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 cutting-edge mass spectrometry to identify, characterize and quantify proteins in cells, tissues and human body fluids. Through robust sample preparation, state of-the-art LC/MS instrumentation, and comprehensive data analysis, the PSR delivers precise and reproducible results for a wide range of applications in both basic and clinical research.

Introduction

Proteomics, the comprehensive study of proteins in biological samples, is playing an increasingly crucial role in biomedical research. With the rapid progress in instrumentation and techniques, there is a growing need for centralized facilities to boost productivity, offer specialized expertise, and manage costs for researchers. The PSR offers access to cutting-edge mass spectrometry equipment, advanced sample preparation, and LC/MS techniques to help move projects toward successful outcomes. Simply drop off your samples and collect your data.

Instrumentation/Informatics Support

- Orbitrap Eclipse Tribrid with ETD
- Orbitrap Fusion Tribrid with ETD
- Q-Exactive HF
- · LTQ Velos linear ion trap
- Nano UPLC systems
- FPLC 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 seed funding for generation of preliminary data for new grant submissions is also available.

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Medical Research Building Room

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Director

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Location

533 and 534

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Web www.ohsu.edu/proteomics



Services

- 1. **Differential Protein Abundance Analysis:** Quantitative proteomic analysis using 18-plex TMT labeling.
- 2. Biomarker Discovery: Identifying biomarkers in human serum/plasma, saliva, urine, tears, cerebrospinal fluid, and amniotic fluid.
- 3. Extracellular Vesicle Analysis: Quantitative proteomics of vesicles from cells, plasma, urine, cerebrospinal fluid, and organoids.
- 4. **Post-translational Modifications:** Detecting and quantifying modifications such as phosphorylation, acetylation, methylation, and ubiquitination.
- 5. **Protein-Protein Interactions:** Identifying interactions in co-immunoprecipitated and proximitylabeled complexes.
- 6. Bioactive Molecule Targets: Identifying protein targets of small bioactive drugs.
- 7. Targeted Protein Quantification: Accurate quantification of specific proteins in biological samples.
- 8. Structural Protein Analysis: Analyzing protein cross-links and disulfide bond localization.
- 9. Sample Quality Assessment: Mass measurement of purified proteins and peptides.
- 10. Protein Identification: Identifying proteins from 1D gel bands.
- 11. Informatics Support: Providing in-house data analysis support for experiments.
- 12. **Research Assistance:** Assisting with experimental design, grant submissions, letters of support, and manuscript preparation.
- 13. Instrumentation Partnership: Collaborating with researchers to acquire new instrumentation for emerging technologies.
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- 14. Proteomics Training: Offering training in proteomics theory and practical applications.