

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGSFESSRPSSR**

Found in **AT4G12770.1**, | Symbols: | heat shock protein binding | chr4:7506733-7511405 REVERSE

Match to Query 8: 1572.447723 from(525.156517,3+)

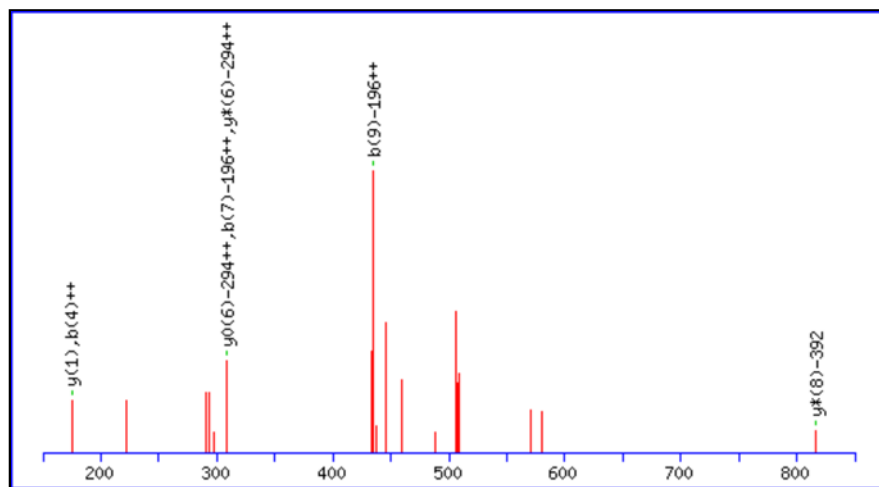
Title: PR470_%_Salt.11572.11572.3.dta

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, 150 to 850 Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1572.4449

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

Variable modifications:

S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

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

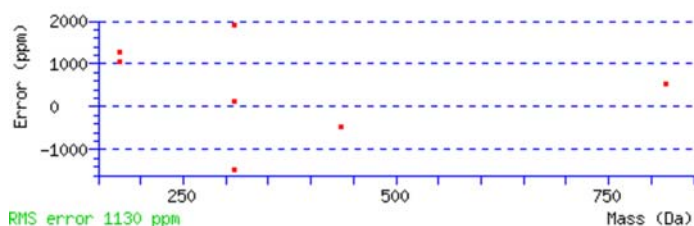
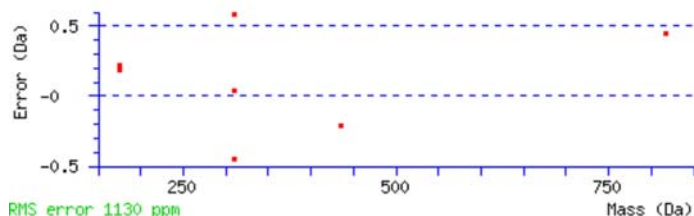
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 12 Expect: 0.15

Matches : 7/204 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							12
2	115.0502	58.0287					G	1124.5232	562.7652	1107.4966	554.2520	1106.5126	553.7599	11
3	202.0822	101.5448			184.0717	92.5395	S	1067.5017	534.2545	1050.4752	525.7412	1049.4911	525.2492	10
4	349.1506	175.0790			331.1401	166.0737	F	980.4697	490.7385	963.4431	482.2252	962.4591	481.7332	9
5	478.1932	239.6003			460.1827	230.5950	E	833.4013	417.2043	816.3747	408.6910	815.3907	408.1990	8
6	547.2147	274.1110			529.2041	265.1057	S	704.3587	352.6830	687.3321	344.1697	686.3481	343.6777	7
7	616.2362	308.6217			598.2256	299.6164	S	635.3372	318.1722	618.3107	309.6590	617.3267	309.1670	6
8	772.3373	386.6723	755.3107	378.1590	754.3267	377.6670	R	566.3158	283.6615	549.2892	275.1482	548.3052	274.6562	5
9	869.3900	435.1987	852.3635	426.6854	851.3795	426.1934	P	410.2146	205.6110	393.1881	197.0977	392.2041	196.6057	4
10	938.4115	469.7094	921.3850	461.1961	920.4009	460.7041	S	313.1619	157.0846	296.1353	148.5713	295.1513	148.0793	3
11	1007.4330	504.2201	990.4064	495.7068	989.4224	495.2148	S	244.1404	122.5738	227.1139	114.0606	226.1299	113.5686	2
12							R	175.1190	88.0631	158.0924	79.5498			1



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

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
12.4	1572.4449	0.0028	GGSFESSRPSSR
6.4	1571.4531	0.9947	VSSGTQTSLGR
5.7	1571.4531	0.9947	VSSGTQTSLGR
5.2	1572.4532	-0.0054	GSSGSYQSSSSGSR
4.7	1572.4548	-0.0071	DVSGTSTVSSTGR
3.6	1571.4531	0.9947	VSSGTQTSLGR
3.6	1571.4531	0.9947	VSSGTQTSLGR
2.9	1572.4532	-0.0054	GSSGSYQSSSSGSR
2.9	1572.4523	-0.0046	TAASWSSMVSAR
2.9	1571.4531	0.9947	VSSGTQTSLGR

MS2: Top score of 12.4 is very low and match probability is just 85%. +3 charge, -98 neutral loss and deduced S6, S7, S10, S11 [-18]; multiply phosphorylated peptides ionize poorly. Low position confidence.

Mascot: [http://w](#)