

### Peptide View

MS/MS Fragmentation of **LSNKPVGMNODGPGSR**

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

Match to Query 10: 1735.769994 from(868.892273,2+)

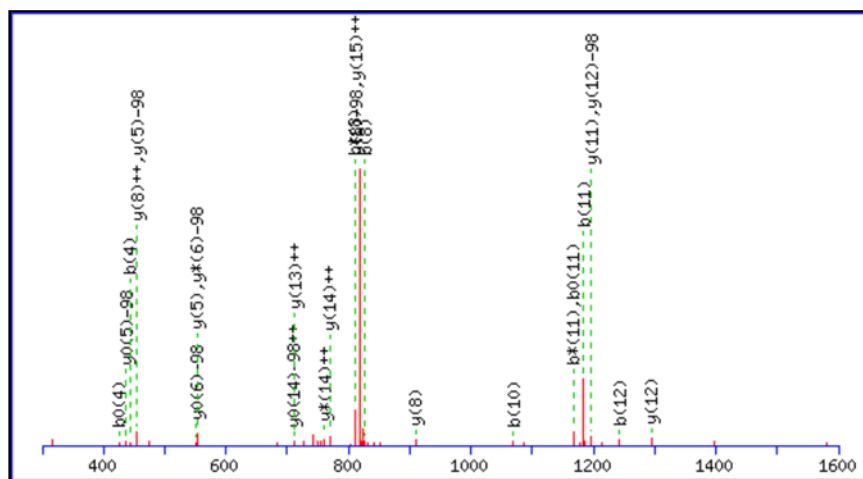
Title: PR460 % Salt.2922.2922.2.dta

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 300 to 1600 Da Full range

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1735.7713

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

Variable modifications:

**S15** : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

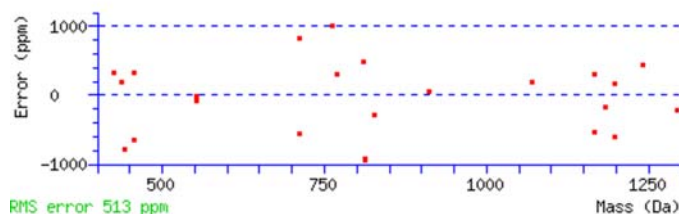
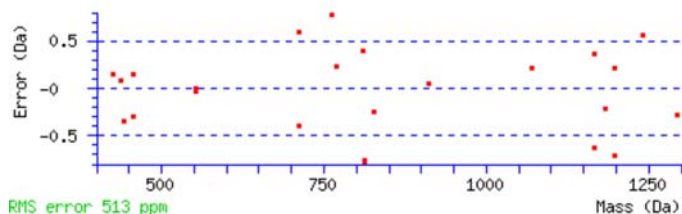
Ions Score: 27 Expect: 0.068

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Matches : 25/262 fragment ions using 33 most intense peaks (help)

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#	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	114.0913	57.5493					L							16
2	201.1234	101.0653			183.1128	92.0600	S	1623.6945	812.3509	1606.6679	803.8376	1605.6839	803.3456	15
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	N	1536.6625	768.8349	1519.6359	760.3216	1518.6519	759.8296	14
4	443.2613	222.1343	426.2347	213.6210	425.2507	213.1290	K	1422.6195	711.8134	1405.5930	703.3001	1404.6090	702.8081	13
5	540.3140	270.6606	523.2875	262.1474	522.3035	261.6554	P	1294.5246	647.7659	1277.4980	639.2527	1276.5140	638.7606	12
6	639.3824	320.1949	622.3559	311.6816	621.3719	311.1896	V	1197.4718	599.2395	1180.4453	590.7263	1179.4612	590.2343	11
7	696.4039	348.7056	679.3774	340.1923	678.3933	339.7003	G	1098.4034	549.7053	1081.3769	541.1921	1080.3928	540.7001	10
8	827.4444	414.2258	810.4178	405.7126	809.4338	405.2205	M	1041.3819	521.1946	1024.3554	512.6813	1023.3714	512.1893	9
9	941.4873	471.2473	924.4608	462.7340	923.4767	462.2420	N	910.3415	455.6744	893.3149	447.1611	892.3309	446.6691	8
10	1069.5459	535.2766	1052.5193	526.7633	1051.5353	526.2713	Q	796.2985	398.6529	779.2720	390.1396	778.2880	389.6476	7
11	1184.5728	592.7901	1167.5463	584.2768	1166.5623	583.7848	D	668.2399	334.6236	651.2134	326.1103	650.2294	325.6183	6
12	1241.5943	621.3008	1224.5677	612.7875	1223.5837	612.2955	G	553.2130	277.1101	536.1865	268.5969	535.2024	268.1049	5
13	1338.6471	669.8272	1321.6205	661.3139	1320.6365	660.8219	P	496.1915	248.5994	479.1650	240.0861	478.1810	239.5941	4
14	1395.6685	698.3379	1378.6420	689.8246	1377.6580	689.3326	G	399.1388	200.0730	382.1122	191.5598	381.1282	191.0677	3
15	1562.6669	781.8371	1545.6403	773.3238	1544.6563	772.8318	S	342.1173	171.5623	325.0908	163.0490	324.1067	162.5570	2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSNKPVG MNQDGP GSR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.7	1735.7713	-0.0013	<a href="#">LSNKPVG MNQDGP GSR</a>
17.8	1735.7851	-0.0151	<a href="#">ELEKSHNEMLEG IK</a>
13.4	1735.7770	-0.0070	<a href="#">MQWGV AQRC DGTP SK</a>
12.5	1735.7562	0.0138	<a href="#">ELVLNNALMDMY SK</a>
12.5	1735.7562	0.0138	<a href="#">ELVLNNALMDMY SK</a>
11.4	1734.7569	1.0131	<a href="#">IVAGMEGTVMTDG KSK</a>
9.4	1735.7641	0.0059	<a href="#">DVVSWNKMINGYS K</a>
7.6	1734.7648	1.0052	<a href="#">GSISFQEQASCKVK</a>
7.0	1735.7543	0.0157	<a href="#">SGGSSAASKGGATIG QLK</a>
7.0	1735.7543	0.0157	<a href="#">SGGSSAASKGGATIG QLK</a>

MS2: Only position assignment is top score of 26.7; match probability of 93%; +2 charge, no -98 neutral loss, S15 [+80] is deduced from other ions. Low positioning confidence.

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