

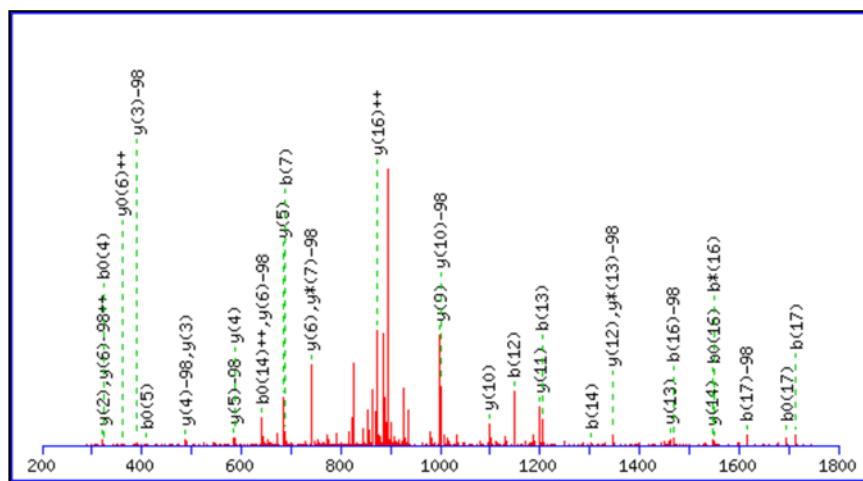
Mascot Search Results**Peptide View**MS/MS Fragmentation of **AAPTSNFTVGSDGPPSFR**Found in **AT5G03280.1**, | Symbols: EIN2, PIR2, CKR1, ERA3, ORE3, ORE2 | EIN2 (ETHYLENE INSENSITIVE 2); transporter | chr5:788588-793065 FORWARD

Match to Query 11: 1886.822364 from(944.418458,2+)

Title: PR3acn_grad.4061.4061.2.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 1800 Da Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1886.8200

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

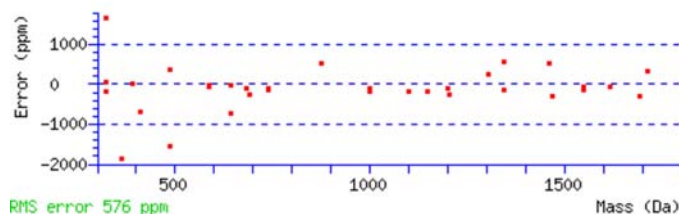
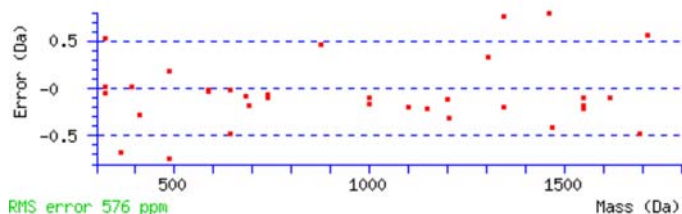
Variable modifications:

S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 73 Expect: 1.6e-006

Matches : 34/286 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	72.0444	36.5258					A							18
2	143.0815	72.0444					A	1816.7902	908.8987	1799.7636	900.3854	1798.7796	899.8934	17
3	240.1343	120.5708					P	1745.7531	873.3802	1728.7265	864.8669	1727.7425	864.3749	16
4	341.1819	171.0946			323.1714	162.0893	T	1648.7003	824.8538	1631.6737	816.3405	1630.6897	815.8485	15
5	428.2140	214.6106			410.2034	205.6053	S	1547.6526	774.3299	1530.6261	765.8167	1529.6420	765.3247	14
6	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	N	1460.6206	730.8139	1443.5940	722.3007	1442.6100	721.8086	13
7	689.3253	345.1663	672.2988	336.6530	671.3148	336.1610	F	1346.5777	673.7925	1329.5511	665.2792	1328.5671	664.7872	12
8	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	T	1199.5092	600.2583	1182.4827	591.7450	1181.4987	591.2530	11
9	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	V	1098.4616	549.7344	1081.4350	541.2211	1080.4510	540.7291	10
10	946.4629	473.7351	929.4363	465.2218	928.4523	464.7298	G	999.3932	500.2002	982.3666	491.6869	981.3826	491.1949	9
11	1033.4949	517.2511	1016.4684	508.7378	1015.4843	508.2458	S	942.3717	471.6895	925.3451	463.1762	924.3611	462.6842	8
12	1148.5218	574.7646	1131.4953	566.2513	1130.5113	565.7593	D	855.3397	428.1735	838.3131	419.6602	837.3291	419.1682	7
13	1205.5433	603.2753	1188.5168	594.7620	1187.5327	594.2700	G	740.3127	370.6600	723.2862	362.1467	722.3022	361.6547	6
14	1302.5961	651.8017	1285.5695	643.2884	1284.5855	642.7964	P	683.2913	342.1493	666.2647	333.6360	665.2807	333.1440	5
15	1399.6488	700.3281	1382.6223	691.8148	1381.6383	691.3228	P	586.2385	293.6229	569.2119	285.1096	568.2279	284.6176	4
16	1566.6472	783.8272	1549.6206	775.3140	1548.6366	774.8220	S	489.1857	245.0965	472.1592	236.5832	471.1752	236.0912	3
17	1713.7156	857.3614	1696.6891	848.8482	1695.7050	848.3562	F	322.1874	161.5973	305.1608	153.0840			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [AAPTSNFTVGSDGPPSFR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.0	1886.8200	0.0023	AAPTSNFTVGSDGPPSFR
41.6	1886.8200	0.0023	AAPTSNFTVGSDGPPSFR
34.1	1886.8200	0.0023	AAPTSNFTVGSDGPPSFR
28.4	1886.8200	0.0023	AAPTSNFTVGSDGPPSFR
23.6	1886.8200	0.0023	AAPTSNFTVGSDGPPSFR
18.5	1886.8362	-0.0139	SQLLSTPLMAVNSNPR
9.7	1886.8128	0.0095	MVGGGAPQRGSAAATASMR
9.7	1886.8128	0.0095	MVGGGAPQRGSAAATASMR
7.8	1886.8128	0.0095	MVGGGAPQRGSAAATASMR
7.2	1886.8274	-0.0050	IEFSNSDMTKFAVFR

no -98 loss, S16 +80
 -98 loss, S11 -18
 -98 loss, T8 -18
 -98 loss, T4 -18
 -98 loss, S5 -18

MS2: high score of 73 and match probability greater than 99%. +2 charge; y ion found for S16 [+80]. Corroborating MS3. High position confidence.

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAPTSNFTVGSDGPPSFR**

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

Match to Query 5: 1789.922724 from(895.968638,2+)

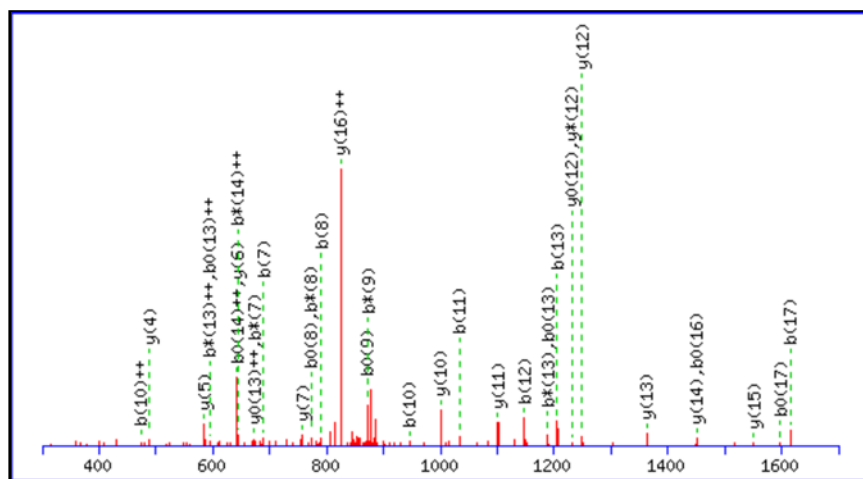
Title: PR3acn_grad.4062.4062.2.dta

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, 300 to 1700 Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1788.8432

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

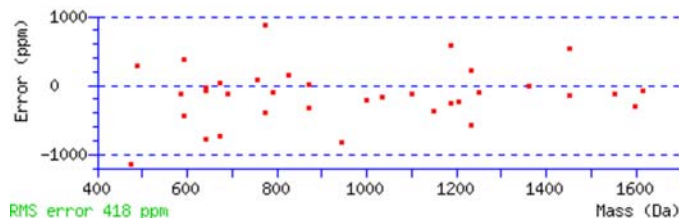
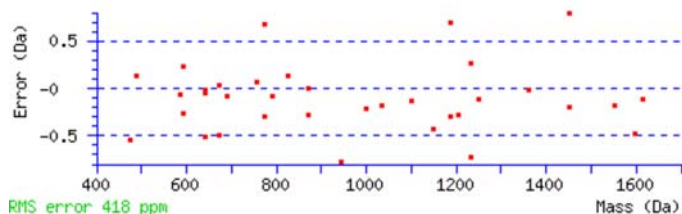
Variable modifications:

S16 : Dehydrated (S)

Ions Score: 65 Expect: 0.00065

Matches : 35/184 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	72.0444	36.5258					A							18
2	143.0815	72.0444					A	1718.8133	859.9103	1701.7867	851.3970	1700.8027	850.9050	17
3	240.1343	120.5708					P	1647.7762	824.3917	1630.7496	815.8784	1629.7656	815.3864	16
4	341.1819	171.0946			323.1714	162.0893	T	1550.7234	775.8653	1533.6968	767.3521	1532.7128	766.8601	15
5	428.2140	214.6106			410.2034	205.6053	S	1449.6757	725.3415	1432.6492	716.8282	1431.6652	716.3362	14
6	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	N	1362.6437	681.8255	1345.6171	673.3122	1344.6331	672.8202	13
7	689.3253	345.1663	672.2988	336.6530	671.3148	336.1610	F	1248.6008	624.8040	1231.5742	616.2907	1230.5902	615.7987	12
8	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	T	1101.5323	551.2698	1084.5058	542.7565	1083.5218	542.2645	11
9	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	V	1000.4847	500.7460	983.4581	492.2327	982.4741	491.7407	10
10	946.4629	473.7351	929.4363	465.2218	928.4523	464.7298	G	901.4163	451.2118	884.3897	442.6985	883.4057	442.2065	9
11	1033.4949	517.2511	1016.4684	508.7378	1015.4843	508.2458	S	844.3948	422.7010	827.3682	414.1878	826.3842	413.6958	8
12	1148.5218	574.7646	1131.4953	566.2513	1130.5113	565.7593	D	757.3628	379.1850	740.3362	370.6717	739.3522	370.1797	7
13	1205.5433	603.2753	1188.5168	594.7620	1187.5327	594.2700	G	642.3358	321.6715	625.3093	313.1583	624.3253	312.6663	6
14	1302.5961	651.8017	1285.5695	643.2884	1284.5855	642.7964	P	585.3144	293.1608	568.2878	284.6475	567.3038	284.1555	5
15	1399.6488	700.3281	1382.6223	691.8148	1381.6383	691.3228	P	488.2616	244.6344	471.2350	236.1212	470.2510	235.6292	4
16	1468.6703	734.8388	1451.6438	726.3255	1450.6597	725.8335	S	391.2088	196.1081	374.1823	187.5948	373.1983	187.1028	3
17	1615.7387	808.3730	1598.7122	799.8597	1597.7281	799.3677	F	322.1874	161.5973	305.1608	153.0840			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [AAPTSNFTVGSDGPPSFR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.5	1788.8432	1.0796	AAPTSNFTVGSDGPPSFR
42.5	1788.8432	1.0796	AAPTSNFTVGSDGPPSFR
37.4	1788.8432	1.0796	AAPTSNFTVGSDGPPSFR
26.5	1788.8151	1.1076	KMTTMIASSTLSPSR
26.5	1788.8151	1.1076	KMTTMIASSTLSPSR
26.5	1788.8151	1.1076	KMTTMIASSTLSPSR
26.5	1788.8151	1.1076	KMTTMIASSTLSPSR
25.0	1788.8151	1.1076	KMTTMIASSTLSPSR
24.1	1788.8151	1.1076	KMTTMIASSTLSPSR
23.2	1788.8151	1.1076	KMTTMIASSTLSPSR

S16 -18
S11 -18
T8 -18

MS3: -98 Da
triggered
consecutive
spectrum; top
position
assignment is
same as in MS2;
S16 [-18]

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