

A full range of proteomic services

About Us

The **Proteomics Core Facility at UMass Boston** offers a full range of proteomic services using the most advanced instrumentation and methodologies. Our services range from sample preparation, bottom-up protein identification, quantification of expression levels using both label free and TMT multiplexing strategies, PTM analysis, 2D fractionation, and top-down proteomic analysis. So that you get the most out of the resulting data, we work with you to learn your needs and formulate the best plan for analyzing your samples. Count on our team for unmatched customer support, rooted in deep expertise in biological mass spectrometry.



Jason Evans, PhD

*Associate Professor of Chemistry
and Proteomics Core Facility Director*

Jason Evans leads a highly skilled team that provides proteomics services to internal and external clients. Dr. Evans has over 25 years of experience in the field of mass spectrometry and proteomics.

State-of-the-Art Equipment

The Proteomics Core Facility's instrumentation offers unique flexibility in designing proteomic experiments to provide the best outcomes for projects. We use the:

- Orbitrap Fusion Lumos Tribrid mass spectrometer, equipped with Easy-ETD, coupled with Easy-nLC 1200 or UltiMate 3000RS HPLC systems for nano- and micro-flow separations
- Thermo Xcalibur software suite to run the instruments and analyze raw data
- Thermo Proteome Discoverer for protein identification and/or quantification in bottom-up workflows
- Bruker timsTOF HT for high-speed, high-sensitivity DIA and DDA analyses
- Bruker ProteoScape integrated with Spectronaut for large-scale DIA and DDA proteomics and real-time data processing
- PEAKS software for database searching and de novo sequencing

Services

- Extraction and Digestion
- 1D-LC-MS (90 min. Gradient)
- 2D-LC-MS
- Intact Protein Analysis
- TMT Labeling
- Label Free Quantification
- Small Molecule Exact Mass/CID
- Complete mAb Characterization