

## Mascot Search Results

### Peptide View

MS/MS Fragmentation of **GMDSQMTSSLYDSLKQQR**

Found in **AT5G03280.1**, | Symbols: EIN2, PIR2, CKR1, ERA3, ORE3, ORE2 | EIN2 (ETHYLENE INSENSITIVE 2); transporter | chr5:788588-793065 FORWARD

Match to Query 15: 2410.791723 from(804.604517,3+)

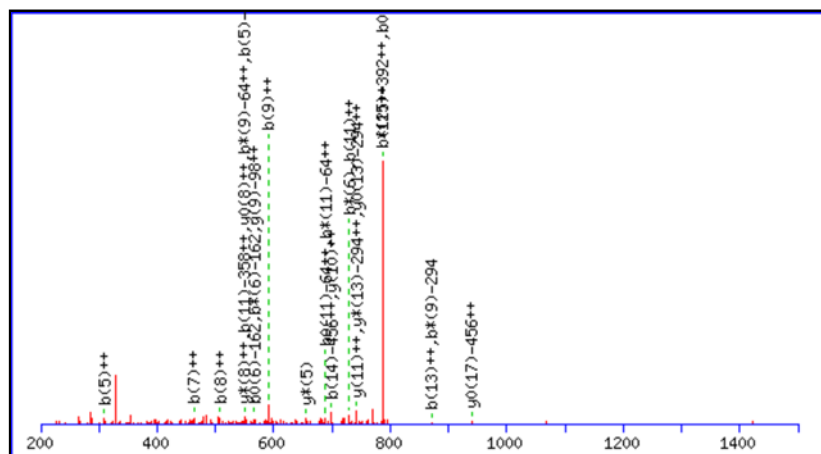
Title: PR4acn\_grad.15974.15974.3.dta

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	1500	Da	Full range
-----	-----------	-----	----	------	----	------------

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 2409.8061

**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

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

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

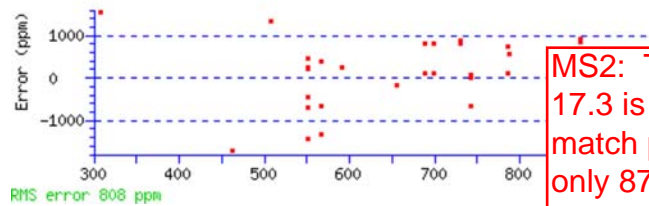
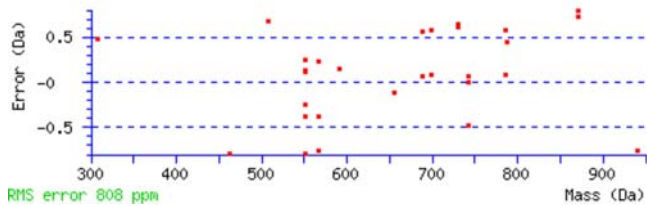
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

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

**Ions Score: 17 Expect: 0.13**

**Matches :** 29/518 fragment ions using 34 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b*	b <sup>*++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	58.0287	29.5180					G							18
2	205.0641	103.0357					M	2353.7920	1177.3996	2336.7654	1168.8864	2335.7814	1168.3944	17
3	320.0911	160.5492			302.0805	151.5439	D	2206.7566	1103.8819	2189.7300	1095.3687	2188.7460	1094.8767	16
4	487.0894	244.0484			469.0789	235.0431	S	2091.7296	1046.3685	2074.7031	1037.8552	2073.7191	1037.3632	15
5	615.1480	308.0776	598.1215	299.5644	597.1375	299.0724	Q	1924.7313	962.8693	1907.7047	954.3560	1906.7207	953.8640	14
6	746.1885	373.5979	729.1620	365.0846	728.1779	364.5926	M	1796.6727	898.8400	1779.6462	890.3267	1778.6621	889.8347	13
7	927.2025	464.1049	910.1760	455.5916	909.1919	455.0996	T	1665.6322	833.3198	1648.6057	824.8065	1647.6217	824.3145	12
8	1014.2345	507.6209	997.2080	499.1076	996.2240	498.6156	S	1484.6182	742.8127	1467.5917	734.2995	1466.6077	733.8075	11
9	1181.2329	591.1201	1164.2064	582.6068	1163.2223	582.1148	S	1397.5862	699.2967	1380.5596	690.7835	1379.5756	690.2915	10
10	1294.3170	647.6621	1277.2904	639.1488	1276.3064	638.6568	L	1230.5878	615.7976	1213.5613	607.2843	1212.5773	606.7923	9
11	1457.3803	729.1938	1440.3537	720.6805	1439.3697	720.1885	Y	1117.5038	559.2555	1100.4772	550.7422	1099.4932	550.2502	8
12	1572.4072	786.7073	1555.3807	778.1940	1554.3967	777.7020	D	954.4404	477.7239	937.4139	469.2106	936.4299	468.7186	7
13	1739.4056	870.2064	1722.3790	861.6932	1721.3950	861.2012	S	839.4135	420.2104	822.3869	411.6971	821.4029	411.2051	6
14	1852.4897	926.7485	1835.4631	918.2352	1834.4791	917.7432	L	672.4151	336.7112	655.3886	328.1979			5
15	1980.5846	990.7960	1963.5581	982.2827	1962.5741	981.7907	K	559.3311	280.1692	542.3045	271.6559			4
16	2108.6432	1054.8252	2091.6167	1046.3120	2090.6326	1045.8200	Q	431.2361	216.1217	414.2096	207.6084			3
17	2236.7018	1118.8545	2219.6752	1110.3413	2218.6912	1109.8492	Q	303.1775	152.0924	286.1510	143.5791			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [GMDSQMTSSLYDSLKQQR](#)

(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	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>
11.2	2410.7979	-0.0061	<a href="#">SSNGGGGGSGSGSSLENQPRR</a>
9.8	2409.7979	0.9938	<a href="#">CTAFPLNGTSMNGVSVISR</a>
9.0	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>
8.8	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>
8.8	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>
8.3	2410.7874	0.0043	<a href="#">NYPSNPNPSTDFTEFFK</a>
6.4	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>
6.4	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>
6.4	2409.8061	0.9856	<a href="#">GMDSQMTSSLYDSLKQQR</a>

no -98 loss; S4, T7, S9, S13 +80, oxM2

no, -98 loss; S4, T7, S9, S13 +80, oxM 6

MS2: Top score of 17.3 is low and match probability only 87%. +3 charge; all sites with +80 deduced. This multiply phosphorylated peptide ionized poorly. Low position confidence

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