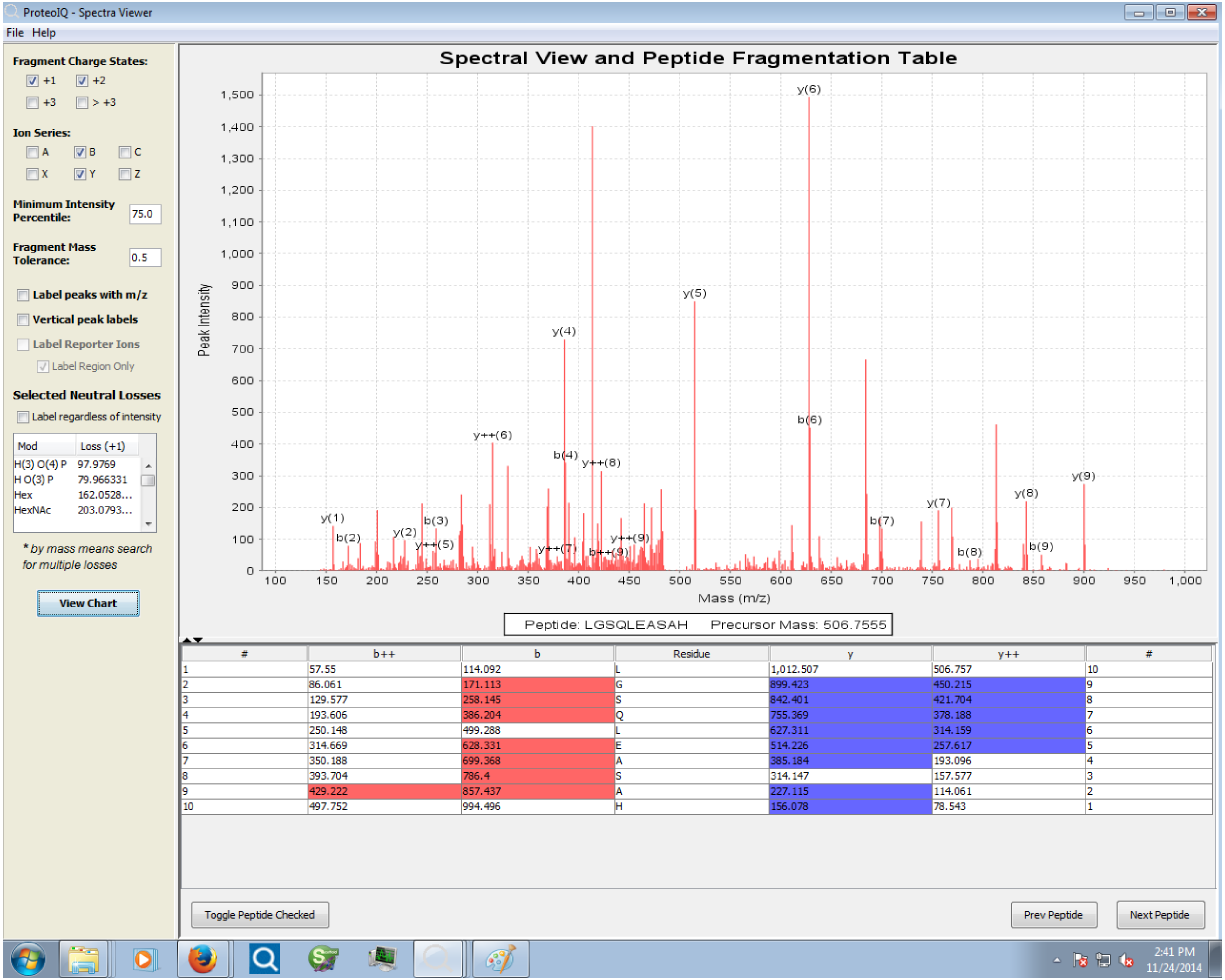

Fragment Charge States:
☑ +1 ☑ +2
☐ +3 ☐ > +3

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*

Peptide: LGSQLEASAH Precursor Mass: 506.7555

#	b++	b	Residue	y	y++	#
1	57.55	114.092	L	1,012.507	506.757	10
2	86.061	171.113	G	899.423	450.215	9
3	129.577	258.145	S	842.401	421.704	8
4	193.606	386.204	Q	755.369	378.188	7
5	250.148	499.288	L	627.311	314.159	6
6	314.669	628.331	E	514.226	257.617	5
7	350.188	699.368	A	385.184	193.096	4
8	393.704	786.4	S	314.147	157.577	3
9	429.222	857.437	A	227.115	114.061	2
10	497.752	994.496	H	156.078	78.543	1