	15
9	933.4312	467.2193	916.4047	458.7060	915.4207	458.2140	G	1555.7863	778.3968	1538.7598	769.8835	1537.7758	769.3915	14
10	1034.4789	517.7431	1017.4524	509.2298	1016.4684	508.7378	T	1498.7649	749.8861	1481.7383	741.3728	1480.7543	740.8808	13
11	1147.5630	574.2851	1130.5364	565.7719	1129.5524	565.2798	I	1397.7172	699.3622	1380.6906	690.8490	1379.7066	690.3569	12
12	1284.6219	642.8146	1267.5953	634.3013	1266.6113	633.8093	H	1284.6331	642.8202	1267.6066	634.3069	1266.6226	633.8149	11
13	1383.6903	692.3488	1366.6638	683.8355	1365.6797	683.3435	V	1147.5742	574.2907	1130.5477	565.7775	1129.5636	565.2855	10
14	1496.7744	748.8908	1479.7478	740.3775	1478.7638	739.8855	L	1048.5058	524.7565	1031.4792	516.2433	1030.4952	515.7513	9
15	1610.8173	805.9123	1593.7907	797.3990	1592.8067	796.9070	N	935.4217	468.2145	918.3952	459.7012	917.4112	459.2092	8
16	1739.8599	870.4336	1722.8333	861.9203	1721.8493	861.4283	E	821.3788	411.1930	804.3523	402.6798	803.3682	402.1878	7
17	1840.9076	920.9574	1823.8810	912.4441	1822.8970	911.9521	T	692.3362	346.6717	675.3097	338.1585	674.3257	337.6665	6
18	2026.9869	1013.9971	2009.9603	1005.4838	2008.9763	1004.9918	W	591.2885	296.1479	574.2620	287.6346	573.2780	287.1426	5
19	2114.0189	1057.5131	2096.9924	1048.9998	2096.0083	1048.5078	S	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	4
20	2228.0618	1114.5346	2211.0353	1106.0213	2210.0513	1105.5293	N	318.1772	159.5922	301.1506	151.0790			3
21	2285.0833	1143.0453	2268.0568	1134.5320	2267.0727	1134.0400	G	204.1343	102.5708	187.1077	94.0575			2
22							K	147.1128	74.0600	130.0863	65.5468			1

AT5G58070.1





NCBI **BLAST** search of ATYTLNPDGTIHVLNETWSNGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.5	2430.1815	-0.0069	ATYTLNPDGTIHVLNETWSNGK
8.8	2430.1703	0.0043	SPLNESQAGGSIDAKTSEFAFFK
4.3	2430.1705	0.0041	GLSGDSLRKLPCYIMSSEMVR
0.9	2430.1737	0.0010	MEEDGSDWGGLAPEILINIISR
0.2	2430.1696	0.0050	VENQDAIDTSIVNMLGDPKEAR
0.1	2430.1717	0.0030	THTGRTGPGYAEEHQLFPASFK

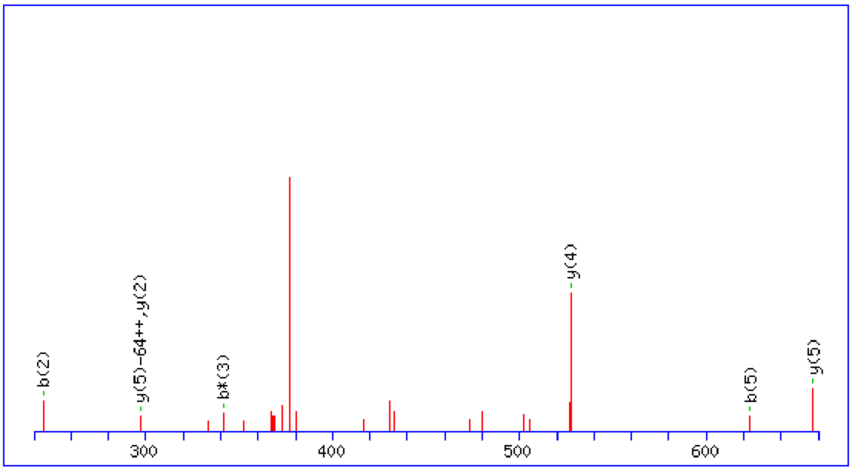
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IKLDMK**
Found in **AT5G58110.1** in **TAIR_Arabidopsis**, Symbols: | ATPase activator/ chaperone activator/ chaperone binding | chr5:23532501-23533705 FORWARD

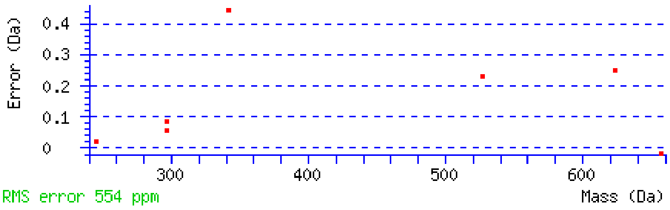
Match to Query 873: 770.408054 from(386.211303,2+) index(3723)
Title: Elution from: 36.078 to 36.078 scan no 4651 cid35.00 polarity:+
Data file D12h-3_1.mgf

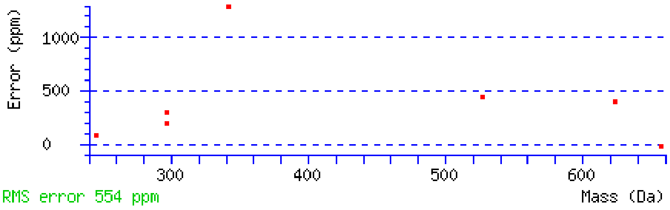
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 240 to 660 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.4072
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.039
Matches : 7/76 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0884	58.0478					I							6
2	***245.1774***	123.0923	227.1538	114.0805			K	***657.3334***	329.1703	639.3098	320.1586	639.3229	320.1651	5
3	359.2585	180.1329	341.2349	171.1211			L	***527.2444***	264.1258	509.2208	255.1140	509.2338	255.1205	4
4	475.2825	238.1449	457.2589	229.1331	457.2719	229.1396	D	413.1633	207.0853	395.1397	198.0735	395.1527	198.0800	3
5	***623.3149***	312.1611	605.2913	303.1493	605.3044	303.1558	M	***297.1393***	149.0733	279.1157	140.0615			2
6							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of IKLDMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.1	770.4072	0.0008	IKLDMK
23.0	770.4072	0.0008	LEMVKK

23.0	770.4072	0.0008	LKDLMK
23.0	770.4072	0.0008	LKDMLK
23.0	770.4072	0.0008	LKEMVK
12.6	770.4072	0.0008	KLVEMK
10.6	770.4072	0.0008	LMLKDK
10.0	770.4072	0.0008	MGVSLLK
10.0	770.4072	0.0008	MKDLIK
9.4	770.4072	0.0008	ELKMVK

AT5G58250.1

Mascot Search Results

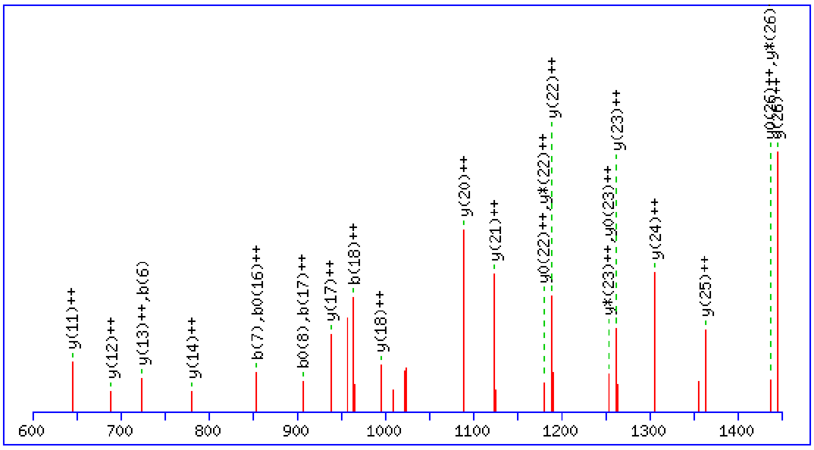
Peptide View

MS/MS Fragmentation of **VLYDSFEATSLDEALASNPTTLEFDKPK**
Found in **AT5G58250.1** in **TAIR_Arabidopsis**, Symbols: | similar to hypothetical protein [Vitis vinifera] (GB:CAN75840.1); contains domain PD020337 (PD020337) | chr5:23576784-23577598 FORWARD

Match to Query 10650: 3100.515846 from(1034.512558,3+) index(9685)
Title: Elution from: 93.469 to 93.469 scan no 13781 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

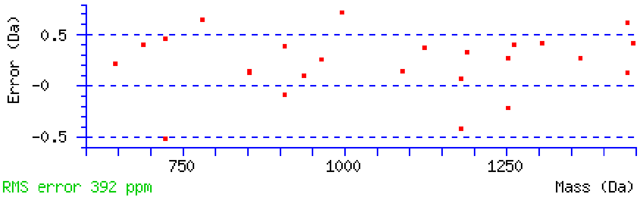
Or, Plot from 600 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

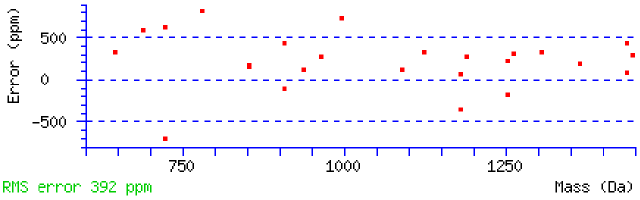


Monoisotopic mass of neutral peptide Mr(calc): 3100.5128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 96 **Expect:** 8e-010
Matches : 25/278 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							28
2	213.1598	107.0835					L	3002.4517	1501.7295	2985.4252	1493.2162	2984.4411	1492.7242	27
3	376.2231	188.6152					Y	2889.3676	1445.1875	2872.3411	1436.6742	2871.3571	1436.1822	26
4	491.2500	246.1287			473.2395	237.1234	D	2726.3043	1363.6558	2709.2778	1355.1425	2708.2937	1354.6505	25
5	578.2821	289.6447			560.2715	280.6394	S	2611.2774	1306.1423	2594.2508	1297.6290	2593.2668	1297.1370	24
6	**725.3505**	363.1789			707.3399	354.1736	F	2524.2453	1262.6263	2507.2188	1254.1130	2506.2348	1253.6210	23
7	**854.3931**	427.7002			836.3825	418.6949	E	2377.1769	1189.0921	2360.1504	1180.5788	2359.1664	1180.0868	22
8	925.4302	463.2187			907.4196	454.2134	A	2248.1343	1124.5708	2231.1078	1116.0575	2230.1238	1115.5655	21
9	1026.4779	513.7426			1008.4673	504.7373	T	2177.0972	1089.0522	2160.0707	1080.5390	2159.0867	1080.0470	20
10	1113.5099	557.2586			1095.4993	548.2533	S	2076.0495	1038.5284	2059.0230	1030.0151	2058.0390	1029.5231	19
11	1226.5939	613.8006			1208.5834	604.7953	L	1989.0175	995.0124	1971.9910	986.4991	1971.0069	986.0071	18
12	1341.6209	671.3141			1323.6103	662.3088	D	1875.9335	938.4704	1858.9069	929.9571	1857.9229	929.4651	17
13	1470.6635	735.8354			1452.6529	726.8301	E	1760.9065	880.9569	1743.8800	872.4436	1742.8959	871.9516	16
14	1541.7006	771.3539			1523.6900	762.3487	A	1631.8639	816.4356	1614.8374	807.9223	1613.8533	807.4303	15
15	1654.7847	827.8960			1636.7741	818.8907	L	1560.8268	780.9170	1543.8003	772.4038	1542.8162	771.9118	14
16	1725.8218	863.4145			1707.8112	854.4092	A	1447.7427	724.3750	1430.7162	715.8617	1429.7322	715.3697	13
17	1812.8538	**906.9305**			1794.8432	897.9253	S	1376.7056	688.8564	1359.6791	680.3432	1358.6951	679.8512	12
18	1926.8967	**963.9520**	1909.8702	955.4387	1908.8862	954.9467	N	1289.6736	645.3404	1272.6470	636.8272	1271.6630	636.3352	11
19	2023.9495	1012.4784	2006.9229	1003.9651	2005.9389	1003.4731	P	1175.6307	588.3190	1158.6041	579.8057	1157.6201	579.3137	10
20	2124.9972	1063.0022	2107.9706	1054.4889	2106.9866	1053.9969	T	1078.5779	539.7926	1061.5514	531.2793	1060.5673	530.7873	9
21	2226.0449	1113.5261	2209.0183	1105.0128	2208.0343	1104.5208	T	977.5302	489.2687	960.5037	480.7555	959.5197	480.2635	8
22	2339.1289	1170.0681	2322.1024	1161.5548	2321.1183	1161.0628	L	876.4825	438.7449	859.4560	430.2316	858.4720	429.7396	7
23	2468.1715	1234.5894	2451.1450	1226.0761	2450.1609	1225.5841	E	763.3985	382.2029	746.3719	373.6896	745.3879	373.1976	6
24	2615.2399	1308.1236	2598.2134	1299.6103	2597.2294	1299.1183	F	634.3559	317.6816	617.3293	309.1683	616.3453	308.6763	5

25	2730.2669	1365.6371	2713.2403	1357.1238	2712.2563	1356.6318	**D**	487.2875	244.1474	470.2609	235.6341	469.2769	235.1421	**4**
26	2858.3618	1429.6846	2841.3353	1421.1713	2840.3513	1420.6793	**K**	372.2605	186.6339	355.2340	178.1206			**3**
27	2955.4146	1478.2109	2938.3880	1469.6977	2937.4040	1469.2057	**P**	244.1656	122.5864	227.1390	114.0731			**2**
28							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VLYDSFEATSLDEALASNPTTLEFDKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.5	3100.5128	0.0030	VLYDSFEATSLDEALASNPTTLEFDKPK
2.4	3100.5070	0.0089	WVQELQAQGNPNMVMALAGNKSDLLDAR
1.8	3100.5142	0.0017	VLKPVGKGYLRYDFFDDGLPEDDEASR
1.3	3100.5175	-0.0017	VALELTRSDYVEAEEALVDMKNWFTR
0.3	3100.5070	0.0089	NNMSMSLVDVSNPDKNNPRLWENIAVK

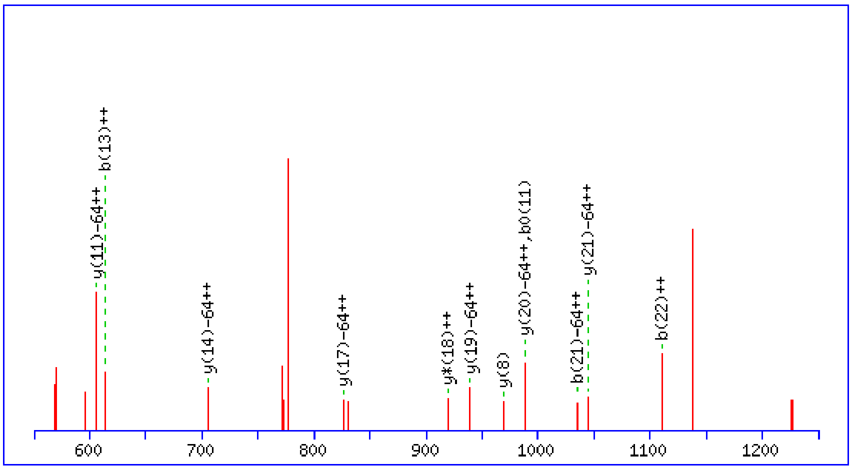
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILVSHSVGGGSMTAAMCLFPSK**
Found in **AT5G58310.1** in **TAIR_Arabidopsis**, Symbols: | hydrolase, alpha/beta fold family protein | chr5:23592353-23593233 REVERSE

Match to Query 10498: 2364.168969 from(789.063599,3+) index(8225)
Title: Elution from: 71.655 to 71.655 scan no 10745 cid35.00 polarity:+
Data file D1d-3_1.mgf

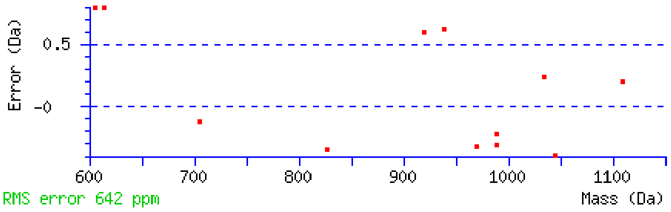
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 550 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

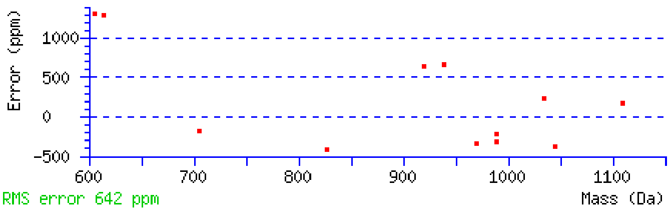


Monoisotopic mass of neutral peptide Mr(calc): 2364.1640
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M17 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.015
Matches : 12/330 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							23
2	213.1598	107.0835			I	2202.1046	1101.5559	2185.0780	1093.0427	2184.0940	1092.5506	22
3	326.2438	163.6255			L	2089.0205	1045.0139	2071.9940	1036.5006	2071.0099	1036.0086	21
4	425.3122	213.1598			V	1975.9364	988.4719	1958.9099	979.9586	1957.9259	979.4666	20
5	512.3443	256.6758	494.3337	247.6705	S	1876.8680	938.9377	1859.8415	930.4244	1858.8575	929.9324	19
6	649.4032	325.2052	631.3926	316.1999	H	1789.8360	895.4216	1772.8095	886.9084	1771.8254	886.4164	18
7	736.4352	368.7212	718.4246	359.7160	S	1652.7771	826.8922	1635.7505	818.3789	1634.7665	817.8869	17
8	835.5036	418.2554	817.4930	409.2502	V	1565.7451	783.3762	1548.7185	774.8629	1547.7345	774.3709	16
9	892.5251	446.7662	874.5145	437.7609	G	1466.6767	733.8420	1449.6501	725.3287	1448.6661	724.8367	15
10	949.5465	475.2769	931.5360	466.2716	G	1409.6552	705.3312	1392.6286	696.8180	1391.6446	696.3259	14
11	1006.5680	503.7876	988.5574	494.7824	G	1352.6337	676.8205	1335.6072	668.3072	1334.6232	667.8152	13
12	1093.6000	547.3037	1075.5895	538.2984	S	1295.6123	648.3098	1278.5857	639.7965	1277.6017	639.3045	12
13	1224.6405	**612.8239**	1206.6300	603.8186	M	1208.5802	604.7938	1191.5537	596.2805	1190.5697	595.7885	11
14	1325.6882	663.3477	1307.6776	654.3425	T	1077.5397	539.2735	1060.5132	530.7602	1059.5292	530.2682	10
15	1396.7253	698.8663	1378.7147	689.8610	A	976.4921	488.7497	959.4655	480.2364	958.4815	479.7444	9
16	1467.7624	734.3849	1449.7519	725.3796	A	905.4550	453.2311	888.4284	444.7178	887.4444	444.2258	8
17	1550.7995	775.9034	1532.7890	766.8981	M	834.4178	417.7126	817.3913	409.1993	816.4073	408.7073	7
18	1710.8302	855.9187	1692.8196	846.9135	C	751.3807	376.1940	734.3542	367.6807	733.3702	367.1887	6
19	1823.9143	912.4608	1805.9037	903.4555	L	591.3501	296.1787	574.3235	287.6654	573.3395	287.1734	5
20	1970.9827	985.9950	1952.9721	976.9897	F	478.2660	239.6366	461.2395	231.1234	460.2554	230.6314	4
21	2068.0354	**1034.5214**	2050.0249	1025.5161	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3

22	2155.0675	1078.0374	2137.0569	1069.0321	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
23					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VILVSHSVGGGSMTAAMCLFPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
24.0	2364.1640	0.0050	VILVSHSVGGGSMTAAMCLFPSK	Oxidation M17 73.94%
23.7	2364.1671	0.0019	KLTESPGLINSSPYEDGWMIK	
19.4	2364.1640	0.0050	VILVSHSVGGGSMTAAMCLFPSK	Oxidation M13 26.06%
5.2	2364.1631	0.0059	SKDIMSDIPTFSAENLQNNLK	
3.1	2364.1752	-0.0062	HMMLLADVMTYRGEVLGIQR	
3.1	2364.1752	-0.0062	HMMLLADVMTYRGEVLGIQR	
2.7	2364.1672	0.0018	VTDMAFFAEDVHLLASVSLDGK	
2.7	2364.1752	-0.0062	HMMLLADVMTYRGEVLGIQR	
0.8	2364.1710	-0.0020	EGDSYSSWLITEAPGSIAAVRR	
0.4	2364.1671	0.0019	LPNAPEMEIYSLYGVGIPTER	

Mascot: http://www.matrixscience.com/

AT5G58330.1

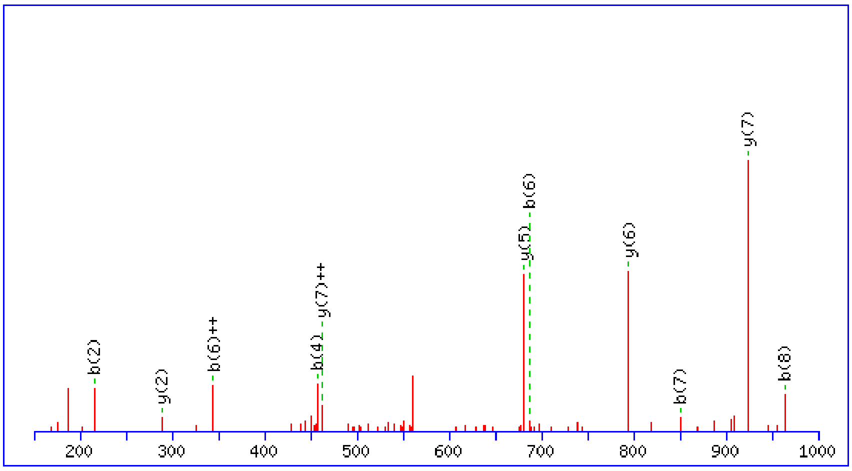
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVEIDDYLR**
Found in **AT5G58330.1** in **TAIR_Arabidopsis**, Symbols: | malate dehydrogenase (NADP), chloroplast, putative | chr5:23597236-23599513 REVERSE

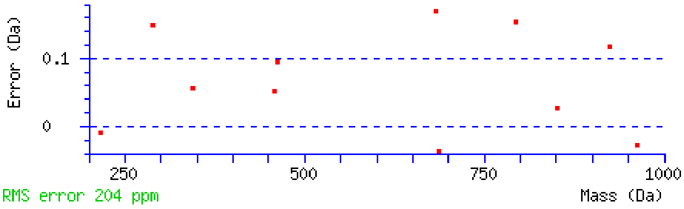
Match to Query 3214: 1136.537068 from(569.275810,2+) index(6454)
Title: Elution from: 60.594 to 60.594 scan no 8508 cid35.00 polarity:+
Data file D1d-2_2.mgf

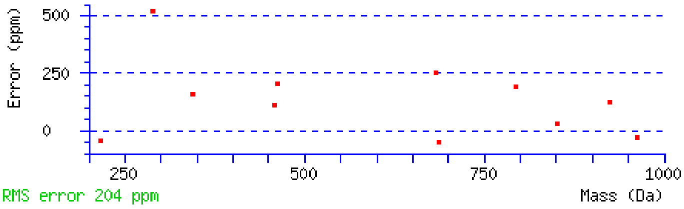
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1136.5350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 5.3e-005
Matches : 12/74 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	***215.1026***	108.0550	197.0921	99.0497	V	1022.5153	511.7613	1005.4888	503.2480	1004.5047	502.7560	8
3	***344.1452***	172.5763	326.1347	163.5710	E	**923.4469**	462.2271	906.4203	453.7138	905.4363	453.2218	7
4	***457.2293***	229.1183	439.2187	220.1130	I	**794.4043**	397.7058	777.3777	389.1925	776.3937	388.7005	6
5	572.2562	286.6318	554.2457	277.6265	D	**681.3202**	341.1638	664.2937	332.6505	663.3097	332.1585	5
6	***687.2832***	344.1452	669.2726	335.1399	D	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
7	***850.3465***	425.6769	832.3359	416.6716	Y	451.2663	226.1368	434.2398	217.6235			3
8	***963.4306***	482.2189	945.4200	473.2136	L	**288.2030**	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DVEIDDYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G58330.1

48.3	1136.5350	0.0021	DVEIDDYLR
9.6	1136.5383	-0.0012	ETIMEETLR
2.0	1136.5403	-0.0032	HEYFSWLR

AT5G58390.1

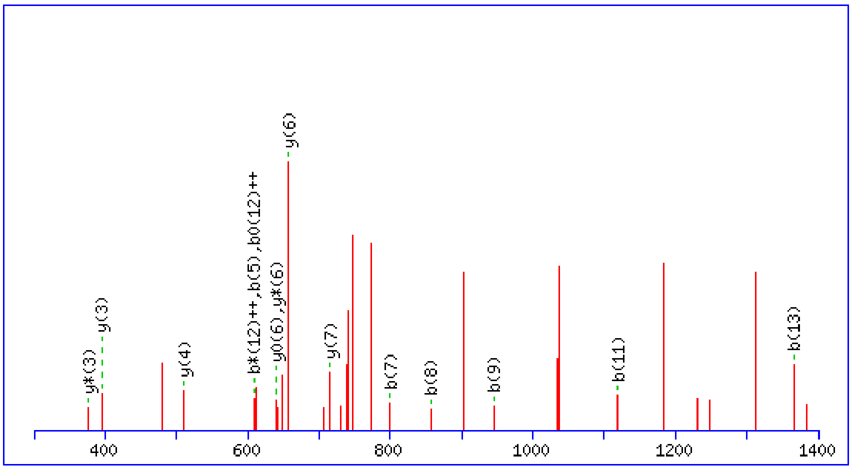
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNCPATSGSGDNKK**
Found in **AT5G58390.1** in **TAIR_Arabidopsis**, Symbols: | peroxidase, putative | chr5:23616981-23618470 REVERSE

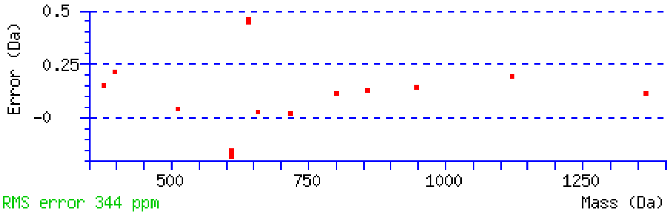
Match to Query 6496: 1512.620544 from(757.317548,2+) index(3060)
Title: Elution from: 29.836 to 29.836 scan no 3793 cid35.00 polarity:+
Data file C7-3_2.mgf

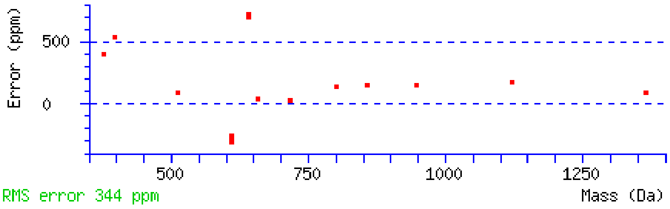
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1512.6244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.01
Matches : 15/140 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							14
2	277.1335	139.0704	259.1099	130.0586			N	1353.5424	677.2748	1335.5188	668.2630	1335.5318	668.2695	13
3	439.1582	220.0828	421.1347	211.0710			C	1237.5054	619.2563	1219.4818	610.2445	1219.4948	610.2510	12
4	537.2080	269.1077	519.1845	260.0959			P	1075.4807	538.2440	1057.4571	529.2322	1057.4701	529.2387	11
5	***609.2422***	305.1247	591.2186	296.1129			A	977.4309	489.2191	959.4073	480.2073	959.4203	480.2138	10
6	711.2869	356.1471	693.2633	347.1353	693.2763	347.1418	T	905.3967	453.2020	887.3731	444.1902	887.3862	444.1967	9
7	***799.3160***	400.1616	781.2924	391.1498	781.3054	391.1563	S	803.3520	402.1796	785.3284	393.1678	785.3414	393.1744	8
8	***857.3345***	429.1709	839.3109	420.1591	839.3239	420.1656	G	**715.3229**	358.1651	697.2994	349.1533	697.3124	349.1598	7
9	***945.3635***	473.1854	927.3399	464.1736	927.3530	464.1801	S	**657.3044**	329.1559	639.2809	320.1441	639.2939	320.1506	6
10	1003.3820	502.1947	985.3584	493.1829	985.3715	493.1894	G	569.2754	285.1413	551.2518	276.1295	551.2648	276.1360	5
11	***1119.4060***	560.2066	1101.3824	551.1948	1101.3954	551.2014	D	**511.2569**	256.1321	493.2333	247.1203	493.2463	247.1268	4
12	1235.4430	618.2251	1217.4194	609.2133	1217.4324	609.2199	N	**395.2329**	198.1201	377.2093	189.1083			3
13	***1365.5320***	683.2697	1347.5085	674.2579	1347.5215	674.2644	K	279.1959	140.1016	261.1723	131.0898			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RNCPATSGSGDNKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G58390.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.1	1512.6244	-0.0038	RNCPATSGSGDNKK
20.2	1512.6212	-0.0007	EESEQVMFGALDK
6.0	1512.6217	-0.0011	EQTCSTGRDIAEK
0.9	1512.6217	-0.0011	MAQEADSRSEGSVK

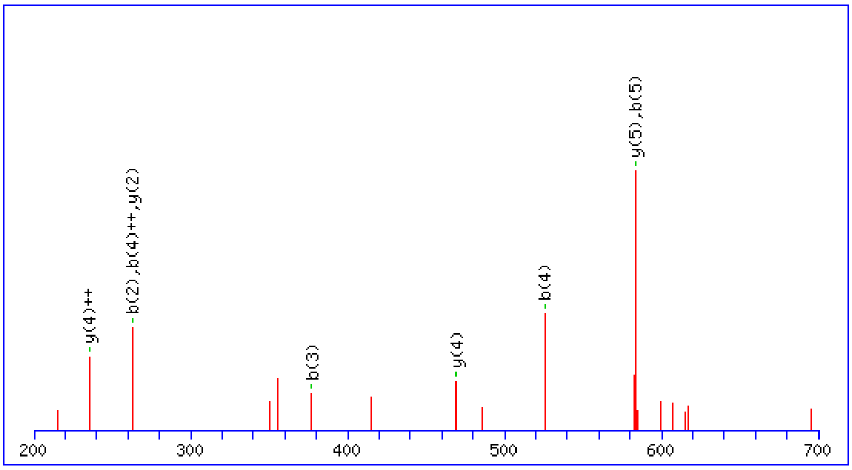
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFLMGLK**
Found in **AT5G58900.1** in **TAIR_Arabidopsis**, Symbols: | myb family transcription factor | chr5:23800501-23801893 REVERSE

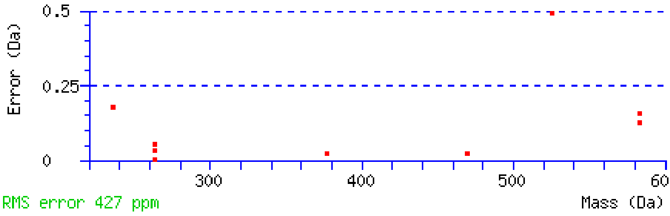
Match to Query 1251: 844.459252 from(423.236902,2+) index(4999)
Title: Elution from: 46.198 to 46.198 scan no 6277 cid35.00 polarity:+
Data file D6h-2_2.mgf

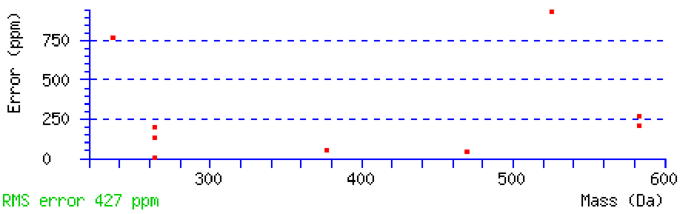
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 844.4593
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21  Expect: 0.033
Matches : 9/54 fragment ions using 14 most intense peaks   (help)
```

#	b	b++	Seq.	y	y++	y*	y*++	#
1	115.0884	58.0478	L					7
2	***263.1538***	132.0805	F	731.3855	366.1964	713.3619	357.1846	6
3	***377.2349***	189.1211	L	**583.3200**	292.1636	565.2964	283.1518	5
4	***525.2674***	263.1373	M	**469.2389**	235.1231	451.2153	226.1113	4
5	***583.2859***	292.1466	G	321.2065	161.1069	303.1829	152.0951	3
6	697.3670	349.1871	L	**263.1880**	132.0976	245.1644	123.0858	2
7			K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of LFLMGLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.2	844.4593	-0.0000	LFLMGLK
13.2	844.4593	-0.0000	MIGYLLK

AT5G58900.1

6.5	844.4593	-0.0000	ILFMLGK
5.2	844.4568	0.0025	RTLRQR
5.2	844.4570	0.0022	SMTKILK
1.3	844.4570	0.0022	STKIMLK
0.6	844.4593	-0.0000	VFLMSLK
0.5	844.4570	0.0022	KVTTMIK
0.5	844.4597	-0.0005	KMSLAKR

AT5G59880.1

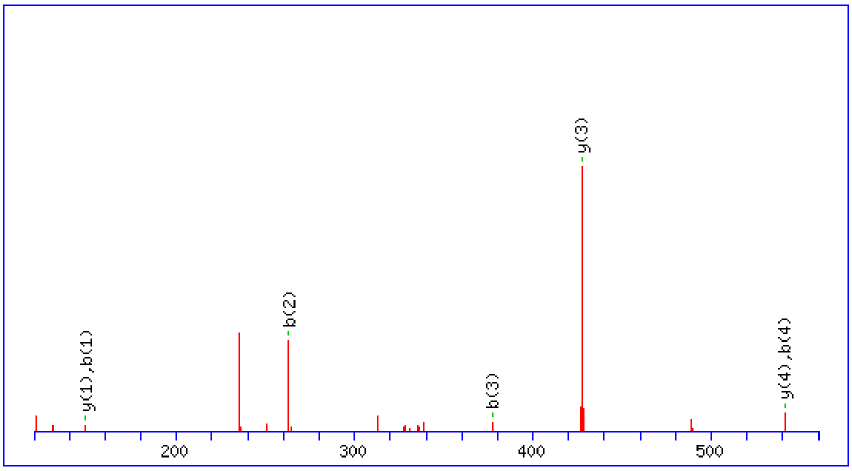
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FIIYK**
Found in **AT5G59880.1** in **TAIR_Arabidopsis**, Symbols: ADF3 | ADF3 (ACTIN DEPOLYMERIZING FACTOR 3); actin binding | chr5:24137608-24138854 FORWARD

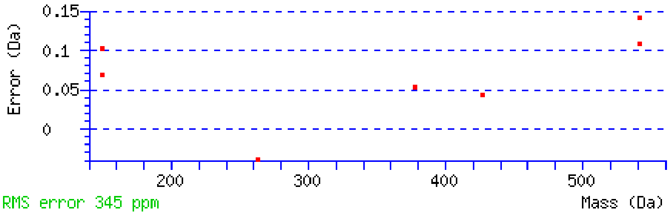
Match to Query 577: 688.387170 from(345.200861,2+) index(3217)
Title: Elution from: 30.932 to 30.932 scan no 3981 cid35.00 polarity:+
Data file C7-3_2.mgf

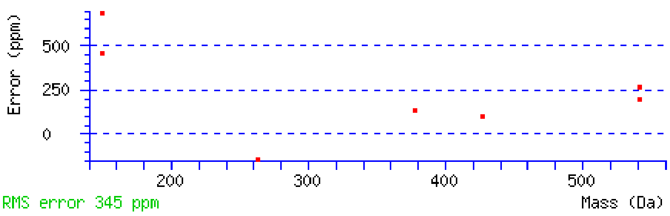
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 560 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 688.3876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0025
Matches : 7/24 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	***149.0727***	75.0400	F					5
2	***263.1538***	132.0805	I	**541.3294**	271.1684	523.3059	262.1566	4
3	***377.2349***	189.1211	I	**427.2483**	214.1278	409.2248	205.1160	3
4	***541.2953***	271.1513	Y	313.1672	157.0873	295.1437	148.0755	2
5			K	**149.1069**	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of FIIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.4	688.3876	-0.0004	FIIYK
31.4	688.3876	-0.0004	FLIYK
31.4	688.3876	-0.0004	FLLYK
31.4	688.3876	-0.0004	FYIIK

AT5G59880.1

29.6	688.3876	-0.0004	FLYLK
20.9	688.3876	-0.0004	IFLYK
20.9	688.3876	-0.0004	YFIIK
11.1	688.3854	0.0018	IDPPIK
11.1	688.3880	-0.0009	RTFKK
11.1	688.3880	-0.0009	TRKFK

AT5G59950.1

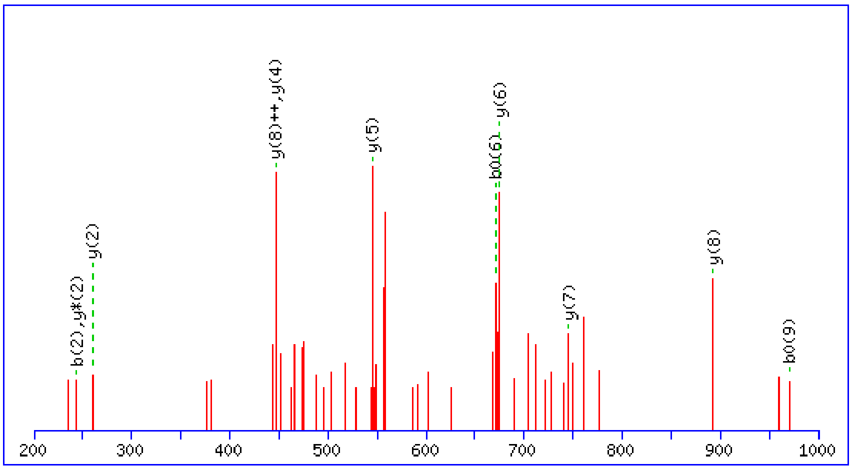
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELFAEVGELK**
Found in **AT5G59950.1** in **TAIR_Arabidopsis**, Symbols: | RNA and export factor-binding protein, putative | chr5:24157461-24158730 FORWARD

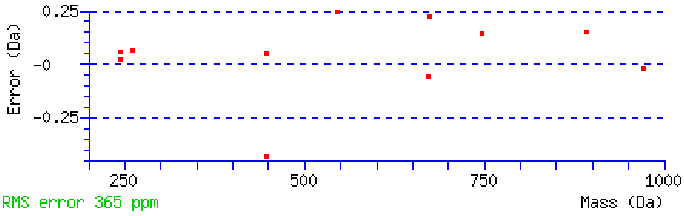
Match to Query 3940: 1133.595666 from(567.805109,2+) index(7088)
Title: Elution from: 61.484 to 61.484 scan no 9066 cid35.00 polarity:+
Data file D6h-1_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

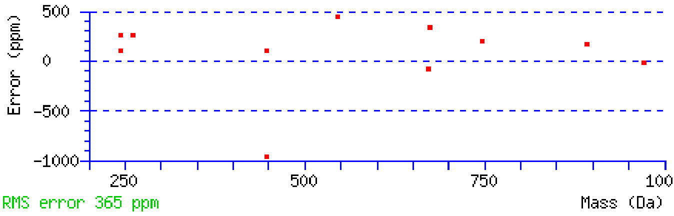


Monoisotopic mass of neutral peptide Mr(calc): 1133.5968
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00061
Matches : 11/86 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	243.1339	122.0706	225.1234	113.0653	L	1005.5615	503.2844	988.5350	494.7711	987.5510	494.2791	9
3	390.2023	195.6048	372.1918	186.5995	F	***892.4775***	446.7424	875.4509	438.2291	874.4669	437.7371	8
4	461.2395	231.1234	443.2289	222.1181	A	***745.4090***	373.2082	728.3825	364.6949	727.3985	364.2029	7
5	590.2821	295.6447	572.2715	286.6394	E	***674.3719***	337.6896	657.3454	329.1763	656.3614	328.6843	6
6	689.3505	345.1789	671.3399	336.1736	V	***545.3293***	273.1683	528.3028	264.6550	527.3188	264.1630	5
7	746.3719	373.6896	728.3614	364.6843	G	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
8	875.4145	438.2109	857.4040	429.2056	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	988.4986	494.7529	970.4880	485.7477	L	***260.1969***	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 365 ppm



RMS error 365 ppm

NCBI **BLAST** search of ELFAEVGELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G59950.1

39.5	1133.5968	-0.0012	ELFAEVGELK
9.7	1133.5968	-0.0012	EIGFLEGEIK
1.2	1133.5968	-0.0012	IYGLELSDPK

AT5G59980.1

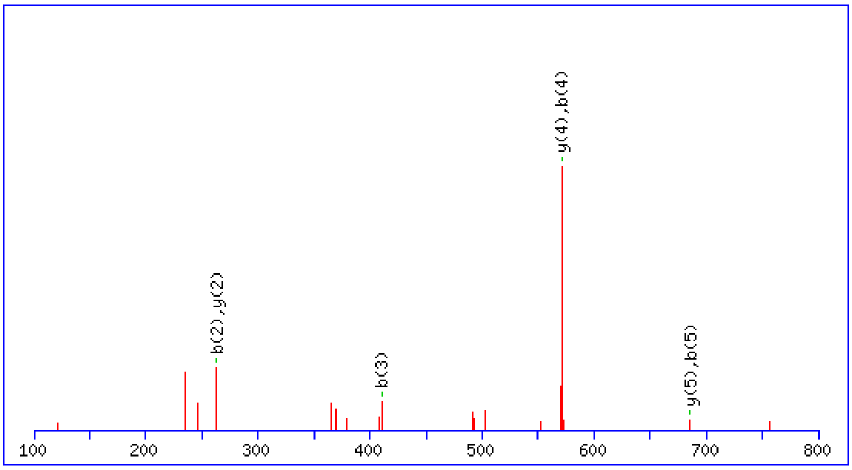
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLFRLK**
Found in **AT5G59980.1** in **TAIR_Arabidopsis**, Symbols: | RNase P subunit p30 family protein | chr5:24164433-24166618 FORWARD

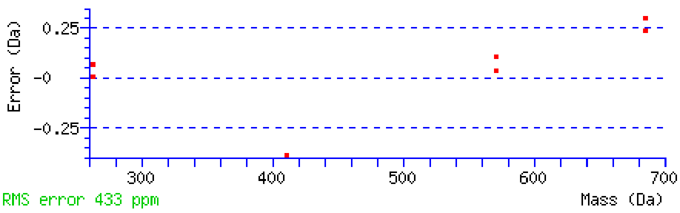
Match to Query 1200: 832.449744 from(417.232148,2+) index(6744)
Title: Elution from: 59.643 to 59.643 scan no 8726 cid35.00 polarity:+
Data file 0-1_3.mgf

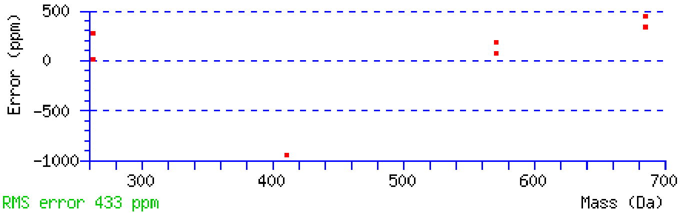
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 832.4489
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 0.0017
Matches : 7/48 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	149.0397	75.0235			M					6
2	***263.1208***	132.0640			L	**685.4238**	343.2155	667.4002	334.2037	5
3	***411.1863***	206.0968			F	**571.3427**	286.1750	553.3191	277.1632	4
4	***571.2755***	286.1414	553.2519	277.1296	R	423.2772	212.1422	405.2536	203.1305	3
5	***685.3566***	343.1819	667.3330	334.1702	L	**263.1880**	132.0976	245.1644	123.0858	2
6					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of MLFRLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.2	832.4489	0.0008	FLRMLK
28.2	832.4489	0.0008	IMFRLK
28.2	832.4489	0.0008	MLFRLK

AT5G59980.1

15.8	832.4489	0.0008	LMFLRK
9.9	832.4489	0.0008	IMRYLK
3.9	832.4489	0.0008	LRMYLK
0.3	832.4489	0.0008	MLYIRK

Mascot: http://www.matrixscience.com/

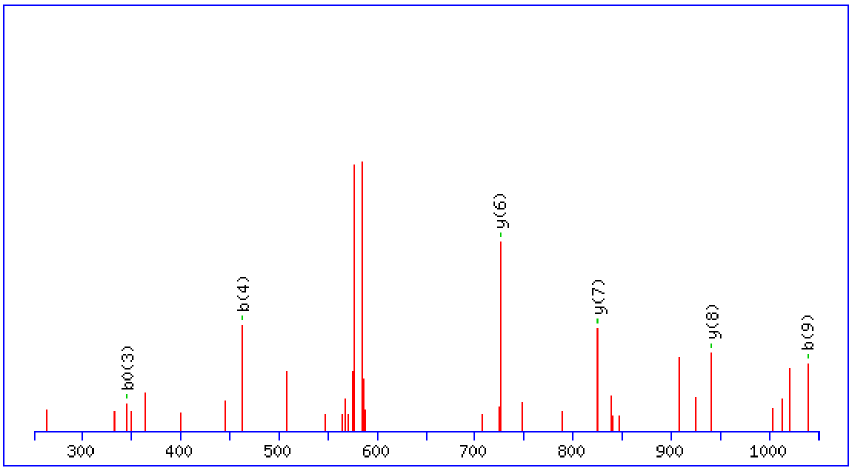
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEDVVDEKVK**
Found in **AT5G60030.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G75335.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN66187.1) | chr5:24189308-24190186 REVERSE

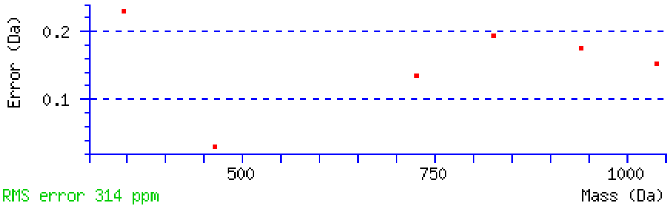
Match to Query 4084: 1186.537262 from(594.275907,2+) index(1343)
Title: Elution from: 20.815 to 20.815 scan no 1917 cid35.00 polarity:+
Data file D6h-2_1.mgf

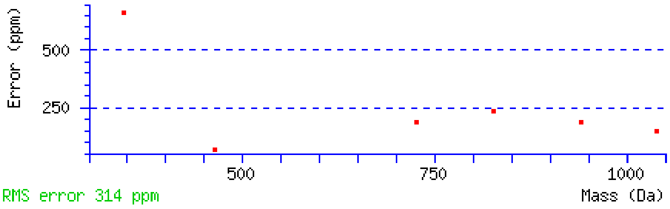
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1186.5361
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 0.023
Matches : 6/88 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							10
2	247.0709	124.0391			229.0603	115.0338	E	1071.5195	536.2634	1053.4959	527.2516	1053.5089	527.2581	9
3	363.0949	182.0511			345.0843	173.0458	D	***941.4798***	471.2436	923.4563	462.2318	923.4693	462.2383	8
4	***463.1603***	232.0838			445.1497	223.0785	V	***825.4559***	413.2316	807.4323	404.2198	807.4453	404.2263	7
5	563.2258	282.1165			545.2152	273.1112	V	***725.3904***	363.1988	707.3668	354.1871	707.3798	354.1936	6
6	679.2497	340.1285			661.2392	331.1232	D	625.3250	313.1661	607.3014	304.1543	607.3144	304.1608	5
7	809.2894	405.1483			791.2788	396.1430	E	509.3010	255.1541	491.2774	246.1423	491.2904	246.1488	4
8	939.3784	470.1928	921.3548	461.1810	921.3678	461.1876	K	379.2614	190.1343	361.2378	181.1225			3
9	***1039.4438***	520.2256	1021.4203	511.2138	1021.4333	511.2203	V	249.1723	125.0898	231.1487	116.0780			2
10							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DEDVVDEKVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G60030.1

Score	Mr(calc)	Delta	Sequence
22.9	1186.5361	0.0011	DEDVVDEKVK
9.8	1186.5388	-0.0016	NVENGDNVAIK
9.4	1186.5397	-0.0024	MVEQCHKLK
9.2	1186.5370	0.0002	ISASMPDVPMK
7.5	1186.5368	0.0005	ESPRQHRMK
7.5	1186.5341	0.0032	EVISRDGHMK
6.7	1186.5388	-0.0016	EDVDLAVNAAR
4.0	1186.5341	0.0032	CTPVPRNLNT
1.3	1186.5388	-0.0016	QKTSDTEHVK
0.9	1186.5370	0.0002	MSPVEPAGIMK

AT5G60040.1

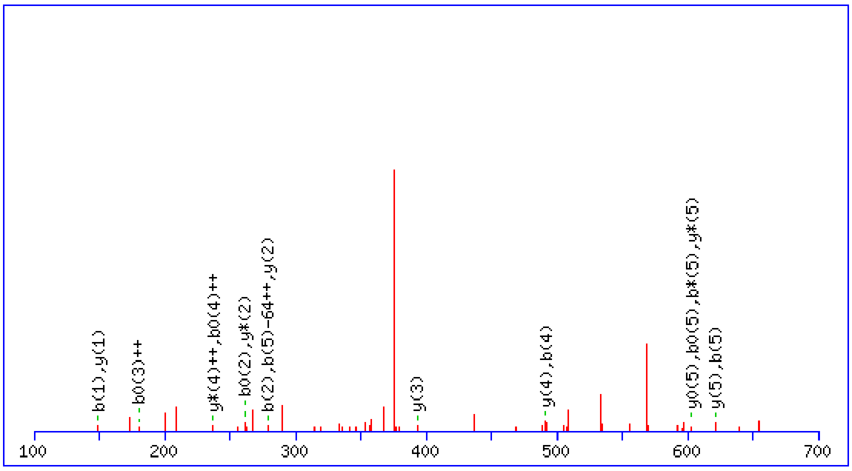
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEPLKK**
Found in **AT5G60040.1** in **TAIR_Arabidopsis**, Symbols: NRPC1 | NRPC1 (nuclear RNA polymerase C 1); DNA binding / DNA-directed RNA polymerase | chr5:24190816-24200495 FORWARD

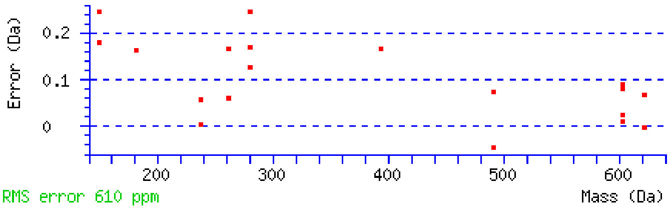
Match to Query 887: 768.393310 from(385.203931,2+) index(438)
Title: Elution from: 10.222 to 10.222 scan no 714 cid35.00 polarity:+
Data file C7-3_1.mgf

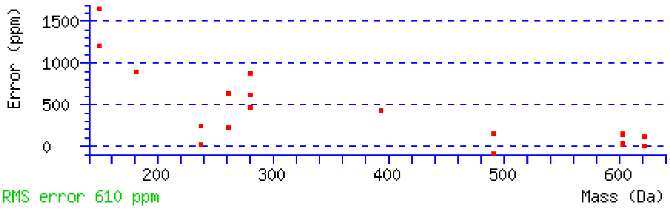
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 768.3916
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21  Expect: 0.04
Matches : 19/62 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**149.0397**	75.0235					**M**							**6**
2	**279.0793**	140.0433			261.0688	131.0380	**E**	***621.3664***	311.1869	603.3428	302.1751	603.3559	302.1816	**5**
3	377.1291	189.0682			359.1186	180.0629	**P**	***491.3268***	246.1670	473.3032	237.1552			**4**
4	**491.2102**	246.1088			473.1997	237.1035	**L**	***393.2770***	197.1421	375.2534	188.1303			**3**
5	**621.2993**	311.1533	603.2757	302.1415	603.2887	302.1480	**K**	***279.1959***	140.1016	261.1723	131.0898			**2**
6							**K**	***149.1069***	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of MEPLKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.5	768.3916	0.0017	MEPLKK
19.6	768.3916	0.0017	MLKPEK

AT5G60040.1

19.6	768.3916	0.0017	EMILQK
19.6	768.3916	0.0017	EMLIQK
18.6	768.3916	0.0017	KMLPEK
11.7	768.3916	0.0017	EIMIAGK
11.7	768.3916	0.0017	LLMPGSK
10.8	768.3943	-0.0010	MKKHSK
10.3	768.3916	0.0017	MLPEKK
9.6	768.3943	-0.0010	MKHKAK

AT5G60050.1

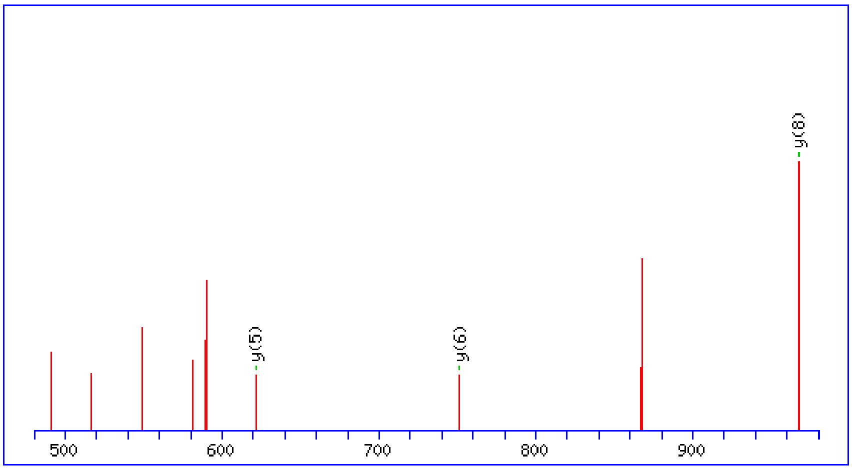
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVLTEPDEPR**
Found in **AT5G60050.1** in **TAIR_Arabidopsis**, Symbols: | PRLI-interacting factor-related | chr5:24200906-24202490 REVERSE

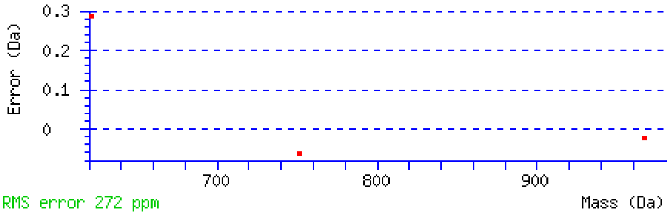
Match to Query 4182: 1196.545964 from(599.280258,2+) index(4273)
Title: Elution from: 39.396 to 39.396 scan no 5352 cid35.00 polarity:+
Data file C7-2_2.mgf

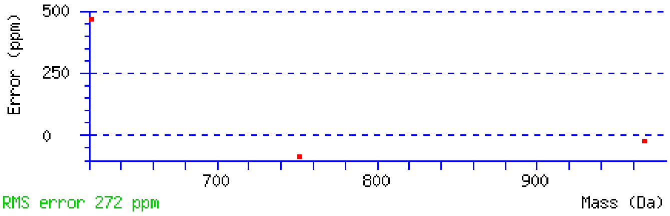
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 480 to 980 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1196.5465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 0.046
Matches : 3/98 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							10
2	231.1254	116.0663	213.1018	107.0545			V	1067.5012	534.2542	1049.4776	525.2424	1049.4906	525.2489	9
3	345.2065	173.1069	327.1829	164.0951			L	***967.4357***	484.2215	949.4122	475.2097	949.4252	475.2162	8
4	447.2512	224.1292	429.2276	215.1174	429.2406	215.1239	T	853.3546	427.1810	835.3311	418.1692	835.3441	418.1757	7
5	577.2908	289.1490	559.2672	280.1373	559.2802	280.1438	E	***751.3099***	376.1586	733.2863	367.1468	733.2994	367.1533	6
6	675.3406	338.1739	657.3170	329.1622	657.3300	329.1687	P	***621.2703***	311.1388	603.2467	302.1270	603.2597	302.1335	5
7	791.3646	396.1859	773.3410	387.1741	773.3540	387.1807	D	523.2205	262.1139	505.1969	253.1021	505.2099	253.1086	4
8	921.4042	461.2057	903.3806	452.1940	903.3937	452.2005	E	407.1965	204.1019	389.1729	195.0901	389.1860	195.0966	3
9	1019.4540	510.2306	1001.4304	501.2189	1001.4435	501.2254	P	277.1569	139.0821	259.1333	130.0703			2
10							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of QVLTEPDEPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G60050.1

20.8	1196.5465	-0.0006	QVLTEPDEPR
19.9	1196.5465	-0.0006	TLLDEHVNDK
0.7	1196.5441	0.0019	GCHVFPPEIK

AT5G60600.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLFDLQEISAEIR**
Found in **AT5G60600.1** in **TAIR_Arabidopsis**, Symbols: ISPG, CSB3, CLB4, GcpE | GcpE (CHLOROPLAST BIOGENESIS 4); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | chr5:24376673-24380500 FORWARD

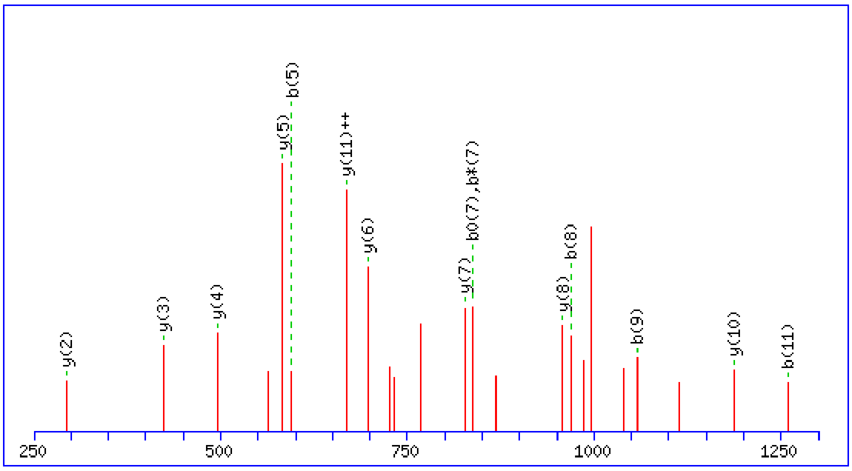
Match to Query 6796: 1550.749302 from(776.381927,2+) index(10033)
Title: Elution from: 92.940 to 92.940 scan no 14016 cid35.00 polarity:+
Data file D12h-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1300 Da Full range

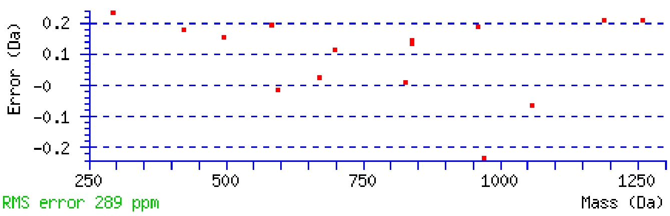
Label all possible matches ○ Label matches used for scoring ●

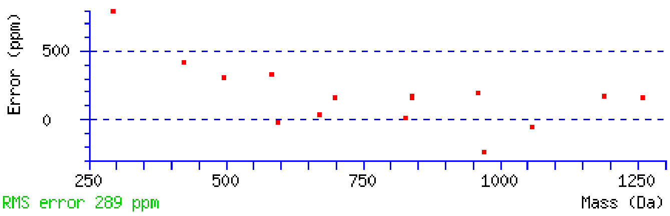
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1550.7534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 9e-007
Matches : 15/130 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	103.0520	52.0296			85.0414	43.0244	T							13
2	217.1331	109.0702			199.1225	100.0649	L	1449.7160	725.3617	1431.6924	716.3499	1431.7055	716.3564	12
3	365.1985	183.1029			347.1880	174.0976	F	1335.6349	668.3211	1317.6113	659.3093	1317.6244	659.3158	11
4	481.2225	241.1149			463.2120	232.1096	D	***1187.5695***	594.2884	1169.5459	585.2766	1169.5589	585.2831	10
5	**595.3036**	298.1554			577.2930	289.1502	L	1071.5455	536.2764	1053.5219	527.2646	1053.5349	527.2711	9
6	725.3563	363.1818	707.3327	354.1700	707.3457	354.1765	Q	***957.4644***	479.2358	939.4408	470.2240	939.4538	470.2306	8
7	855.3959	428.2016	837.3723	419.1898	837.3853	419.1963	E	***827.4118***	414.2095	809.3882	405.1977	809.4012	405.2042	7
8	**969.4770**	485.2421	951.4534	476.2303	951.4664	476.2368	I	***697.3721***	349.1897	679.3485	340.1779	679.3616	340.1844	6
9	**1057.5061**	529.2567	1039.4825	520.2449	1039.4955	520.2514	S	***583.2910***	292.1492	565.2674	283.1374	565.2805	283.1439	5
10	1129.5402	565.2737	1111.5166	556.2619	1111.5296	556.2685	A	***495.2620***	248.1346	477.2384	239.1228	477.2514	239.1293	4
11	**1259.5798**	630.2936	1241.5562	621.2818	1241.5693	621.2883	E	***423.2278***	212.1175	405.2042	203.1058	405.2173	203.1123	3
12	1373.6609	687.3341	1355.6373	678.3223	1355.6504	678.3288	I	***293.1882***	147.0977	275.1646	138.0859			2
13							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of TLFDLQEISAEIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G60600.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.6	1550.7534	-0.0041	TLFDLQEISAEIR
7.6	1550.7465	0.0028	EKIEAMELEIRR
6.8	1550.7487	0.0006	ALQEKFPACSIAAK
6.6	1550.7487	0.0006	MDILFAQIQADLR
5.0	1550.7465	0.0028	MGKISPLTGSSGEIR
1.2	1550.7487	0.0006	LKPVVSFDCAEIR
0.8	1550.7491	0.0002	MSTAAAARPVAGTGLR
0.6	1550.7539	-0.0046	QNSRVSSQVLVDAK
0.2	1550.7512	-0.0019	TDNSEALSKLEKAK
0.2	1550.7521	-0.0028	SMVKMGNISPLTGAK

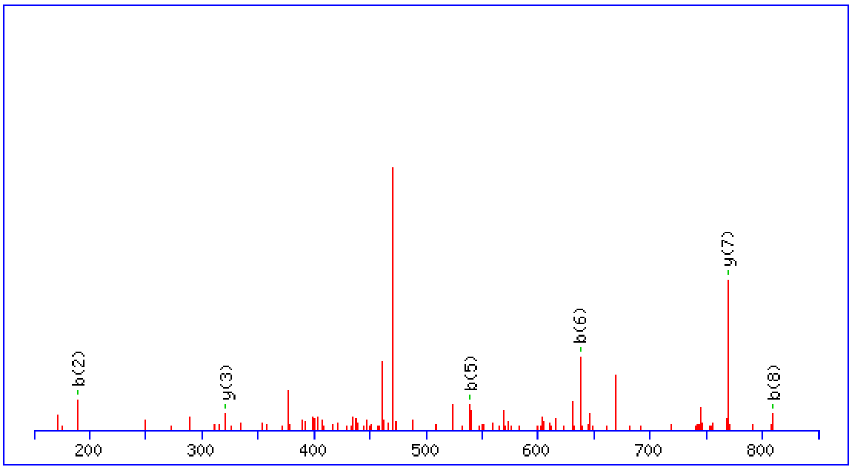
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANGCKPGIK**
Found in **AT5G60960.1** in **TAIR_Arabidopsis**, Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:24545649-24547214 REVERSE

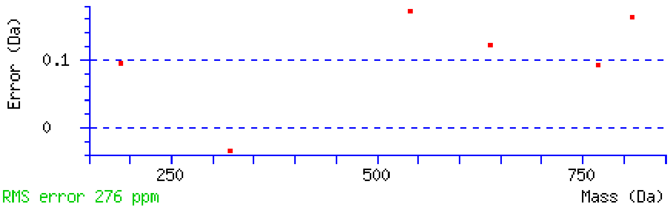
Match to Query 2038: 956.455150 from(479.234851,2+) index(3002)
Title: Elution from: 30.037 to 30.037 scan no 3749 cid35.00 polarity:+
Data file D6h-3_2.mgf

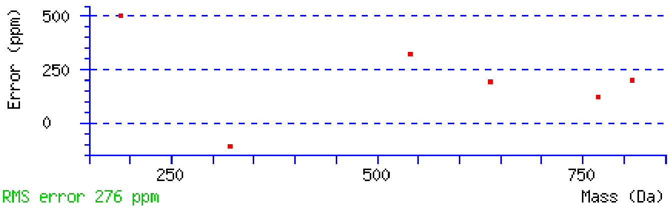
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 956.4524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0014
Matches : 6/62 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	73.0414	37.0244			A					9
2	***189.0784***	95.0428	171.0548	86.0311	N	885.4255	443.2164	867.4019	434.2046	8
3	247.0969	124.0521	229.0733	115.0403	G	**769.3885**	385.1979	751.3649	376.1861	7
4	409.1216	205.0645	391.0981	196.0527	C	711.3700	356.1886	693.3464	347.1769	6
5	***539.2107***	270.1090	521.1871	261.0972	K	549.3453	275.1763	531.3217	266.1645	5
6	***637.2605***	319.1339	619.2369	310.1221	P	419.2563	210.1318	401.2327	201.1200	4
7	695.2790	348.1431	677.2554	339.1313	G	**321.2065**	161.1069	303.1829	152.0951	3
8	***809.3601***	405.1837	791.3365	396.1719	I	263.1880	132.0976	245.1644	123.0858	2
9					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of ANGCKPGIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.2	956.4524	0.0028	ANGCKPGIK

AT5G60960.1

22.4	956.4571	-0.0020	QGDKEAVAK
9.3	956.4524	0.0028	MVTKNSHK
8.1	956.4545	0.0007	ESTLEELK
7.4	956.4571	-0.0020	GENALKDAK
5.8	956.4524	0.0028	DMRLANPK
4.8	956.4571	-0.0020	NDSEKKPK
2.6	956.4571	-0.0020	ADEALKGNK
2.6	956.4571	-0.0020	DARVEVEK
2.6	956.4571	-0.0020	GQTIDIGNK

AT5G61140.1

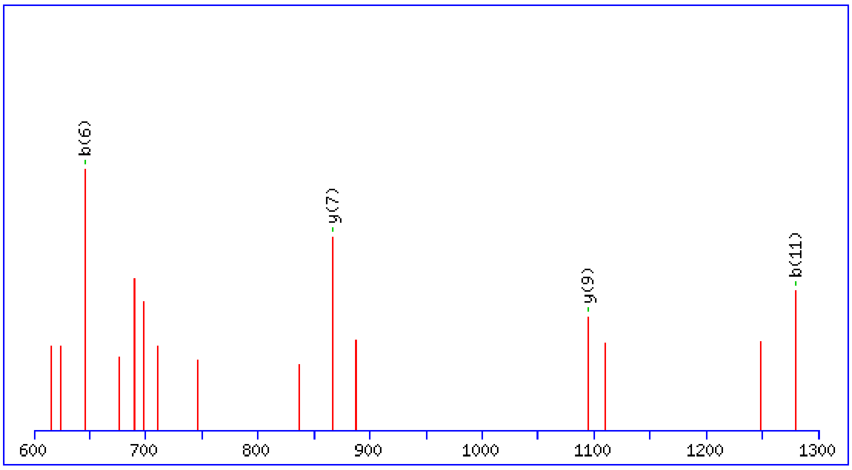
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLGMLDVMQIFGR**
Found in **AT5G61140.1** in **TAIR_Arabidopsis**, Symbols: | DEAD box RNA helicase, putative | chr5:24607225-24620537 FORWARD

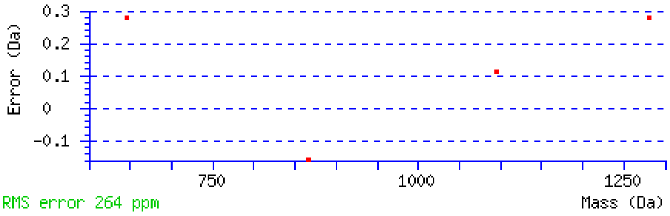
Match to Query 6889: 1509.736378 from(755.875465,2+) index(8167)
Title: Elution from: 70.920 to 70.920 scan no 10488 cid35.00 polarity:+
Data file 0-1_1.mgf

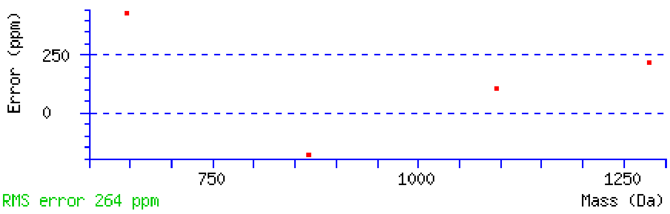
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 600 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1509.7320
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 19 **Expect:** 0.049
Matches : 4/180 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							13
2	229.1183	115.0628			211.1077	106.0575	L	1395.7123	698.3598	1378.6858	689.8465	1377.7017	689.3545	12
3	286.1397	143.5735			268.1292	134.5682	G	1282.6282	641.8178	1265.6017	633.3045	1264.6177	632.8125	11
4	417.1802	209.0938			399.1697	200.0885	M	1225.6068	613.3070	1208.5802	604.7938	1207.5962	604.3017	10
5	530.2643	265.6358			512.2537	256.6305	L	***1094.5663***	547.7868	1077.5397	539.2735	1076.5557	538.7815	9
6	***645.2912***	323.1493			627.2807	314.1440	D	981.4822	491.2448	964.4557	482.7315	963.4717	482.2395	8
7	744.3597	372.6835			726.3491	363.6782	V	***866.4553***	433.7313	849.4287	425.2180			7
8	891.3951	446.2012			873.3845	437.1959	M	767.3869	384.1971	750.3603	375.6838			6
9	1019.4536	510.2305	1002.4271	501.7172	1001.4431	501.2252	Q	620.3515	310.6794	603.3249	302.1661			5
10	1132.5377	566.7725	1115.5111	558.2592	1114.5271	557.7672	I	492.2929	246.6501	475.2663	238.1368			4
11	***1279.6061***	640.3067	1262.5796	631.7934	1261.5955	631.3014	F	379.2088	190.1081	362.1823	181.5948			3
12	1336.6276	668.8174	1319.6010	660.3042	1318.6170	659.8121	G	232.1404	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DLGMLDVMQIFGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G61140.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.8	1509.7320	0.0044	DLGMLDVMQIFGR
5.4	1509.7353	0.0011	LSMEMKNPLKCK
4.1	1509.7398	-0.0035	YFGQCPIITAQGR

AT5G61410.1

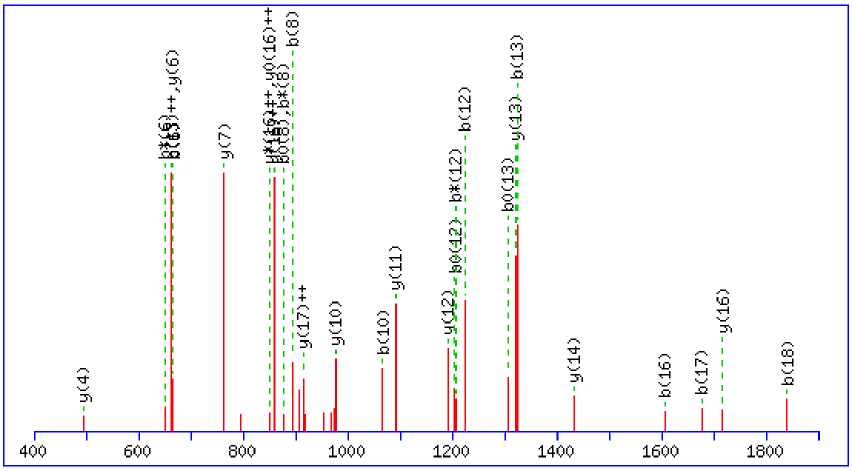
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNPWIEVDGGVTPANAYK**
Found in **AT5G61410.1** in **TAIR_Arabidopsis**, Symbols: EMB2728, RPE | RPE (EMBRYO DEFECTIVE 2728); ribulose-phosphate 3-epimerase | chr5:24701311-24703062 REVERSE

Match to Query 8861: 1985.985452 from(994.000002,2+) index(7315)
Title: Elution from: 65.687 to 65.687 scan no 9641 cid35.00 polarity:+
Data file D1d-2_3.mgf

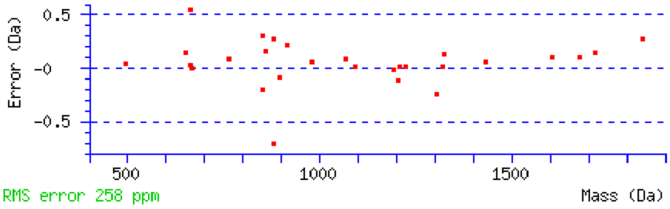
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

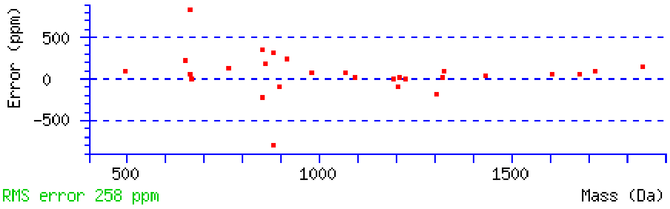


Monoisotopic mass of neutral peptide Mr(calc): 1985.9847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 114 **Expect:** 1.4e-011
Matches : 28/188 fragment ions using 25 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							19
2	157.0972	79.0522					V	1929.9705	965.4889	1912.9440	956.9756	1911.9599	956.4836	18
3	271.1401	136.0737	254.1135	127.5604			N	1830.9021	915.9547	1813.8755	907.4414	1812.8915	906.9494	17
4	368.1928	184.6001	351.1663	176.0868			P	***1716.8592***	858.9332	1699.8326	850.4199	1698.8486	849.9279	16
5	554.2722	277.6397	537.2456	269.1264			W	1619.8064	810.4068	1602.7799	801.8936	1601.7958	801.4016	15
6	***667.3562***	334.1817	650.3297	325.6685			I	***1433.7271***	717.3672	1416.7005	708.8539	1415.7165	708.3619	14
7	796.3988	398.7030	779.3723	390.1898	778.3882	389.6978	E	***1320.6430***	660.8251	1303.6165	652.3119	1302.6325	651.8199	13
8	***895.4672***	448.2373	878.4407	439.7240	877.4567	439.2320	V	***1191.6004***	596.3039	1174.5739	587.7906	1173.5899	587.2986	12
9	1010.4942	505.7507	993.4676	497.2374	992.4836	496.7454	D	***1092.5320***	546.7696	1075.5055	538.2564	1074.5215	537.7644	11
10	***1067.5156***	534.2615	1050.4891	525.7482	1049.5051	525.2562	G	***977.5051***	489.2562	960.4785	480.7429	959.4945	480.2509	10
11	1124.5371	562.7722	1107.5106	554.2589	1106.5265	553.7669	G	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	9
12	***1223.6055***	612.3064	1206.5790	603.7931	1205.5949	603.3011	V	863.4621	432.2347	846.4356	423.7214	845.4516	423.2294	8
13	***1324.6532***	662.8302	1307.6266	654.3170	1306.6426	653.8250	T	***764.3937***	382.7005	747.3672	374.1872	746.3832	373.6952	7
14	1421.7060	711.3566	1404.6794	702.8433	1403.6954	702.3513	P	***663.3461***	332.1767	646.3195	323.6634			6
15	1492.7431	746.8752	1475.7165	738.3619	1474.7325	737.8699	A	566.2933	283.6503	549.2667	275.1370			5
16	***1606.7860***	803.8966	1589.7594	795.3834	1588.7754	794.8914	N	***495.2562***	248.1317	478.2296	239.6185			4
17	***1677.8231***	839.4152	1660.7966	830.9019	1659.8125	830.4099	A	381.2132	191.1103	364.1867	182.5970			3
18	***1840.8864***	920.9469	1823.8599	912.4336	1822.8759	911.9416	Y	310.1761	155.5917	293.1496	147.0784			2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT5G61410.1





NCBI **BLAST** search of GVNPWIEVDGGVTPANAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
113.7	1985.9847	0.0008	GVNPWIEVDGGVTPANAYK

Mascot: http://www.matrixscience.com/

AT5G61580.1

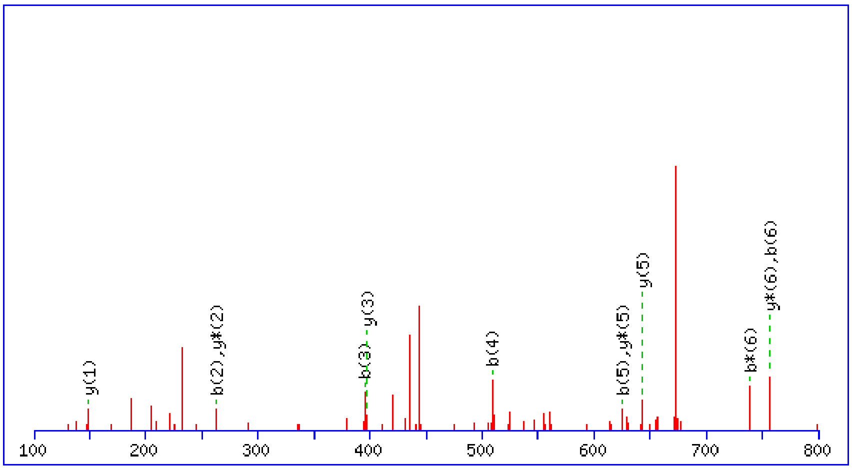
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KMMINMK**
Found in **AT5G61580.1** in **TAIR_Arabidopsis**, Symbols: | phosphofructokinase family protein | chr5:24778376-24781053 FORWARD

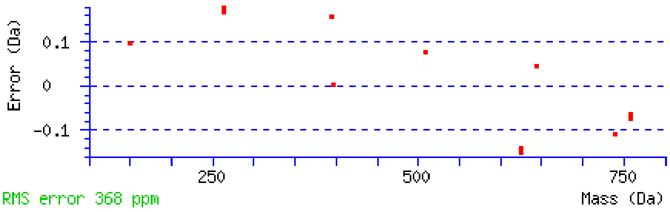
Match to Query 1681: 904.417690 from(453.216121,2+) index(5038)
Title: Elution from: 45.911 to 45.911 scan no 6316 cid35.00 polarity:+
Data file D12h-3_1.mgf

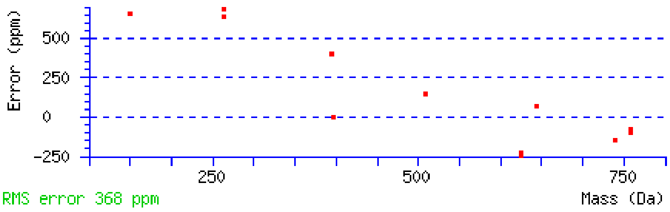
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 904.4193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.02
Matches : 12/48 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	131.0963	66.0518	113.0727	57.0400	K					7
2	*263.1338*	132.0706	245.1102	123.0588	M	775.3375	388.1724	757.3139	379.1606	6
3	*395.1713*	198.0893	377.1478	189.0775	M	643.3000	322.1536	625.2764	313.1419	5
4	*509.2524*	255.1299	491.2289	246.1181	I	511.2625	256.1349	493.2389	247.1231	4
5	*625.2894*	313.1484	607.2659	304.1366	N	397.1814	199.0943	379.1578	190.0825	3
6	*757.3270*	379.1671	739.3034	370.1553	M	281.1444	141.0758	263.1208	132.0640	2
7					K	149.1069	75.0571	131.0833	66.0453	1





NCBI **BLAST** search of KMMINMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.2	904.4193	-0.0016	KMMINMK
23.1	904.4184	-0.0007	MISAASTAK
16.8	904.4150	0.0027	QTYELNK

15.3	904.4155	0.0022	REESSRK
14.1	904.4150	0.0027	TKQFDEK
12.9	904.4184	-0.0007	MATSLQTK
10.9	904.4150	0.0027	TKFDEQK
10.4	904.4151	0.0026	SGGSYSPLK
10.0	904.4184	-0.0007	METKDKK
9.9	904.4173	0.0004	TFDWSLK

Mascot: http://www.matrixscience.com/

AT5G61780.1

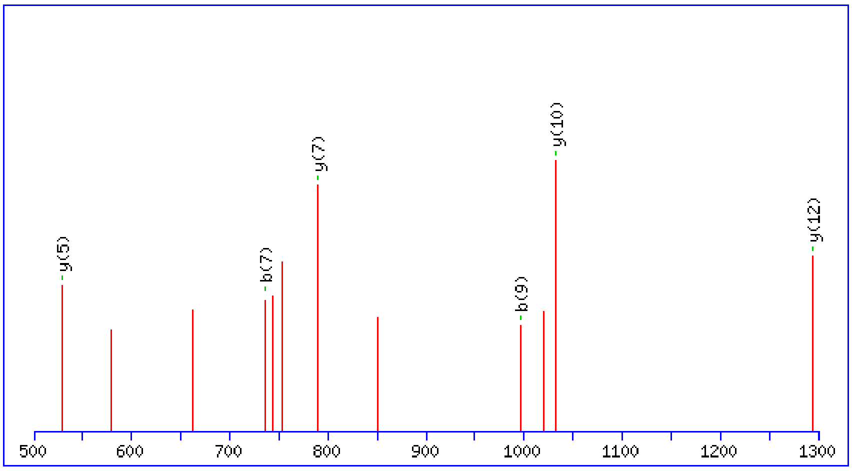
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMDFGSVFLPSPTK**
Found in **AT5G61780.1** in **TAIR_Arabidopsis**, Symbols: | tudor domain-containing protein / nuclease family protein | chr5:24839238-24843867 FORWARD

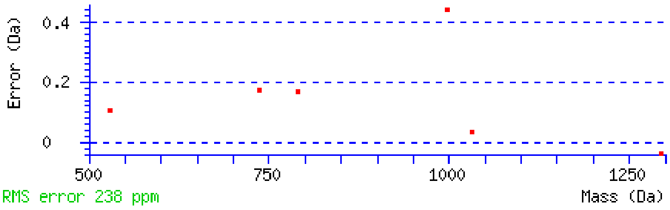
Match to Query 6374: 1523.771246 from(762.892899,2+) index(9069)
Title: Elution from: 82.034 to 82.034 scan no 12344 cid35.00 polarity:+
Data file D12h-3_2.mgf

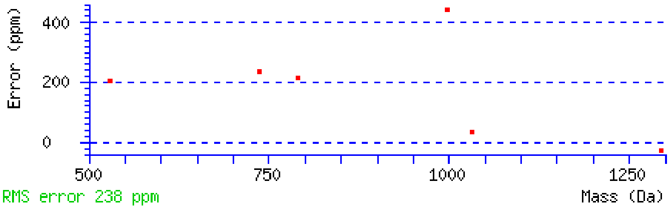
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 500 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1523.7694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 0.012
Matches : 6/124 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							14
2	231.1162	116.0617			M	1425.7083	713.3578	1408.6817	704.8445	1407.6977	704.3525	13
3	346.1431	173.5752	328.1326	164.5699	D	***1294.6678***	647.8375	1277.6412	639.3243	1276.6572	638.8322	12
4	493.2115	247.1094	475.2010	238.1041	F	1179.6408	590.3241	1162.6143	581.8108	1161.6303	581.3188	11
5	550.2330	275.6201	532.2224	266.6149	G	***1032.5724***	516.7898	1015.5459	508.2766	1014.5619	507.7846	10
6	637.2650	319.1362	619.2545	310.1309	S	975.5510	488.2791	958.5244	479.7658	957.5404	479.2738	9
7	**736.3334**	368.6704	718.3229	359.6651	V	888.5189	444.7631	871.4924	436.2498	870.5084	435.7578	8
8	883.4019	442.2046	865.3913	433.1993	F	***789.4505***	395.2289	772.4240	386.7156	771.4400	386.2236	7
9	**996.4859**	498.7466	978.4754	489.7413	L	642.3821	321.6947	625.3556	313.1814	624.3715	312.6894	6
10	1093.5387	547.2730	1075.5281	538.2677	P	***529.2980***	265.1527	512.2715	256.6394	511.2875	256.1474	5
11	1180.5707	590.7890	1162.5601	581.7837	S	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
12	1277.6235	639.3154	1259.6129	630.3101	P	345.2132	173.1103	328.1867	164.5970	327.2027	164.1050	3
13	1378.6712	689.8392	1360.6606	680.8339	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
14					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VMDFGSVFLPSPTK

AT5G61780.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.6	1523.7694	0.0018	VMDFGSVFLPSPTK

Mascot: http://www.matrixscience.com/

AT5G61790.1

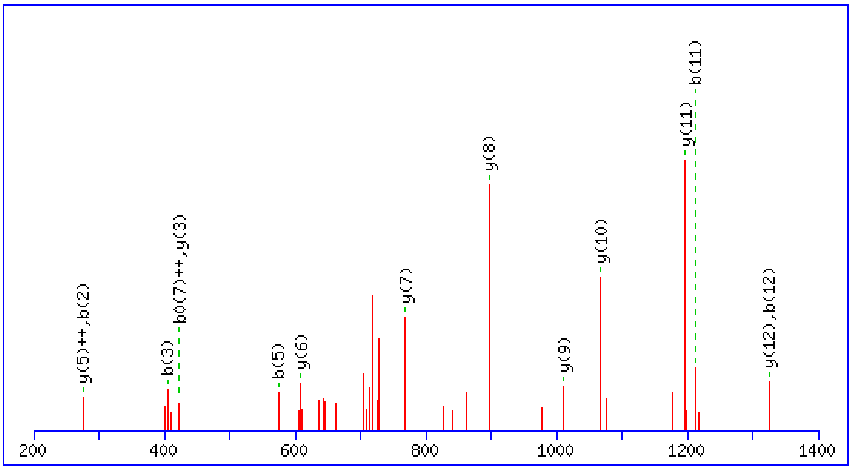
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQEGLECGGAYLK**
Found in **AT5G61790.1** in **TAIR_Arabidopsis**, Symbols: | calnexin 1 (CNX1) | chr5:24844620-24846868 REVERSE

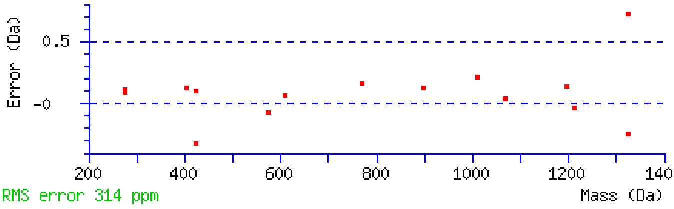
Match to Query 6048: 1470.680522 from(736.347537,2+) index(4825)
Title: Elution from: 44.561 to 44.561 scan no 6118 cid35.00 polarity:+
Data file 0-1_2.mgf

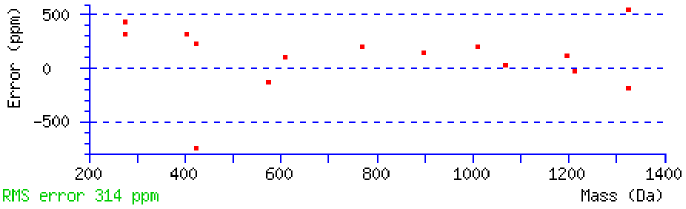
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1470.6813
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 1.7e-007
Matches : 15/124 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							13
2	***276.1343***	138.5708	259.1077	130.0575			Q	***1324.6202***	662.8137	1307.5936	654.3005	1306.6096	653.8084	12
3	***405.1769***	203.0921	388.1503	194.5788	387.1663	194.0868	E	***1196.5616***	598.7844	1179.5351	590.2712	1178.5510	589.7792	11
4	462.1983	231.6028	445.1718	223.0895	444.1878	222.5975	G	***1067.5190***	534.2631	1050.4925	525.7499	1049.5084	525.2579	10
5	***575.2824***	288.1448	558.2558	279.6316	557.2718	279.1395	L	***1010.4975***	505.7524	993.4710	497.2391	992.4870	496.7471	9
6	704.3250	352.6661	687.2984	344.1529	686.3144	343.6608	E	***897.4135***	449.2104	880.3869	440.6971	879.4029	440.2051	8
7	864.3556	432.6815	847.3291	424.1682	846.3451	423.6762	C	***768.3709***	384.6891	751.3443	376.1758			7
8	921.3771	461.1922	904.3505	452.6789	903.3665	452.1869	G	***608.3402***	304.6738	591.3137	296.1605			6
9	978.3986	489.7029	961.3720	481.1896	960.3880	480.6976	G	551.3188	276.1630	534.2922	267.6498			5
10	1049.4357	525.2215	1032.4091	516.7082	1031.4251	516.2162	A	494.2973	247.6523	477.2708	239.1390			4
11	***1212.4990***	606.7531	1195.4725	598.2399	1194.4884	597.7479	Y	***423.2602***	212.1337	406.2336	203.6205			3
12	***1325.5831***	663.2952	1308.5565	654.7819	1307.5725	654.2899	L	260.1969	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FQEGLECGGAYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G61790.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.3	1470.6813	-0.0008	FQEGLECGGAYLK
23.1	1470.6847	-0.0041	GAFELMREMVEK
19.7	1470.6847	-0.0041	FKESVMECANLK
8.1	1470.6773	0.0032	ADDHDDVMQGIKK
1.3	1470.6846	-0.0041	SNMEQIFKSMEK
0.5	1470.6847	-0.0042	LCTVAYQSLCEK
0.1	1470.6811	-0.0006	RHSDSRVEDNEK

AT5G61920.1

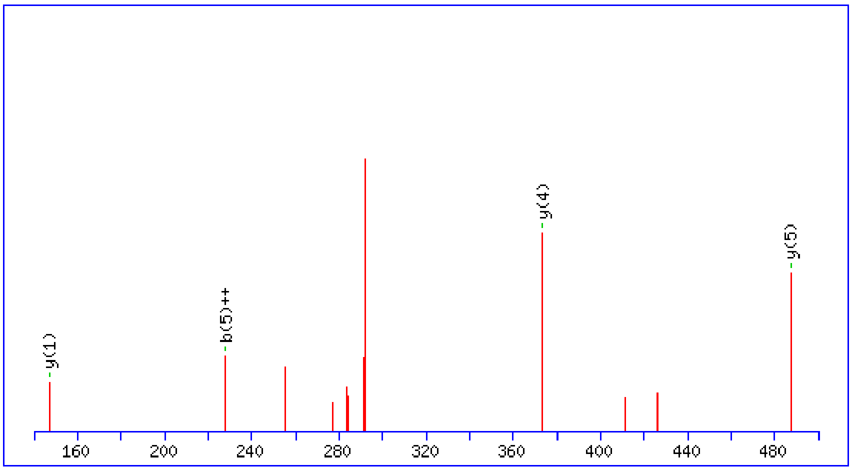
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGAVK**
Found in **AT5G61920.1** in **TAIR_Arabidopsis**, Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G14750.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN62085.1) | chr5:24882056-24882854 FORWARD

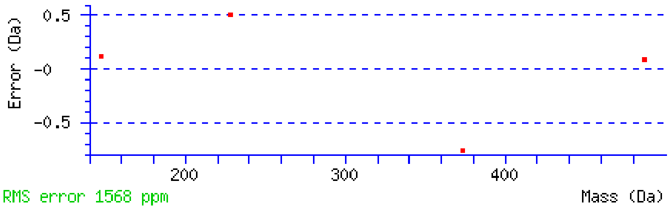
Match to Query 471: 599.400836 from(300.707694,2+) index(2738)
Title: Elution from: 28.029 to 28.029 scan no 3410 cid35.00 polarity:+
Data file C7-1_1.mgf

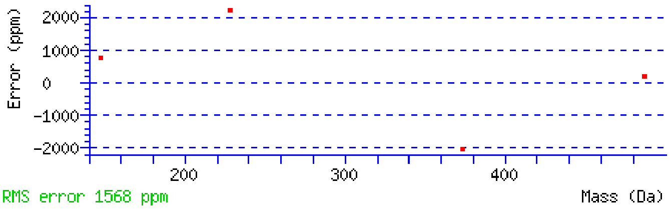
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 599.4006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 0.031
Matches : 4/30 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493	I					6
2	227.1754	114.0913	I	***487.3239***	244.1656	470.2973	235.6523	5
3	284.1969	142.6021	G	***374.2398***	187.6235	357.2132	179.1103	4
4	355.2340	178.1206	A	317.2183	159.1128	300.1918	150.5995	3
5	454.3024	227.6548	V	246.1812	123.5942	229.1547	115.0810	2
6			K	***147.1128***	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of IIGAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	599.4006	0.0002	IGGILK
24.4	599.4006	0.0002	IIGAVK
24.4	599.4006	0.0002	IIIGGK

AT5G61920.1

24.4	599.4006	0.0002	IILNK
24.4	599.4006	0.0002	IINIK
24.4	599.4006	0.0002	IINLK
24.4	599.4006	0.0002	IIQVK
24.4	599.4006	0.0002	ILINK
24.4	599.4006	0.0002	ILNIK
24.4	599.4006	0.0002	ILNLK

AT5G62690.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGPYGQTFRPDNFVFGQSGAGNNWAK**
Found in **AT5G62690.1** in **TAIR_Arabidopsis**, Symbols: TUB2 | TUB2 (Tubulin beta-2); structural molecule | chr5:25198786-25200727 FORWARD

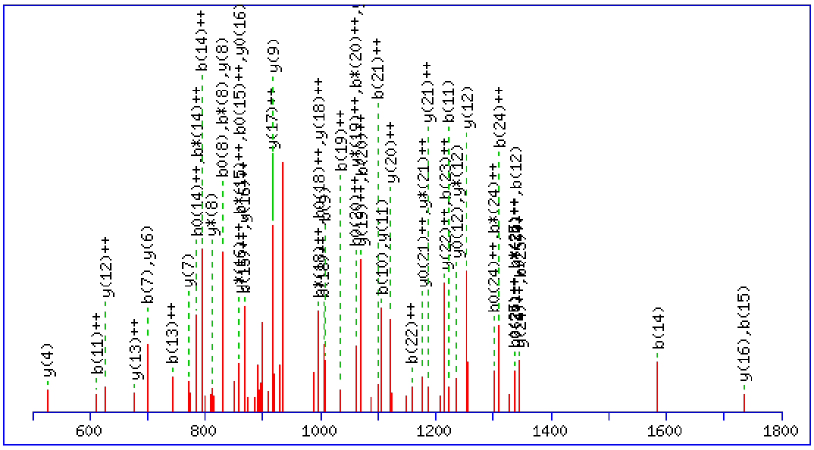
Match to Query 10609: 2837.187474 from(946.736434,3+) index(7982)
Title: Elution from: 70.603 to 70.603 scan no 10515 cid35.00 polarity:+
Data file 0-3_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 500 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

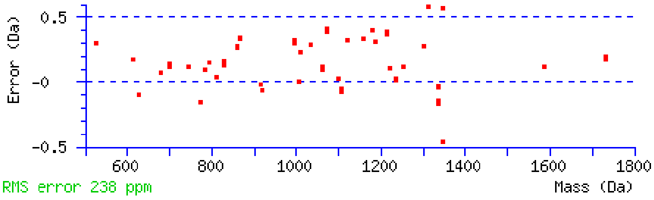
Show Y-axis ☐

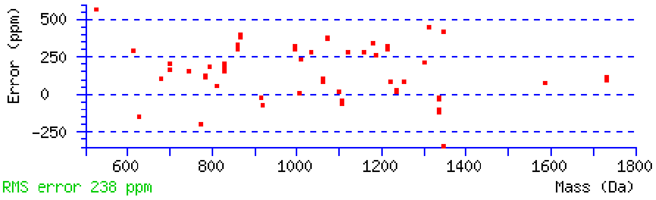


Monoisotopic mass of neutral peptide Mr(calc): 2837.1879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 7.1e-012
Matches : 62/274 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	89.0363	45.0218			71.0258	36.0165	S							26
2	147.0548	74.0311			129.0443	65.0258	G	2750.1661	1375.5867	2732.1425	1366.5749	2732.1555	1366.5814	25
3	245.1046	123.0560			227.0941	114.0507	P	2692.1476	1346.5774	2674.1240	1337.5656	2674.1370	1337.5722	24
4	409.1650	205.0861			391.1544	196.0809	Y	2594.0978	1297.5525	2576.0742	1288.5407	2576.0872	1288.5473	23
5	467.1835	234.0954			449.1729	225.0901	G	2430.0374	1215.5224	2412.0139	1206.5106	2412.0269	1206.5171	22
6	597.2361	299.1217	579.2126	290.1099	579.2256	290.1164	Q	2372.0189	1186.5131	2353.9954	1177.5013	2354.0084	1177.5078	21
7	**699.2809**	350.1441	681.2573	341.1323	681.2703	341.1388	T	2241.9663	1121.4868	2223.9427	1112.4750	2223.9557	1112.4815	20
8	847.3463	424.1768	829.3227	415.1650	829.3357	415.1715	F	2139.9216	1070.4644	2121.8980	1061.4526	2121.9110	1061.4591	19
9	**1007.4356**	504.2214	989.4120	495.2096	989.4250	495.2161	R	1991.8561	996.4317	1973.8325	987.4199	1973.8456	987.4264	18
10	**1105.4854**	553.2463	1087.4618	544.2345	1087.4748	544.2410	P	1831.7669	916.3871	1813.7433	907.3753	1813.7563	907.3818	17
11	**1221.5093**	***611.2583***	1203.4858	602.2465	1203.4988	602.2530	D	**1733.7171**	867.3622	1715.6935	858.3504	1715.7065	858.3569	16
12	**1337.5463**	669.2768	1319.5227	660.2650	1319.5358	660.2715	N	1617.6931	809.3502	1599.6695	800.3384	1599.6825	800.3449	15
13	1485.6118	***743.3095***	1467.5882	734.2977	1467.6012	734.3042	F	1501.6561	751.3317	1483.6325	742.3199	1483.6455	742.3264	14
14	**1585.6772**	***793.3423***	1567.6536	784.3305	1567.6667	784.3370	V	1353.5907	677.2990	1335.5671	668.2872	1335.5801	668.2937	13
15	**1733.7427**	***867.3750***	1715.7191	858.3632	1715.7321	858.3697	F	**1253.5252**	627.2662	1235.5016	618.2544	1235.5146	618.2610	12
16	1791.7612	896.3842	1773.7376	887.3724	1773.7506	887.3789	G	**1105.4598**	553.2335	1087.4362	544.2217	1087.4492	544.2282	11
17	1921.8138	961.4106	1903.7902	952.3988	1903.8033	952.4053	Q	1047.4413	524.2243	1029.4177	515.2125	1029.4307	515.2190	10
18	2009.8429	***1005.4251***	1991.8193	996.4133	1991.8323	996.4198	S	**917.3886**	459.1979	899.3650	450.1862	899.3780	450.1927	9
19	2067.8614	***1034.4343***	2049.8378	1025.4225	2049.8508	1025.4290	G	**829.3595**	415.1834	811.3360	406.1716			8
20	2139.8955	***1070.4514***	2121.8720	1061.4396	2121.8850	1061.4461	A	**771.3410**	386.1742	753.3175	377.1624			7
21	2197.9140	***1099.4607***	2179.8905	1090.4489	2179.9035	1090.4554	G	**699.3069**	350.1571	681.2833	341.1453			6
22	2313.9510	***1157.4792***	2295.9274	1148.4674	2295.9405	1148.4739	N	641.2884	321.1478	623.2648	312.1360			5
23	2429.9880	***1215.4977***	2411.9644	1206.4859	2411.9775	1206.4924	N	**525.2514**	263.1293	507.2278	254.1175			4
24	2618.0614	***1309.5343***	2600.0378	1300.5226	2600.0508	1300.5291	W	409.2144	205.1108	391.1908	196.0990			3
25	2690.0956	***1345.5514***	2672.0720	1336.5396	2672.0850	1336.5461	A	221.1410	111.0741	203.1174	102.0624			2

26							**K**	149.1069	75.0571	131.0833	66.0453			**1**





NCBI **BLAST** search of SGPYGQTFRPDNFVFGQSGAGNNWAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
117.0	2837.1879	-0.0004	SGPYGQTFRPDNFVFGQSGAGNNWAK
7.6	2837.1798	0.0077	KECGKCCYHIVYNVFTMLPDQK
0.1	2837.1812	0.0063	QFVSEDVEWMHIDMAGPVWNEKK

Mascot: http://www.matrixscience.com/

AT5G62790.1

Mascot Search Results

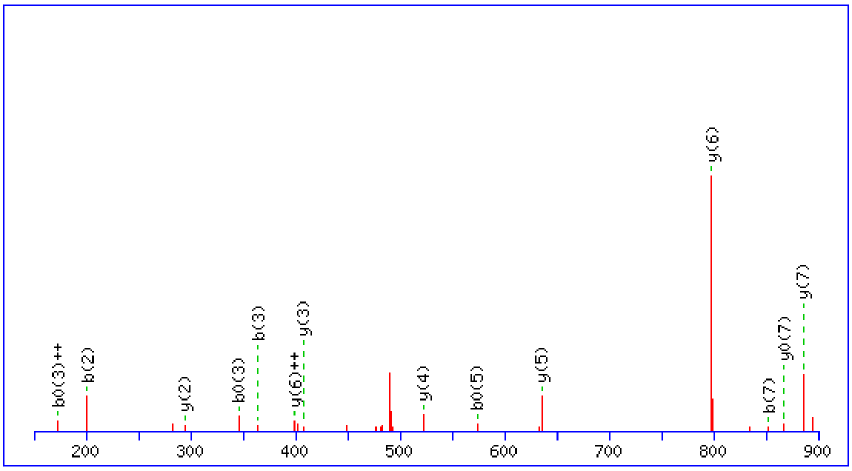
Peptide View

MS/MS Fragmentation of **ISYLDIFK**
Found in **AT5G62790.1** in **TAIR_Arabidopsis**, Symbols: PDE129, DXR | DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE) | chr5:25231584-25234518 REVERSE

Match to Query 2072: 997.548760 from(499.781656,2+) index(8590)
Title: Elution from: 80.316 to 80.316 scan no 11723 cid35.00 polarity:+
Data file D1d-2_2.mgf

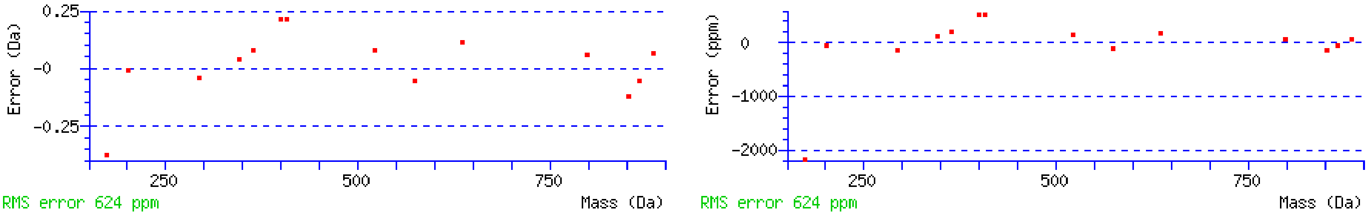
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 997.5484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 4.9e-005
Matches : 14/62 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							8
2	**201.1234**	101.0653	183.1128	92.0600	S	***885.4716***	443.2395	868.4451	434.7262	867.4611	434.2342	7
3	**364.1867**	182.5970	346.1761	173.5917	Y	***798.4396***	399.7234	781.4131	391.2102	780.4291	390.7182	6
4	477.2708	239.1390	459.2602	230.1337	L	***635.3763***	318.1918	618.3497	309.6785	617.3657	309.1865	5
5	592.2977	296.6525	574.2871	287.6472	D	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
6	705.3818	353.1945	687.3712	344.1892	I	***407.2653***	204.1363	390.2387	195.6230			3
7	**852.4502**	426.7287	834.4396	417.7234	F	***294.1812***	147.5942	277.1547	139.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of ISYLDIFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.9	997.5484	0.0003	ISYLDIFK

AT5G62790.1

10.4	997.5484	0.0003	ISIVEYFK

Mascot: http://www.matrixscience.com/

AT5G62860.1

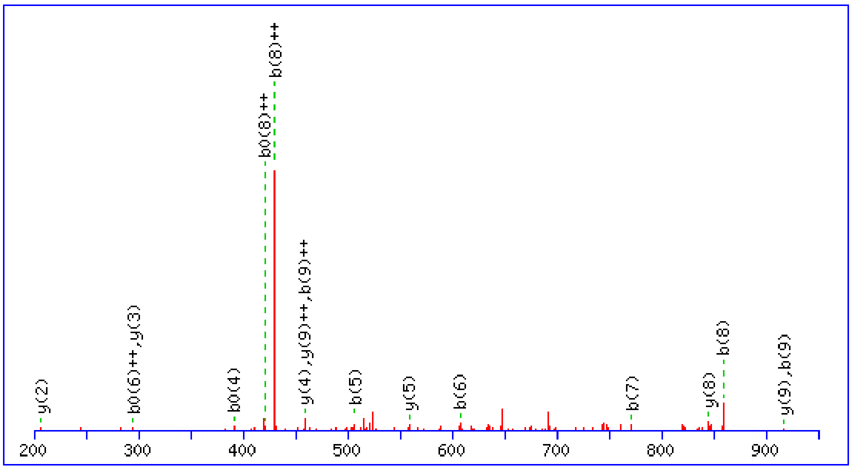
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FASVPVYSGK**
Found in **AT5G62860.1** in **TAIR_Arabidopsis**, Symbols: | F-box family protein-related | chr5:25249858-25251793 FORWARD

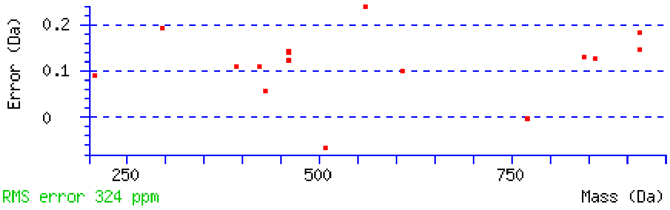
Match to Query 3143: 1064.514454 from(533.264503,2+) index(5186)
Title: Elution from: 45.165 to 45.165 scan no 6505 cid35.00 polarity:+
Data file D1d-3_3.mgf

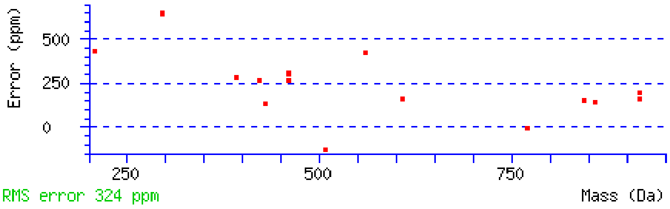
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1064.5169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 0.0096
Matches : 17/82 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	149.0727	75.0400			F							10
2	221.1069	111.0571			A	***917.4587***	459.2330	899.4351	450.2212	899.4481	450.2277	9
3	309.1359	155.0716	291.1254	146.0663	S	***845.4246***	423.2159	827.4010	414.2041	827.4140	414.2106	8
4	409.2014	205.1043	391.1908	196.0990	V	757.3955	379.2014	739.3719	370.1896	739.3849	370.1961	7
5	**507.2512**	254.1292	489.2406	245.1239	P	657.3300	329.1687	639.3065	320.1569	639.3195	320.1634	6
6	**607.3166**	304.1620	589.3061	295.1567	V	***559.2802***	280.1438	541.2567	271.1320	541.2697	271.1385	5
7	**771.3770**	386.1921	753.3664	377.1869	Y	***459.2148***	230.1110	441.1912	221.0992	441.2042	221.1058	4
8	**859.4061**	430.2067	841.3955	421.2014	S	***295.1544***	148.0809	277.1309	139.0691	277.1439	139.0756	3
9	**917.4246**	459.2159	899.4140	450.2106	G	***207.1254***	104.0663	189.1018	95.0545			2
10					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of FASVPVYSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G62860.1

29.5	1064.5169	-0.0024	FASVPVYSGK
15.6	1064.5146	-0.0002	AFSSTGSVLGK
13.2	1064.5169	-0.0024	SVFPAVSYGK
12.1	1064.5146	-0.0002	LGVPVGDDPGK
5.0	1064.5169	-0.0024	LYQFGIEGK
4.9	1064.5146	-0.0002	EPPQSTPAVK
4.6	1064.5146	-0.0002	KQLYSETGK
4.6	1064.5169	-0.0024	YSDKPIFGK
2.1	1064.5173	-0.0028	GFRSLLDSR
1.2	1064.5169	-0.0024	NDALLSFFK

AT5G63310.1

Mascot Search Results

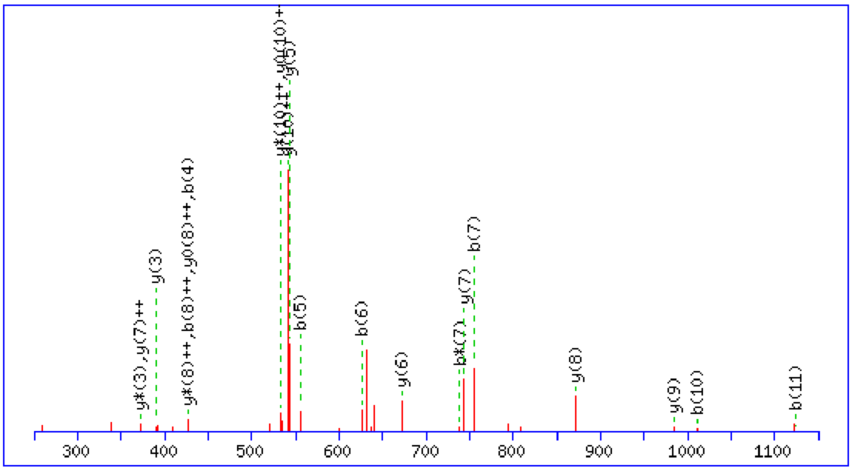
Peptide View

MS/MS Fragmentation of **TDPLQAEPGTIR**
Found in **AT5G63310.1** in **TAIR_Arabidopsis**, Symbols: NDPK1A, NDPK IA IA, NDPK IA, NDPK2 | NDPK2 (NUCLEOSIDE DIPHOSPHATE KINASE 2); ATP binding / nucleoside diphosphate kinase | chr5:25389348-25391064 REVERSE

Match to Query 4885: 1296.666522 from(649.340537,2+) index(3306)
Title: Elution from: 31.132 to 31.132 scan no 4048 cid35.00 polarity:+
Data file D1d-3_2.mgf

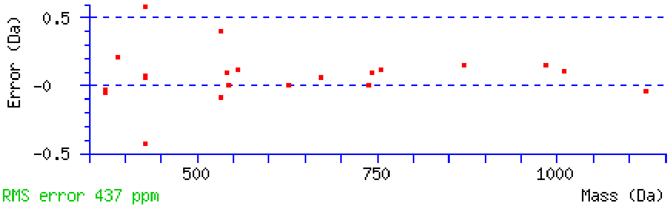
Click mouse within plot area to zoom in by factor of two about that point

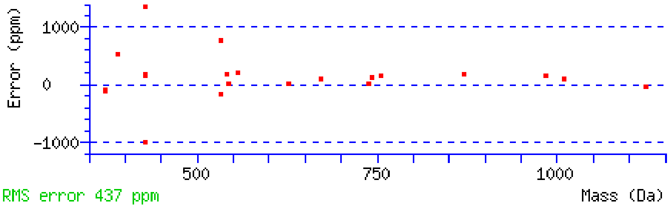
Or, Plot from 250 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1296.6674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 5.8e-006
Matches : 21/120 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	217.0819	109.0446			199.0713	100.0393	D	1196.6270	598.8171	1179.6004	590.3039	1178.6164	589.8118	11
3	314.1347	157.5710			296.1241	148.5657	P	1081.6000	541.3037	1064.5735	532.7904	1063.5895	532.2984	10
4	***427.2187***	214.1130			409.2082	205.1077	L	***984.5473***	492.7773	967.5207	484.2640	966.5367	483.7720	9
5	***555.2773***	278.1423	538.2508	269.6290	537.2667	269.1370	Q	***871.4632***	436.2352	854.4367	427.7220	853.4526	427.2300	8
6	***626.3144***	313.6608	609.2879	305.1476	608.3039	304.6556	A	***743.4046***	372.2060	726.3781	363.6927	725.3941	363.2007	7
7	***755.3570***	378.1821	738.3305	369.6689	737.3464	369.1769	E	***672.3675***	336.6874	655.3410	328.1741	654.3570	327.6821	6
8	852.4098	426.7085	835.3832	418.1953	834.3992	417.7032	P	***543.3249***	272.1661	526.2984	263.6528	525.3144	263.1608	5
9	909.4312	455.2193	892.4047	446.7060	891.4207	446.2140	G	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
10	***1010.4789***	505.7431	993.4524	497.2298	992.4684	496.7378	T	***389.2507***	195.1290	372.2241	186.6157	371.2401	186.1237	3
11	***1123.5630***	562.2851	1106.5364	553.7719	1105.5524	553.2798	I	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TDPLQAEPGTIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G63310.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.9	1296.6674	-0.0009	TDPLQAEPGTIR

Mascot: http://www.matrixscience.com/

AT5G63400.1

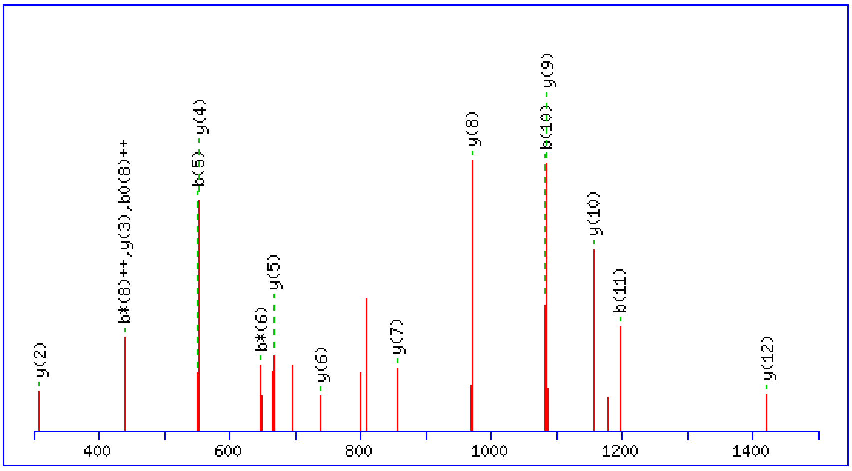
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLNFAIDDAILEER**
Found in **AT5G63400.1** in **TAIR_Arabidopsis**, Symbols: ADK1 | ADK1 (ADENYLATE KINASE 1); adenylate kinase | chr5:25410500-25412043 REVERSE

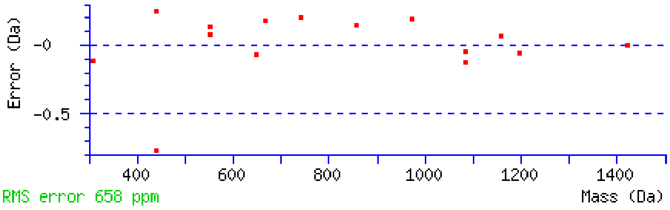
Match to Query 7672: 1634.786680 from(818.400616,2+) index(9600)
Title: Elution from: 86.446 to 86.446 scan no 12968 cid35.00 polarity:+
Data file C7-3_1.mgf

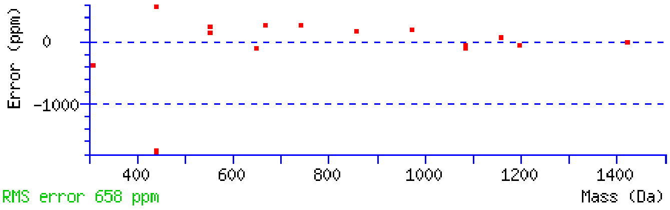
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1634.7876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 104 **Expect:** 3.1e-010
Matches : 16/138 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0727	51.0400					V							14
2	215.1538	108.0805					L	1535.7294	768.3684	1517.7059	759.3566	1517.7189	759.3631	13
3	331.1908	166.0990	313.1672	157.0873			N	***1421.6483***	711.3278	1403.6248	702.3160	1403.6378	702.3225	12
4	479.2563	240.1318	461.2327	231.1200			F	1305.6113	653.3093	1287.5878	644.2975	1287.6008	644.3040	11
5	**551.2904**	276.1488	533.2668	267.1371			A	***1157.5459***	579.2766	1139.5223	570.2648	1139.5353	570.2713	10
6	665.3715	333.1894	647.3479	324.1776			I	***1085.5117***	543.2595	1067.4882	534.2477	1067.5012	534.2542	9
7	781.3955	391.2014	763.3719	382.1896	763.3849	382.1961	D	***971.4307***	486.2190	953.4071	477.2072	953.4201	477.2137	8
8	897.4195	449.2134	879.3959	440.2016	879.4089	440.2081	D	***855.4067***	428.2070	837.3831	419.1952	837.3961	419.2017	7
9	969.4536	485.2304	951.4300	476.2187	951.4431	476.2252	A	***739.3827***	370.1950	721.3591	361.1832	721.3721	361.1897	6
10	**1083.5347**	542.2710	1065.5111	533.2592	1065.5242	533.2657	I	***667.3485***	334.1779	649.3250	325.1661	649.3380	325.1726	5
11	**1197.6158**	599.3115	1179.5922	590.2998	1179.6053	590.3063	L	***553.2674***	277.1374	535.2439	268.1256	535.2569	268.1321	4
12	1327.6554	664.3314	1309.6319	655.3196	1309.6449	655.3261	E	***439.1863***	220.0968	421.1628	211.0850	421.1758	211.0915	3
13	1457.6951	729.3512	1439.6715	720.3394	1439.6845	720.3459	E	***309.1467***	155.0770	291.1231	146.0652	291.1362	146.0717	2
14							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of VLNFAIDDAILEER

AT5G63400.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
104.0	1634.7876	-0.0009	VLNFAIDDAILEER
7.8	1634.7903	-0.0036	VYGDIIPPNLSDRR
7.5	1634.7880	-0.0014	INEIQQESQLQRK
7.5	1634.7854	0.0013	TKTVISNPETLEER
4.9	1634.7903	-0.0036	IVKAQIWDTAGQER
4.9	1634.7903	-0.0036	LVKAQIWDTAGQER
4.9	1634.7903	-0.0036	VIKAQIWDTAGQER
0.6	1634.7903	-0.0036	EDWGDVRTLIAALR
0.1	1634.7829	0.0038	VVPCGEFTASPALLR

AT5G63400.2

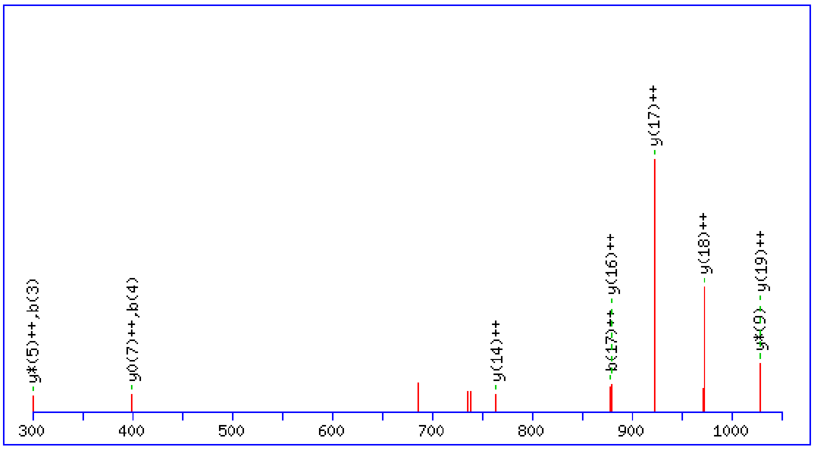
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GELVSDDLVVGIIDEAMNKPK**
Found in **AT5G63400.2** in **TAIR_Arabidopsis**, Symbols: ADK1 | ADK1 (ADENYLATE KINASE 1); adenylate kinase | chr5:25410728-25412043 REVERSE

Match to Query 10368: 2241.159234 from(748.060354,3+) index(11158)
Title: Elution from: 110.708 to 110.708 scan no 15986 cid35.00 polarity:+
Data file D12h-1_1.mgf

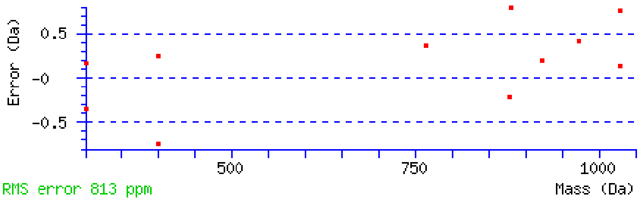
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

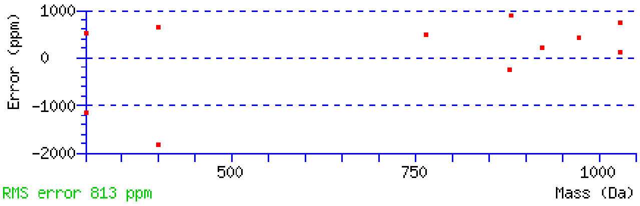


Monoisotopic mass of neutral peptide Mr(calc): 2241.1562
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0028
Matches : 11/192 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							21
2	187.0713	94.0393			169.0608	85.0340	E	2185.1421	1093.0747	2168.1155	1084.5614	2167.1315	1084.0694	20
3	**300.1554**	150.5813			282.1448	141.5761	L	2056.0995	1028.5534	2039.0729	1020.0401	2038.0889	1019.5481	19
4	**399.2238**	200.1155			381.2132	191.1103	V	1943.0154	972.0113	1925.9889	963.4981	1925.0048	963.0061	18
5	486.2558	243.6316			468.2453	234.6263	S	1843.9470	922.4771	1826.9204	913.9639	1825.9364	913.4719	17
6	601.2828	301.1450			583.2722	292.1397	D	1756.9150	878.9611	1739.8884	870.4478	1738.9044	869.9558	16
7	716.3097	358.6585			698.2992	349.6532	D	1641.8880	821.4476	1624.8615	812.9344	1623.8775	812.4424	15
8	829.3938	415.2005			811.3832	406.1952	L	1526.8611	763.9342	1509.8345	755.4209	1508.8505	754.9289	14
9	928.4622	464.7347			910.4516	455.7295	V	1413.7770	707.3921	1396.7505	698.8789	1395.7664	698.3869	13
10	1027.5306	514.2689			1009.5201	505.2637	V	1314.7086	657.8579	1297.6820	649.3447	1296.6980	648.8527	12
11	1084.5521	542.7797			1066.5415	533.7744	G	1215.6402	608.3237	1198.6136	599.8105	1197.6296	599.3184	11
12	1197.6361	599.3217			1179.6256	590.3164	I	1158.6187	579.8130	1141.5922	571.2997	1140.6082	570.8077	10
13	1310.7202	655.8637			1292.7096	646.8585	I	1045.5347	523.2710	1028.5081	514.7577	1027.5241	514.2657	9
14	1425.7472	713.3772			1407.7366	704.3719	D	932.4506	466.7289	915.4240	458.2157	914.4400	457.7237	8
15	1554.7897	777.8985			1536.7792	768.8932	E	817.4236	409.2155	800.3971	400.7022	799.4131	400.2102	7
16	1625.8269	813.4171			1607.8163	804.4118	A	688.3811	344.6942	671.3545	336.1809			6
17	1756.8673	878.9373			1738.8568	869.9320	M	617.3439	309.1756	600.3174	300.6623			5
18	1870.9103	935.9588	1853.8837	927.4455	1852.8997	926.9535	N	486.3035	243.6554	469.2769	235.1421			4
19	1999.0052	1000.0063	1981.9787	991.4930	1980.9947	991.0010	K	372.2605	186.6339	355.2340	178.1206			3
20	2096.0580	1048.5326	2079.0314	1040.0194	2078.0474	1039.5274	P	244.1656	122.5864	227.1390	114.0731			2
21							K	147.1128	74.0600	130.0863	65.5468			1

AT5G63400.2





NCBI **BLAST** search of GELVSDDLVVGIIDEAMNKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.7	2241.1562	0.0030	GELVSDDLVVGIIDEAMNKPK
3.9	2241.1535	0.0057	AIVDNAREENTQGIVNMVLR

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYLEAAWRDGK**
Found in **AT5G63420.1** in **TAIR_Arabidopsis**, Symbols: EMB2746 | EMB2746 (EMBRYO DEFECTIVE 2746); catalytic | chr5:25417741-25423033 FORWARD

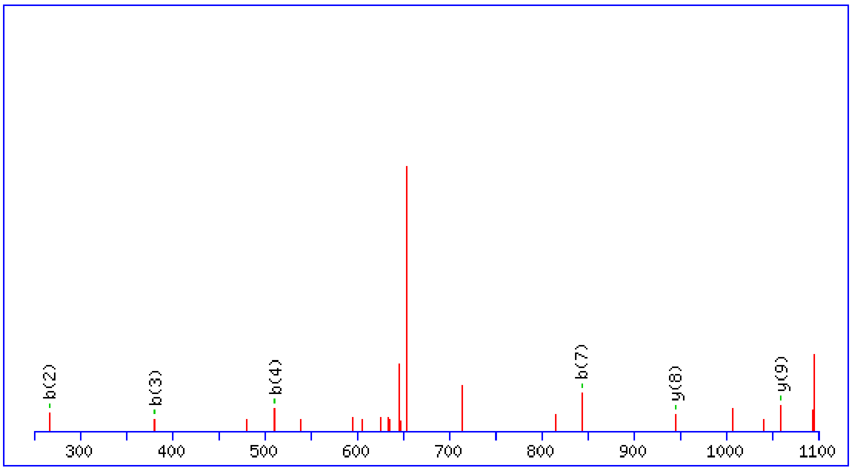
Match to Query 5151: 1324.598334 from(663.306443,2+) index(4768)
Title: Elution from: 43.615 to 43.615 scan no 5961 cid35.00 polarity:+
Data file C7-2_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1100 Da Full range

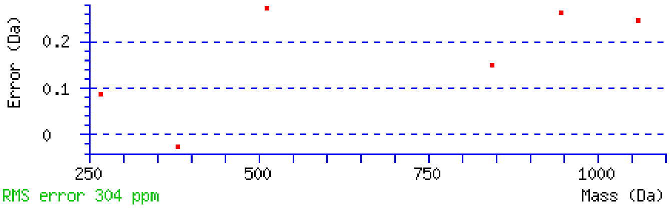
Label all possible matches ○ Label matches used for scoring ●

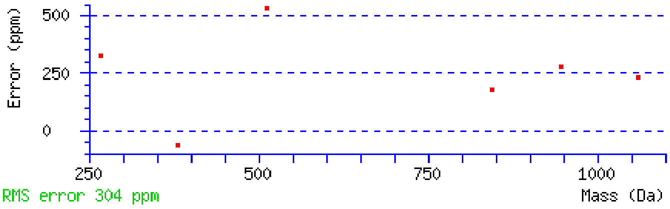
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1324.5988
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.016
Matches : 6/102 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	103.0520	52.0296			85.0414	43.0244	T							11
2	*267.1124*	134.0598			249.1018	125.0545	Y	1223.5614	612.2843	1205.5378	603.2725	1205.5508	603.2790	10
3	*381.1935*	191.1004			363.1829	182.0951	L	**1059.5010**	530.2541	1041.4774	521.2424	1041.4904	521.2489	9
4	*511.2331*	256.1202			493.2225	247.1149	E	**945.4199**	473.2136	927.3963	464.2018	927.4093	464.2083	8
5	583.2672	292.1373			565.2567	283.1320	A	815.3803	408.1938	797.3567	399.1820	797.3697	399.1885	7
6	655.3014	328.1543			637.2908	319.1490	A	743.3461	372.1767	725.3226	363.1649	725.3356	363.1714	6
7	*843.3748*	422.1910			825.3642	413.1857	W	671.3120	336.1596	653.2884	327.1478	653.3014	327.1543	5
8	1003.4640	502.2356	985.4404	493.2239	985.4534	493.2304	R	483.2386	242.1229	465.2150	233.1111	465.2280	233.1177	4
9	1119.4880	560.2476	1101.4644	551.2358	1101.4774	551.2424	D	323.1494	162.0783	305.1258	153.0665	305.1388	153.0730	3
10	1177.5065	589.2569	1159.4829	580.2451	1159.4959	580.2516	G	207.1254	104.0663	189.1018	95.0545			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TYLEAAWRDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G63420.1

Score	Mr(calc)	Delta	Sequence
28.5	1324.5988	-0.0005	TYLEAAWRDGK
12.5	1324.5999	-0.0016	MSENTKVEAKR
12.0	1324.5973	0.0011	MVSATTSEKDVK
5.5	1324.5952	0.0031	CTNIECRVKK
4.1	1324.6022	-0.0038	LVMYPRGTGDGK
3.5	1324.6010	-0.0027	FSFPKSFDHAK
3.0	1324.6022	-0.0038	LMAFEREELR
2.5	1324.6022	-0.0038	VLGFECTNLTR
2.5	1324.5966	0.0018	SLVTASFANENR
2.1	1324.5988	-0.0005	FSVAWDTISGAR

AT5G63510.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLTNEETLEIPK**
Found in **AT5G63510.1** in **TAIR_Arabidopsis**, Symbols: GAMMA CAL1 | GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase | chr5:25441280-25442838 FORWARD

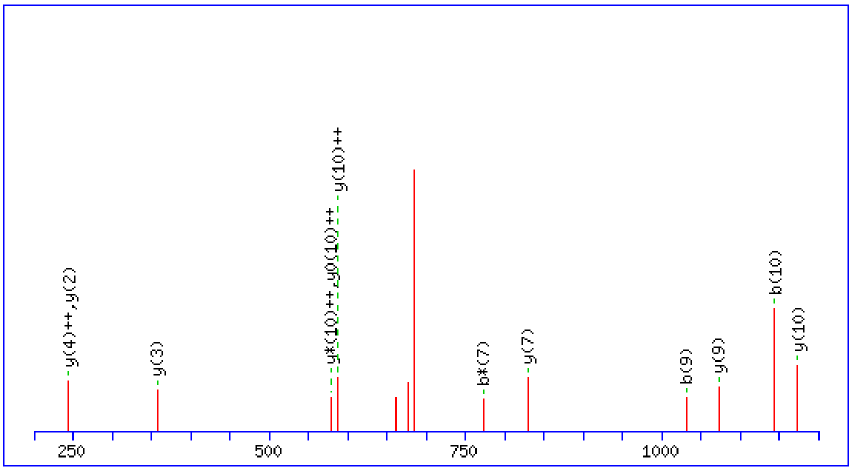
Match to Query 4867: 1386.724330 from(694.369441,2+) index(4463)
Title: Elution from: 43.933 to 43.933 scan no 5731 cid35.00 polarity:+
Data file D1d-2_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1200 Da Full range

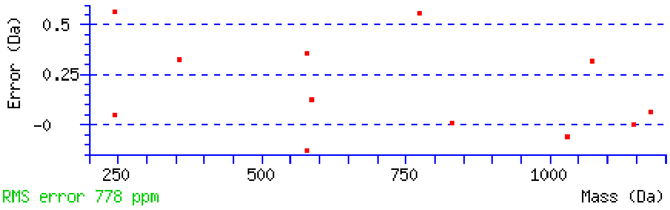
Label all possible matches ○ Label matches used for scoring ●

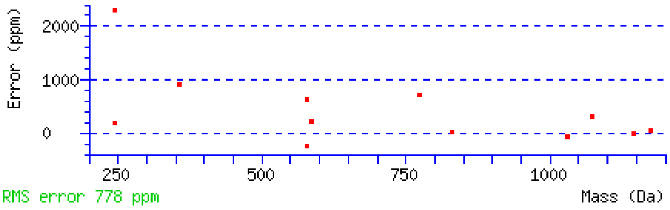
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1386.7242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 3.7e-005
Matches : 12/120 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	215.1390	108.0731			197.1285	99.0679	L	1286.6838	643.8456	1269.6573	635.3323	1268.6733	634.8403	11
3	316.1867	158.5970			298.1761	149.5917	T	***1173.5998***	587.3035	1156.5732	578.7902	1155.5892	578.2982	10
4	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	N	***1072.5521***	536.7797	1055.5255	528.2664	1054.5415	527.7744	9
5	559.2722	280.1397	542.2457	271.6265	541.2617	271.1345	E	958.5092	479.7582	941.4826	471.2449	940.4986	470.7529	8
6	688.3148	344.6610	671.2883	336.1478	670.3042	335.6558	E	***829.4666***	415.2369	812.4400	406.7236	811.4560	406.2316	7
7	789.3625	395.1849	772.3359	386.6716	771.3519	386.1796	T	700.4240	350.7156	683.3974	342.2023	682.4134	341.7103	6
8	902.4466	451.7269	885.4200	443.2136	884.4360	442.7216	L	599.3763	300.1918	582.3497	291.6785	581.3657	291.1865	5
9	**1031.4891**	516.2482	1014.4626	507.7349	1013.4786	507.2429	E	486.2922	243.6498	469.2657	235.1365	468.2817	234.6445	4
10	**1144.5732**	572.7902	1127.5467	564.2770	1126.5626	563.7850	I	***357.2496***	179.1285	340.2231	170.6152			3
11	1241.6260	621.3166	1224.5994	612.8034	1223.6154	612.3113	P	***244.1656***	122.5864	227.1390	114.0731			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TLTNEETLEIPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G63510.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.4	1386.7242	0.0001	TLTNEETLEIPK
3.7	1386.7255	-0.0012	RSHYEEVINLK
3.4	1386.7215	0.0028	AENTAVEAIRSAR
1.1	1386.7256	-0.0012	TDGNVSLIGLWGR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AATSDTLTAPYNDLEAVEK**
Found in **AT5G63570.1** in **TAIR_Arabidopsis**, Symbols: GSA1 | GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase | chr5:25469183-25470846 FORWARD

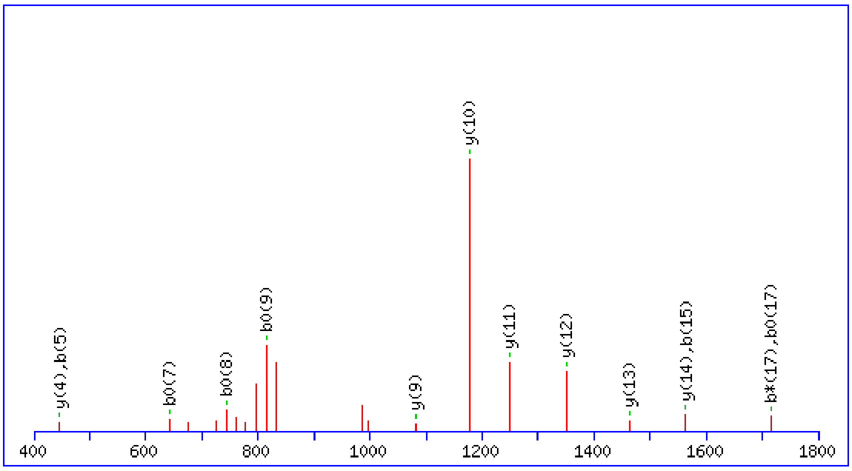
Match to Query 8877: 2007.963292 from(1004.988922,2+) index(6609)
Title: Elution from: 62.434 to 62.434 scan no 8734 cid35.00 polarity:+
Data file D1d-1-2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

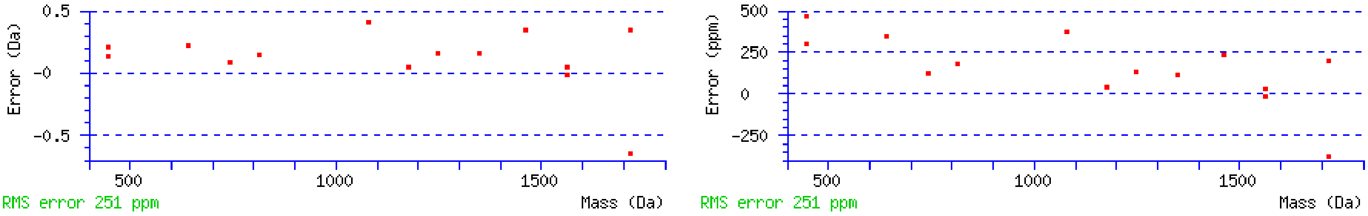
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2007.9637
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 1e-006
Matches : 14/188 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							19
2	143.0815	72.0444					A	1937.9338	969.4706	1920.9073	960.9573	1919.9233	960.4653	18
3	244.1292	122.5682			226.1186	113.5629	T	1866.8967	933.9520	1849.8702	925.4387	1848.8862	924.9467	17
4	331.1612	166.0842			313.1506	157.0790	S	1765.8491	883.4282	1748.8225	874.9149	1747.8385	874.4229	16
5	**446.1882**	223.5977			428.1776	214.5924	D	1678.8170	839.9122	1661.7905	831.3989	1660.8065	830.9069	15
6	547.2358	274.1216			529.2253	265.1163	T	***1563.7901***	782.3987	1546.7635	773.8854	1545.7795	773.3934	14
7	660.3199	330.6636			642.3093	321.6583	L	***1462.7424***	731.8748	1445.7159	723.3616	1444.7318	722.8696	13
8	761.3676	381.1874			743.3570	372.1821	T	***1349.6583***	675.3328	1332.6318	666.8195	1331.6478	666.3275	12
9	832.4047	416.7060			814.3941	407.7007	A	***1248.6107***	624.8090	1231.5841	616.2957	1230.6001	615.8037	11
10	929.4575	465.2324			911.4469	456.2271	P	***1177.5735***	589.2904	1160.5470	580.7771	1159.5630	580.2851	10
11	1092.5208	546.7640			1074.5102	537.7587	Y	***1080.5208***	540.7640	1063.4942	532.2508	1062.5102	531.7587	9
12	1206.5637	603.7855	1189.5372	595.2722	1188.5531	594.7802	N	917.4575	459.2324	900.4309	450.7191	899.4469	450.2271	8
13	1321.5907	661.2990	1304.5641	652.7857	1303.5801	652.2937	D	803.4145	402.2109	786.3880	393.6976	785.4040	393.2056	7
14	1434.6747	717.8410	1417.6482	709.3277	1416.6642	708.8357	L	688.3876	344.6974	671.3610	336.1842	670.3770	335.6921	6
15	**1563.7173**	782.3623	1546.6908	773.8490	1545.7067	773.3570	E	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
16	1634.7544	817.8809	1617.7279	809.3676	1616.7439	808.8756	A	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
17	1733.8228	867.4151	1716.7963	858.9018	1715.8123	858.4098	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
18	1862.8654	931.9364	1845.8389	923.4231	1844.8549	922.9311	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
19							K	147.1128	74.0600	130.0863	65.5468			1

AT5G63570.1



NCBI **BLAST** search of AATSDTLTAPYNDLEAVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.6	2007.9637	-0.0004	AATSDTLTAPYNDLEAVEK
2.9	2007.9610	0.0023	QQADYIISQADSDKDRR

Mascot: http://www.matrixscience.com/

AT5G63690.1

{MATRIX SCIENCE} Mascot Search Results

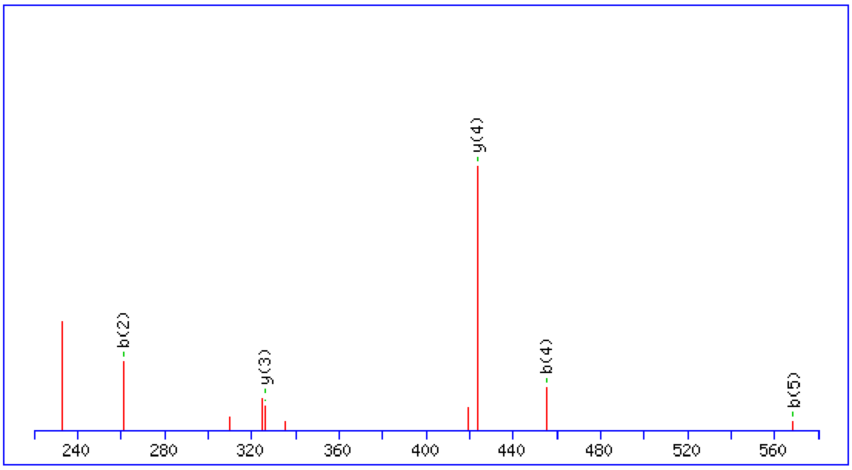
Peptide View

MS/MS Fragmentation of **IFPPLP**
Found in **AT5G63690.1** in **TAIR_Arabidopsis**, Symbols: | similar to hypothetical protein [Vitis vinifera] (GB:CAN67844.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22434.1); contains InterPro domain Nucleic acid-binding, OB-fold (InterPro:IPR012340); contains InterPro domain

Match to Query 553: 682.405236 from(342.209894,2+) index(3094)
Title: Elution from: 29.775 to 29.775 scan no 3828 cid35.00 polarity:+
Data file 0-2_3.mgf

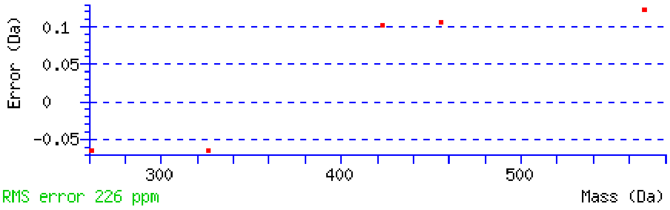
Click mouse within plot area to zoom in by factor of two about that point

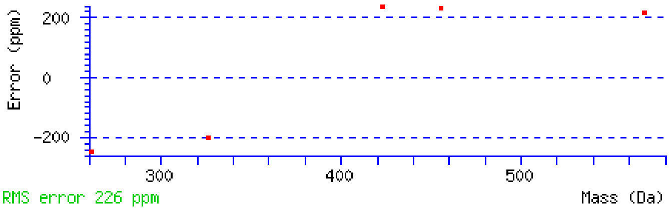
Or, [Plot from] [220] to [580] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 682.4054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.011
Matches : 5/20 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*++}	#
1	114.0913	57.5493	I				6
2	***261.1598***	131.0835	F	570.3286	285.6679		5
3	358.2125	179.6099	P	***423.2602***	212.1337		4
4	***455.2653***	228.1363	P	***326.2074***	163.6074		3
5	***568.3493***	284.6783	L	229.1547	115.0810		2
6			P	116.0706	58.5389		1





NCBI **BLAST** search of IFPPLP
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	682.4054	-0.0002	IFPPLP
3.2	682.4054	-0.0001	FIIYK

3.2	682.4054	-0.0001	FLIYK
3.2	682.4054	-0.0001	FLLYK
3.2	682.4054	-0.0001	IFLYK

AT5G64040.1

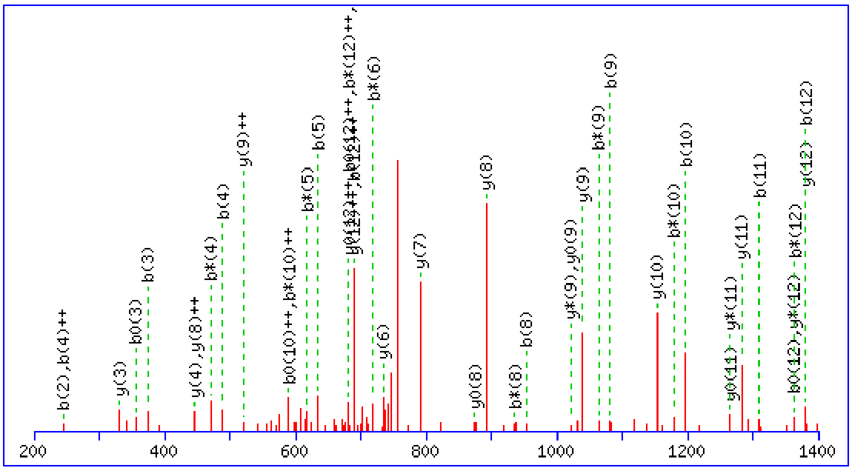
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPENFTGCQDLAK**
Found in **AT5G64040.1** in **TAIR_Arabidopsis**, Symbols: PSAN | PSAN (photosystem I reaction center subunit PSI-N); calmodulin binding | chr5:25645950-25646635 REVERSE

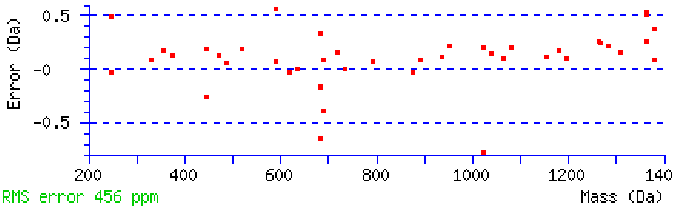
Match to Query 6466: 1525.688328 from(763.851440,2+) index(5159)
Title: Elution from: 48.547 to 48.547 scan no 6582 cid35.00 polarity:+
Data file D1d-2_1.mgf

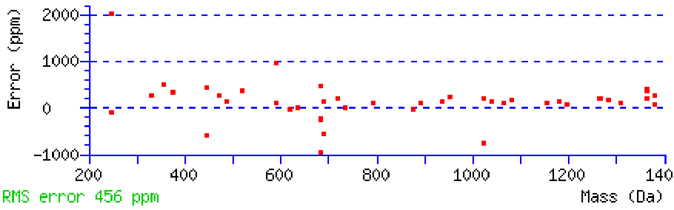
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1525.6871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 3.3e-009
Matches : 44/128 fragment ions using 46 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					**F**							**13**
2	***245.1285***	123.0679					**P**	***1379.6260***	690.3166	1362.5994	681.8034	1361.6154	681.3114	**12**
3	***374.1710***	187.5892			356.1605	178.5839	**E**	***1282.5732***	641.7903	1265.5467	633.2770	1264.5627	632.7850	**11**
4	***488.2140***	244.6106	471.1874	236.0974	470.2034	235.6053	**N**	***1153.5306***	577.2690	1136.5041	568.7557	1135.5201	568.2637	**10**
5	***635.2824***	318.1448	618.2558	309.6316	617.2718	309.1395	**F**	***1039.4877***	520.2475	1022.4612	511.7342	1021.4771	511.2422	**9**
6	736.3301	368.6687	719.3035	360.1554	718.3195	359.6634	**T**	***892.4193***	446.7133	875.3927	438.2000	874.4087	437.7080	**8**
7	793.3515	397.1794	776.3250	388.6661	775.3410	388.1741	**G**	***791.3716***	396.1894	774.3451	387.6762	773.3611	387.1842	**7**
8	***953.3822***	477.1947	936.3556	468.6815	935.3716	468.1894	**C**	***734.3502***	367.6787	717.3236	359.1654	716.3396	358.6734	**6**
9	***1081.4408***	541.2240	1064.4142	532.7107	1063.4302	532.2187	**Q**	574.3195	287.6634	557.2930	279.1501	556.3089	278.6581	**5**
10	***1196.4677***	598.7375	1179.4412	590.2242	1178.4571	589.7322	**D**	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	**4**
11	***1309.5518***	655.2795	1292.5252	646.7662	1291.5412	646.2742	**L**	***331.2340***	166.1206	314.2074	157.6074			**3**
12	***1380.5889***	690.7981	1363.5623	682.2848	1362.5783	681.7928	**A**	218.1499	109.5786	201.1234	101.0653			**2**
13							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of FPENFTGCQDLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

AT5G64040.1

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
87.4	1525.6871	0.0012	FPENFTGCQDLAK
13.1	1525.6871	0.0012	MSRDSPPAFDPYK
6.5	1525.6873	0.0010	MACRGCLECLLK
4.5	1525.6905	-0.0022	VTDGCTIGGCYVPK

Mascot: http://www.matrixscience.com/

AT5G64040.2

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFTVQFGSCK**
Found in **AT5G64040.2** in **TAIR_Arabidopsis**, Symbols: PSAN | PSAN (photosystem I reaction center subunit PSI-N); calmodulin binding | chr5:25645916-25646635 REVERSE

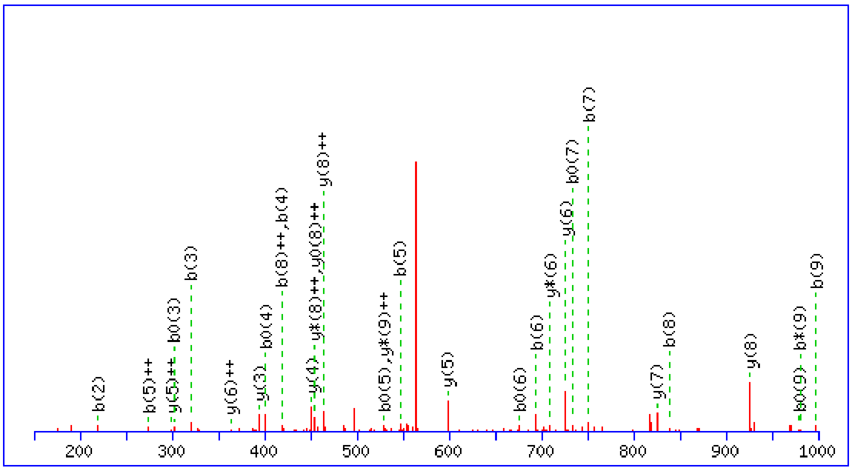
Match to Query 3814: 1143.538812 from(572.776682,2+) index(4525)
Title: Elution from: 40.168 to 40.168 scan no 5658 cid35.00 polarity:+
Data file D1d-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 150 to 1000 Da Full range

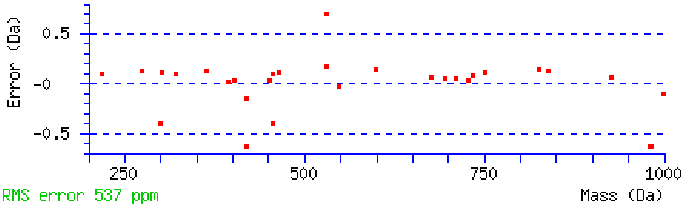
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

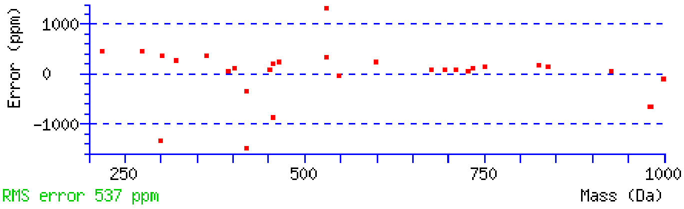


Monoisotopic mass of neutral peptide Mr(calc): 1143.5383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 1.5e-005
Matches : 30/92 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							10
2	***219.1128***	110.0600					F	1073.5084	537.2579	1056.4819	528.7446	1055.4979	528.2526	9
3	***320.1605***	160.5839			302.1499	151.5786	T	**926.4400**	463.7237	909.4135	455.2104	908.4295	454.7184	8
4	***419.2289***	210.1181			401.2183	201.1128	V	**825.3924**	413.1998	808.3658	404.6865	807.3818	404.1945	7
5	***547.2875***	274.1474	530.2609	265.6341	529.2769	265.1421	Q	**726.3239**	363.6656	709.2974	355.1523	708.3134	354.6603	6
6	***694.3559***	347.6816	677.3293	339.1683	676.3453	338.6763	F	**598.2654**	299.6363	581.2388	291.1230	580.2548	290.6310	5
7	***751.3774***	376.1923	734.3508	367.6790	733.3668	367.1870	G	**451.1969**	226.1021	434.1704	217.5888	433.1864	217.0968	4
8	***838.4094***	419.7083	821.3828	411.1951	820.3988	410.7030	S	**394.1755**	197.5914	377.1489	189.0781	376.1649	188.5861	3
9	***998.4400***	499.7237	981.4135	491.2104	980.4295	490.7184	C	307.1435	154.0754	290.1169	145.5621			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 537 ppm



RMS error 537 ppm

NCBI **BLAST** search of AFTVQFGSCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G64040.2

Score	Mr(calc)	Delta	Sequence
52.0	1143.5383	0.0005	AFTVQFGSCK

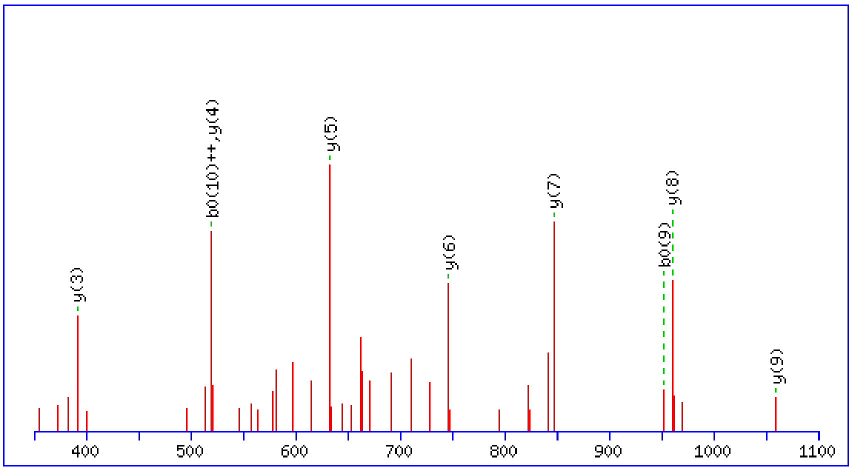
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDVLTLLESER**
Found in **AT5G64140.1** in **TAIR_Arabidopsis**, Symbols: RPS28 | RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome | chr5:25684755-25684949 REVERSE

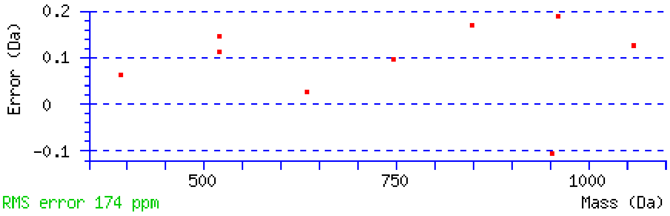
Match to Query 4762: 1359.686442 from(680.850497,2+) index(8312)
Title: Elution from: 74.946 to 74.946 scan no 11143 cid35.00 polarity:+
Data file D1d-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

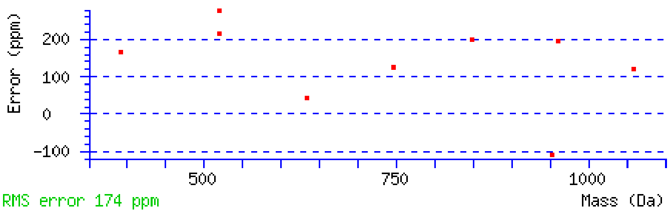


Monoisotopic mass of neutral peptide Mr(calc): 1359.6882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 1.2e-006
Matches : 9/108 fragment ions using 8 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	112.0393	56.5233	E							12
2	187.0713	94.0393	169.0608	85.0340	G	1231.6529	616.3301	1214.6263	607.8168	1213.6423	607.3248	11
3	302.0983	151.5528	284.0877	142.5475	D	1174.6314	587.8193	1157.6048	579.3061	1156.6208	578.8141	10
4	401.1667	201.0870	383.1561	192.0817	V	***1059.6045***	530.3059	1042.5779	521.7926	1041.5939	521.3006	9
5	514.2508	257.6290	496.2402	248.6237	L	***960.5360***	480.7717	943.5095	472.2584	942.5255	471.7664	8
6	615.2984	308.1529	597.2879	299.1476	T	***847.4520***	424.2296	830.4254	415.7164	829.4414	415.2243	7
7	728.3825	364.6949	710.3719	355.6896	L	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
8	841.4666	421.2369	823.4560	412.2316	L	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
9	970.5092	485.7582	952.4986	476.7529	E	***520.2362***	260.6217	503.2096	252.1084	502.2256	251.6164	4
10	1057.5412	529.2742	1039.5306	520.2689	S	***391.1936***	196.1004	374.1670	187.5872	373.1830	187.0951	3
11	1186.5838	593.7955	1168.5732	584.7902	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 174 ppm



RMS error 174 ppm

NCBI **BLAST** search of EGDVLTLLESER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G64140.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.9	1359.6882	-0.0017	EGDVLTLLESER
9.0	1359.6857	0.0008	TPTEWLIDVMR
7.0	1359.6881	-0.0017	GEDVLKAEETAAK

AT5G64690.1

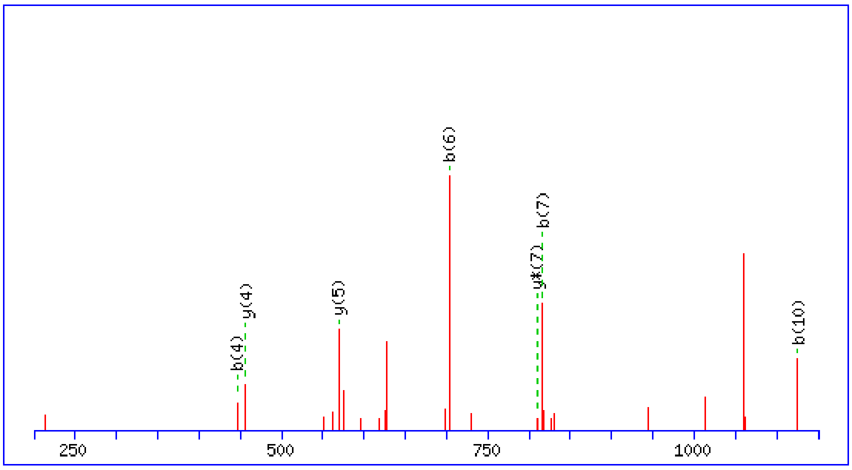
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDQDKEIVLPK**
Found in **AT5G64690.1** in **TAIR_Arabidopsis**, Symbols: | neurofilament triplet H protein-related | chr5:25880195-25881747 FORWARD

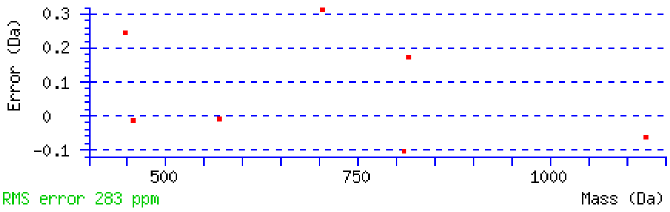
Match to Query 4345: 1270.680660 from(636.347606,2+) index(7528)
Title: Elution from: 68.699 to 68.699 scan no 9932 cid35.00 polarity:+
Data file D1d-2_1.mgf

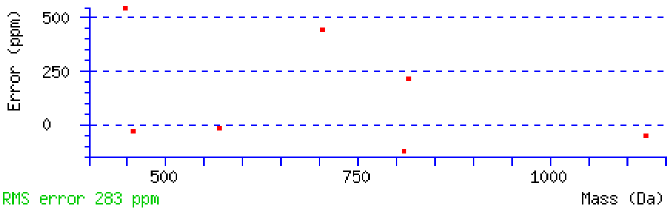
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1270.6769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 0.046
Matches : 7/106 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	203.0662	102.0368			185.0557	93.0315	D	1184.6521	592.8297	1167.6256	584.3164	1166.6416	583.8244	10
3	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	Q	1069.6252	535.3162	1052.5986	526.8030	1051.6146	526.3109	9
4	***446.1518***	223.5795	429.1252	215.0662	428.1412	214.5742	D	941.5666	471.2869	924.5401	462.7737	923.5560	462.2817	8
5	574.2467	287.6270	557.2202	279.1137	556.2362	278.6217	K	826.5397	413.7735	809.5131	405.2602	808.5291	404.7682	7
6	***703.2893***	352.1483	686.2628	343.6350	685.2788	343.1430	E	698.4447	349.7260	681.4182	341.2127	680.4341	340.7207	6
7	***816.3734***	408.6903	799.3468	400.1771	798.3628	399.6850	I	**569.4021**	285.2047	552.3756	276.6914			5
8	915.4418	458.2245	898.4153	449.7113	897.4312	449.2193	V	**456.3180**	228.6627	439.2915	220.1494			4
9	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	L	357.2496	179.1285	340.2231	170.6152			3
10	***1125.5786***	563.2930	1108.5521	554.7797	1107.5681	554.2877	P	244.1656	122.5864	227.1390	114.0731			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SDQDKEIVLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G64690.1

Score	Mr(calc)	Delta	Sequence
19.1	1270.6769	0.0038	SDQDKEIVLPK
5.7	1270.6822	-0.0016	AAQALFHSWLK

AT5G64760.1

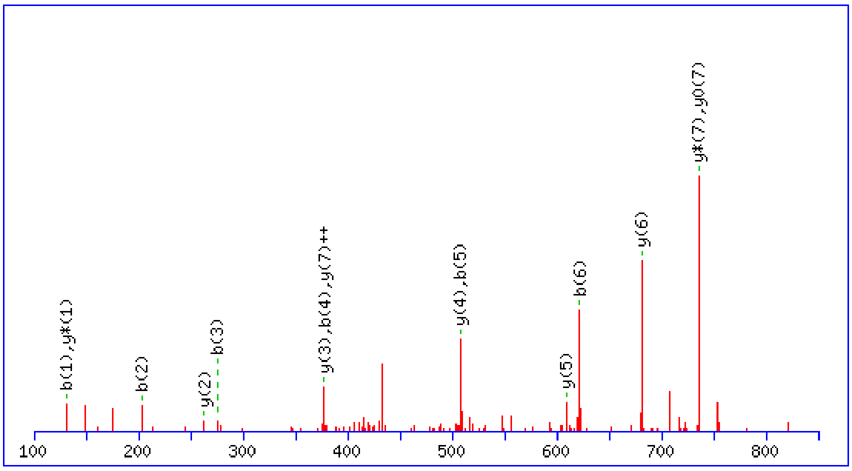
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAATEILK**
Found in **AT5G64760.1** in **TAIR_Arabidopsis**, Symbols: | 26S proteasome regulatory subunit, putative (RPN5) | chr5:25911253-25913671 REVERSE

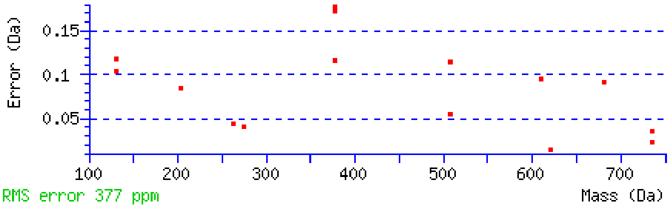
Match to Query 1465: 882.504570 from(442.259561,2+) index(1926)
Title: Elution from: 23.027 to 23.027 scan no 2504 cid35.00 polarity:+
Data file C7-1_2.mgf

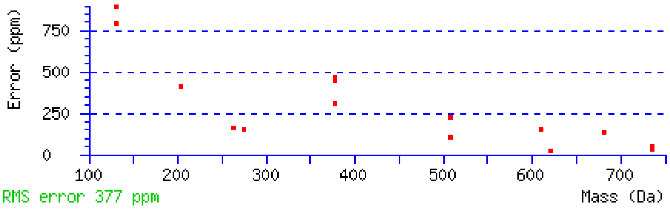
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 882.5035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 1.2e-006
Matches : 16/72 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	***131.0963***	66.0518	113.0727	57.0400			K							8
2	***203.1305***	102.0689	185.1069	93.0571			A	753.4217	377.2145	735.3981	368.2027	735.4111	368.2092	7
3	***275.1646***	138.0859	257.1410	129.0741			A	**681.3876**	341.1974	663.3640	332.1856	663.3770	332.1921	6
4	***377.2093***	189.1083	359.1857	180.0965	359.1988	180.1030	T	**609.3534**	305.1803	591.3298	296.1686	591.3428	296.1751	5
5	***507.2489***	254.1281	489.2254	245.1163	489.2384	245.1228	E	**507.3087**	254.1580	489.2851	245.1462	489.2981	245.1527	4
6	***621.3300***	311.1687	603.3065	302.1569	603.3195	302.1634	I	**377.2691**	189.1382	359.2455	180.1264			3
7	***735.4111***	368.2092	717.3876	359.1974	717.4006	359.2039	L	**263.1880**	132.0976	245.1644	123.0858			2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KAATEILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.6	882.5035	0.0011	KAATEILK

AT5G64760.1

36.4	882.5034	0.0011	GLTTQLLK
35.5	882.5061	-0.0016	GAAALARLK
33.9	882.5035	0.0011	DSGKLLLK
33.9	882.5034	0.0011	GTVDKIIK
24.1	882.5035	0.0011	ISVKDALK
22.4	882.5035	0.0011	ATIQSLLK
22.4	882.5035	0.0011	DVAKSILK
22.4	882.5035	0.0011	GKSDLLIK
22.4	882.5061	-0.0016	RNGGLLLK

AT5G65010.1

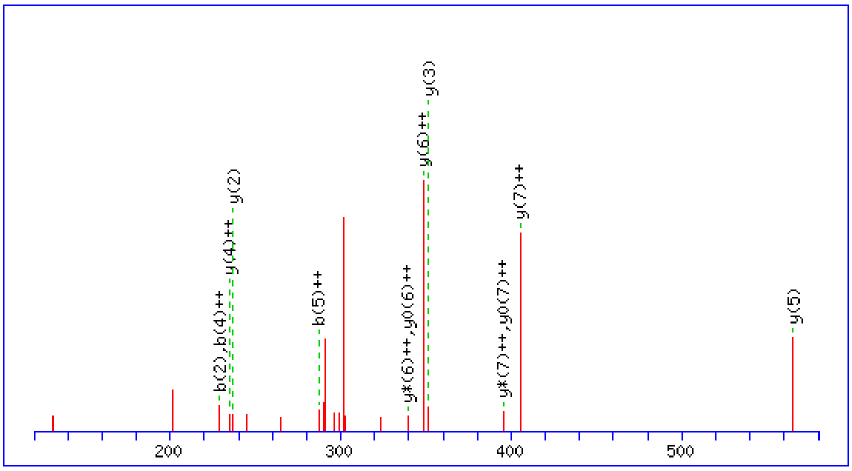
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIKPDLGR**
Found in **AT5G65010.1** in **TAIR_Arabidopsis**, Symbols: ASN2 | ASN2 (ASPARAGINE SYNTHETASE 2); asparagine synthase (glutamine-hydrolyzing) | chr5:25986450-25989504 FORWARD

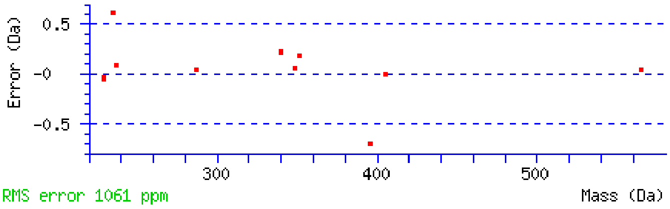
Match to Query 1424: 922.524315 from(308.515381,3+) index(1456)
Title: Elution from: 21.195 to 21.195 scan no 1995 cid35.00 polarity:+
Data file D1d-1_3.mgf

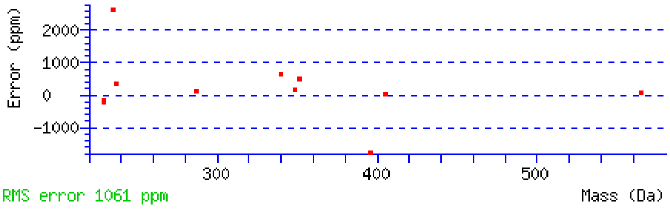
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 120 to 580 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 922.5244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 0.0099
Matches : 13/66 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							8
2	229.1695	115.0884					I	809.4506	405.2289	791.4270	396.2171	791.4400	396.2237	7
3	359.2585	180.1329	341.2349	171.1211			K	695.3695	348.1884	677.3459	339.1766	677.3589	339.1831	6
4	457.3083	**229.1578**	439.2847	220.1460			P	***565.2805***	283.1439	547.2569	274.1321	547.2699	274.1386	5
5	573.3323	**287.1698**	555.3087	278.1580	555.3217	278.1645	D	467.2307	234.1190	449.2071	225.1072	449.2201	225.1137	4
6	687.4134	344.2103	669.3898	335.1985	669.4028	335.2050	L	***351.2067***	176.1070	333.1831	167.0952			3
7	745.4319	373.2196	727.4083	364.2078	727.4213	364.2143	G	***237.1256***	119.0664	219.1020	110.0546			2
8							R	179.1071	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of LIKPDLGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.7	922.5244	-0.0001	LIKPDLGR

AT5G65010.1

17.6	922.5217	0.0026	LLLILDAEK
17.6	922.5217	0.0026	LLLIDAEK
13.6	922.5244	-0.0001	ILAKPVDR
7.8	922.5244	-0.0001	EPLGVRIK
7.6	922.5244	-0.0001	IKVVHTSK
6.9	922.5271	-0.0028	ILGKRGHK
6.9	922.5271	-0.0028	LLGKRGHK
3.7	922.5267	-0.0023	IIPPLGFR
3.0	922.5244	-0.0001	LLSQVVPR

AT5G65220.1

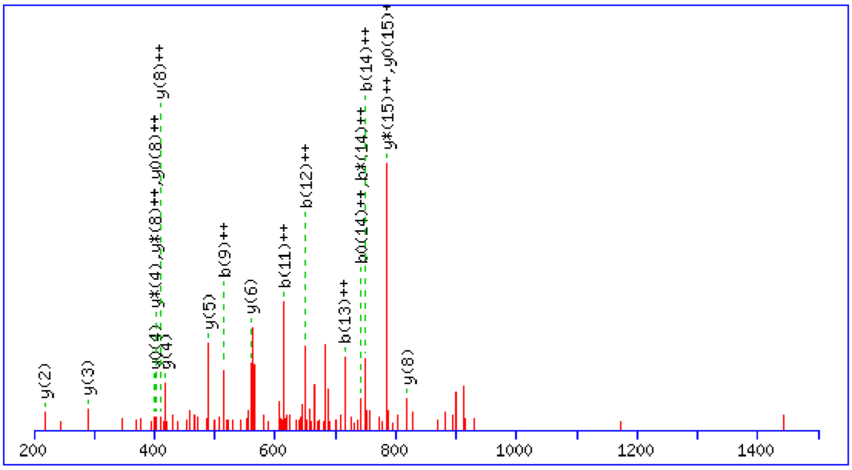
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLQEEEAAEEAAEAAK**
Found in **AT5G65220.1** in **TAIR_Arabidopsis**, Symbols: | ribosomal protein L29 family protein | chr5:26078527-26079732 FORWARD

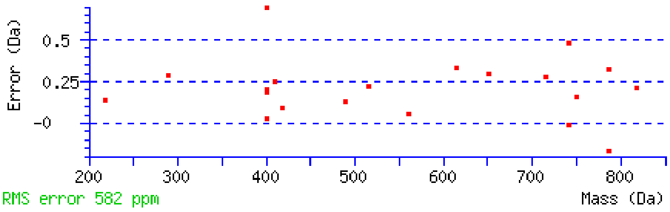
Match to Query 8491: 1715.819103 from(572.946977,3+) index(3675)
Title: Elution from: 35.350 to 35.350 scan no 4553 cid35.00 polarity:+
Data file 0-2_1.mgf

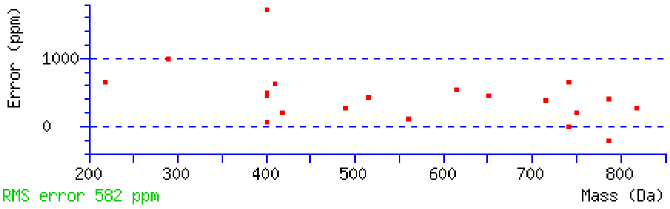
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1715.8213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00039
Matches : 21/168 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							16
2	242.1863	121.5968	225.1598	113.0835			L	1588.7337	794.8705	1571.7071	786.3572	1570.7231	785.8652	15
3	370.2449	185.6261	353.2183	177.1128			Q	1475.6496	738.3284	1458.6231	729.8152	1457.6391	729.3232	14
4	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	E	1347.5910	674.2992	1330.5645	665.7859	1329.5805	665.2939	13
5	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	E	1218.5485	609.7779	1201.5219	601.2646	1200.5379	600.7726	12
6	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	E	1089.5059	545.2566	1072.4793	536.7433	1071.4953	536.2513	11
7	828.4098	414.7085	811.3832	406.1953	810.3992	405.7032	A	960.4633	480.7353	943.4367	472.2220	942.4527	471.7300	10
8	899.4469	450.2271	882.4203	441.7138	881.4363	441.2218	A	889.4262	445.2167	872.3996	436.7034	871.4156	436.2114	9
9	1028.4895	***514.7484***	1011.4629	506.2351	1010.4789	505.7431	E	***818.3890***	409.6982	801.3625	401.1849	800.3785	400.6929	8
10	1157.5321	579.2697	1140.5055	570.7564	1139.5215	570.2644	E	689.3464	345.1769	672.3199	336.6636	671.3359	336.1716	7
11	1228.5692	***614.7882***	1211.5426	606.2750	1210.5586	605.7829	A	***560.3039***	280.6556	543.2773	272.1423	542.2933	271.6503	6
12	1299.6063	***650.3068***	1282.5798	641.7935	1281.5957	641.3015	A	***489.2667***	245.1370	472.2402	236.6237	471.2562	236.1317	5
13	1428.6489	***714.8281***	1411.6223	706.3148	1410.6383	705.8228	E	***418.2296***	209.6185	401.2031	201.1052	400.2191	200.6132	4
14	1499.6860	***750.3466***	1482.6595	741.8334	1481.6754	741.3414	A	***289.1870***	145.0972	272.1605	136.5839			3
15	1570.7231	***785.8652***	1553.6966	777.3519	1552.7126	776.8599	A	***218.1499***	109.5786	201.1234	101.0653			2
16							K	147.1128	74.0600	130.0863	65.5468			1





AT5G65220.1

NCBI **BLAST** search of KLQEEEAAEEAAEAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.1	1715.8213	-0.0022	KLQEEEAAEEAAEAAK
7.2	1715.8209	-0.0018	HHRMHANCNIVVGR
1.6	1715.8162	0.0029	RHYCPELGTNADRK
1.1	1715.8187	0.0004	QKSNSSHSGVSESINR

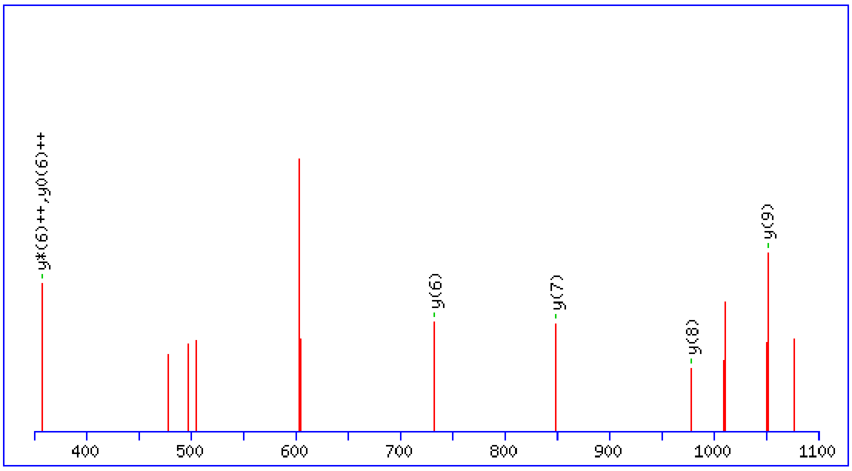
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAAEDTMIAYK**
Found in **AT5G65430.1** in **TAIR_Arabidopsis**, Symbols: GF14 KAPPA, GRF8 | GRF8 (GENERAL REGULATORY FACTOR 8); protein phosphorylated amino acid binding | chr5:26165772-26167481 REVERSE

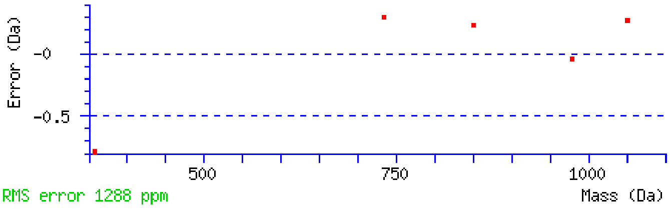
Match to Query 4189: 1224.535882 from(613.275217,2+) index(3407)
Title: Elution from: 32.937 to 32.937 scan no 4238 cid35.00 polarity:+
Data file 0-1_3.mgf

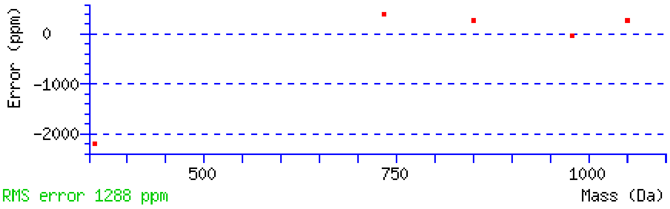
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1224.5340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.039
Matches : 6/90 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	103.0520	52.0296	85.0414	43.0244	T							11
2	175.0861	88.0467	157.0756	79.0414	A	1123.4966	562.2519	1105.4730	553.2402	1105.4861	553.2467	10
3	247.1203	124.0638	229.1097	115.0585	A	***1051.4625***	526.2349	1033.4389	517.2231	1033.4519	517.2296	9
4	377.1599	189.0836	359.1494	180.0783	E	***979.4283***	490.2178	961.4047	481.2060	961.4178	481.2125	8
5	493.1839	247.0956	475.1733	238.0903	D	***849.3887***	425.1980	831.3651	416.1862	831.3781	416.1927	7
6	595.2286	298.1179	577.2180	289.1127	T	***733.3647***	367.1860	715.3411	358.1742	715.3542	358.1807	6
7	727.2661	364.1367	709.2556	355.1314	M	631.3200	316.1636	613.2964	307.1518			5
8	841.3472	421.1773	823.3367	412.1720	I	499.2825	250.1449	481.2589	241.1331			4
9	913.3814	457.1943	895.3708	448.1890	A	385.2014	193.1043	367.1778	184.0925			3
10	1077.4417	539.2245	1059.4312	530.2192	Y	313.1672	157.0873	295.1437	148.0755			2
11					K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of TAAEDTMIAYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G65430.1

Score	Mr(calc)	Delta	Sequence
22.4	1224.5340	0.0018	TAAEDTMIAYK
22.4	1224.5340	0.0018	TAAEDTMLAYK
1.9	1224.5394	-0.0035	AGNMPVQYRR
1.7	1224.5345	0.0014	ETMKSQKADR
1.3	1224.5390	-0.0031	GCAKSYGPFPK

AT5G65860.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMDSESKGVMMAWEKPLMEAHAK**
Found in **AT5G65860.1** in **TAIR_Arabidopsis**, Symbols: | ankyrin repeat family protein | chr5:26364932-26365972 REVERSE

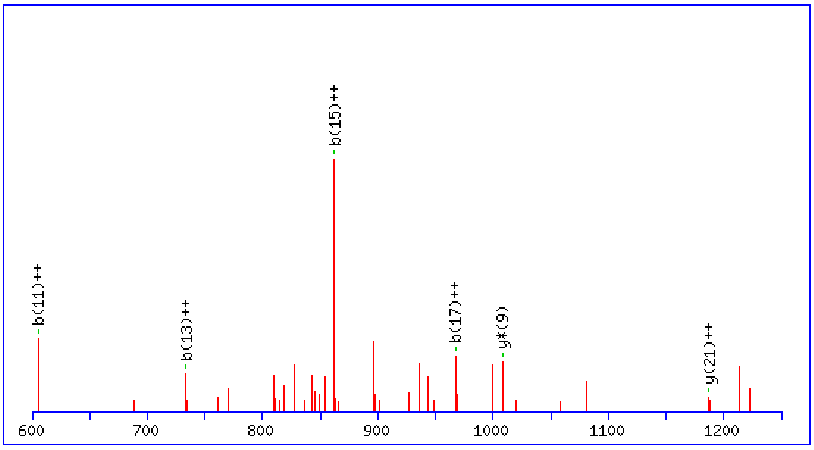
Match to Query 10140: 2618.231700 from(873.751176,3+) index(7074)
Title: Elution from: 62.436 to 62.436 scan no 9274 cid35.00 polarity:+
Data file 0-3_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 600 to 1250 Da Full range

Label all possible matches ○ Label matches used for scoring ●

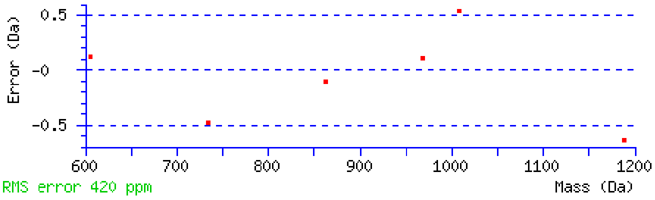
Show Y-axis ☐

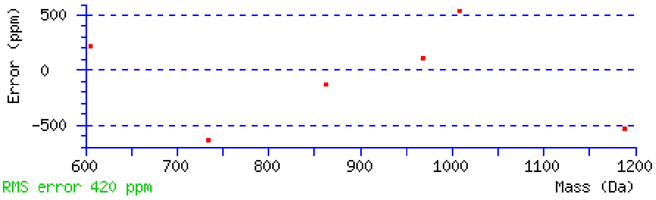


```
Monoisotopic mass of neutral peptide Mr(calc): 2618.2364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19  Expect: 0.032
Matches : 6/240 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							23
2	245.1318	123.0696					M	2506.1597	1253.5835	2489.1332	1245.0702	2488.1492	1244.5782	22
3	360.1588	180.5830			342.1482	171.5777	D	2375.1192	1188.0633	2358.0927	1179.5500	2357.1087	1179.0580	21
4	447.1908	224.0990			429.1802	215.0938	S	2260.0923	1130.5498	2243.0657	1122.0365	2242.0817	1121.5445	20
5	576.2334	288.6203			558.2228	279.6151	E	2173.0603	1087.0338	2156.0337	1078.5205	2155.0497	1078.0285	19
6	663.2654	332.1363			645.2549	323.1311	S	2044.0177	1022.5125	2026.9911	1013.9992	2026.0071	1013.5072	18
7	791.3604	396.1838	774.3338	387.6706	773.3498	387.1785	K	1956.9856	978.9965	1939.9591	970.4832	1938.9751	969.9912	17
8	848.3818	424.6946	831.3553	416.1813	830.3713	415.6893	G	1828.8907	914.9490	1811.8641	906.4357	1810.8801	905.9437	16
9	947.4503	474.2288	930.4237	465.7155	929.4397	465.2235	V	1771.8692	886.4382	1754.8427	877.9250	1753.8587	877.4330	15
10	1078.4907	539.7490	1061.4642	531.2357	1060.4802	530.7437	M	1672.8008	836.9040	1655.7743	828.3908	1654.7902	827.8988	14
11	1209.5312	***605.2693***	1192.5047	596.7560	1191.5207	596.2640	M	1541.7603	771.3838	1524.7338	762.8705	1523.7498	762.3785	13
12	1280.5683	640.7878	1263.5418	632.2745	1262.5578	631.7825	A	1410.7198	705.8636	1393.6933	697.3503	1392.7093	696.8583	12
13	1466.6477	***733.8275***	1449.6211	725.3142	1448.6371	724.8222	W	1339.6827	670.3450	1322.6562	661.8317	1321.6722	661.3397	11
14	1595.6902	798.3488	1578.6637	789.8355	1577.6797	789.3435	E	1153.6034	577.3053	1136.5769	568.7921	1135.5928	568.3001	10
15	1723.7852	***862.3962***	1706.7587	853.8830	1705.7746	853.3910	K	1024.5608	512.7840	1007.5343	504.2708	1006.5502	503.7788	9
16	1820.8380	910.9226	1803.8114	902.4094	1802.8274	901.9173	P	896.4659	448.7366	879.4393	440.2233	878.4553	439.7313	8
17	1933.9220	***967.4647***	1916.8955	958.9514	1915.9115	958.4594	L	799.4131	400.2102	782.3865	391.6969	781.4025	391.2049	7
18	2064.9625	1032.9849	2047.9360	1024.4716	2046.9520	1023.9796	M	686.3290	343.6681	669.3025	335.1549	668.3185	334.6629	6
19	2194.0051	1097.5062	2176.9786	1088.9929	2175.9946	1088.5009	E	555.2885	278.1479	538.2620	269.6346	537.2780	269.1426	5
20	2265.0422	1133.0248	2248.0157	1124.5115	2247.0317	1124.0195	A	426.2459	213.6266	409.2194	205.1133			4
21	2402.1011	1201.5542	2385.0746	1193.0409	2384.0906	1192.5489	H	355.2088	178.1081	338.1823	169.5948			3
22	2473.1383	1237.0728	2456.1117	1228.5595	2455.1277	1228.0675	A	218.1499	109.5786	201.1234	101.0653			2
23							K	147.1128	74.0600	130.0863	65.5468			1

AT5G65860.1





NCBI **BLAST** search of LMDSESKGVMMAWEKPLMEAHAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.7	2618.2364	-0.0047	LMDSESKGVMMAWEKPLMEAHAK
8.4	2618.2395	-0.0078	AQQTLAGYSSSNLGMDFARTELSR
0.5	2618.2322	-0.0005	FWSSESNELITADQLAEMKYTR
0.3	2618.2262	0.0055	GYQFWSKADENGSFSINNVRSGR

AT5G66120.2

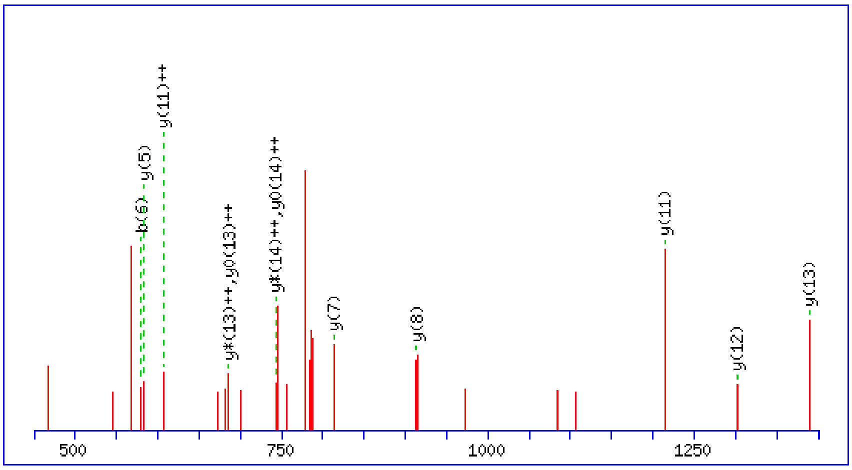
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SISSPTVVEVDLGDR**
Found in **AT5G66120.2** in **TAIR_Arabidopsis**, Symbols: | 3-dehydroquinate synthase, putative | chr5:26448742-26450875 REVERSE

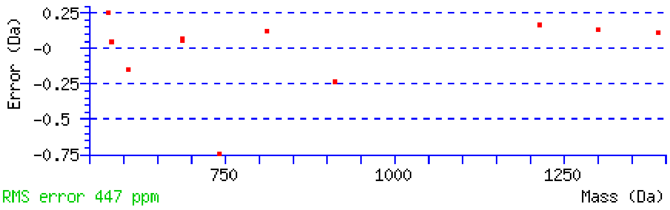
Match to Query 7112: 1590.746680 from(796.380616,2+) index(6047)
Title: Elution from: 53.890 to 53.890 scan no 7755 cid35.00 polarity:+
Data file 0-2_2.mgf

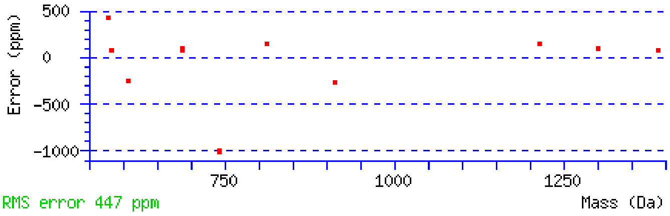
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 450 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1590.7461
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.012
Matches : 12/138 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	89.0363	45.0218	71.0258	36.0165	**S**							**15**
2	203.1174	102.0624	185.1069	93.0571	**I**	1503.7244	752.3658	1485.7008	743.3540	1485.7138	743.3605	**14**
3	291.1465	146.0769	273.1359	137.0716	**S**	***1389.6433***	695.3253	1371.6197	686.3135	1371.6327	686.3200	**13**
4	379.1756	190.0914	361.1650	181.0861	**S**	***1301.6142***	651.3107	1283.5906	642.2989	1283.6036	642.3055	**12**
5	477.2254	239.1163	459.2148	230.1110	**P**	***1213.5851***	607.2962	1195.5615	598.2844	1195.5746	598.2909	**11**
6	579.2701	290.1387	561.2595	281.1334	**T**	1115.5353	558.2713	1097.5117	549.2595	1097.5248	549.2660	**10**
7	679.3355	340.1714	661.3250	331.1661	**V**	1013.4906	507.2489	995.4670	498.2372	995.4801	498.2437	**9**
8	779.4010	390.2041	761.3904	381.1988	**V**	***913.4252***	457.2162	895.4016	448.2044	895.4146	448.2109	**8**
9	909.4406	455.2239	891.4300	446.2187	**E**	***813.3597***	407.1835	795.3361	398.1717	795.3492	398.1782	**7**
10	1009.5061	505.2567	991.4955	496.2514	**V**	683.3201	342.1637	665.2965	333.1519	665.3095	333.1584	**6**
11	1125.5300	563.2687	1107.5195	554.2634	**D**	***583.2546***	292.1310	565.2311	283.1192	565.2441	283.1257	**5**
12	1239.6111	620.3092	1221.6006	611.3039	**L**	467.2307	234.1190	449.2071	225.1072	449.2201	225.1137	**4**
13	1297.6296	649.3185	1279.6191	640.3132	**G**	353.1496	177.0784	335.1260	168.0666	335.1390	168.0731	**3**
14	1413.6536	707.3304	1395.6430	698.3252	**D**	295.1311	148.0692	277.1075	139.0574	277.1205	139.0639	**2**
15					**R**	179.1071	90.0572	161.0835	81.0454			**1**





NCBI **BLAST** search of SISSPTVVEVDLGDR

AT5G66120.2

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.8	1590.7461	0.0006	SISSPTVVEVDLGDR
1.1	1590.7506	-0.0039	SFIDDLVDPAGWLK
0.1	1590.7461	0.0006	KRDIDAEIEEVEK

AT5G66190.1

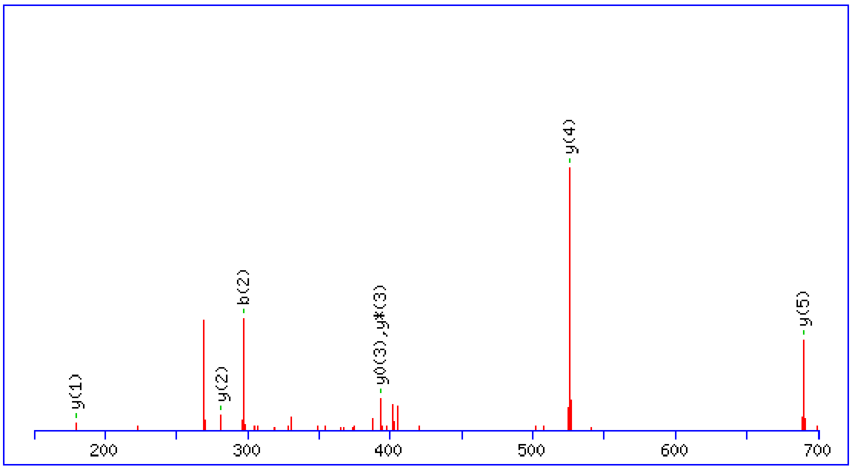
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MYIQTR**
Found in **AT5G66190.1** in **TAIR_Arabidopsis**, Symbols: ATLFNR1 | ATLFNR1 (LEAF FNR 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron tr

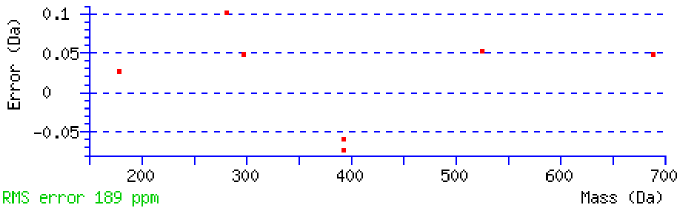
Match to Query 1113: 820.376372 from(411.195462,2+) index(1032)
Title: Elution from: 16.021 to 16.021 scan no 1435 cid35.00 polarity:+
Data file 0-3_2.mgf

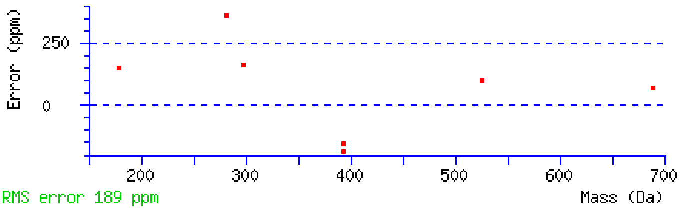
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 820.3761
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.04
Matches : 7/44 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	133.0448	67.0260					**M**							6
2	297.1052	149.0562					**Y**	***689.3459***	345.1766	671.3223	336.1648	671.3354	336.1713	5
3	411.1863	206.0968					**I**	***525.2856***	263.1464	507.2620	254.1346	507.2750	254.1411	4
4	541.2389	271.1231	523.2153	262.1113			**Q**	411.2045	206.1059	393.1809	197.0941	393.1939	197.1006	3
5	643.2836	322.1454	625.2600	313.1337	625.2731	313.1402	**T**	***281.1518***	141.0795	263.1282	132.0677	263.1412	132.0743	2
6							**R**	***179.1071***	90.0572	161.0835	81.0454			1





NCBI **BLAST** search of MYIQTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.1	820.3761	0.0002	MYIQTR
11.0	820.3761	0.0002	MYKDVR

AT5G66190.1

6.5	820.3762	0.0002	MPVPDPR
4.9	820.3762	0.0002	GSKNMFK
1.4	820.3762	0.0002	KFNQMK

AT5G66400.1

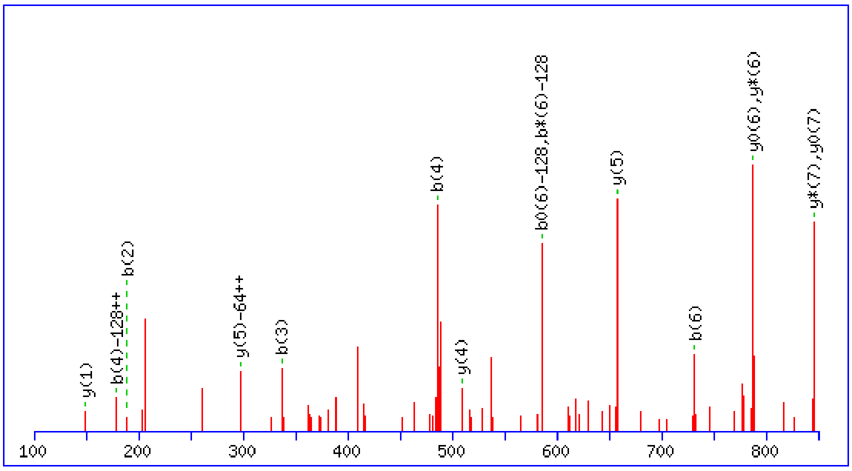
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGMMDKIK**
Found in **AT5G66400.1** in **TAIR_Arabidopsis**, Symbols: ATDI8, RAB18 | RAB18 (RESPONSIVE TO ABA 18) | chr5:26535737-26536379 REVERSE

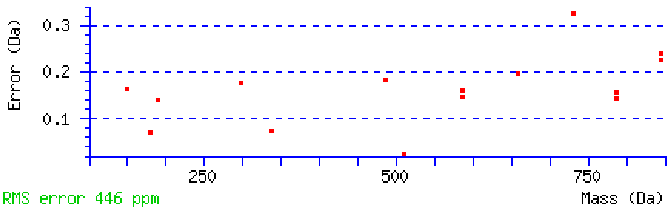
Match to Query 2537: 992.466268 from(497.240410,2+) index(7003)
Title: Elution from: 61.362 to 61.362 scan no 8939 cid35.00 polarity:+
Data file C7-3_1.mgf

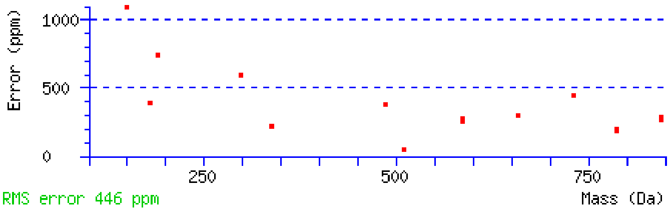
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 992.4661
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.031
Matches : 16/114 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	131.0963	66.0518	113.0727	57.0400			K							8
2	***189.1148***	95.0610	171.0912	86.0492			G	863.3844	432.1958	845.3608	423.1840	845.3738	423.1905	7
3	***337.1472***	169.0773	319.1237	160.0655			M	805.3659	403.1866	787.3423	394.1748	787.3553	394.1813	6
4	***485.1797***	243.0935	467.1561	234.0817			M	**657.3334**	329.1703	639.3098	320.1586	639.3229	320.1651	5
5	601.2037	301.1055	583.1801	292.0937	583.1931	292.1002	D	**509.3010**	255.1541	491.2774	246.1423	491.2904	246.1488	4
6	***731.2927***	366.1500	713.2691	357.1382	713.2821	357.1447	K	393.2770	197.1421	375.2534	188.1303			3
7	***845.3738***	423.1905	827.3502	414.1787	827.3632	414.1852	I	263.1880	132.0976	245.1644	123.0858			2
8							K	**149.1069**	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of KGMMDKIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G66400.1

Score	Mr(calc)	Delta	Sequence
20.1	992.4661	0.0002	KGMMDKIK
17.7	992.4661	0.0002	AMLTSMKGK
17.1	992.4661	0.0002	AMLTSMKGK
11.8	992.4650	0.0013	FWMKVEK
8.1	992.4675	-0.0012	KETYDTVK
5.4	992.4654	0.0009	FRCLDLR
5.4	992.4654	0.0009	FVRLCER
2.6	992.4658	0.0004	MVNQRRR

AT5G66470.1

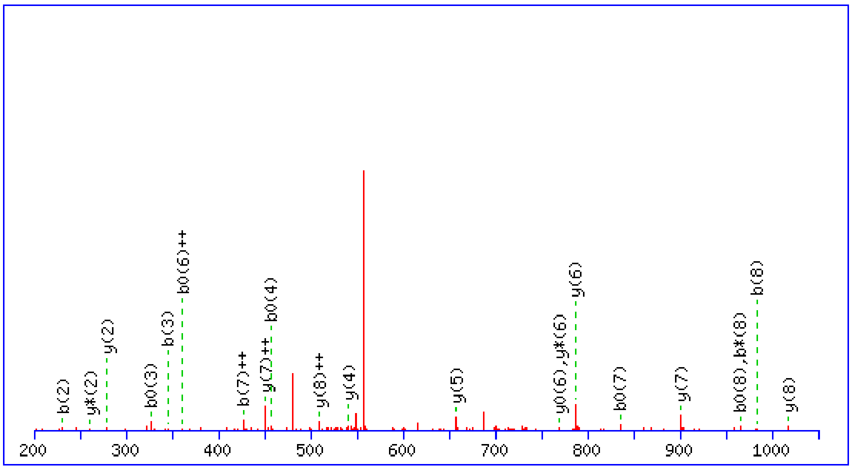
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDIEDFLQK**
Found in **AT5G66470.1** in **TAIR_Arabidopsis**, Symbols: | GTP binding / RNA binding | chr5:26559212-26561528 REVERSE

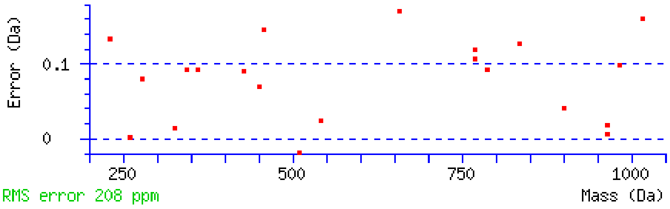
Match to Query 3357: 1130.549196 from(566.281874,2+) index(5690)
Title: Elution from: 53.630 to 53.630 scan no 7355 cid35.00 polarity:+
Data file D12h-2_1.mgf

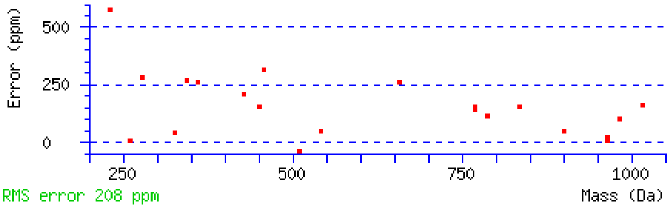
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1130.5486
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.019
Matches : 21/72 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0884	58.0478					L							9
2	**231.1124**	116.0598			213.1018	107.0545	D	***1017.4748***	509.2410	999.4512	500.2292	999.4642	500.2357	8
3	**345.1935**	173.1004			327.1829	164.0951	I	***901.4508***	451.2290	883.4272	442.2172	883.4402	442.2237	7
4	475.2331	238.1202			457.2225	229.1149	E	***787.3697***	394.1885	769.3461	385.1767	769.3591	385.1832	6
5	591.2571	296.1322			573.2465	287.1269	D	***657.3300***	329.1687	639.3065	320.1569	639.3195	320.1634	5
6	739.3225	370.1649			721.3119	361.1596	F	***541.3061***	271.1567	523.2825	262.1449			4
7	853.4036	427.2054			835.3930	418.2002	L	393.2406	197.1239	375.2170	188.1122			3
8	**983.4563**	492.2318	965.4327	483.2200	965.4457	483.2265	Q	***279.1595***	140.0834	261.1359	131.0716			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of LDIEDFLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.1	1130.5486	0.0006	LDIEDFLQK

AT5G66470.1

18.7	1130.5463	0.0029	LKIDDSEATK
13.7	1130.5486	0.0006	DIELFLNEK
13.5	1130.5519	-0.0027	LVKDIEEMK
12.3	1130.5463	0.0029	LPEETSSKTK
10.9	1130.5519	-0.0027	LIDEKEMVK
10.4	1130.5463	0.0029	LQAITESETK
9.5	1130.5463	0.0029	LDTTLAKDDK
9.1	1130.5513	-0.0021	IDYHSKNIK
7.9	1130.5486	0.0006	LPTDASFIEK

Mascot: http://www.matrixscience.com/

AT5G66530.1

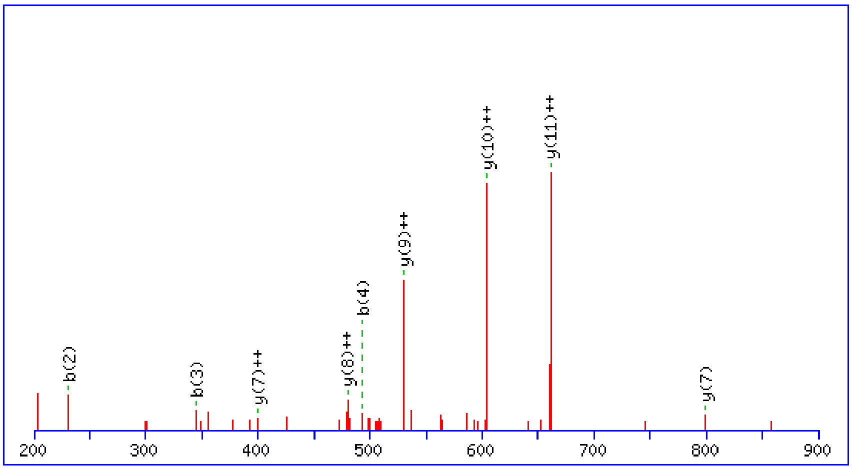
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLLFVRPDAVFNK**
Found in **AT5G66530.1** in **TAIR_Arabidopsis**, Symbols: | aldose 1-epimerase family protein | chr5:26571047-26572801 REVERSE

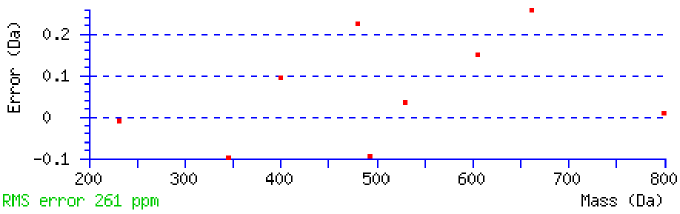
Match to Query 6264: 1550.785266 from(517.935698,3+) index(8314)
Title: Elution from: 78.300 to 78.300 scan no 11319 cid35.00 polarity:+
Data file D1d-1-2.mgf

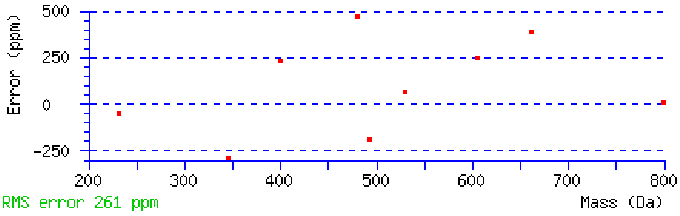
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1550.7817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.015
Matches : 9/124 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	117.0313	59.0193			99.0207	50.0140	D							13
2	231.1124	116.0598			213.1018	107.0545	L	1435.7650	718.3862	1417.7415	709.3744	1417.7545	709.3809	12
3	345.1935	173.1004			327.1829	164.0951	L	1321.6839	661.3456	1303.6604	652.3338	1303.6734	652.3403	11
4	493.2589	247.1331			475.2483	238.1278	F	1207.6028	604.3051	1189.5793	595.2933	1189.5923	595.2998	10
5	593.3244	297.1658			575.3138	288.1605	V	1059.5374	530.2723	1041.5138	521.2605	1041.5268	521.2671	9
6	753.4136	377.2104	735.3900	368.1986	735.4030	368.2052	R	959.4719	480.2396	941.4484	471.2278	941.4614	471.2343	8
7	851.4634	426.2353	833.4398	417.2235	833.4528	417.2301	P	799.3827	400.1950	781.3591	391.1832	781.3721	391.1897	7
8	967.4874	484.2473	949.4638	475.2355	949.4768	475.2420	D	701.3329	351.1701	683.3093	342.1583	683.3223	342.1648	6
9	1039.5215	520.2644	1021.4979	511.2526	1021.5110	511.2591	A	585.3089	293.1581	567.2853	284.1463			5
10	1139.5870	570.2971	1121.5634	561.2853	1121.5764	561.2918	V	513.2748	257.1410	495.2512	248.1292			4
11	1287.6524	644.3299	1269.6288	635.3181	1269.6419	635.3246	F	413.2093	207.1083	395.1857	198.0965			3
12	1403.6894	702.3483	1385.6658	693.3366	1385.6789	693.3431	N	265.1439	133.0756	247.1203	124.0638			2
13							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of DLLFVRPDAVFNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

AT5G66530.1

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.3	1550.7817	0.0035	DLLFVRPDAVFNK
12.5	1550.7898	-0.0046	INTVYQAALSVVEK
4.5	1550.7885	-0.0032	KVMLGVDRLDMIK
3.7	1550.7898	-0.0046	DIIGDFLTVISSVR
2.8	1550.7851	0.0002	TEMVKLYSKHIGK
0.5	1550.7844	0.0009	VKSPPFPTARGFAR
0.2	1550.7851	0.0001	NLNVMLKLNPYAK

AT5G66540.1

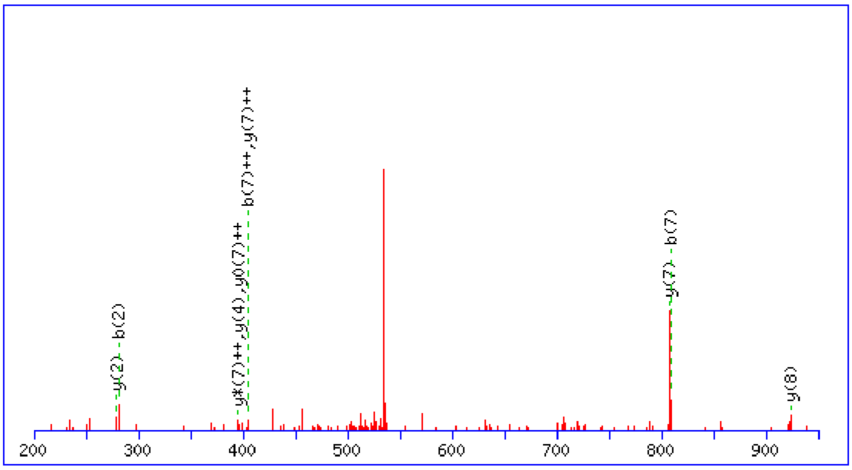
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDDFFGGKK**
Found in **AT5G66540.1** in **TAIR_Arabidopsis**, Symbols: | similar to hypothetical protein OsI_036143 [Oryza sativa (indica cultivar-group)] (GB:EAY82184.1); similar to hypothetical protein OsJ_031573 [Oryza sativa (japonica cultivar-group)] (GB:EAZ17364.1); similar to Os12g0133900 [Oryza sativ

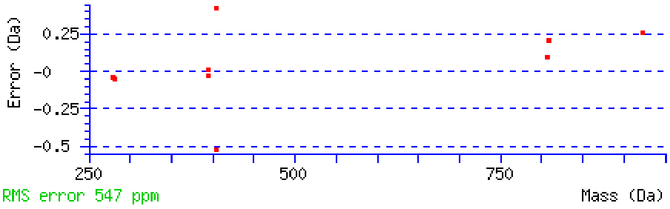
Match to Query 3442: 1086.467122 from(544.240837,2+) index(3270)
Title: Elution from: 32.643 to 32.643 scan no 4056 cid35.00 polarity:+
Data file 0-1_1.mgf

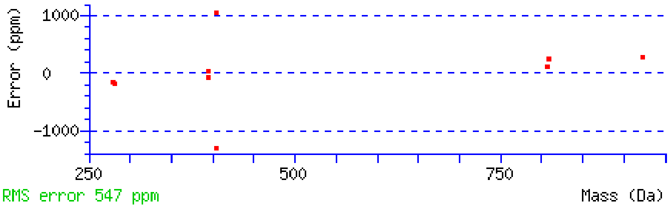
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1086.4648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 0.023
Matches : 10/68 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	165.0676	83.0375					Y							9
2	**281.0916**	141.0494			263.0811	132.0442	D	***923.4118***	462.2095	905.3882	453.1977	905.4012	453.2042	8
3	397.1156	199.0614			379.1050	190.0562	D	***807.3878***	404.1975	789.3642	395.1857	789.3772	395.1922	7
4	545.1810	273.0942			527.1705	264.0889	F	691.3638	346.1855	673.3402	337.1737			6
5	693.2465	347.1269			675.2359	338.1216	F	543.2984	272.1528	525.2748	263.1410			5
6	751.2650	376.1361			733.2544	367.1309	G	***395.2329***	198.1201	377.2093	189.1083			4
7	**809.2835**	405.1454			791.2729	396.1401	G	337.2144	169.1108	319.1908	160.0990			3
8	939.3725	470.1899	921.3489	461.1781	921.3620	461.1846	K	***279.1959***	140.1016	261.1723	131.0898			2
9							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of YDDFFGGKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G66540.1

Score	Mr(calc)	Delta	Sequence
21.6	1086.4648	0.0023	YDDFFGGKK
10.2	1086.4660	0.0011	MQSDSGLPPK
9.6	1086.4660	0.0012	GGEPDLMTGAK
7.3	1086.4653	0.0019	YGHPTEAAAR
4.3	1086.4660	0.0011	VSDPMVNDAK
3.9	1086.4639	0.0032	MFRSKSCR
3.1	1086.4653	0.0019	HTSGEWVTR
3.1	1086.4660	0.0011	SGDINDPVMK
2.6	1086.4687	-0.0015	MRFSSSSVR
1.2	1086.4660	0.0012	DVPDEIMTR

AT5G66570.1

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLDASGKPDSFTGK**
Found in **AT5G66570.1** in **TAIR_Arabidopsis**, Symbols: PSBO-1, OEE1, OEE33, OE33, PSBO1 | OE33/OEE1/OEE33/PSBO-1/PSBO1 (OXYGEN-EVOLVING ENHANCER 33); oxygen evolving/ poly(U) binding | chr5:26585970-26587350 FORWARD

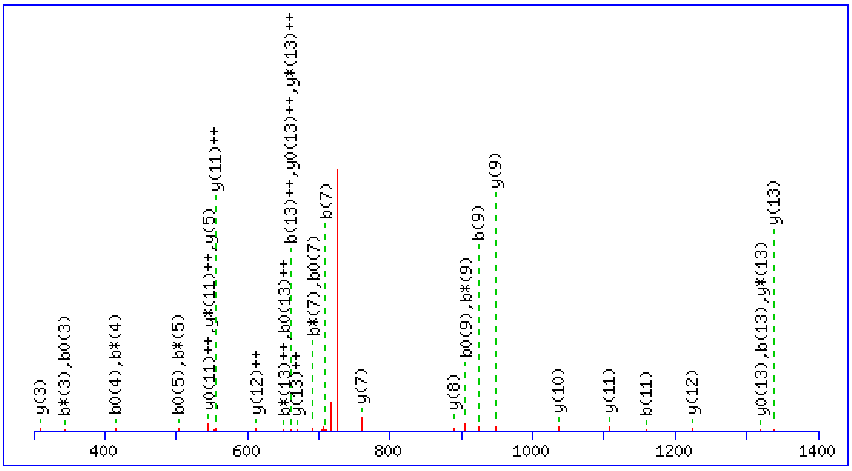
Match to Query 6031: 1466.659720 from(734.337136,2+) index(1557)
Title: Elution from: 20.616 to 20.616 scan no 2092 cid35.00 polarity:+
Data file C7-1_2.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 300 to 1400 Da Full range

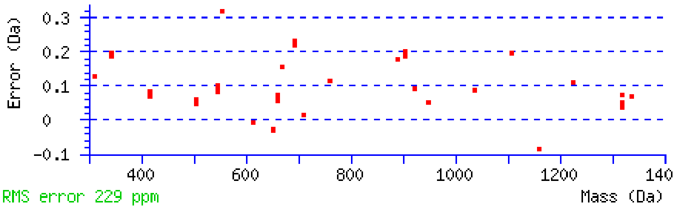
Label all possible matches ○ Label matches used for scoring ●

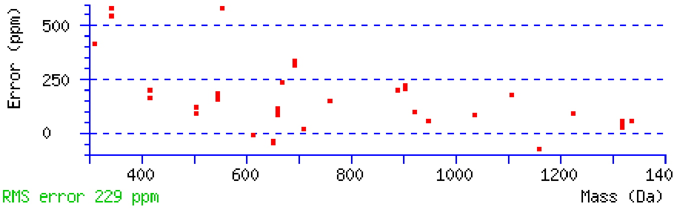
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1466.6595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 3e-009
Matches : 35/148 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	131.0599	66.0336	113.0363	57.0218			Q							14
2	245.1410	123.0741	227.1174	114.0624			L	***1337.6142***	669.3107	1319.5906	660.2989	1319.6036	660.3055	13
3	361.1650	181.0861	343.1414	172.0743	343.1544	172.0809	D	***1223.5331***	612.2702	1205.5095	603.2584	1205.5225	603.2649	12
4	433.1991	217.1032	415.1756	208.0914	415.1886	208.0979	A	***1107.5091***	554.2582	1089.4855	545.2464	1089.4986	545.2529	11
5	521.2282	261.1177	503.2046	252.1060	503.2176	252.1125	S	***1035.4750***	518.2411	1017.4514	509.2293	1017.4644	509.2358	10
6	579.2467	290.1270	561.2231	281.1152	561.2361	281.1217	G	***947.4459***	474.2266	929.4223	465.2148	929.4353	465.2213	9
7	**709.3357**	355.1715	691.3122	346.1597	691.3252	346.1662	K	***889.4274***	445.2173	871.4038	436.2055	871.4168	436.2121	8
8	807.3855	404.1964	789.3620	395.1846	789.3750	395.1911	P	***759.3384***	380.1728	741.3148	371.1610	741.3278	371.1675	7
9	**923.4095**	462.2084	905.3859	453.1966	905.3990	453.2031	D	661.2886	331.1479	643.2650	322.1361	643.2780	322.1426	6
10	1011.4386	506.2229	993.4150	497.2111	993.4280	497.2176	S	***545.2646***	273.1359	527.2410	264.1241	527.2540	264.1307	5
11	**1159.5040**	580.2557	1141.4804	571.2439	1141.4935	571.2504	F	457.2355	229.1214	439.2120	220.1096	439.2250	220.1161	4
12	1261.5487	631.2780	1243.5252	622.2662	1243.5382	622.2727	T	***309.1701***	155.0887	291.1465	146.0769	291.1595	146.0834	3
13	**1319.5672**	660.2873	1301.5437	651.2755	1301.5567	651.2820	G	207.1254	104.0663	189.1018	95.0545			2
14							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of QLDASGKPDSFTGK

AT5G66570.1

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.0	1466.6595	0.0002	QLDASGKPDSFTGK
20.4	1466.6573	0.0024	KIDGSDNTGEKASK
16.5	1466.6622	-0.0025	QNSAFENGSLPRK
16.3	1466.6573	0.0024	TPTKTNGPSSSSGTK
14.9	1466.6573	0.0024	EIKSNNQSLDSSK
13.0	1466.6582	0.0015	MLPQVEMTANKR
12.1	1466.6555	0.0042	ELCLIDESMKAK
11.3	1466.6622	-0.0025	SIWEKGNQDSKR
10.8	1466.6596	0.0001	VEENSIESYPRK
10.1	1466.6604	-0.0007	MLDMGFDPQIRK

AT5G66760.1

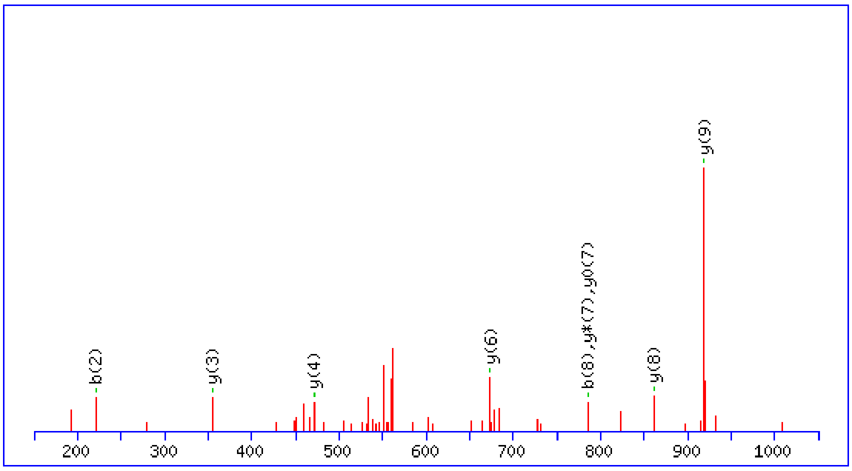
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFGGQSLDFGK**
Found in **AT5G66760.1** in **TAIR_Arabidopsis**, Symbols: SDH1-1 | SDH1-1 (Succinate dehydrogenase 1-1) | chr5:26671002-26674450 FORWARD

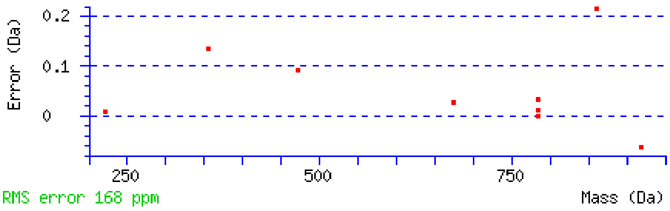
Match to Query 3588: 1138.503858 from(570.259205,2+) index(4821)
Title: Elution from: 43.586 to 43.586 scan no 6048 cid35.00 polarity:+
Data file 0-3_2.mgf

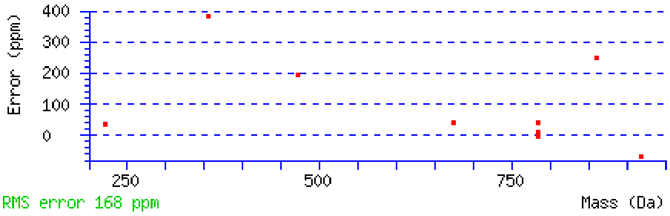
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1138.5069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00022
Matches : 9/96 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							11
2	**221.1069**	111.0571					F	1067.4801	534.2437	1049.4565	525.2319	1049.4695	525.2384	10
3	279.1254	140.0663					G	***919.4146***	460.2109	901.3910	451.1991	901.4040	451.2057	9
4	337.1439	169.0756					G	***861.3961***	431.2017	843.3725	422.1899	843.3855	422.1964	8
5	467.1965	234.1019	449.1729	225.0901			Q	803.3776	402.1924	785.3540	393.1807	785.3670	393.1872	7
6	555.2256	278.1164	537.2020	269.1046	537.2150	269.1111	S	***673.3250***	337.1661	655.3014	328.1543	655.3144	328.1608	6
7	669.3067	335.1570	651.2831	326.1452	651.2961	326.1517	L	585.2959	293.1516	567.2723	284.1398	567.2853	284.1463	5
8	**785.3307**	393.1690	767.3071	384.1572	767.3201	384.1637	D	***471.2148***	236.1110	453.1912	227.0992	453.2042	227.1058	4
9	933.3961	467.2017	915.3725	458.1899	915.3855	458.1964	F	***355.1908***	178.0990	337.1672	169.0873			3
10	991.4146	496.2109	973.3910	487.1991	973.4040	487.2057	G	207.1254	104.0663	189.1018	95.0545			2
11							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of AFGGQSLDFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G66760.1

Score	Mr(calc)	Delta	Sequence
43.6	1138.5069	-0.0030	AFGGQSLDFGK
10.0	1138.5069	-0.0031	FQQYLNDAK
4.1	1138.5022	0.0017	GYWCVANKK
2.8	1138.5033	0.0005	RVMTGNMTAK
1.6	1138.5033	0.0005	MSMTDRVLR
0.2	1138.5033	0.0005	RVMTGNMTAK

AT5G67030.1

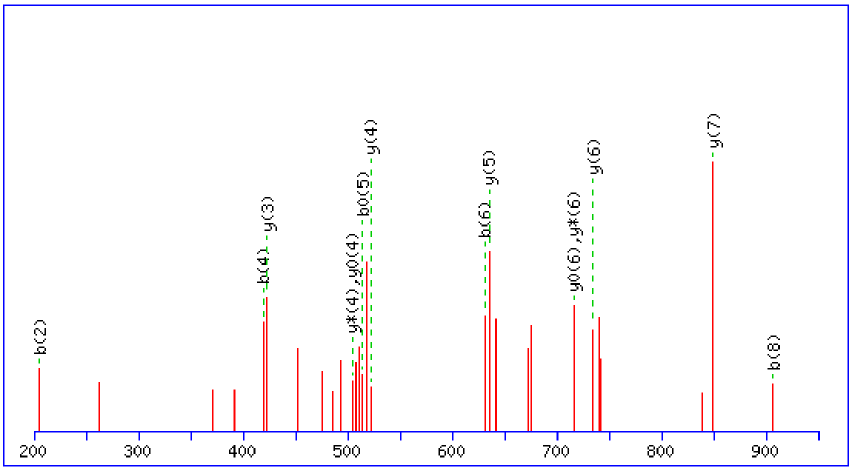
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFDVLVFEK**
Found in **AT5G67030.1** in **TAIR_Arabidopsis**, Symbols: LOS6, NPQ2, ATABA1, ZEP, IBS3, ATZEP, ABA1 | ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase | chr5:26770971-26774316 REVERSE

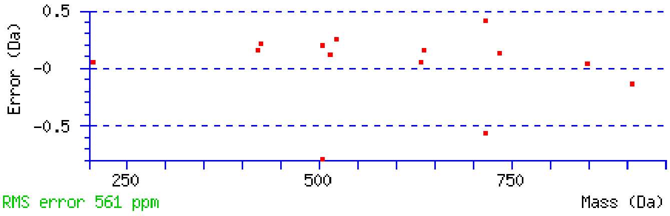
Match to Query 3108: 1052.555038 from(527.284795,2+) index(8394)
Title: Elution from: 73.911 to 73.911 scan no 10989 cid35.00 polarity:+
Data file C7-3_1.mgf

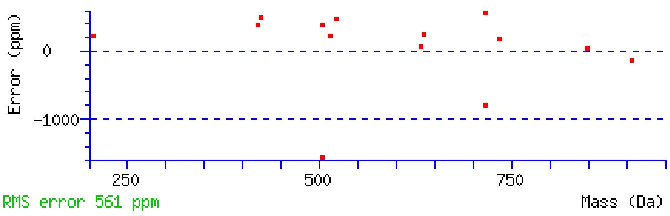
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1052.5543
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 0.0056
Matches : 14/74 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180			G							9
2	***205.0972***	103.0522			F	996.5401	498.7737	979.5135	490.2604	978.5295	489.7684	8
3	320.1241	160.5657	302.1135	151.5604	D	***849.4716***	425.2395	832.4451	416.7262	831.4611	416.2342	7
4	***419.1925***	210.0999	401.1819	201.0946	V	***734.4447***	367.7260	717.4182	359.2127	716.4341	358.7207	6
5	532.2766	266.6419	514.2660	257.6366	L	***635.3763***	318.1918	618.3497	309.6785	617.3657	309.1865	5
6	***631.3450***	316.1761	613.3344	307.1709	V	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
7	778.4134	389.7103	760.4028	380.7051	F	***423.2238***	212.1155	406.1973	203.6023	405.2132	203.1103	3
8	***907.4560***	454.2316	889.4454	445.2264	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GFDVLVFEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence

AT5G67030.1

26.8	1052.5543	0.0008	GFDVLVFEK

Mascot: http://www.matrixscience.com/

AT5G67230.1

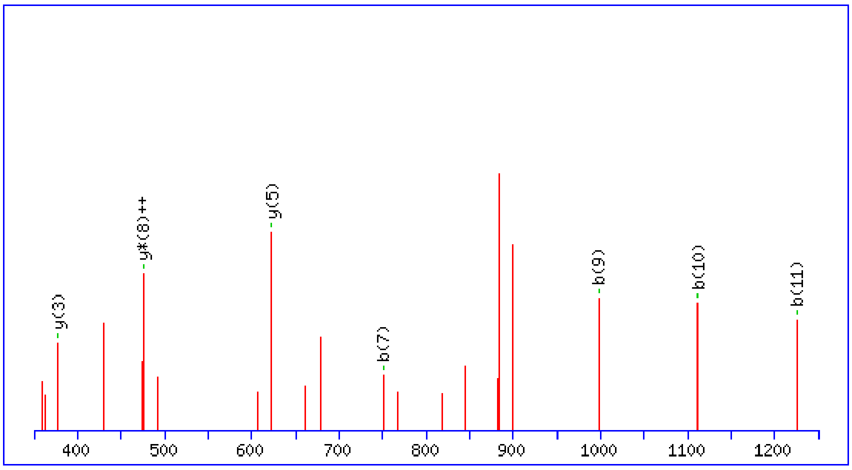
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADSKFPPGWIIK**
Found in **AT5G67230.1** in **TAIR_Arabidopsis**, Symbols: | glycosyl transferase family 43 protein | chr5:26839732-26841407 FORWARD

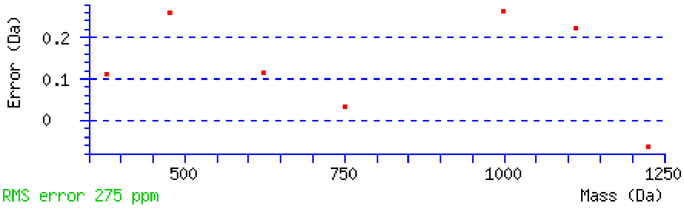
Match to Query 4715: 1372.690856 from(687.352704,2+) index(10124)
Title: Elution from: 101.553 to 101.553 scan no 14794 cid35.00 polarity:+
Data file D1d-1-2.mgf

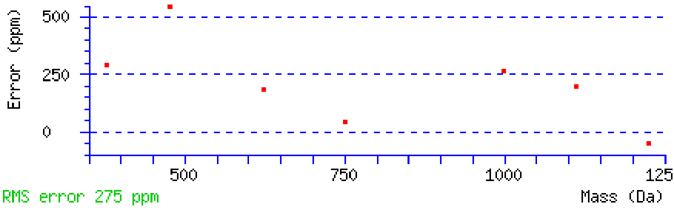
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 350 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1372.6949
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.042
Matches : 7/106 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	73.0414	37.0244					A							12
2	189.0654	95.0363			171.0548	86.0311	D	1301.6681	651.3377	1283.6445	642.3259	1283.6575	642.3324	11
3	277.0945	139.0509			259.0839	130.0456	S	1185.6441	593.3257	1167.6205	584.3139	1167.6335	584.3204	10
4	407.1835	204.0954	389.1599	195.0836	389.1729	195.0901	K	1097.6150	549.3112	1079.5915	540.2994			9
5	555.2489	278.1281	537.2254	269.1163	537.2384	269.1228	F	967.5260	484.2666	949.5024	475.2548			8
6	653.2987	327.1530	635.2752	318.1412	635.2882	318.1477	P	819.4606	410.2339	801.4370	401.2221			7
7	***751.3485***	376.1779	733.3250	367.1661	733.3380	367.1726	P	721.4108	361.2090	703.3872	352.1972			6
8	809.3670	405.1872	791.3435	396.1754	791.3565	396.1819	G	**623.3610**	312.1841	605.3374	303.1723			5
9	***997.4404***	499.2239	979.4168	490.2121	979.4299	490.2186	W	565.3425	283.1749	547.3189	274.1631			4
10	***1111.5215***	556.2644	1093.4979	547.2526	1093.5110	547.2591	I	**377.2691**	189.1382	359.2455	180.1264			3
11	***1225.6026***	613.3050	1207.5790	604.2932	1207.5921	604.2997	I	263.1880	132.0976	245.1644	123.0858			2
12							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of ADSKFPPGWIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

AT5G67230.1

Score	Mr(calc)	Delta	Sequence
20.5	1372.6949	-0.0041	ADSKFPPGWIIK
17.6	1372.6905	0.0004	STAQEVDPRLLK
16.1	1372.6927	-0.0018	GSAIGFHLDSLLK
7.8	1372.6931	-0.0023	VRNLPSRGETPK
5.6	1372.6931	-0.0023	QKLVHATASRDK
3.8	1372.6900	0.0008	AYLPSETPELIK
3.8	1372.6880	0.0029	MYGRKGYQLIK
1.9	1372.6905	0.0004	GLVNNKDLDQLK
1.6	1372.6884	0.0024	SLRLRMQHPSK
0.9	1372.6905	0.0004	NEIERLVNELK

AT5G67500.1

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSTNENTITVGGLYAIDHSTAVK**
Found in **AT5G67500.1** in **TAIR_Arabidopsis**, Symbols: | porin, putative | chr5:26952449-26954349 FORWARD

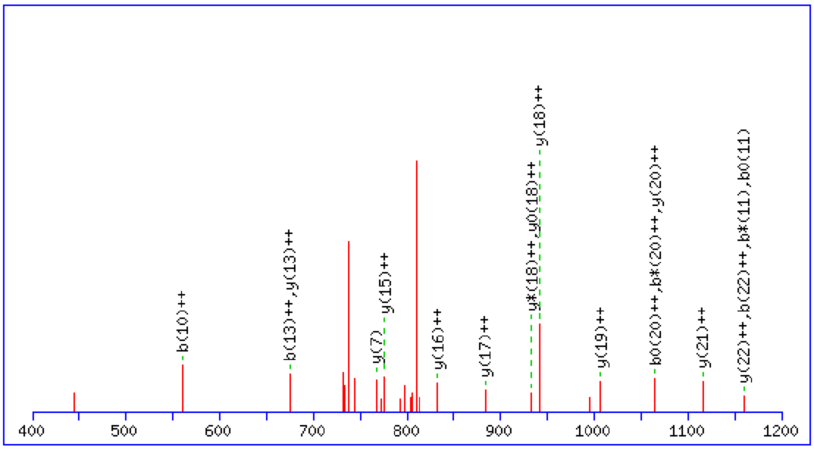
Match to Query 10095: 2465.131254 from(822.717694,3+) index(7003)
Title: Elution from: 63.111 to 63.111 scan no 9205 cid35.00 polarity:+
Data file D12h-2_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 400 to 1200 Da Full range

Label all possible matches ○ Label matches used for scoring ●

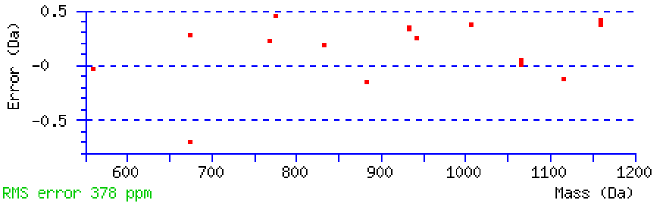
Show Y-axis ☐

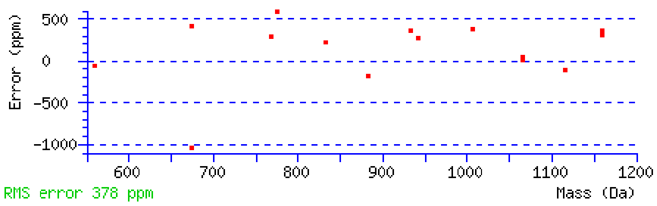


Monoisotopic mass of neutral peptide Mr(calc): 2465.1295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 8.2e-005
Matches : 19/250 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	149.0727	75.0400					F							23
2	237.1018	119.0545			219.0912	110.0492	S	2318.0713	1159.5393	2300.0477	1150.5275	2300.0608	1150.5340	22
3	339.1465	170.0769			321.1359	161.0716	T	2230.0423	1115.5248	2212.0187	1106.5130	2212.0317	1106.5195	21
4	455.1835	228.0954	437.1599	219.0836	437.1729	219.0901	N	2127.9975	1064.5024	2109.9740	1055.4906	2109.9870	1055.4971	20
5	585.2231	293.1152	567.1995	284.1034	567.2126	284.1099	E	2011.9606	1006.4839	1993.9370	997.4721	1993.9500	997.4786	19
6	701.2601	351.1337	683.2365	342.1219	683.2496	342.1284	N	1881.9209	941.4641	1863.8973	932.4523	1863.9104	932.4588	18
7	803.3048	402.1561	785.2813	393.1443	785.2943	393.1508	T	1765.8839	883.4456	1747.8603	874.4338	1747.8734	874.4403	17
8	917.3859	459.1966	899.3624	450.1848	899.3754	450.1913	I	1663.8392	832.4232	1645.8156	823.4115	1645.8286	823.4180	16
9	1019.4306	510.2190	1001.4071	501.2072	1001.4201	501.2137	T	1549.7581	775.3827	1531.7345	766.3709	1531.7475	766.3774	15
10	1119.4961	**560.2517**	1101.4725	551.2399	1101.4855	551.2464	V	1447.7134	724.3603	1429.6898	715.3485	1429.7028	715.3551	14
11	1177.5146	589.2609	1159.4910	580.2491	1159.5040	580.2557	G	1347.6480	674.3276	1329.6244	665.3158	1329.6374	665.3223	13
12	1235.5331	618.2702	1217.5095	609.2584	1217.5225	609.2649	G	1289.6295	645.3184	1271.6059	636.3066	1271.6189	636.3131	12
13	1349.6142	**675.3107**	1331.5906	666.2989	1331.6036	666.3055	L	1231.6110	616.3091	1213.5874	607.2973	1213.6004	607.3038	11
14	1513.6746	757.3409	1495.6510	748.3291	1495.6640	748.3356	Y	1117.5299	559.2686	1099.5063	550.2568	1099.5193	550.2633	10
15	1585.7087	793.3580	1567.6851	784.3462	1567.6981	784.3527	A	953.4695	477.2384	935.4459	468.2266	935.4589	468.2331	9
16	1699.7898	850.3985	1681.7662	841.3867	1681.7792	841.3933	I	881.4353	441.2213	863.4118	432.2095	863.4248	432.2160	8
17	1815.8138	908.4105	1797.7902	899.3987	1797.8032	899.4052	D	767.3542	384.1808	749.3307	375.1690	749.3437	375.1755	7
18	1955.8638	978.4355	1937.8402	969.4237	1937.8532	969.4303	H	651.3303	326.1688	633.3067	317.1570	633.3197	317.1635	6
19	2043.8929	1022.4501	2025.8693	1013.4383	2025.8823	1013.4448	S	511.2802	256.1438	493.2567	247.1320	493.2697	247.1385	5
20	2145.9376	1073.4724	2127.9140	1064.4606	2127.9270	1064.4671	T	423.2512	212.1292	405.2276	203.1174	405.2406	203.1239	4
21	2217.9717	1109.4895	2199.9481	1100.4777	2199.9612	1100.4842	A	321.2065	161.1069	303.1829	152.0951			3
22	2318.0372	**1159.5222**	2300.0136	1150.5104	2300.0266	1150.5169	V	249.1723	125.0898	231.1487	116.0780			2
23							K	149.1069	75.0571	131.0833	66.0453			1

AT5G67500.1





NCBI **BLAST** search of FSTNENTITVGGLYAIDHSTAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.8	2465.1295	0.0018	FSTNENTITVGGLYAIDHSTAVK
8.0	2465.1326	-0.0013	IYKAACKEPFPLDAVCGSVWK
5.7	2465.1302	0.0011	ELDVYDTCLLSSLPEVSKSGTK
3.2	2465.1355	-0.0043	MKYENELALRQGVEADINGLR
2.6	2465.1344	-0.0031	WTNYLRPDIKRGPFTADEEK
1.0	2465.1281	0.0031	AGKALEEHDILSHMLMNIGETK
1.0	2465.1281	0.0031	GMEKDSVSWAAMIKGLAQNGLAK
0.2	2465.1355	-0.0043	VEIGDLGNNFMVDAKSVGQSRAK

AT5G67580.1

Mascot Search Results

Peptide View

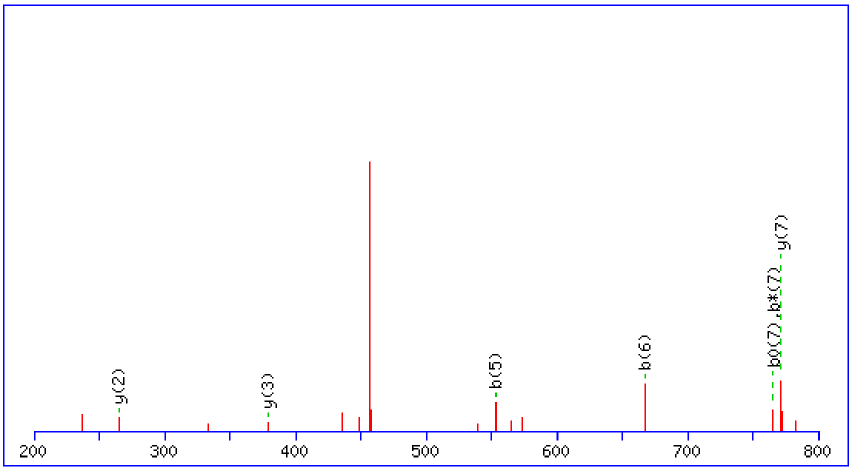
MS/MS Fragmentation of **RSITSLDK**
Found in **AT5G67580.1** in **TAIR_Arabidopsis**, Symbols: TRB2, ATTRB2 | ATTRB2/TRB2 (TELOMERE REPEAT BINDING FACTOR 2); DNA binding / transcription factor | chr5:26973069-26974299 REVERSE

Match to Query 1892: 930.477214 from(466.245883,2+) index(7635)
Title: Elution from: 67.646 to 67.646 scan no 10043 cid35.00 polarity:+
Data file 0-1_3.mgf

Click mouse within plot area to zoom in by factor of two about that point

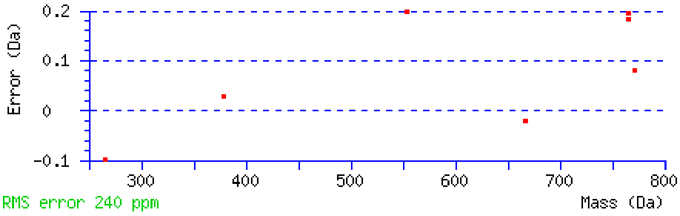
Or, Plot from 200 to 800 Da Full range

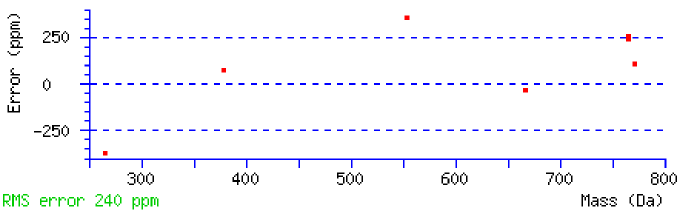
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 930.4779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 0.024
Matches : 7/80 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0965	81.0519	143.0729	72.0401			R							8
2	249.1256	125.0664	231.1020	116.0546	231.1150	116.0612	S	***771.3959***	386.2016	753.3723	377.1898	753.3853	377.1963	7
3	363.2067	182.1070	345.1831	173.0952	345.1961	173.1017	I	683.3668	342.1871	665.3432	333.1753	665.3563	333.1818	6
4	465.2514	233.1293	447.2278	224.1175	447.2408	224.1241	T	569.2857	285.1465	551.2621	276.1347	551.2752	276.1412	5
5	**553.2805**	277.1439	535.2569	268.1321	535.2699	268.1386	S	467.2410	234.1241	449.2174	225.1124	449.2304	225.1189	4
6	**667.3616**	334.1844	649.3380	325.1726	649.3510	325.1791	L	***379.2120***	190.1096	361.1884	181.0978	361.2014	181.1043	3
7	783.3855	392.1964	765.3620	383.1846	765.3750	383.1911	D	***265.1309***	133.0691	247.1073	124.0573	247.1203	124.0638	2
8							K	149.1069	75.0571	131.0833	66.0453			1





NCBI **BLAST** search of RSITSLDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.5	930.4779	-0.0006	RSITSLDK

8.9	930.4779	-0.0006	STKLTAGNK
8.8	930.4778	-0.0006	SLRTVTDK
8.6	930.4779	-0.0006	VDTNKKSK
2.1	930.4779	-0.0006	TKETAKNK
1.9	930.4779	-0.0007	AESSKAKAK
1.9	930.4787	-0.0015	KRIMPMK
1.9	930.4779	-0.0007	SKSKDNLK
1.5	930.4779	-0.0006	KTQSSLQK
1.5	930.4753	0.0019	MVVWTRK

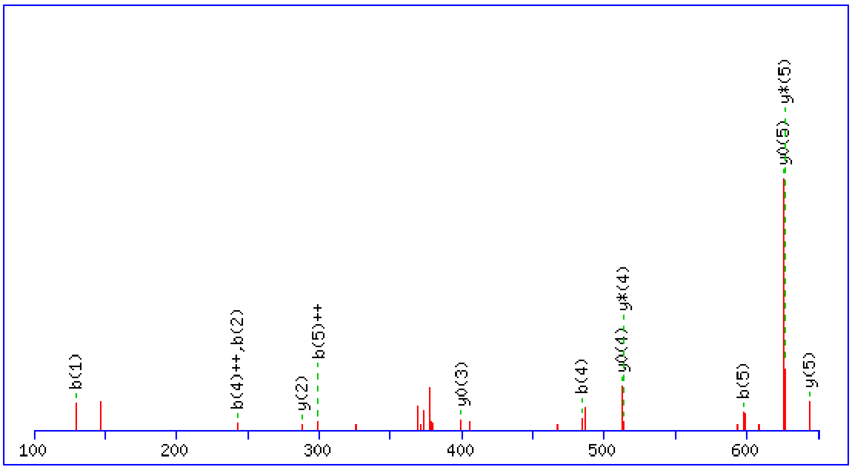
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KILEIR**
Found in **AT5G67630.1** in **TAIR_Arabidopsis**, Symbols: | DNA helicase, putative | chr5:26984761-26986532 REVERSE

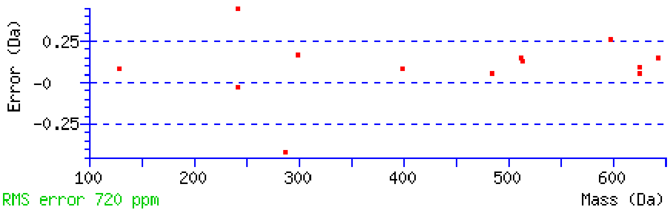
Match to Query 915: 770.501454 from(386.258003,2+) index(1136)
Title: Elution from: 17.593 to 17.593 scan no 1607 cid35.00 polarity:+
Data file 0-2_1.mgf

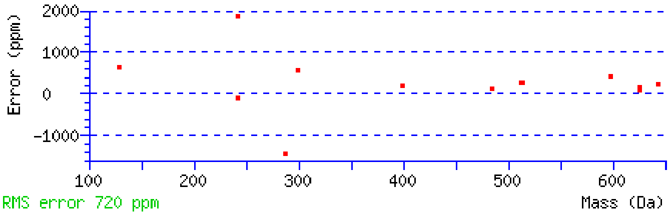
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 770.5014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 0.017
Matches : 13/50 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.1022***	65.0548	112.0757	56.5415			K							6
2	***242.1863***	121.5968	225.1598	113.0835			I	**643.4137**	322.2105	626.3872	313.6972	625.4032	313.2052	5
3	355.2704	178.1388	338.2438	169.6255			L	530.3297	265.6685	513.3031	257.1552	512.3191	256.6632	4
4	***484.3130***	**242.6601**	467.2864	234.1468	466.3024	233.6548	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
5	***597.3970***	**299.2022**	580.3705	290.6889	579.3865	290.1969	I	**288.2030**	144.6051	271.1765	136.0919			2
6							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KILEIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.6	770.5014	0.0001	KILEIR
22.8	770.5014	0.0001	ELLRLK
20.4	770.5014	0.0001	IERIIK
20.3	770.5014	0.0001	RELLLK

AT5G67630.1

19.1	770.5014	0.0001	KELILR
18.8	770.5014	0.0001	KVLNGLK
18.8	770.5014	0.0001	QAIKAIK
18.3	770.5014	0.0001	GKNIVIK
17.5	770.5014	0.0000	GGGKIVLK
16.8	770.5014	0.0001	RIEILK