GMSBI793 Lecture 9 Problem set

Due by email to on 4/15/25

Please read "Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics"; Anal Chem; (2020), available as a pdf file in the lecture 9 folder.

1. What are the strengths and limitations of the SPS-MS^3 method?

2. Explain how ΦSDM resolves TMT reporter ions at lower resolution that with HRMS^2.

3. How did the investigators avoid acquiring SPS-MS^3 scans that produce unidentifiable scans?

4. How was shorter ion injection times achieved on the Eclipse instrument?

5. How will the use of FAIMS with the Eclipse improve speed and performance of multiplexed quantitative proteomics workflows?