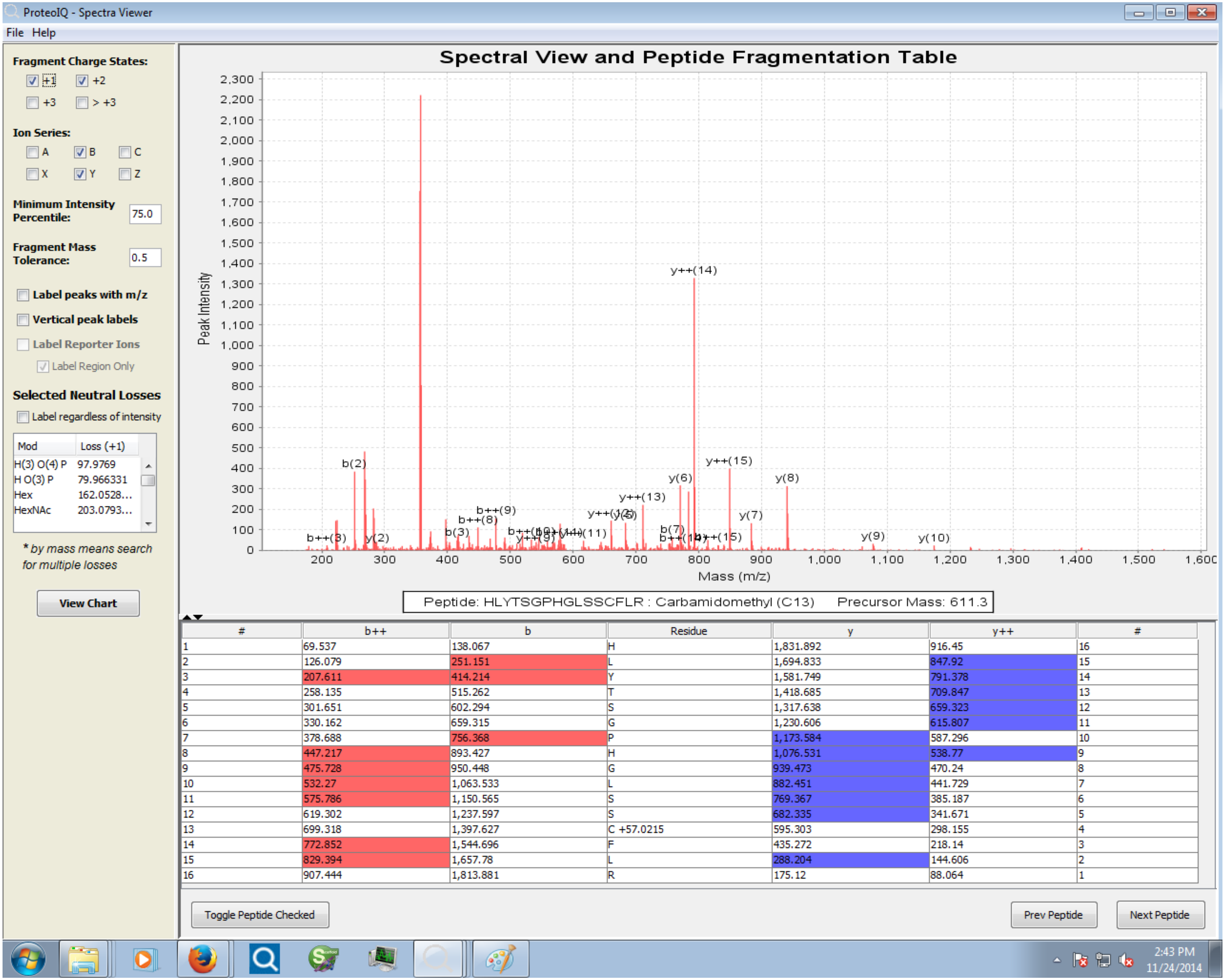

Fragment Charge States:

☑ +1 ☑ +2

☐ +3 ☐ > +3

Ion Series:

☐ A ☑ B ☐ C

☐ X ☑ Y ☐ Z

Minimum Intensity Percentile: 75.0

Fragment Mass Tolerance: 0.5

☐ **Label peaks with m/z**

☐ **Vertical peak labels**

☐ **Label Reporter Ions**

☑ Label Region Only

Selected Neutral Losses

☐ Label regardless of intensity

Mod	Loss (+1)
H(3) O(4) P	97.9769
H O(3) P	79.966331
Hex	162.0528...
HexNAc	203.0793...

** by mass means search for multiple losses*

Spectral View and Peptide Fragmentation Table

Peptide: HLYTSGPHGLSSCFLR : Carbamidomethyl (C13)   Precursor Mass: 611.3

#	b++	b	Residue	y	y++	#
1	69.537	138.067	H	1,831.892	916.45	16
2	126.079	251.151	L	1,694.833	847.92	15
3	207.611	414.214	Y	1,581.749	791.378	14
4	258.135	515.262	T	1,418.685	709.847	13
5	301.651	602.294	S	1,317.638	659.323	12
6	330.162	659.315	G	1,230.606	615.807	11
7	378.688	756.368	P	1,173.584	587.296	10
8	447.217	893.427	H	1,076.531	538.77	9
9	475.728	950.448	G	939.473	470.24	8
10	532.27	1,063.533	L	882.451	441.729	7
11	575.786	1,150.565	S	769.367	385.187	6
12	619.302	1,237.597	S	682.335	341.671	5
13	699.318	1,397.627	C +57.0215	595.303	298.155	4
14	772.852	1,544.696	F	435.272	218.14	3
15	829.394	1,657.78	L	288.204	144.606	2
16	907.444	1,813.881	R	175.12	88.064	1