2/24/12

Mascot Search Results: Peptide View

## (MATRIX) Mascot Search Results

## Peptide View

MS/MS Fragmentation of VSTPVPGVVAPGSR

Found in AT2G35530.1, Symbols: | bZIP transcription factor family protein | chr2:14923280-14926025 REVERSE

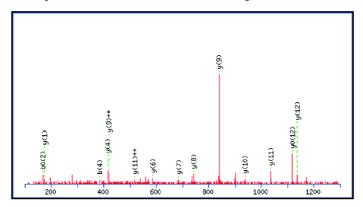
Match to Query 1: 1321.732724 from(661.873638,2+)

Data file Jihad Sample 661.8c.dta

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1300 Da Label all possible matches 

Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1321.7354 Ions Score: 39 Expect: 0.0032 Matches: 14/126 fragment ions using 39 most intense peaks

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	у	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	100.0757	50.5415			V							14
2	187.1077	94.0575	169.0972	85.0522	S	1223.6743	612.3408	1206.6477	603.8275	1205.6637	603.3355	13
3	288.1554	144.5813	270.1448	135.5761	T	1136.6422	568.8248	1119.6157	560.3115	1118.6317	559.8195	12
4	385.2082	193.1077	367.1976	184.1024	P	1035.5946	518.3009	1018.5680	509.7876	1017.5840	509.2956	11
5	484.2766	242.6419	466.2660	233.6366	V	938.5418	469.7745	921.5152	461.2613	920.5312	460.7693	10
6	581.3293	291.1683	563.3188	282.1630	P	839.4734	420.2403	822.4468	411.7271	821.4628	411.2350	9
7	638.3508	319.6790	620.3402	310.6738	G	742.4206	371.7139	725.3941	363.2007	724.4100	362.7087	8
8	737.4192	369.2132	719.4087	360.2080	V	685.3991	343.2032	668.3726	334.6899	667.3886	334.1979	7
9	836.4876	418.7475	818.4771	409.7422	V	586.3307	293.6690	569.3042	285.1557	568.3202	284.6637	6
10	907.5247	454.2660	889.5142	445.2607	A	487.2623	244.1348	470.2358	235.6215	469.2518	235.1295	5
11	1004.5775	502.7924	986.5669	493.7871	P	416.2252	208.6162	399.1987	200.1030	398.2146	199.6110	4
12	1061.5990	531.3031	1043.5884	522.2978	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
13	1148.6310	574.8191	1130.6204	565.8139	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14					R	175.1190	88.0631	158.0924	79.5498			1

