

Mascot Search Results**Peptide View**MS/MS Fragmentation of **GMDSQMTSSLYDSLK**Found in **AT5G03280.1**, | Symbols: EIN2, PIR2, CKR1, ERA3, ORE3, ORE2 | EIN2 (ETHYLENE INSENSITIVE 2); transporter | chr5:788588-793065 FORWARD

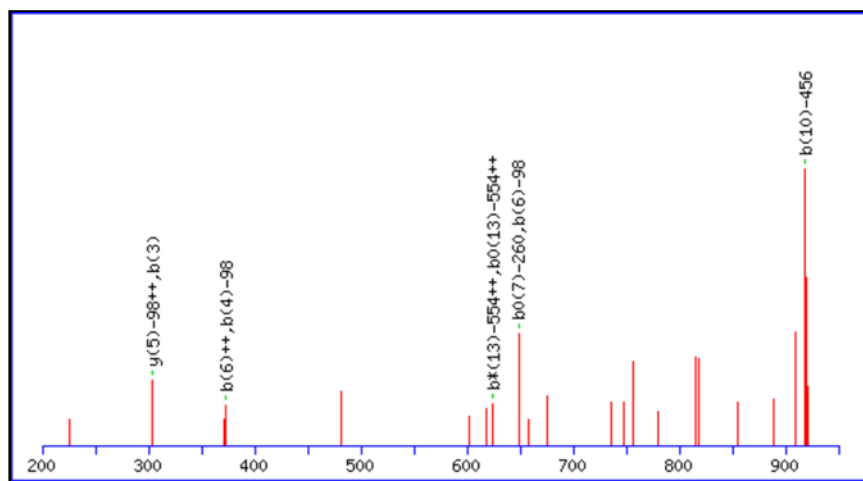
Match to Query 12: 2078.573724 from(693.865184,3+)

Title: PR240_%_Salt.6140.6140.3.dta

Data file C:\Users\CooperB\Desktop\Ray\mgfs\MS2special.txt

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 ☒

Monoisotopic mass of neutral peptide Mr(calc): 2077.5542

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

M6 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000

T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

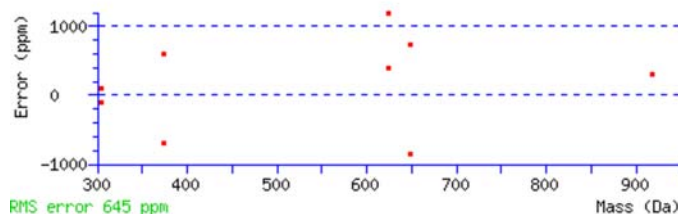
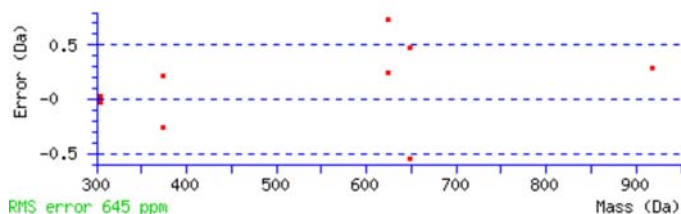
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 14 Expect: 0.046

Matches : 9/456 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	58.0287	29.5180					G							15
2	189.0692	95.0383					M	1467.6573	734.3323	1450.6307	725.8190	1449.6467	725.3270	14
3	304.0962	152.5517			286.0856	143.5464	D	1336.6168	668.8120	1319.5903	660.2988	1318.6062	659.8068	13
4	373.1176	187.0625			355.1071	178.0572	S	1221.5899	611.2986	1204.5633	602.7853	1203.5793	602.2933	12
5	501.1762	251.0917	484.1497	242.5785	483.1656	242.0865	Q	1152.5684	576.7878	1135.5419	568.2746	1134.5578	567.7826	11
6	584.2133	292.6103	567.1868	284.0970	566.2028	283.6050	M	1024.5098	512.7585	1007.4833	504.2453	1006.4993	503.7533	10
7	667.2504	334.1289	650.2239	325.6156	649.2399	325.1236	T	941.4727	471.2400	924.4462	462.7267	923.4621	462.2347	9
8	736.2719	368.6396	719.2454	360.1263	718.2613	359.6343	S	858.4356	429.7214	841.4090	421.2082	840.4250	420.7162	8
9	805.2934	403.1503	788.2668	394.6370	787.2828	394.1450	S	789.4141	395.2107	772.3876	386.6974	771.4036	386.2054	7
10	918.3774	459.6924	901.3509	451.1791	900.3669	450.6871	L	720.3927	360.7000	703.3661	352.1867	702.3821	351.6947	6
11	1081.4408	541.2240	1064.4142	532.7107	1063.4302	532.2187	Y	607.3086	304.1579	590.2821	295.6447	589.2980	295.1527	5
12	1196.4677	598.7375	1179.4412	590.2242	1178.4571	589.7322	D	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	4
13	1265.4892	633.2482	1248.4626	624.7349	1247.4786	624.2429	S	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	3
14	1378.5732	689.7903	1361.5467	681.2770	1360.5627	680.7850	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 [GMDSQMTSSLYDSLK](#)

(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	2077.5542	1.0195	GMDSQMTSSLYDSLK
10.3	2078.5623	0.0114	MTTMIASSTLSPSR
10.3	2078.5623	0.0114	MTTMIASSTLSPSR
4.8	2078.5623	0.0114	MTTMIASSTLSPSR
4.8	2078.5623	0.0114	MTTMIASSTLSPSR
4.8	2077.5676	1.0062	ASSNTTIGVDNTERK
0.9	2077.5598	1.0139	SGSCSCSGNISASDVDR

neutral loss -98, S4, T7, S8, S9 -18

MS2: Match probability 95% but top score of 14.2 is low. +3 charge; S4 [-18] ion found but others deduced. Multiply phosphorylated peptides ionize poorly. Moderate confidence for site positioning.

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