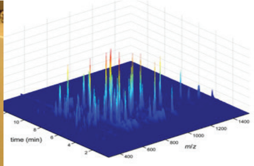
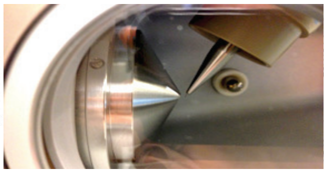
OHSU Research Cores and Shared Resources

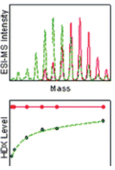
Proteomics

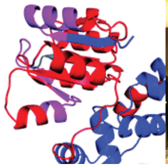
OHSU's cores are your campus technology partners dedicated to the success of your project. For optimal results, take advantage of the state-of-the-art scientific resources within the OHSU community.

www.ohsu.edu/cores









The Proteomics Shared Resource (PSR) provides expertise and instrumentation to assist the OHSU research community with mass spectrometric analysis of proteins.

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Introduction

Proteomics, the global analysis of proteins in biological samples, is becoming an increasingly important discipline in biomedical research. The rapid advances in instrumentation and methodology requires centralization of facilities to enhance productivity, provide expertise, and control costs for investigators. The PSR provides access to the very latest instrumentation and techniques in proteomics to OHSU researchers. The highly experienced staff work collaboratively with faculty, post-docs and students to move projects to a successful completion.

Instrumentation/Informatics Support

- Orbitrap Fusion Tribrid instrument with ETD fragmentation
- Q-Exactive HF
  LTQ Velos linear ion trap
- Forte Bio Octet Red Biolayer Interferometer
- Nano and capillary HPLC and UPLC systems
- HPLC for sample prep (ion exchange, gel filtration, and reverse phase)
- Computers and a large suite of software for informatics support

Consultation and Preliminary Results

Free initial consultations with PSR staff are strongly encouraged before beginning projects. Limited funds for generation of preliminary data for new grant submissions are also available.

Services

1. Analysis of differential protein abundance in complex mixtures using multinotch 16-plex TMT labeling
2. Biomarker discovery in human serum/plasma, saliva, urine, tears, cerebrospinal and amniotic fluids
3. Analysis of extracellular vesicles isolated from human plasma, urine, cerebrospinal fluid and organoids
4. Detection and quantification of post-translational modifications, such as phosphorylation, acetylation, methylation, and ubiquination
5. Identification of protein-protein interactions in co-immunoprecipitated complexes
6. Targeted quantitation of specific proteins in biological samples
7. Structural analysis of proteins, including disulfide bond localization and hydrogen deuterium exchange measurements
8. Mass measurement of purified proteins and peptides to assess sample quality
9. Protein identification from 1D gel bands and 2D gel spots
10. In house informatics support for all experiments
11. Assistance in experimental design, letter of support, grant submissions and manuscript preparation
12. Partnering with investigators to secure new instrumentation to support emerging technologies
13. Training in proteomics theory and practice

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