

Fragment Charge States:

- +1 +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

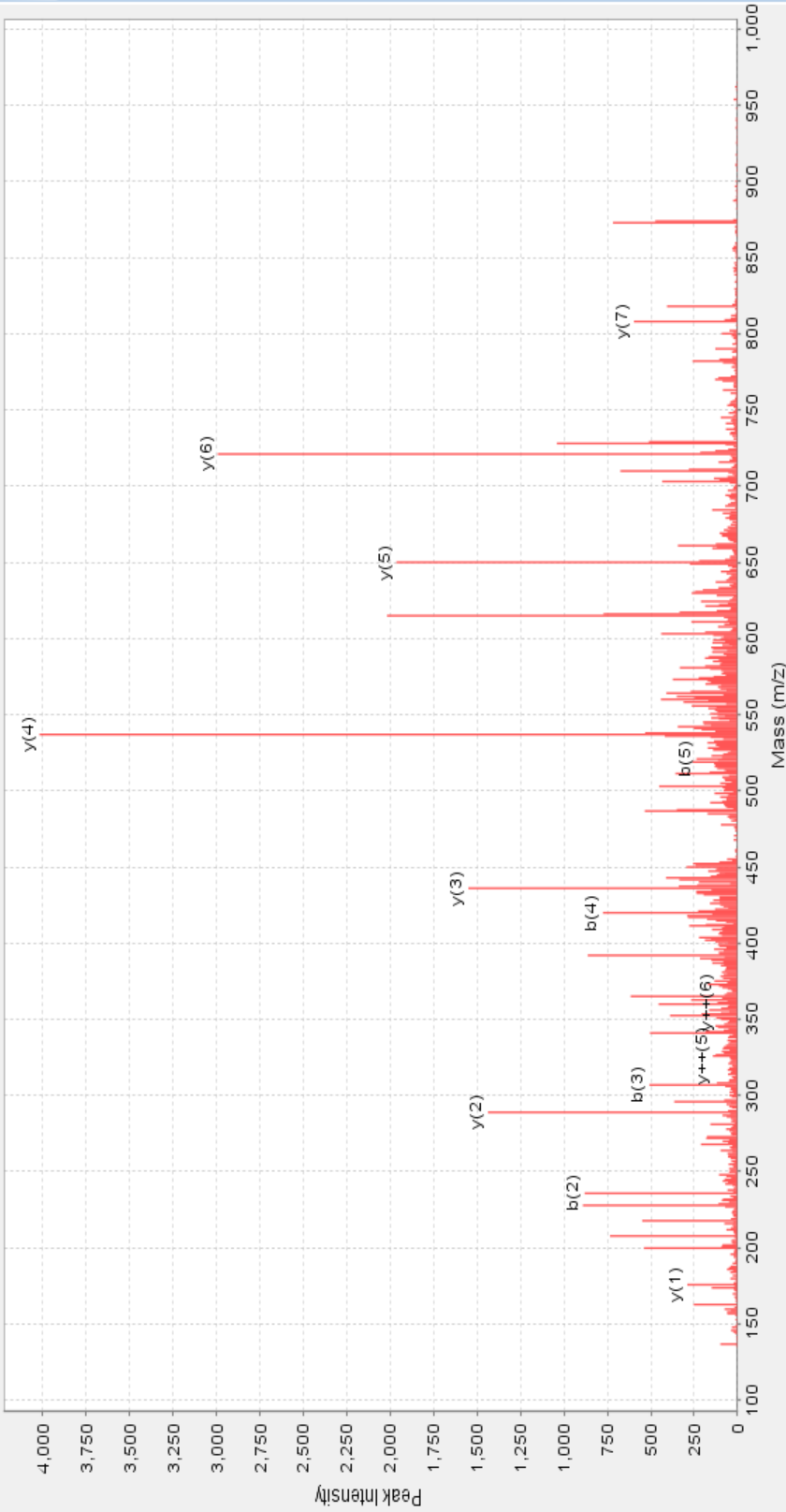
Selected Neutral Losses

- Label regardless of intensity
- | Mod | Loss (+) |
|-------------|-------------|
| H(3) O(4) P | 97.9789 |
| 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: FSALTFLR Precursor Mass: 477.7742

#	b++	b	Residue	y	y++	#
1	74.542	148.076	F	954.542	477.775	8
2	118.058	235.108	S	807.473	404.241	7
3	153.577	306.145	A	720.441	360.725	6
4	210.119	419.229	L	649.404	325.206	5
5	260.642	520.277	T	536.32	268.664	4
6	334.177	667.346	F	435.272	218.14	3
7	390.719	780.43	L	288.204	144.606	2
8	468.769	936.531	R	175.12	88.064	1

Toggle Peptide Checked

Prev Peptide

Next Peptide