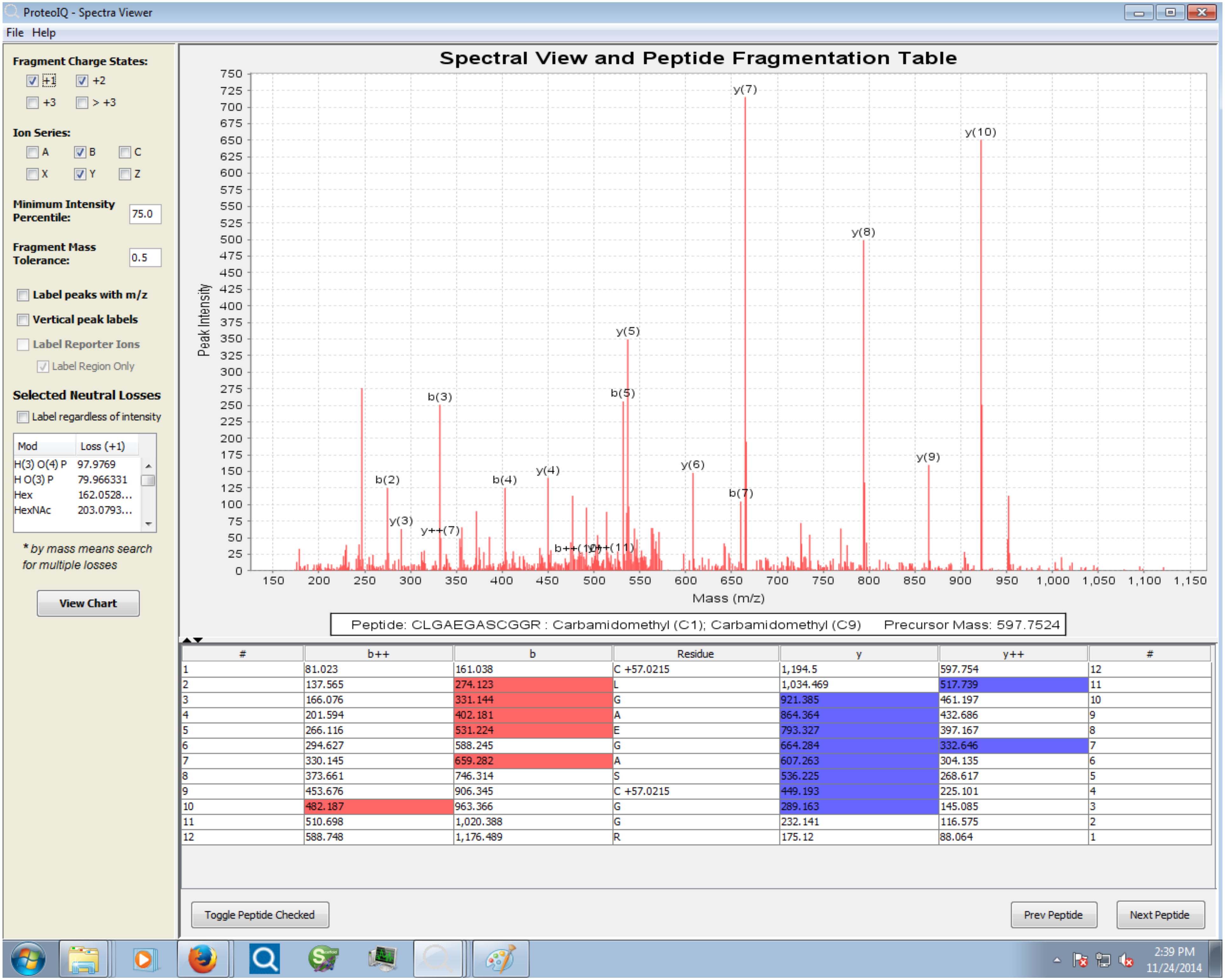

Fragment Charge States:

☑ +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: CLGAEGASCGGR : Carbamidomethyl (C1); Carbamidomethyl (C9)   Precursor Mass: 597.7524

#	b++	b	Residue	y	y++	#
1	81.023	161.038	C +57.0215	1,194.5	597.754	12
2	137.565	274.123	L	1,034.469	517.739	11
3	166.076	331.144	G	921.385	461.197	10
4	201.594	402.181	A	864.364	432.686	9
5	266.116	531.224	E	793.327	397.167	8
6	294.627	588.245	G	664.284	332.646	7
7	330.145	659.282	A	607.263	304.135	6
8	373.661	746.314	S	536.225	268.617	5
9	453.676	906.345	C +57.0215	449.193	225.101	4
10	482.187	963.366	G	289.163	145.085	3
11	510.698	1,020.388	G	232.141	116.575	2
12	588.748	1,176.489	R	175.12	88.064	1