

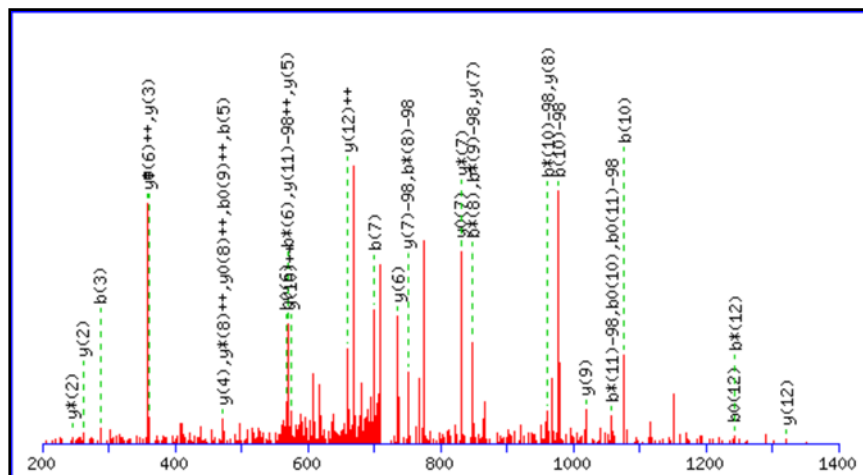
Mascot Search Results**Peptide View**MS/MS Fragmentation of **LSSQGLSPIPSR**Found in **AT2G39130.1**, | Symbols: | amino acid transporter family protein | chr2:16330249-16333822 REVERSE

Match to Query 4: 1433.727884 from(717.871218,2+)

Title: FR420_%_Salt.7600.7600.2.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 1400 Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1433.7279

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

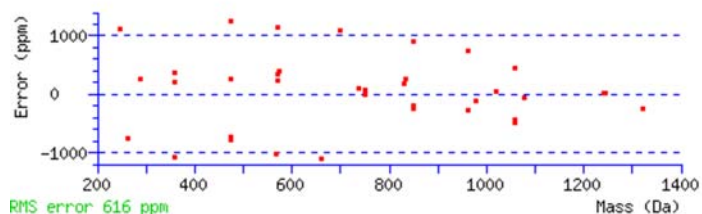
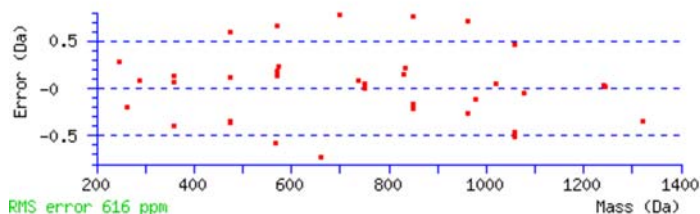
Variable modifications:

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

Ions score: 51 Expect: 0.00024

Matches : 37/206 fragment ions using 46 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							13
2	201.1234	101.0653			183.1128	92.0600	S	1321.6512	661.3292	1304.6246	652.8159	1303.6406	652.3239	12
3	288.1554	144.5813			270.1448	135.5761	S	1234.6191	617.8132	1217.5926	609.2999	1216.6086	608.8079	11
4	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	Q	1147.5871	574.2972	1130.5606	565.7839	1129.5765	565.2919	10
5	473.2354	237.1214	456.2089	228.6081	455.2249	228.1161	G	1019.5285	510.2679	1002.5020	501.7546	1001.5180	501.2626	9
6	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	L	962.5071	481.7572	945.4805	473.2439	944.4965	472.7519	8
7	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	L	849.4230	425.2151	832.3964	416.7019	831.4124	416.2099	7
8	866.4019	433.7046	849.3754	425.1913	848.3914	424.6993	S	736.3389	368.6731	719.3124	360.1598	718.3284	359.6678	6
9	963.4547	482.2310	946.4281	473.7177	945.4441	473.2257	P	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	5
10	1076.5388	538.7730	1059.5122	530.2597	1058.5282	529.7677	I	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
11	1173.5915	587.2994	1156.5650	578.7861	1155.5810	578.2941	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
12	1260.6235	630.8154	1243.5970	622.3021	1242.6130	621.8101	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSSQGLLSPIPSR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.1	1433.7279	-0.0000	LSSQGLLSPIPSR
18.4	1433.7279	-0.0000	LSSQGLLSPIPSR
18.4	1433.7279	-0.0000	LSSQGLLSPIPSR
17.8	1433.7279	-0.0000	LSSQGLLSPIPSR
7.9	1432.7133	1.0146	LYCSGHIIDSLR
7.2	1433.7337	-0.0058	LKCAIDLDFPSR
5.7	1432.7340	0.9939	IQVPYVSHVRR
5.6	1433.7319	-0.0040	TKFLPLEELHK
4.5	1433.7263	0.0016	VLFSDGRSTSTHK
2.4	1433.7184	0.0095	VIADAGTMTDLAR

no -98 neutral loss, S8 +80
 -98 neutral loss, S3 -18
 -98 neutral loss, S2 -18
 no -98 neutral loss, S12 +80

MS2: Top score 51.1, match probability greater than 99%; +2 charge; b and y ions found for S8 [+80]. High positioning confidence.

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