

RESOURCES

Mass Spectrometry Facility

Laboratory: The Mass Spectrometry Facility, a University Research Resource Facility, resides within the MUSC Proteomics Center, 4200 sq. ft. of laboratory space on the 3rd floor of the Children's Research Institute that houses state-of-the-art instrumentation and expertise for proteomics and imaging mass spectrometry.

Mass Spectrometry Facility staff is comprised of the Scientific Director, Lauren E. Ball, Ph.D., Facility Manager, Jennifer Bethard, M.S., and three research assistants with expertise in protein chemistry, LC-MS/MS, and quantitative proteomics who provide consultation and assistance with experimental design, sample preparation, data acquisition, and data interpretation. Data archiving and computing infrastructure are maintained by Mr. Anthony Scott, Information Resources Consultant II. The Facility is supported, in part, by the Vice President for Research at MUSC, the College of Medicine, the Hollings Cancer Center, and NIH grants (S10 OD010731, S10 OD025126, P20 GM103542, and P30 CA138313).

Computational Resources and Data Archiving:

Quantitative proteomic experiments for differential protein expression, regulated post-translational modifications, and protein/drug interactions using label free (MaxLFQ), stable isotope labeling (SILAC), or isobaric tagging (TMT/iTRAQ) approaches are performed on the ThermoScientific Orbitrap Fusion Lumos ETD/UVPD or Orbitrap Elite ETD LC-MS/MS instrumentation. Protein identification and quantification are determined using database searching algorithms within MaxQuant (Max Planck Institute) or Proteome Discoverer 2.3 (Thermo Scientific) software platforms. For detection of unanticipated or complex post-translational modifications, Protein Prospector (University of California, San Francisco), Byonic (Protein Metrics), BioPharma Finder (ThermoScientific) are also available. Large-scale proteomic experiments are searched using 36 core 128 GB RAM high performance servers (2) and processed using Perseus (Max Planck Institute), Proteome Discoverer, or Skyline (University of Washington). Statistical analyses (both parametric and non-parametric) can be performed within most of these programs, as well as R-packages from Bioconductor. Data are temporarily stored on high-speed NAS servers with automated backup and archived off-site through CommVault. The Mass Spectrometry Facility shares a license for Advaita Bioinformatics software with the MUSC Bioinformatics Core for downstream data analysis.