

Fragment Charge States:

- #
- +2
- +3
- > +3

Ion Series:

- A
- B
- C
- X
- Y
- Z

Minimum Intensity Percentile:

Fragment Mass Tolerance:

- Label peaks with m/z
- Vertical peak labels
- Label Reporter Ions
- Label Region Only

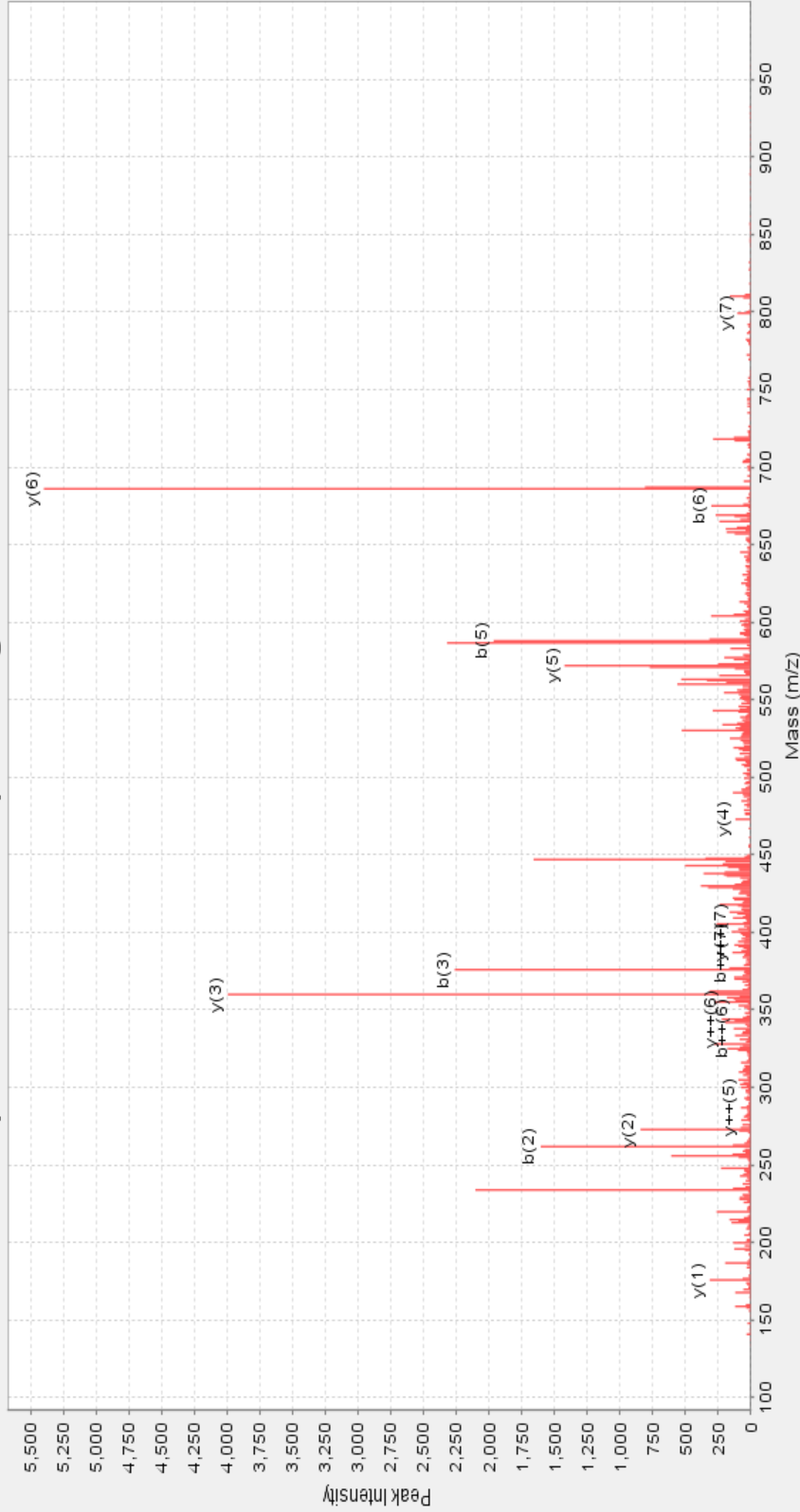
Selected Neutral Losses

- Label regardless of intensity
- | Mod | Loss (+) |
|-------------|-------------|
| 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: FLNVLSPR Precursor Mass: 473.2799

#	b++	b	Residue	Y	Y++	#
1	74.542	148.076	F	945.553	473.28	8
2	131.084	261.16	L	798.484	399.746	7
3	188.106	375.203	N	685.4	343.204	6
4	237.64	474.272	V	571.357	286.182	5
5	294.182	587.356	L	472.289	236.648	4
6	337.698	674.388	S	359.205	180.106	3
7	386.224	771.441	P	272.173	136.59	2
8	464.275	927.542	R	175.12	88.064	1

Toggle Peptide Checked

Prev Peptide

Next Peptide