

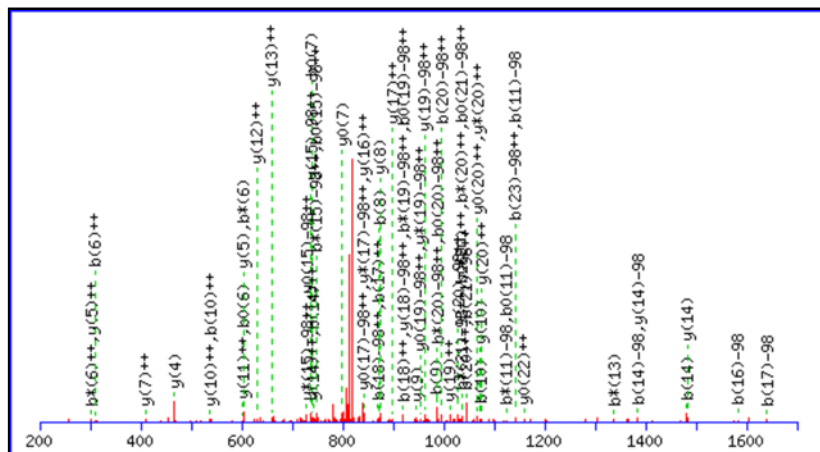
Mascot Search Results**Peptide View**MS/MS Fragmentation of **MSGQESHDISSGGEQAGVDHPPPR**Found in **AT5G64330.1** | Symbols: JK218, RPT3, NPH3 | NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); signal transducer | chr5:25744794-25747451 FORWARD

Match to Query 16: 2554.046724 from(852.356184,3+)

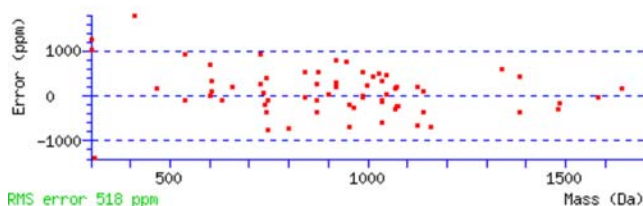
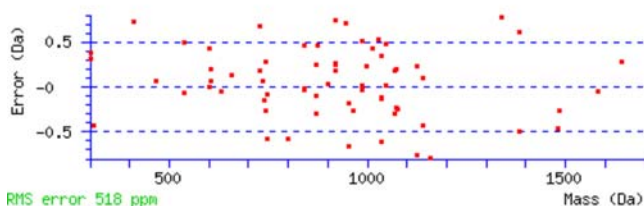
Title: PR1100_%_Salt.2789.2789.3.dta

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

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

Or, 200 1700 Label all possible matches ☐ Label matches used for scoring ☒

22	2185.9203	1093.4638	2168.8938	1084.9505	2167.9098	1084.4585	P	369.2245	185.1159	352.1979	176.6026			3
23	2282.9731	1141.9902	2265.9466	1133.4769	2264.9625	1132.9849	P	272.1717	136.5895	255.1452	128.0762			2
24							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [MSGQESHDISSGGEQAGVDHPPPR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.3	2554.0544	-0.0077	MSGQESHDISSGGEQAGVDHPPPR
30.5	2554.0544	-0.0077	MSGQESHDISSGGEQAGVDHPPPR
22.3	2554.0544	-0.0077	MSGQESHDISSGGEQAGVDHPPPR
17.6	2553.0564	0.9903	RGSGNSTAPTSRPVPASQPFGR
16.8	2554.0544	-0.0077	MSGQESHDISSGGEQAGVDHPPPR
11.4	2553.0564	0.9903	RGSGNSTAPTSRPVPASQPFGR
7.6	2553.0522	0.9945	ISPERPMRGHGFYGEHQHR
7.1	2554.0293	0.0174	GYFVEPAIVSNVTTSMEIWR
7.1	2554.0293	0.0174	GYFVEPAIVSNVTTSMEIWR
7.0	2553.0190	1.0277	TELAETTTVGSSSSSASSMSKR

-98 neutral loss, S11 -18

-98 neutral loss, S10 -18

-98 neutral loss, S6 -18

MS2: Top score of 36.3, match probability greater than 99%. +3 charge and b and y ions for S11 [-18], supported by MS3. High position confidence.

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

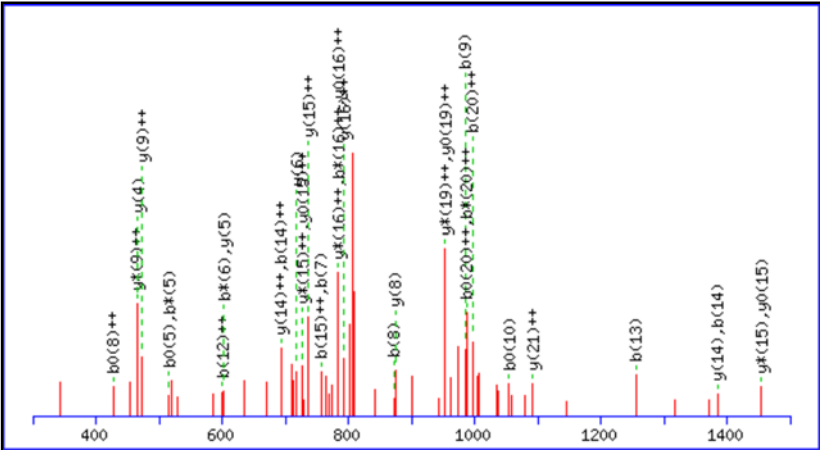
Mascot Search Results

Peptide View

MS/MS Fragmentation of MSGQESHDISSGGEQAGVDHPPPR
Found in AT5G64330.1 | Symbols: JK218, RPT3, NPH3 | NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); signal transducer |
chr5:25744794-25747451 FORWARD

Match to Query 6: 2456.342724 from(819.788184,3+)
Title: PR1100_%.Salt.2790.2790.3.dta
Data file C:\Users\CooperB\Desktop\Ray\mgfs\MS3special.txt

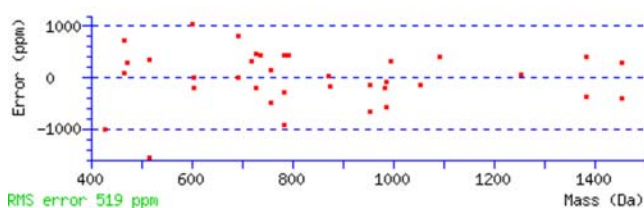
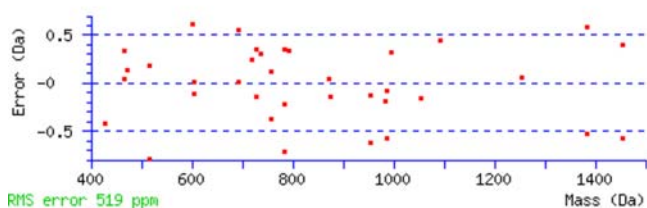
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2456.0775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Dehydrated (S)
Ions Score: 25 Expect: 8.6
Matches : 36/258 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	132.0478	66.5275					M							24
2	219.0798	110.0435			201.0692	101.0382	S	2326.0443	1163.5258	2309.0177	1155.0125	2308.0337	1154.5205	23
3	276.1013	138.5543			258.0907	129.5490	G	2239.0123	1120.0098	2221.9857	1111.4965	2221.0017	1111.0045	22
4	404.1598	202.5836	387.1333	194.0703	386.1493	193.5783	Q	2181.9908	1091.4990	2164.9642	1082.9858	2163.9802	1082.4938	21
5	533.2024	267.1049	516.1759	258.5916	515.1919	258.0996	E	2053.9322	1027.4697	2036.9057	1018.9565	2035.9217	1018.4645	20
6	620.2345	310.6209	603.2079	302.1076	602.2239	301.6156	S	1924.8896	962.9485	1907.8631	954.4352	1906.8791	953.9432	19
7	757.2934	379.1503	740.2668	370.6370	739.2828	370.1450	H	1837.8576	919.4324	1820.8311	910.9192	1819.8470	910.4272	18
8	872.3203	436.6638	855.2938	428.1505	854.3097	427.6585	D	1700.7987	850.9030	1683.7721	842.3897	1682.7881	841.8977	17
9	985.4044	493.2058	968.3778	484.6925	967.3938	484.2005	I	1585.7717	793.3895	1568.7452	784.8762	1567.7612	784.3842	16
10	1072.4364	536.7218	1055.4099	528.2086	1054.4258	527.7166	S	1472.6877	736.8475	1455.6611	728.3342	1454.6771	727.8422	15
11	1141.4579	571.2326	1124.4313	562.7193	1123.4473	562.2273	S	1385.6557	693.3315	1368.6291	684.8182	1367.6451	684.3262	14
12	1198.4793	599.7433	1181.4528	591.2300	1180.4688	590.7380	G	1316.6342	658.8207	1299.6076	650.3075	1298.6236	649.8155	13
13	1255.5008	628.2540	1238.4742	619.7408	1237.4902	619.2488	G	1259.6127	630.3100	1242.5862	621.7967	1241.6022	621.3047	12
14	1384.5434	692.7753	1367.5168	684.2621	1366.5328	683.7700	E	1202.5913	601.7993	1185.5647	593.2860	1184.5807	592.7940	11
15	1512.6020	756.8046	1495.5754	748.2913	1494.5914	747.7993	Q	1073.5487	537.2780	1056.5221	528.7647	1055.5381	528.2727	10
16	1583.6391	792.3232	1566.6125	783.8099	1565.6285	783.3179	A	945.4901	473.2487	928.4635	464.7354	927.4795	464.2434	9
17	1640.6605	820.8339	1623.6340	812.3206	1622.6500	811.8286	G	874.4530	437.7301	857.4264	429.2169	856.4424	428.7248	8
18	1739.7290	870.3681	1722.7024	861.8548	1721.7184	861.3628	V	817.4315	409.2194	800.4050	400.7061	799.4209	400.2141	7
19	1854.7559	927.8816	1837.7293	919.3683	1836.7453	918.8763	D	718.3631	359.6852	701.3365	351.1719	700.3525	350.6799	6
20	1991.8148	996.4110	1974.7883	987.8978	1973.8042	987.4058	H	603.3362	302.1717	586.3096	293.6584			5
21	2088.8676	1044.9374	2071.8410	1036.4241	2070.8570	1035.9321	P	466.2772	233.6423	449.2507	225.1290			4

22	2185.9203	1093.4638	2168.8938	1084.9505	2167.9098	1084.4585	P	369.2245	185.1159	352.1979	176.6026			3
23	2282.9731	1141.9902	2265.9466	1133.4769	2264.9625	1132.9849	P	272.1717	136.5895	255.1452	128.0762			2
24							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [MSGQESHDISSGGEQAGVDHPPPR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.6	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
26.6	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
26.5	2456.0775	0.2652	MSGQESHDISSGGEQAGVDHPPPR
24.6	2456.0775	0.2652	MSGQESHDISSGGEQAGVDHPPPR
21.0	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
21.0	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
20.7	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
20.7	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
20.7	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR
20.7	2455.0742	1.2685	SSSTPTSTVYNSGGVTGSRMSITR

S11 -18

MS3: -98 Da triggered consecutive spectrum with corroborating ions for MS2. This is 3rd ranked match but first two have big mass delta. y ion found for S11 [-18]

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