ProteoIQ - Spectra Viewer

File Help

Fragment Charge States:

☑ +1 ☑ +2

☐ +3 ☐ > +3

Ion Series:

☐ A ☑ B ☐ C

☐ X ☑ Y ☐ Z

Minimum Intensity Percentile: 75

Fragment Mass Tolerance: 0.5

☐ **Label peaks with m/z**

☐ **Vertical peak labels**

☐ **Label Reporter Ions**

☑ Label Region Only

Selected Neutral Losses

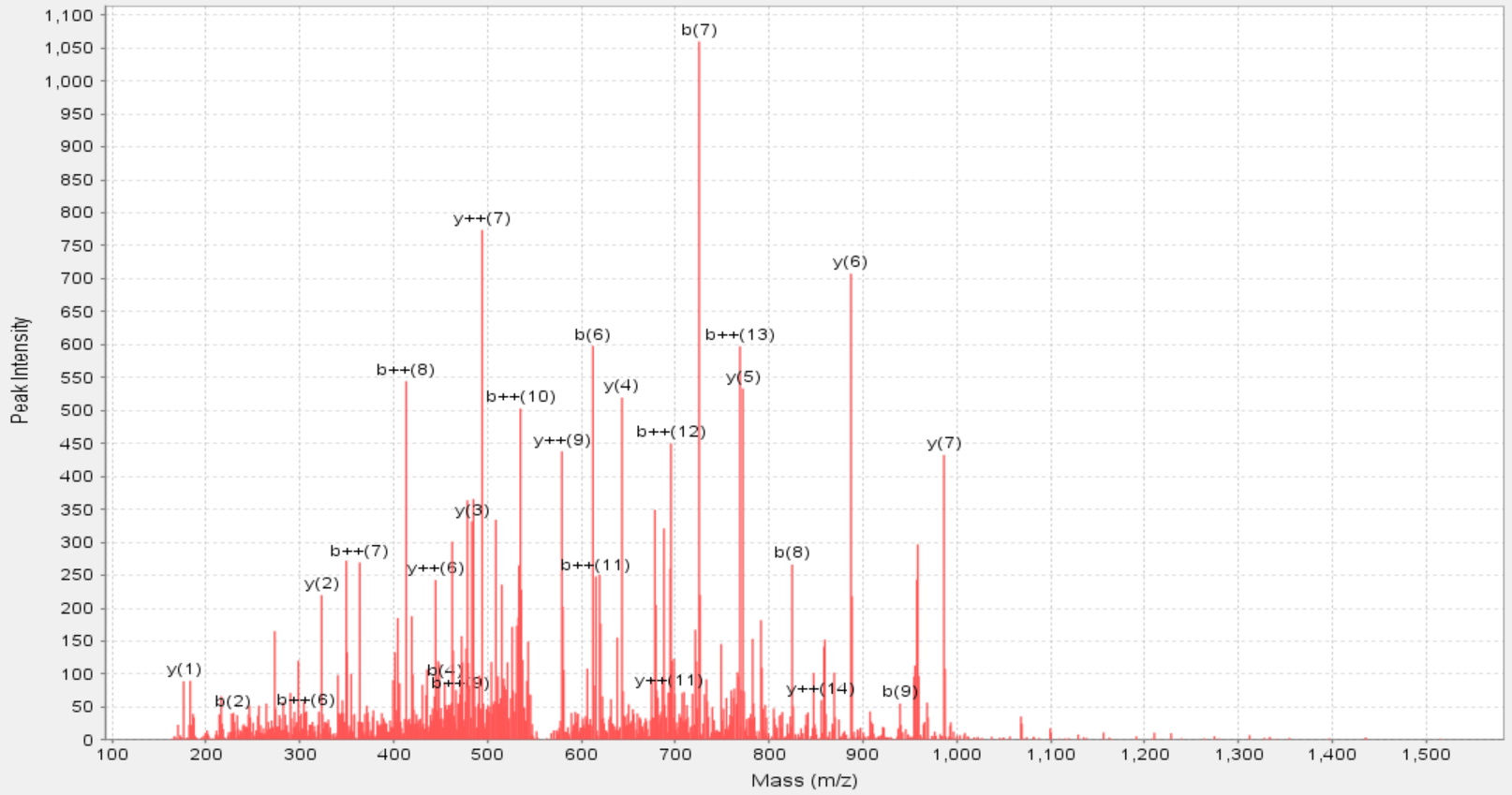
☐ Label regardless of intensity

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*

View Chart

Spectral View and Peptide Fragmentation Table



Peptide: RAPQTGIVDECCFR : Carbamidomethyl (C11); Carbamidomethyl (C12) Precursor Mass: 570.2684

#	b++	b	Residue	y	y++	#
1	79.058	157.109	R	1,708.79	854.899	14
2	114.577	228.146	A	1,552.689	776.849	13
3	163.103	325.199	P	1,481.652	741.33	12
4	227.133	453.257	Q	1,384.599	692.804	11
5	277.656	554.305	T	1,256.541	628.774	10
6	306.167	611.327	G	1,155.493	578.25	9
7	362.709	724.411	I	1,098.472	549.74	8
8	412.243	823.479	V	985.388	493.198	7
9	469.757	938.506	D	886.319	443.663	6
10	534.278	1,067.549	E	771.292	386.15	5
11	614.294	1,227.579	C +57.0215	642.25	321.629	4
12	694.309	1,387.61	C +57.0215	482.219	241.613	3
13	767.843	1,534.678	F	322.188	161.598	2
14	845.894	1,690.779	R	175.12	88.064	1

Toggle Peptide Checked

Prev Peptide Next Peptide

2:33 PM
11/24/2014