

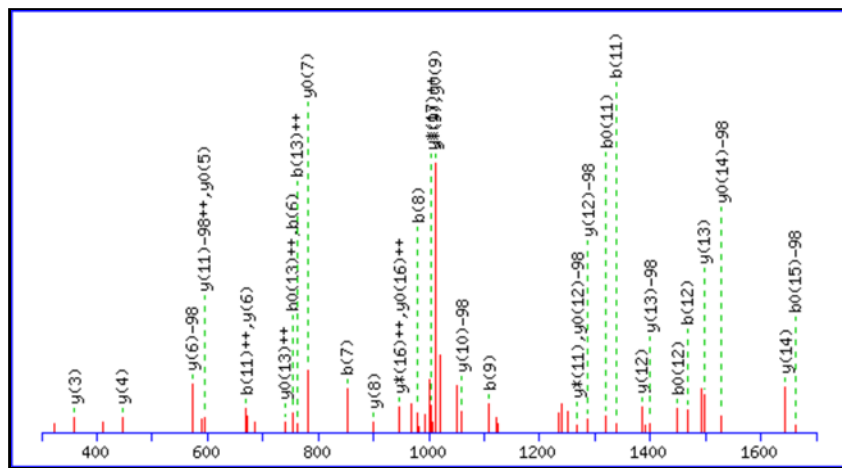
Mascot Search Results**Peptide View**MS/MS Fragmentation of **LLEHFLVQEQTGSSPSR**Found in **AT5G64330.1**, | Symbols: JK218, RPT3, NPH3 | NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); signal transducer | chr5:25744794-25747451 FORWARD

Match to Query 13: 2135.986724 from(1069.000638,2+)

Title: PR180_%_Salt.6604.6604.2.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, 300 1700 Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2135.9888

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

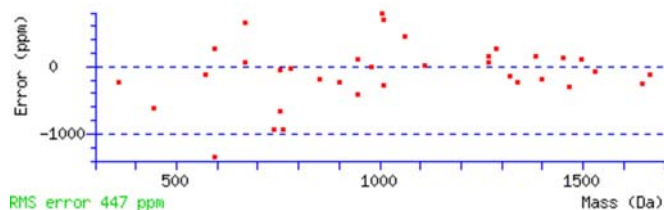
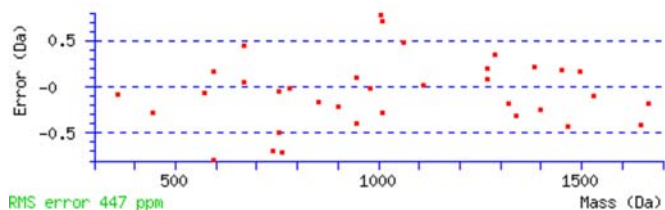
Variable modifications:

S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 38 Expect: 0.0058

Matches : 35/286 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	114.0913	57.5493					L							18
2	227.1754	114.0913					L	2023.9121	1012.4597	2006.8855	1003.9464	2005.9015	1003.4544	17
3	356.2180	178.6126			338.2074	169.6074	E	1910.8280	955.9176	1893.8015	947.4044	1892.8174	946.9124	16
4	493.2769	247.1421			475.2663	238.1368	H	1781.7854	891.3963	1764.7589	882.8831	1763.7749	882.3911	15
5	640.3453	320.6763			622.3348	311.6710	F	1644.7265	822.8669	1627.7000	814.3536	1626.7159	813.8616	14
6	753.4294	377.2183			735.4188	368.2130	L	1497.6581	749.3327	1480.6315	740.8194	1479.6475	740.3274	13
7	852.4978	426.7525			834.4872	417.7473	V	1384.5740	692.7907	1367.5475	684.2774	1366.5635	683.7854	12
8	980.5564	490.7818	963.5298	482.2686	962.5458	481.7765	Q	1285.5056	643.2564	1268.4791	634.7432	1267.4951	634.2512	11
9	1109.5990	555.3031	1092.5724	546.7898	1091.5884	546.2978	E	1157.4470	579.2272	1140.4205	570.7139	1139.4365	570.2219	10
10	1237.6576	619.3324	1220.6310	610.8191	1219.6470	610.3271	Q	1028.4044	514.7059	1011.3779	506.1926	1010.3939	505.7006	9
11	1338.7052	669.8563	1321.6787	661.3430	1320.6947	660.8510	T	900.3459	450.6766	883.3193	442.1633	882.3353	441.6713	8
12	1467.7478	734.3775	1450.7213	725.8643	1449.7373	725.3723	E	799.2982	400.1527	782.2716	391.6395	781.2876	391.1474	7
13	1524.7693	762.8883	1507.7427	754.3750	1506.7587	753.8830	G	670.2556	335.6314	653.2290	327.1182	652.2450	326.6262	6
14	1691.7676	846.3875	1674.7411	837.8742	1673.7571	837.3822	S	613.2341	307.1207	596.2076	298.6074	595.2236	298.1154	5
15	1778.7997	889.9035	1761.7731	881.3902	1760.7891	880.8982	S	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
16	1875.8524	938.4299	1858.8259	929.9166	1857.8419	929.4246	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
17	1962.8845	981.9459	1945.8579	973.4326	1944.8739	972.9406	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
18							R	175.1190	88.0631	158.0924	79.5498			1



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

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	2135.9888	-0.0021	LLEHFLVQEQTGSSPSR
31.2	2135.9888	-0.0021	LLEHFLVQEQTGSSPSR
27.4	2135.9888	-0.0021	LLEHFLVQEQTGSSPSR
26.3	2135.9888	-0.0021	LLEHFLVQEQTGSSPSR
7.7	2134.9745	1.0122	DYSCESGTLTLLVIDELTK
4.9	2135.9870	-0.0003	LFQGVHGRMTDLCRPNR
2.2	2135.9962	-0.0095	LKQIQQLFSFADEMSGSK
2.0	2134.9783	1.0084	HEGSSTLVNLEGDAKEELK
2.0	2134.9783	1.0084	HEGSSTLVNLEGDAKEELK
1.6	2135.9963	-0.0095	SFSTGKSPATFSVVAMAPQK

no -98 neutral loss, S14 +80
no -98 neutral loss, S15 +80
-98 neutral loss, T11 -18
no -98 neutral loss, S17 +80

MS2: Top score of 37.8, match probability greater than 99%; +2 charge, deduced S14 [+80]. Moderate confidence in position assignment.

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