

# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KISGILDDGSVGFR**

Found in **AT5G49890.1**, | Symbols: ATCLC-C, CLC-C | CLC-C (chloride channel C); anion channel/ voltage-gated chloride channel | chr5:20305715-20309369 REVERSE

Match to Query 7: 1542.739594 from(772.377073,2+)

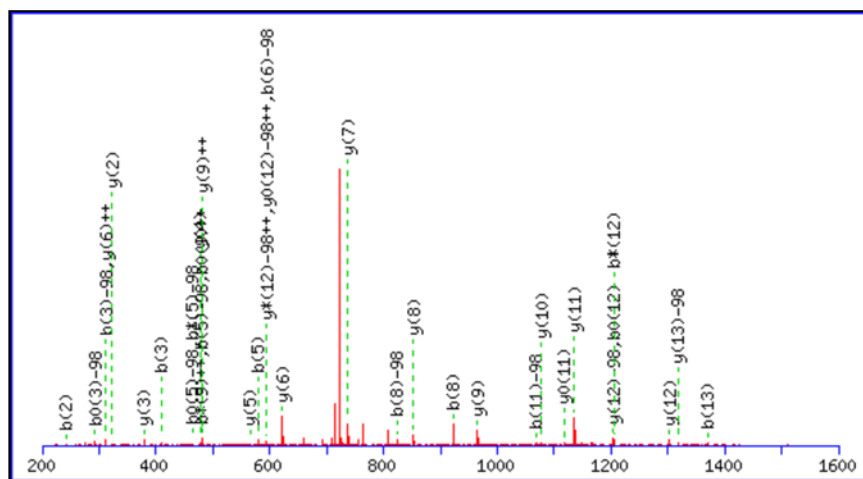
Title: PR1acn\_grad.4511.4511.2.dta

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  Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1542.7443

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

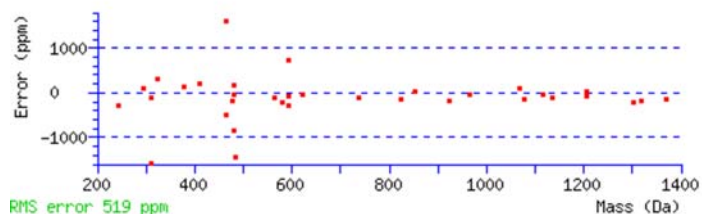
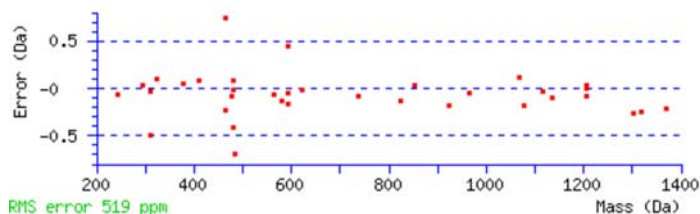
Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 89 Expect: 3.9e-008

Matches : 35/222 fragment ions using 51 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	<b>242.1863</b>	121.5968	225.1598	113.0835			I	<b>1317.6797</b>	659.3435	1300.6532	650.8302	1299.6692	650.3382	13
3	<b>311.2078</b>	156.1075	294.1812	147.5942	<b>293.1972</b>	147.1022	S	<b>1204.5957</b>	602.8015	1187.5691	<b>594.2882</b>	1186.5851	<b>593.7962</b>	12
4	368.2292	184.6183	351.2027	176.1050	350.2187	175.6130	G	<b>1135.5742</b>	568.2907	1118.5477	559.7775	<b>1117.5636</b>	559.2855	11
5	<b>481.3133</b>	241.1603	<b>464.2867</b>	232.6470	<b>463.3027</b>	232.1550	I	<b>1078.5528</b>	539.7800	1061.5262	531.2667	1060.5422	530.7747	10
6	<b>594.3974</b>	297.7023	577.3708	289.1890	576.3868	288.6970	L	<b>965.4687</b>	<b>483.2380</b>	948.4421	474.7247	947.4581	474.2327	9
7	709.4243	355.2158	692.3978	346.7025	691.4137	346.2105	D	<b>852.3846</b>	426.6959	835.3581	418.1827	834.3741	417.6907	8
8	<b>824.4512</b>	412.7293	807.4247	404.2160	806.4407	403.7240	D	<b>737.3577</b>	369.1825	720.3311	360.6692	719.3471	360.1772	7
9	881.4727	441.2400	864.4462	432.7267	863.4621	432.2347	G	<b>622.3307</b>	<b>311.6690</b>	605.3042	303.1557	604.3202	302.6637	6
10	968.5047	484.7560	951.4782	476.2427	950.4942	475.7507	S	<b>565.3093</b>	283.1583	548.2827	274.6450	547.2987	274.1530	5
11	<b>1067.5732</b>	534.2902	1050.5466	525.7769	1049.5626	525.2849	V	<b>478.2772</b>	239.6423	461.2507	231.1290			4
12	1124.5946	562.8009	1107.5681	554.2877	1106.5840	553.7957	G	<b>379.2088</b>	190.1081	362.1823	181.5948			3
13	1271.6630	636.3352	1254.6365	627.8219	1253.6525	627.3299	F	<b>322.1874</b>	161.5973	305.1608	153.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [KISGILDDGSVGFR](#)

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

Other BLAST [web gateways](#)

**All matches to this query**

Score	Mr(calc):	Delta	Sequence
89.5	1542.7443	-0.0047	<a href="#">KISGILDDGSVGFR</a>
16.3	1542.7443	-0.0047	<a href="#">KISGILDDGSVGFR</a>
9.5	1542.7331	0.0065	<a href="#">GTGLILGTEFVDNK</a>
5.5	1542.7443	-0.0047	<a href="#">IQASVVLDATGFSR</a>
3.7	1542.7443	-0.0047	<a href="#">KVTEAVIGFENTR</a>
3.5	1541.7504	0.9892	<a href="#">HFTDIKQLAPHR</a>
2.9	1542.7418	-0.0022	<a href="#">VYIMTVHFVQAR</a>
2.6	1541.7392	1.0004	<a href="#">TDALNKPFWRSK</a>
0.6	1541.7313	1.0083	<a href="#">LTGLIPESLCFGR</a>
0.5	1541.7474	0.9922	<a href="#">DKPSALKPDDWDR</a>

neutral loss -98, S3 -18  
neutral loss -98, S10 -18

MS2: Top ranked score of 89.5 and match probability greater than 99%. +2 charge; b and y ions found for S3 [-18] and supported by MS3. High match confidence.

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

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Match to Query 4: 1446.077724 from(724.046138,2+)

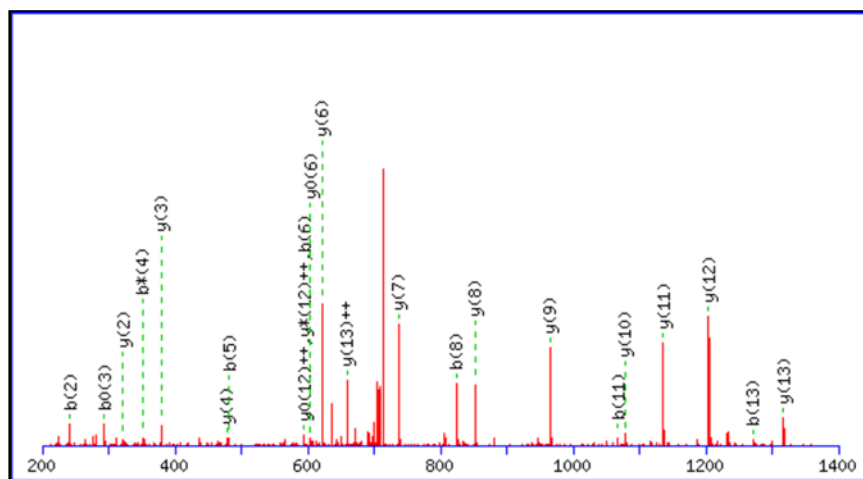
Title: PR1acn\_grad.4512.4512.2.dta

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,  200 to  Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1444.7675

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

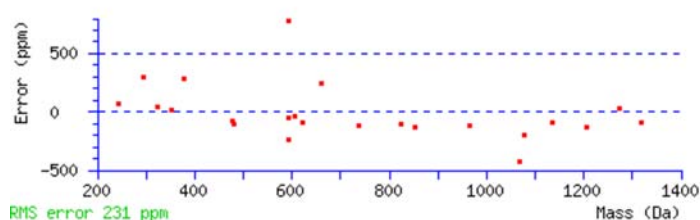
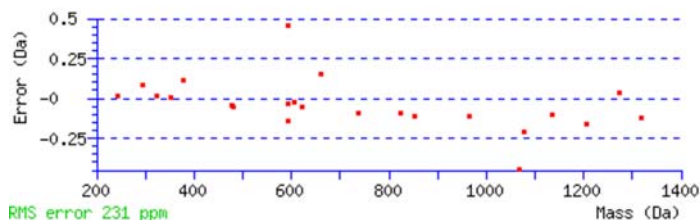
Variable modifications:

S3 : Dehydrated (S)

Ions Score: 86 Expect: 3.9e-006

Matches : 23/144 fragment ions using 36 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>*++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	129.1022	65.0548	112.0757	56.5415			K							14
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(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.7	1444.7675	1.3103	<a href="#">KISGILDDGSVGFR</a>
31.2	1444.7675	1.3103	<a href="#">KISGILDDGSVGFR</a>
16.8	1445.8243	0.2535	<a href="#">LKVLSESLNSTSK</a>
16.7	1445.8243	0.2535	<a href="#">LKVLSESLNSTSK</a>
16.1	1445.8144	0.2633	<a href="#">ITATLLPPPPTSHR</a>
15.1	1445.6817	0.3960	<a href="#">QLSSLSHTSITHK</a>
15.1	1445.6817	0.3960	<a href="#">QLSSLSHTSITHK</a>
15.1	1445.7895	0.2883	<a href="#">IKPLSTSPSLKTL</a>
14.4	1445.7895	0.2883	<a href="#">IKPLSTSPSLKTL</a>
14.3	1446.5446	-0.4669	<a href="#">KDSGMSSNTESSR</a>

S3 -18  
S10 -18

MS3: -98 Da  
triggered  
consecutive  
spectrum.  
Corroborating ions,  
y ion found for S3  
[-18].

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