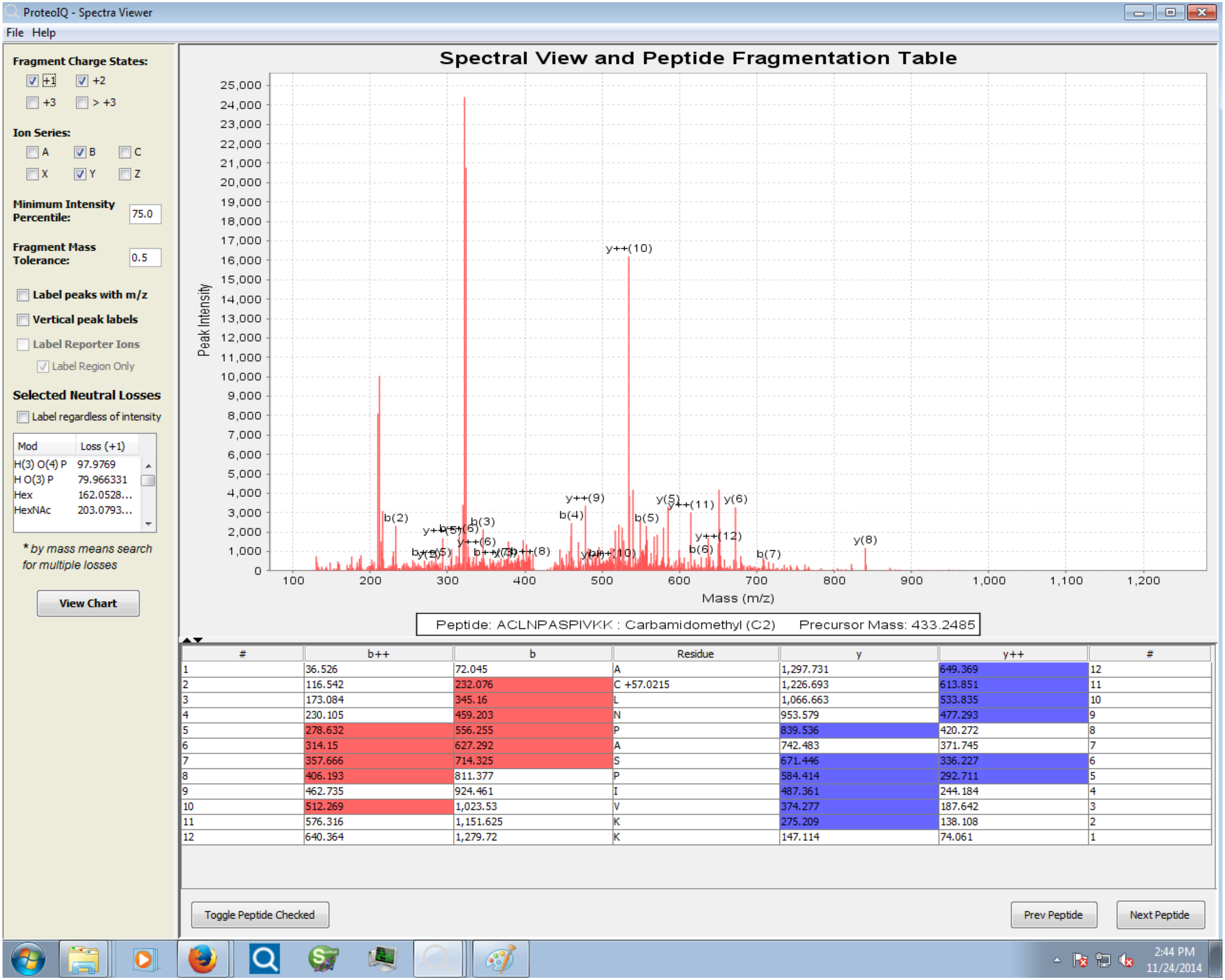

Fragment Charge States:
☑ +1 ☑ +2
☐ +3 ☐ > +3

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: ACLNPASPIVKK : Carbamidomethyl (C2) Precursor Mass: 433.2485

#	b++	b	Residue	y	y++	#
1	36.526	72.045	A	1,297.731	649.369	12
2	116.542	232.076	C +57.0215	1,226.693	613.851	11
3	173.084	345.16	L	1,066.663	533.835	10
4	230.105	459.203	N	953.579	477.293	9
5	278.632	556.255	P	839.536	420.272	8
6	314.15	627.292	A	742.483	371.745	7
7	357.666	714.325	S	671.446	336.227	6
8	406.193	811.377	P	584.414	292.711	5
9	462.735	924.461	I	487.361	244.184	4
10	512.269	1,023.53	V	374.277	187.642	3
11	576.316	1,151.625	K	275.209	138.108	2
12	640.364	1,279.72	K	147.114	74.061	1