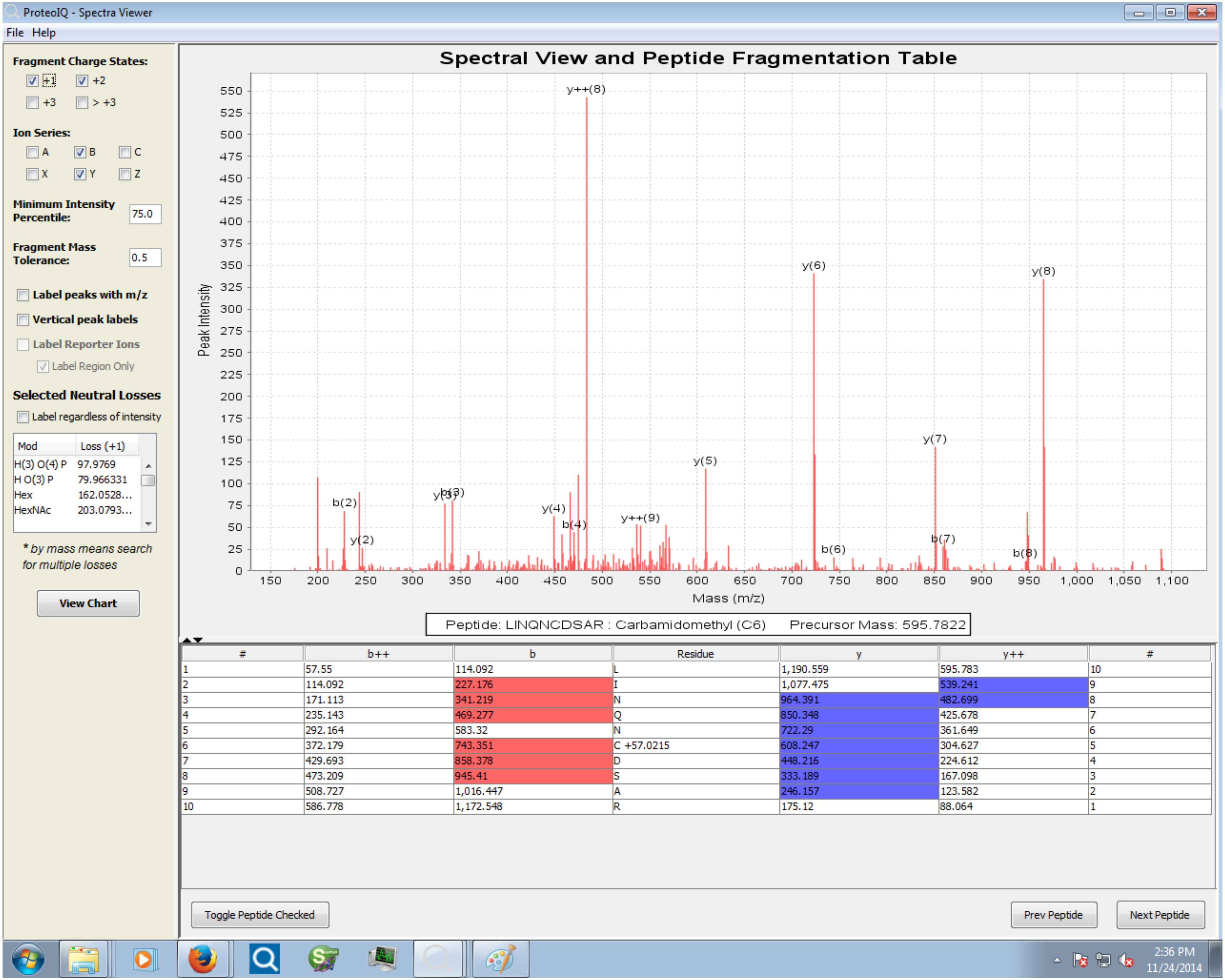

Fragment Charge States:

☑ +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: LINQNCDSAR : Carbamidomethyl (C6)   Precursor Mass: 595.7822

#	b++	b	Residue	y	y++	#
1	57.55	114.092	L	1,190.559	595.783	10
2	114.092	227.176	I	1,077.475	539.241	9
3	171.113	341.219	N	964.391	482.699	8
4	235.143	469.277	Q	850.348	425.678	7
5	292.164	583.32	N	722.29	361.649	6
6	372.179	743.351	C +57.0215	608.247	304.627	5
7	429.693	858.378	D	448.216	224.612	4
8	473.209	945.41	S	333.189	167.098	3
9	508.727	1,016.447	A	246.157	123.582	2
10	586.778	1,172.548	R	175.12	88.064	1