

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSQGLLSPIPSR**

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

Match to Query 6: 1514.699804 from(758.357178,2+)

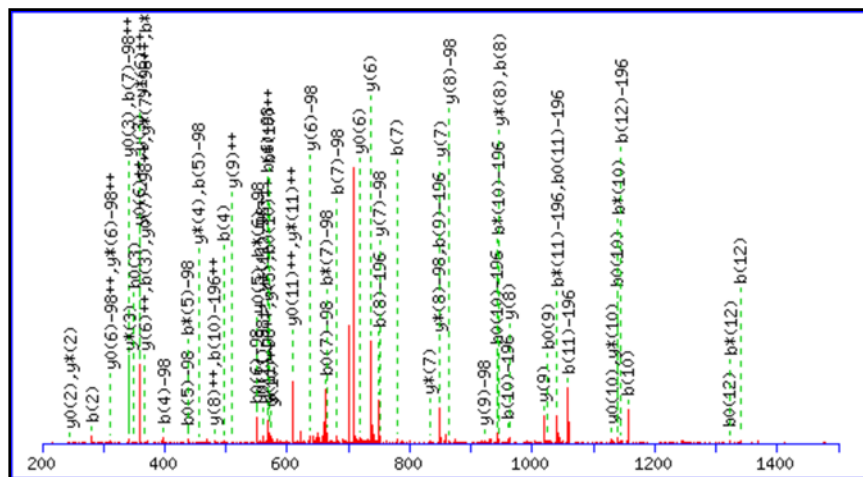
Title: PR2acn_grad.4671.4671.2.dta

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 1500

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1513.6942

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

Variable modifications:

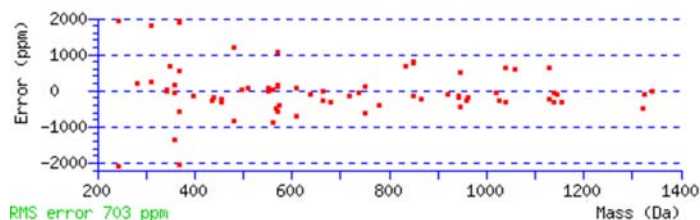
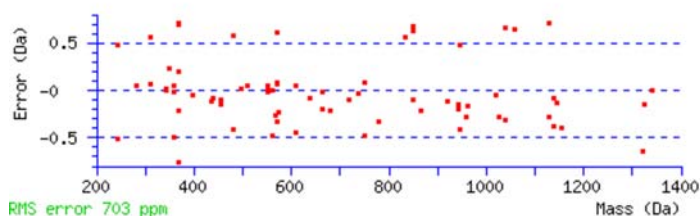
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

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

Ions Score: 32 Expect: 0.024

Matches : 74/238 fragment ions using 123 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	183.1128	92.0600			165.1022	83.0548	S	1205.6637	603.3355	1188.6371	594.8222	1187.6531	594.3302	12
3	270.1448	135.5761			252.1343	126.5708	S	1136.6422	568.8248	1119.6157	560.3115	1118.6317	559.8195	11
4	398.2034	199.6053	381.1769	191.0921	380.1928	190.6001	Q	1049.6102	525.3087	1032.5837	516.7955	1031.5996	516.3035	10
5	455.2249	228.1161	438.1983	219.6028	437.2143	219.1108	G	921.5516	461.2795	904.5251	452.7662	903.5411	452.2742	9
6	568.3089	284.6581	551.2824	276.1448	550.2984	275.6528	L	864.5302	432.7687	847.5036	424.2554	846.5196	423.7634	8
7	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	L	751.4461	376.2267	734.4195	367.7134	733.4355	367.2214	7
8	750.4145	375.7109	733.3879	367.1976	732.4039	366.7056	S	638.3620	319.6847	621.3355	311.1714	620.3515	310.6794	6
9	847.4672	424.2373	830.4407	415.7240	829.4567	415.2320	P	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	5
10	960.5513	480.7793	943.5247	472.2660	942.5407	471.7740	I	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
11	1057.6041	529.3057	1040.5775	520.7924	1039.5935	520.3004	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
12	1144.6361	572.8217	1127.6095	564.3084	1126.6255	563.8164	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
31.7	1513.6942	1.0056	LSSQGLLSPIPSR
30.6	1513.6942	1.0056	LSSQGLLSPIPSR
18.3	1513.6942	1.0056	LSSQGLLSPIPSR
17.4	1513.6942	1.0056	LSSQGLLSPIPSR
16.1	1513.6942	1.0056	LSSQGLLSPIPSR
11.3	1513.6831	1.0167	SRVYSDEMTSSPR
8.7	1514.6986	0.0012	MEVVAVGSMKTQR
6.2	1514.6905	0.0093	YPELTTEGSPTIK
5.8	1513.6814	1.0184	FGGPTEVTSGGNALK
5.8	1513.6814	1.0184	FGGPTEVTSGGNALK

-98 neutral loss; S2, S8 -18
 -98 neutral loss; S3, S8 -18
 -98 neutral loss; S2, S12 -18
 -98 neutral loss; S3, S12 -18
 -98 neutral loss; S2, S3 -18

MS2: Top match score of 31.7 has probability of 97% but is close to second score for a different position assignment; b and y ions found for S8 [-18] in each but only deduced for S2 [-18] or S3 [-18]. However, in MS3, b and y ions found for S8 [-18] and y ion found for unmodified S3, meaning that S2 [-18]. High position confidence.

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSQGLSPIR**

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

Match to Query 3: 1415.806724 from(708.910638,2+)

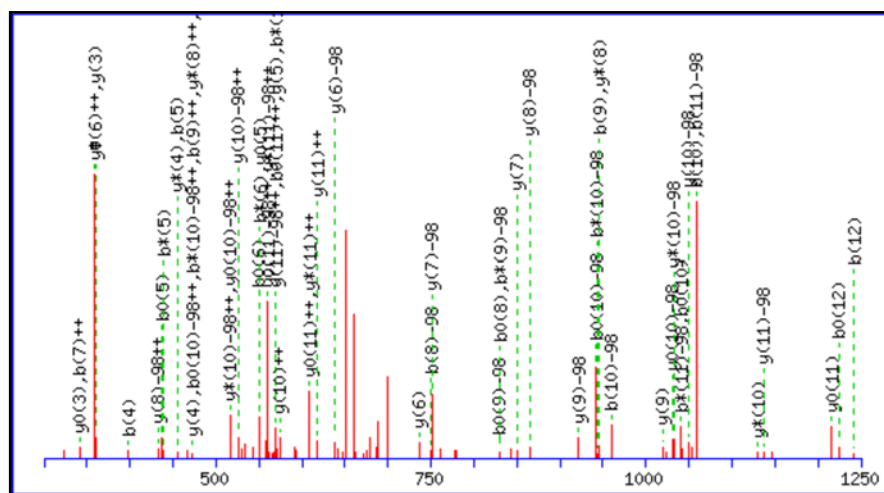
Title: PR2acn_grad.4672.4672.2.dta

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 1250 Da Full range

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1415.7174

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

Variable modifications:

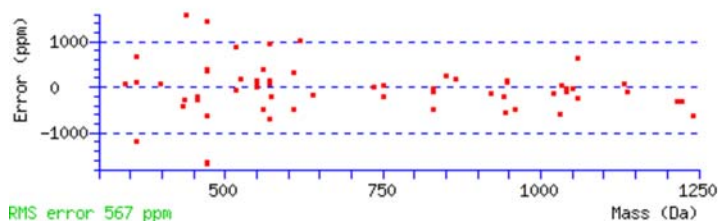
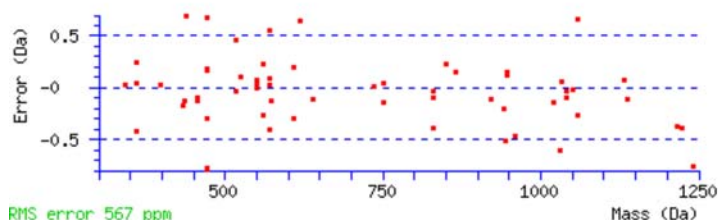
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S2      : Dehydrated (S)
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s8      : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
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Ions Score: 63 Expect: 0.00064

Matches : 61/206 fragment ions using 63 most intense peaks ([help](#))

#	b	b⁺⁺	b*	b^{*++}	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y^{*++}	y⁰	y⁰⁺⁺
1	114.0913	57.5493					L						
2	183.1128	92.0600			165.1022	83.0548	S	1205.6637	603.3355	1188.6371	594.8222	1187.6531	594.3302
3	270.1448	135.5761			252.1343	126.5708	S	1136.6422	568.8248	1119.6157	560.3115	1118.6317	559.8195
4	398.2034	199.6053	381.1769	191.0921	380.1928	190.6001	Q	1049.6102	525.3087	1032.5837	516.7955	1031.5996	516.3035
5	455.2249	228.1161	438.1983	219.6028	437.2143	219.1108	G	921.5516	461.2795	904.5251	452.7662	903.5411	452.2742
6	568.3089	284.6581	551.2824	276.1448	550.2984	275.6528	L	864.5302	432.7687	847.5036	424.2554	846.5196	423.7634
7	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	L	751.4461	376.2267	734.4196	367.7134	733.4355	367.2214
8	750.4145	375.7109	733.3879	367.1976	732.4039	366.7056	S	638.3620	319.6847	621.3355	311.1714	620.3515	310.6794
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11	1057.6041	529.3057	1040.5775	520.7924	1039.5935	520.3004	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002
12	1144.6361	572.8217	1127.6095	564.3084	1126.6255	563.8164	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738
13							R	175.1190	88.0631	158.0924	79.5498		



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
63.4	1415.7174	0.0893	LSSQGLLSPIPSR
57.7	1415.7174	0.0893	LSSQGLLSPIPSR
52.7	1415.7174	0.0893	LSSQGLLSPIPSR
48.7	1415.7174	0.0893	LSSQGLLSPIPSR
44.8	1415.7174	0.0893	LSSQGLLSPIPSR
40.1	1415.7174	0.0893	LSSQGLLSPIPSR
35.0	1415.7174	0.0893	LSSQGLLSPIPSR
31.9	1415.7174	0.0893	LSSQGLLSPIPSR
22.8	1415.7174	0.0893	LSSQGLLSPIPSR
22.8	1415.7174	0.0893	LSSQGLLSPIPSR

S2 -18; neutral loss -98, so S8 -18
 neutral loss -98, so S2 -18; S8 -18
 S3 -18; neutral loss -98, so S8 -18
 neutral loss -98, so S3 -18; S8 -18
 S2 -18; neutral loss -98, so S12 -18

MS3: -98 Da
 triggered
 consecutive
 spectrum. Top
 match
 phosphorylation
 position
 assignment
 corroborates top
 MS2 assignment. b
 and y ions found
 for S8 [-18]; y ion
 found for
 unmodified S3, so
 S2 must be [-18].

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