**[Mass Spectrometry and Proteomics Resource Laboratory](http://cbmi.catalyst.harvard.edu/cores/cat/core.html?core_id=92&uri_id=0000012b-00c0-1e2d-db6e-7a3f80000000&category_id=19&navMode=cat)**

**URL:** <http://proteomics.fas.harvard.edu/>

**Laboratory Director:** Bogdan Budnik

**Description:**

*Square Footage:* N/A

*Facility Location:* Northwest Labs, Room B247

The Mass Spectrometry and Proteomics Resource Laboratory provides mass spectrometry and strategic consulting in Proteomics analysis for life science and chemical biology researchers at Harvard as well as others worldwide. This resource brings together the state-of-the-art expertise and instrumentation from across the Faculty of Arts and Sciences, leveraging the lab’s breadth of experience to provide the best possible support for research.

**Major Equipment:**

* ThermoFisher LTQ-Orbitrap Elite
* Thermo Fisher Lumos Orbitrap
* (3) Waters nanoAcquity UPLCs
* Thermo Easy 100 UPLC Pump
* Agilent 1200 HPLC
* Agilent ChemStation
* HFX Orbitra

**Services:**

* Protein identification service: After an in-depth project discussion, the sample is prepared by the user following simple protocols, and submitted to the facility for analysis. Samples are enzymatically digested, run on nano-capillary HPLC/MSMS, and the MSMS spectra are correlated against a specific database for peptide identification. When applicable, N-terminal Edman sequencing is also available.
* Complex protein mixture analysis service: Complex mixtures of proteins are identified by a number of single- and multi-dimensional approaches. For example, GeLC, in which an entire lane of an SDS-PAGE gel is excised into sections, affords the user a two dimensional separation of the protein mixture based on protein intact molecular weight (SDS-PAGE) and then individual peptide hydrophobicity by reversed phase chromatography (RPLC). An analogous liquid based analysis 2D-method known as MUDPIT (Multidimensional Protein Identification Technology) starts with a solution digestion of the sample (direct or filter-aided (FASP)), electrostatic repulsion hydrophilic interaction chromatography (ERLIC) followed by reversed phase chromatography (RPLC).
* Quantitative proteomics services
* TMT stable isotope labeling a well-established method here that includes up to 10 isotopic labels for multiplexing experimental variables. The technique is based upon chemically tagging the N-terminus of peptides generated from protein. The labeled samples are then combined (post labeling), fractionated by nano-LC and analyzed by tandem mass spectrometry. Peptides are chromatographically resolved as single peaks with identical full MS masses. Fragmentation of the labeled peptides generates a low molecular mass reporter ion that is unique to the tag used to label each of the samples. Measurement of the intensity of these reporter ions, enables relative quantification of the peptides in each digest and hence the proteins from where they originate. This process has the advantage of no chromatographic interference from the labels but requires a low mass MSMS scan to observe the reporter ions.
* SILAC: Quantitative mass spectrometry with stable isotope labeling in cell culture at the whole cell level, intact protein level or peptide level. There are several well-established techniques to do this, and a detailed project consultation prior to beginning an experiment with this goal is recommended.
* MRM: Multiple reaction monitoring for quantitative measurements of proteins across, for example, a time course, multiple conditions and dilutions are performed on an Orbitrap mass spectrometer. Such experiments are also well suited when large numbers of repetitive measurements will be made.
* “AQUA” method of absolute quantitation with stable isotope synthetic peptide standards.
* Posttranslational modification site determination service: Starting with a single highly purified protein from a Gel or solution sample, multiple sites of modification, e.g. phosphorylation, acetylation and others, can be determined. This process involves a detailed project discussion and careful selection of multiple enzymes to maximize peptide coverage for specific sites of interest. Global modification analyses on large-scale proteomics experiments can also be performed. Enrichment schemes such as TiO2, IMAC, etc. are employed as needed.
* C-terminal sequence analysis service: In this lab, we use multiple enzymes to obtain redundant peptides that exhaustively define the C-terminal region of a purified protein. Multiple instrument runs are combined with custom bioinformatics tools to orthogonally map the C-terminal amino acids.
* Exact mass MS and MS/MS electrospray for structural elucidation service: Fees depend upon the nature of the experiments. Please contact our facility for more details.
* Data analysis service: Data Analysis is an essential part of mass spectrometry, and we encourage our customers to discuss their results with us when this is helpful. Custom processing is always available on an as needed basis. We use our own integrated suite of software applications MaxQuant, Proteome Discoverer, Mascot and statistical analysis using Scaffold package and Perseus.