

Mascot Search Results**Peptide View**MS/MS Fragmentation of **TPGSIDSLYGLQR**

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

Match to Query 5: 1485.690724 from(743.852638,2+)

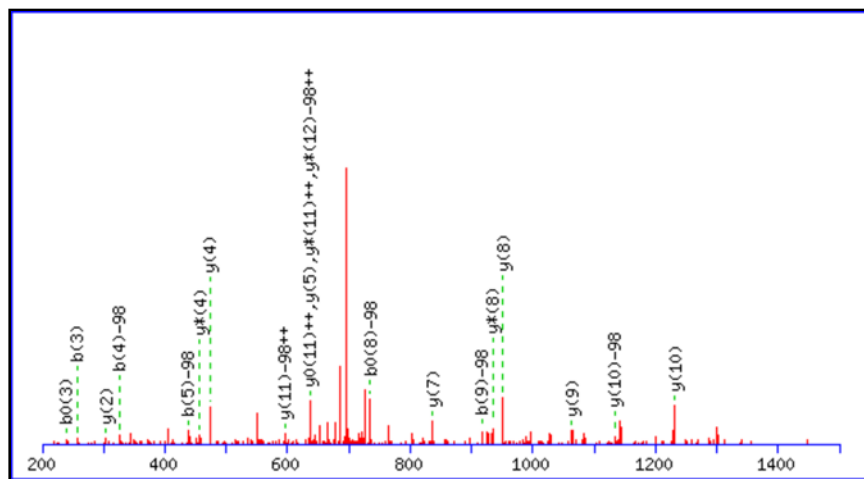
Title: PR4acn_grad.4271.4271.2.dta

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, 200 to Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide **Mr(calc)**: 1485.6865

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

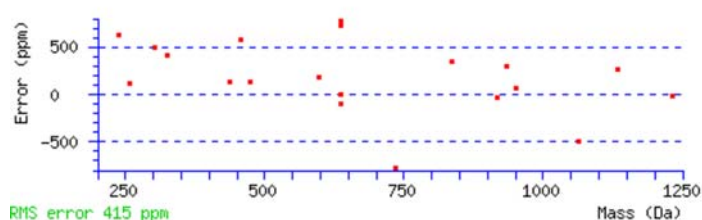
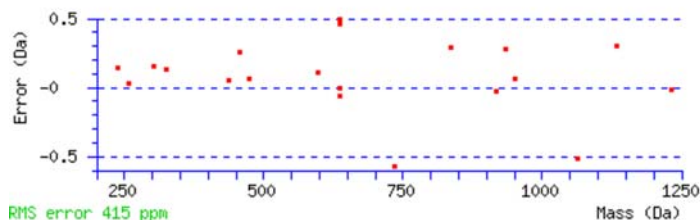
Variable modifications:

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

Ions Score: 36 **Expect**: 0.0087

Matches : 20/166 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							13
2	199.1077	100.0575			181.0972	91.0522	P	1287.6692	644.3382	1270.6426	635.8250	1269.6586	635.3329	12
3	256.1292	128.5682			238.1186	119.5629	G	1190.6164	595.8118	1173.5899	587.2986	1172.6058	586.8066	11
4	325.1506	163.0790			307.1401	154.0737	S	1133.5949	567.3011	1116.5684	558.7878	1115.5844	558.2958	10
5	438.2347	219.6210			420.2241	210.6157	I	1064.5735	532.7904	1047.5469	524.2771	1046.5629	523.7851	9
6	553.2617	277.1345			535.2511	268.1292	D	951.4894	476.2483	934.4629	467.7351	933.4789	467.2431	8
7	640.2937	320.6505			622.2831	311.6452	S	836.4625	418.7349	819.4359	410.2216	818.4519	409.7296	7
8	753.3777	377.1925			735.3672	368.1872	L	749.4305	375.2189	732.4039	366.7056			6
9	916.4411	458.7242			898.4305	449.7189	Y	636.3464	318.6768	619.3198	310.1636			5
10	973.4625	487.2349			955.4520	478.2296	G	473.2831	237.1452	456.2565	228.6319			4
11	1086.5466	543.7769			1068.5360	534.7717	L	416.2616	208.6344	399.2350	200.1212			3
12	1214.6052	607.8062	1197.5786	599.2930	1196.5946	598.8009	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 [TPGSIDSLYGLQR](#)

(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	1485.6865	0.0043	TPGSIDSLYGLQR
26.1	1485.6865	0.0043	TPGSIDSLYGLQR
13.9	1485.6865	0.0043	TPGSIDSLYGLQR
11.2	1484.6872	1.0036	GTSNSILEEATKR
7.8	1484.6872	1.0036	GTSNSILEEATKR
7.0	1484.6768	1.0139	DACGSVMPLKSLK
6.0	1484.6789	1.0118	SRLVLHAVSESK
5.8	1485.6843	0.0064	ENVIMFLSDMSGK
5.6	1484.6969	0.9938	KYEIEQGSAMWK
5.3	1484.6789	1.0118	SRLVLHAVSESK

neutral loss -98, S4 -18
neutral loss -98, T1 -18
neutral loss -98, S7 -18

MS2: +2 charge; b and y ions found for S4 [-18]; top ranked score of 35.6; match probability >99%; high confidence in position assignment

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

Mascot Search Results

Peptide View

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Match to Query 2: 1387.789724 from(694.902138,2+)

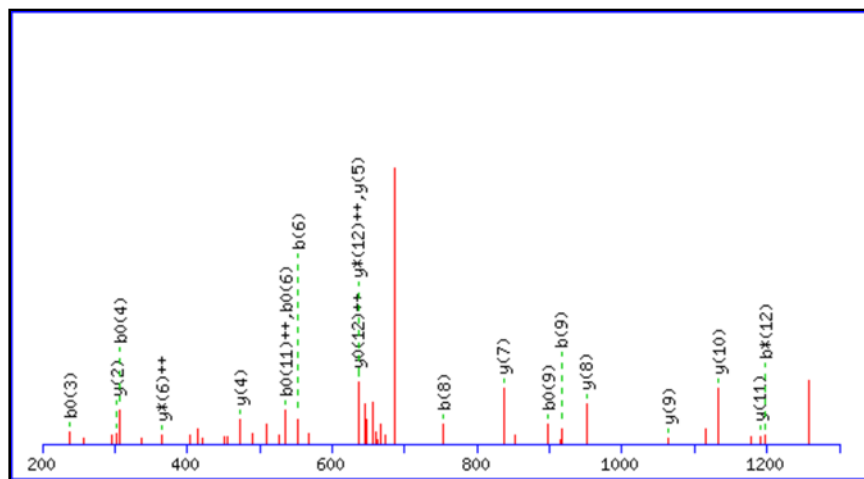
Title: PR4acn_grad.4272.4272.2.dta

Data file C:\Users\CooperB\Desktop\Ray\mgfs\MS3special.txt

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

Or, 200 to Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide **Mr(calc)**: 1387.7096

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

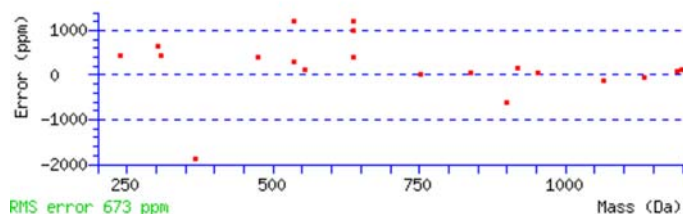
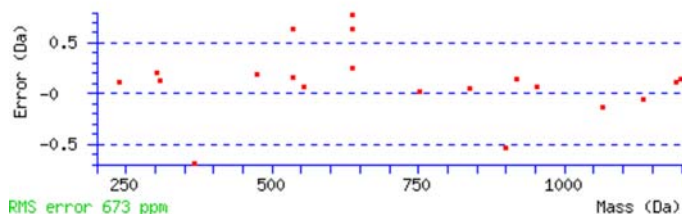
Variable modifications:

S4 : Dehydrated (S)

Ions Score: 57 **Expect:** 0.0025

Matches : 20/110 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							13
2	199.1077	100.0575			181.0972	91.0522	P	1287.6692	644.3382	1270.6426	635.8250	1269.6586	635.3329	12
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(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.3	1387.7096	0.0801	TPGSIDSLYGLQR
36.8	1387.7096	0.0801	TPGSIDSLYGLQR
19.4	1387.7096	0.0801	TPGSIDSLYGLQR
17.1	1386.4619	1.3278	SSSLSGSSSTRK
16.1	1386.4619	1.3278	SSSLSGSSSTRK
16.1	1386.4619	1.3278	SSSLSGSSSTRK
16.1	1386.4619	1.3278	SSSLSGSSSTRK
15.8	1388.5624	-0.7727	SSSVSPTTSGSQHR
15.8	1388.5624	-0.7727	SSSVSPTTSGSQHR
15.8	1388.5624	-0.7727	SSSVSPTTSGSQHR

S4 -18
T1 -18
S7 -18

MS3: -98 Da
triggered
consecutive
spectrum; top
position
assignment is
same as in MS2; y
ion found for S4
[-18]

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