

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IHFMLSSYAPVISA**AK

Found in **AT5G19770.1**, | Symbols: TUA3 | TUA3 (tubulin alpha-3) | chr5:6682763-6684476 REVERSE

Match to Query 12: 1813.900484 from(907.957518,2+)

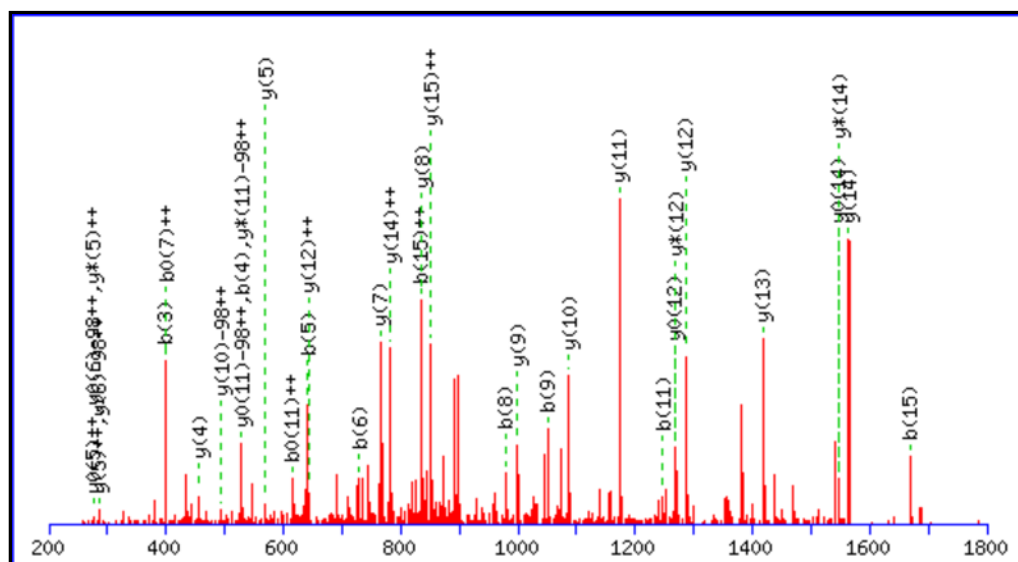
Title: FR190_%_Salt_two.9639.9639.2.dta

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 to 1800 Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1813.8838

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

Variable modifications:

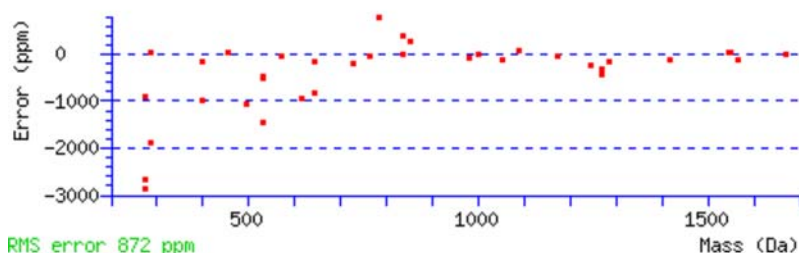
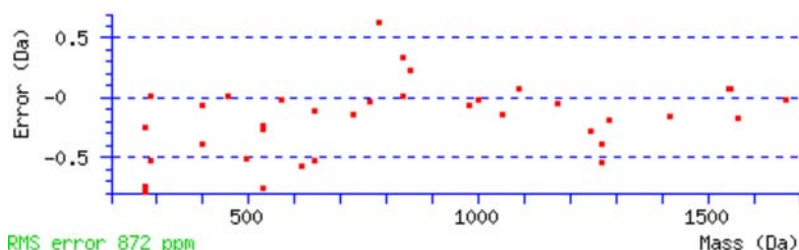
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 43 Expect: 0.0015

Matches : 36/218 fragment ions using 76 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							16
2	251.1503	126.0788			H	1701.8070	851.4071	1684.7805	842.8939	1683.7964	842.4019	15
3	398.2187	199.6130			F	1564.7481	782.8777	1547.7215	774.3644	1546.7375	773.8724	14
4	529.2592	265.1332			M	1417.6797	709.3435	1400.6531	700.8302	1399.6691	700.3382	13
5	642.3432	321.6752			L	1286.6392	643.8232	1269.6126	635.3100	1268.6286	634.8180	12
6	729.3752	365.1913	711.3647	356.1860	S	1173.5551	587.2812	1156.5286	578.7679	1155.5446	578.2759	11
7	816.4073	408.7073	798.3967	399.7020	S	1086.5231	543.7652	1069.4966	535.2519	1068.5125	534.7599	10
8	979.4706	490.2389	961.4600	481.2337	Y	999.4911	500.2492	982.4645	491.7359	981.4805	491.2439	9
9	1050.5077	525.7575	1032.4971	516.7522	A	836.4277	418.7175	819.4012	410.2042	818.4172	409.7122	8
10	1147.5605	574.2839	1129.5499	565.2786	P	765.3906	383.1990	748.3641	374.6857	747.3801	374.1937	7
11	1246.6289	623.8181	1228.6183	614.8128	V	668.3379	334.6726	651.3113	326.1593	650.3273	325.6673	6

12	1359.7130	680.3601	1341.7024	671.3548	I	569.2695	285.1384	552.2429	276.6251	551.2589	276.1331	5
13	1526.7113	763.8593	1508.7008	754.8540	S	456.1854	228.5963	439.1588	220.0831	438.1748	219.5911	4
14	1597.7484	799.3779	1579.7379	790.3726	A	289.1870	145.0972	272.1605	136.5839			3
15	1668.7855	834.8964	1650.7750	825.8911	A	218.1499	109.5786	201.1234	101.0653			2
16					K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [IHFMLSSYAPVISA AK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	1813.8838	0.0167	IHFMLSSYAPVISA AK
24.5	1813.8838	0.0167	IHFMLSSYAPVISA AK
16.7	1813.8838	0.0167	IHFMLSSYAPVISA AK
4.8	1813.8862	0.0142	YDLNTVISAKPKEEK
4.0	1813.8872	0.0133	KFTGKPLPLTCTPMK
2.5	1813.9128	-0.0123	GRWTPIFLTTLGLSSAK
2.5	1813.9128	-0.0123	GRWTPIFLTTLGLSSAK
1.8	1813.8862	0.0143	ALAAALEAEELYSKQK
1.3	1813.8862	0.0142	YDLNTVISAKPKEEK
0.7	1813.8872	0.0133	KFTGKPLPLTCTPMK

no -98 neutral loss, S13 +80
no -98 neutral loss, S7 +80
no -98 neutral loss, S6 +80

MS2: top score of 42.8 and match probability of 99%; +2 charge; y ion found for S13 [+80]. High confidence in positioning.

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