

Mass Spectrometry Facility Resource Sharing Plan

The goal of the MUSC Mass Spectrometry Facility is to provide LC-MS/MS-based proteomic services and customized methodology to advance the research efforts of our investigators. Upon request, raw LC-MS/MS data files accompanied by a detailed description of the experimental design are uploaded to the ProteomeXchange Consortium via the PRIDE partner repository. A link providing direct access to the raw data will be provided for inclusion in publications. To ensure acquisition and publication of high-quality proteomics data, we follow the guidelines provided by the American Society for Biochemistry and Molecular Biology Journal: *Molecular and Cellular Proteomics*. To ensure reproducibility, detailed methodological information regarding sample preparation, data acquisition, data processing, and statistical evaluation are provided as well. Regarding the identification of novel and regulated sites of post-translational modification, manually annotated tandem mass spectra are provided upon request. Our goal is to provide curated information regarding post-translational modifications that can be uploaded into publicly accessible databases, such as the PhosphositePlus Database or the Swiss Institute of Bioinformatics NextProt Database. Newly developed and optimized methodology are made available to all users of the Mass Spectrometry Facility.