

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGSSFLSSGLIR**

Found in **AT2G39130.1**, | Symbols: | amino acid transporter family protein | chr2:16330249-16333822 REVERSE

Match to Query 2: 1349.634984 from(675.824768,2+)

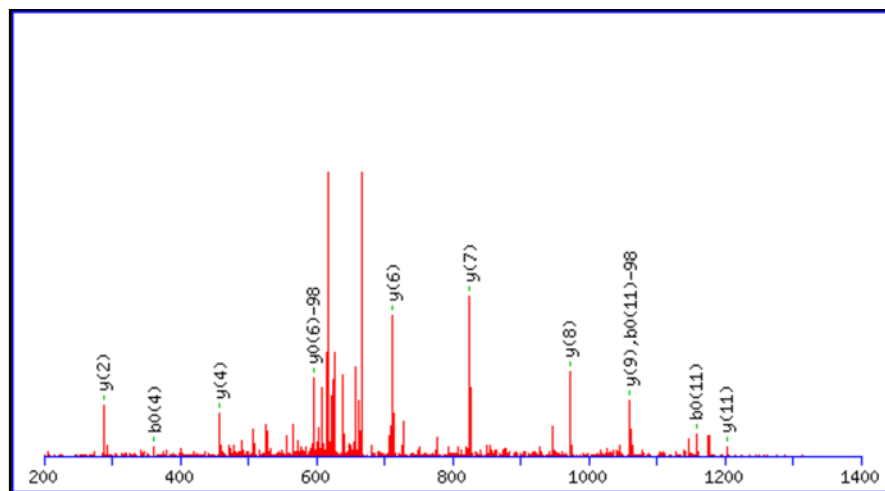
Title: 20_%_Salt.9993.9993.2.dta

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): 1349.6381

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

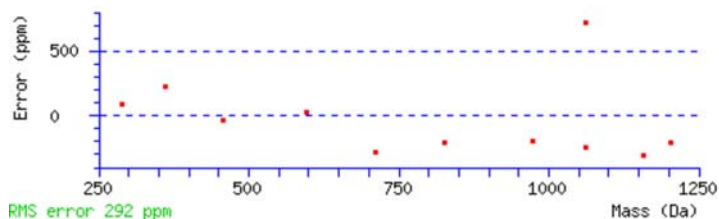
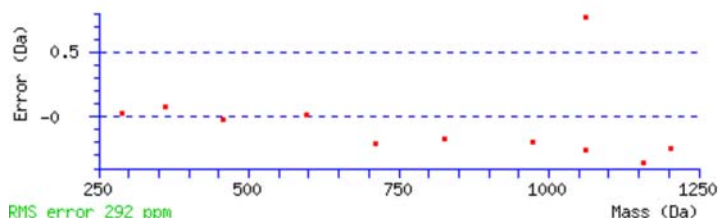
Variable modifications:

S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 51 Expect: 0.00025

Matches : 11/154 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							12
2	205.0972	103.0522			G	1203.5769	602.2921	1186.5504	593.7788	1185.5664	593.2868	11
3	292.1292	146.5682	274.1186	137.5629	S	1146.5555	573.7814	1129.5289	565.2681	1128.5449	564.7761	10
4	379.1612	190.0842	361.1506	181.0790	S	1059.5234	530.2654	1042.4969	521.7521	1041.5129	521.2601	9
5	526.2296	263.6185	508.2191	254.6132	F	972.4914	486.7493	955.4649	478.2361	954.4808	477.7441	8
6	639.3137	320.1605	621.3031	311.1552	L	825.4230	413.2151	808.3964	404.7019	807.4124	404.2099	7
7	806.3120	403.6597	788.3015	394.6544	S	712.3389	356.6731	695.3124	348.1598	694.3284	347.6678	6
8	893.3441	447.1757	875.3335	438.1704	S	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	5
9	950.3655	475.6864	932.3550	466.6811	G	458.3085	229.6579	441.2820	221.1446			4
10	1063.4496	532.2284	1045.4390	523.2232	L	401.2871	201.1472	384.2605	192.6339			3
11	1176.5337	588.7705	1158.5231	579.7652	I	288.2030	144.6051	271.1765	136.0919			2
12					R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [FGSSFLSSGLIR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.9	1349.6381	-0.0031	FGSSFLSSGLIR
50.9	1349.6381	-0.0031	FGSSFLSSGLIR
19.9	1349.6381	-0.0031	FGSSFLSSGLIR
12.7	1349.6381	-0.0031	FGSSFLSSGLIR
7.5	1348.6388	0.9962	VADNSVGPLEIR
5.1	1349.6354	-0.0004	DYRRPHTGLR
3.4	1349.6452	-0.0103	TIAAAPARQTDR
2.0	1348.6428	0.9922	ERFTIESLFK
1.7	1349.6479	-0.0130	SEGELLPSPTLK
1.5	1349.6479	-0.0130	IEAPEATTPTLK

no -98 neutral loss, S7 +80
no -98 neutral loss, S8 +80
no -98 neutral loss, S4 +80
no -98 neutral loss, S3 +80

MS2: +2 charge;
alternative
positions S7 [+80]
and S8 [+80] have
the same mascot
score with match
probability of
greater than 99%.
But the y ion for S7
[+80] was found
but only deduced
for S8 +80.
Therefore S7 [+80]
is correct. High
position
confidence.

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