

Proteomics 102

Data Acquisition

Thursday April 27, 10-11 am in NMS 1.120

Join us for the second of three interactive classes when the CBRs Biological Mass Spectrometry Facility staff will present how MS and MS/MS data are generated using our Orbitrap Fusion instruments in

Data acquisition for Proteomics and Mass Spectrometry.

Topics for discussion will include:

- LC and MS principles
- Peptide characteristics
- Fragmentation modalities (HCD/CID)
- Data dependent acquisition
- Contamination issues
- LC-MS/MS method set up

Later this Spring, our final class, “**Proteomics 103 - Data analysis and interpretation**” will cover how to analyze MS and MS/MS data using the suite of software available in the core facility.

Proteomics 101
*Experimental design
and sample prep*

Proteomics 103
*Data analysis
and interpretation*



Proteomics 102
Data acquisition

To register and pay for this class, scan the QR code.
Any questions? Come and talk to us in MBB 1.420 B.

