

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

Found in **AT1G45688.2**, | Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42860.1); similar to H0814G11.12 [Oryza sativa (indica cultivar-group)] (GB:CAJ86345.1); similar to CAA30379.1 protein [Oryza sativa] (GB:CAB53482.1) | chr1:17193942-17194904

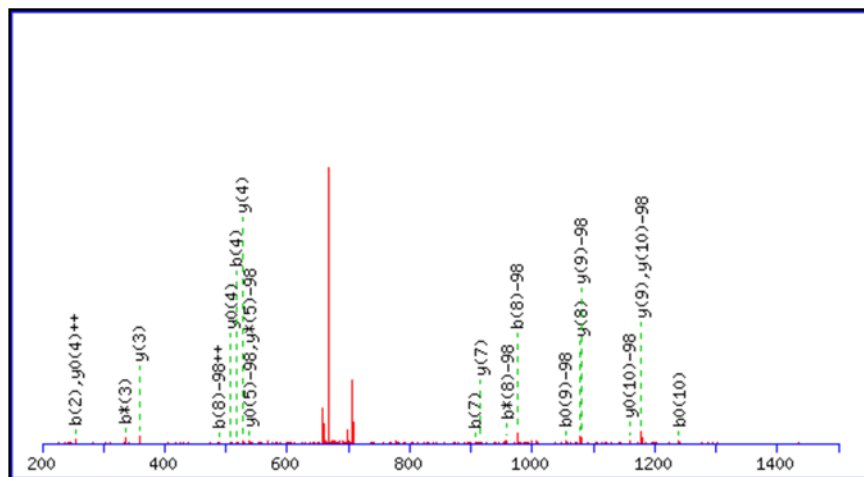
Match to Query 2: 1430.668434 from(716.341493,2+)

Title: PR170\_%\_Salt.3216.3216.2.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, Plot from 200 to 1500 Da Full range

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1430.6707

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

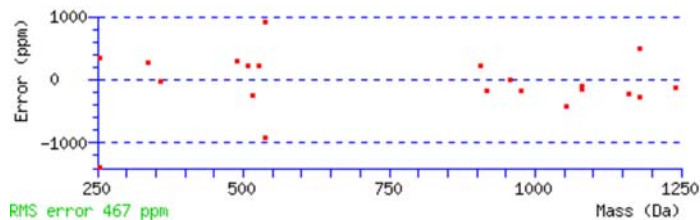
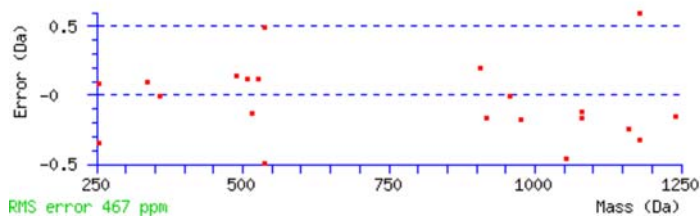
Variable modifications:

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

Ions Score: 24 Expect: 0.11

Matches : 22/164 fragment ions using 33 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>*++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	157.1084	79.0578	140.0818	70.5446			R							11
2	254.1612	127.5842	237.1346	119.0709			P	1177.6000	589.3037	1160.5735	580.7904	1159.5895	580.2984	10
3	353.2296	177.1184	336.2030	168.6051			V	1080.5473	540.7773	1063.5207	532.2640	1062.5367	531.7720	9
4	516.2929	258.6501	499.2663	250.1368			Y	981.4789	491.2431	964.4523	482.7298	963.4683	482.2378	8
5	679.3562	340.1817	662.3297	331.6685			Y	818.4155	409.7114	801.3890	401.1981	800.4050	400.7061	7
6	778.4246	389.7160	761.3981	381.2027			V	655.3522	328.1797	638.3257	319.6665	637.3416	319.1745	6
7	906.4832	453.7452	889.4567	445.2320			Q	556.2838	278.6455	539.2572	270.1323	538.2732	269.6402	5
8	975.5047	488.2560	958.4781	479.7427	957.4941	479.2507	S	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	4
9	1072.5574	536.7824	1055.5309	528.2691	1054.5469	527.7771	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
10	1159.5895	580.2984	1142.5629	571.7851	1141.5789	571.2931	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 [RPVYYVQSPSR](#)

(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	1430.6707	-0.0023	<a href="#">RPVYYVQSPSR</a>
17.5	1430.6707	-0.0023	<a href="#">RPVYYVQSPSR</a>
9.7	1429.6755	0.9929	<a href="#">WLGSKTIFENR</a>
7.8	1429.6710	0.9974	<a href="#">QVLMMEIVSLR</a>
7.5	1430.6752	-0.0067	<a href="#">EFTFVMEAQVSK</a>
3.5	1430.6595	0.0089	<a href="#">LTGGVPNYFVER</a>
3.4	1429.6548	1.0136	<a href="#">FSAMAGAGVDDFVK</a>
2.8	1430.6568	0.0116	<a href="#">WASNQHSRLPR</a>
2.7	1430.6629	0.0055	<a href="#">LAGVDKTCNFVK</a>
2.7	1429.6626	1.0058	<a href="#">YFDIGAAAAGGFDR</a>

-98 neutral loss, S8 -18  
-98 neutral loss, S10 -18

MS2: top score of 24.5, match probability of 90%; +2 charge, b ion found for S8 [-18], supported by MS3. moderate position confidence because of match probability.

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

# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RPVYYVQSPSR**

Found in **AT1G45688.1**, | Symbols: | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42860.1); similar to H0814G11.12 [Oryza sativa (indica cultivar-group)] (GB:CAJ86345.1); similar to CAA30379.1 protein [Oryza sativa] (GB:CAB53482.1) | chr1:17193942-17195310

Match to Query 1: 1332.970724 from(667.492638,2+)

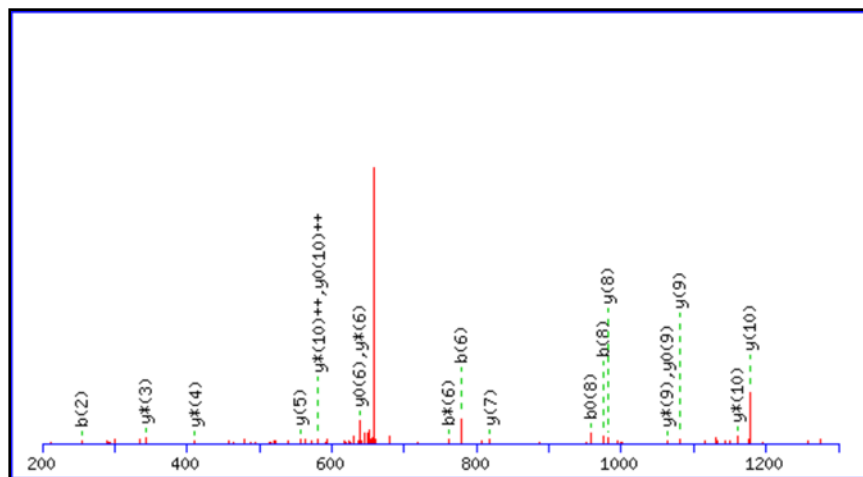
Title: PR170\_%\_Salt.3217.3217.2.dta

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 1300 Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide **Mr(calc):** 1332.6939

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

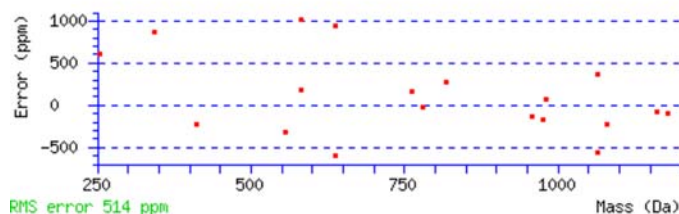
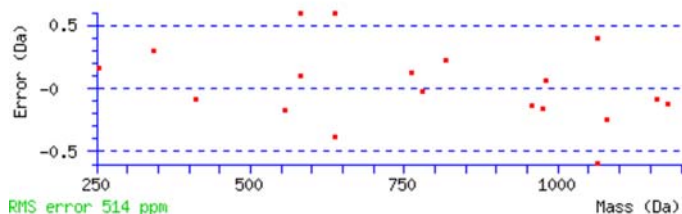
**Variable modifications:**

S8 : Dehydrated (S)

**Ions Score:** 24 **Expect:** 5.5

**Matches :** 20/104 fragment ions using 31 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	157.1084	79.0578	140.0818	70.5446			R							11
2	<b>254.1612</b>	127.5842	237.1346	119.0709			P	<b>1177.6000</b>	589.3037	<b>1160.5735</b>	<b>580.7904</b>	1159.5895	<b>580.2984</b>	10
3	353.2296	177.1184	336.2030	168.6051			V	<b>1080.5473</b>	540.7773	<b>1063.5207</b>	532.2640	<b>1062.5367</b>	531.7720	9
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6	<b>778.4246</b>	389.7160	<b>761.3981</b>	381.2027			V	655.3522	328.1797	<b>638.3256</b>	319.6665	<b>637.3416</b>	319.1745	6
7	906.4832	453.7452	889.4567	445.2320			Q	<b>556.2838</b>	278.6455	539.2572	270.1323	538.2732	269.6402	5
8	<b>975.5047</b>	488.2560	958.4781	479.7427	<b>957.4941</b>	479.2507	S	428.2252	214.6162	<b>411.1987</b>	206.1030	410.2146	205.6110	4
9	1072.5574	536.7824	1055.5309	528.2691	1054.5469	527.7771	P	359.2037	180.1055	<b>342.1772</b>	171.5922	341.1932	171.1002	3
10	1159.5895	<b>580.2984</b>	1142.5629	571.7851	1141.5789	571.2931	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
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NCBI BLAST search of [RPVYYVQSPSR](#)

(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	1332.6939	0.2768	<a href="#">RPVYYVQSPSR</a>
20.1	1332.6939	0.2768	<a href="#">RPVYYVQSPSR</a>
19.7	1333.5412	-0.5705	<a href="#">GQSETQNSKSSR</a>
19.7	1333.5412	-0.5705	<a href="#">GQSETQNSKSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>
18.7	1333.5123	-0.5416	<a href="#">SLSSPTSACSSSR</a>

S8 -18  
S10 -18

MS3: -98 Da  
triggered  
consecutive  
spectrum with  
corroborating ions.  
b ion found for S8  
[-18].

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