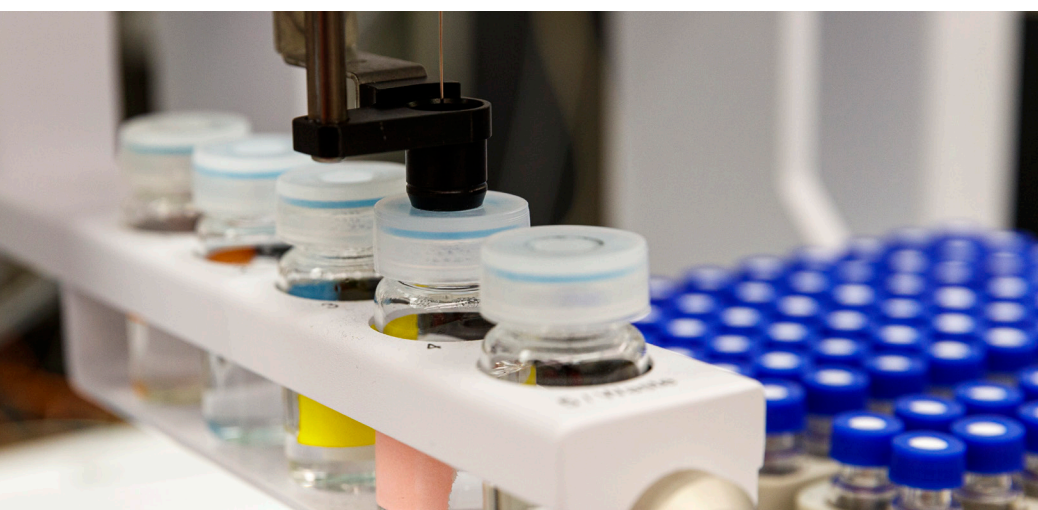


WHO WE ARE

The Proteomics and Metabolomics Facility (PMF) provides University of Nebraska faculty, staff, students, and external academic and industry, nation-wide, with high quality proteomics and metabolomics services. With our specialized platforms, the core facility's broad impact on research includes advancing world-class research, supporting grant proposals, assisting in the education of future scientists and supporting economic and scientific advancements. We offer both full-service and self-service options to meet the unique needs, time requirements and budgets of our users. Our outreach and education program includes workshops, seminars and courses.

OUR SKILLSET

With our technological platforms and decades of experience in the fields of proteomics and metabolomics, we can offer a range of technical services in the identification and relative quantification of proteins through mass spectrometry, as well as advanced methods for the profiling and quantification of small molecules.



INSTRUMENTATION

- 1290 Agilent UPLC Infinity II quaternary pump system equipped with three different detectors: DAD, fluorescence and ELSD; and a fraction collector
- Agilent GC-MS, 7890B GC system/5977A MSD and a PAL RS185 equipped with liquid, headspace and SPME injections
- Sciex QTRAP 6500+ coupled to a Shimadzu Nexera X2 UPLC
- Thermo Q Exactive-HF coupled to a Thermo Vanquish H binary UPLC
- Thermo Orbitrap Eclipse Tribrid with FAIMS and ETD coupled to a Dionex U3000 RSLCnano

WORK WITH US

Sophie Alvarez
402-472-4575
salvarez@unl.edu

Learn more about our services, fees, policies, procedures, training opportunities and more:

go.unl.edu/pmf

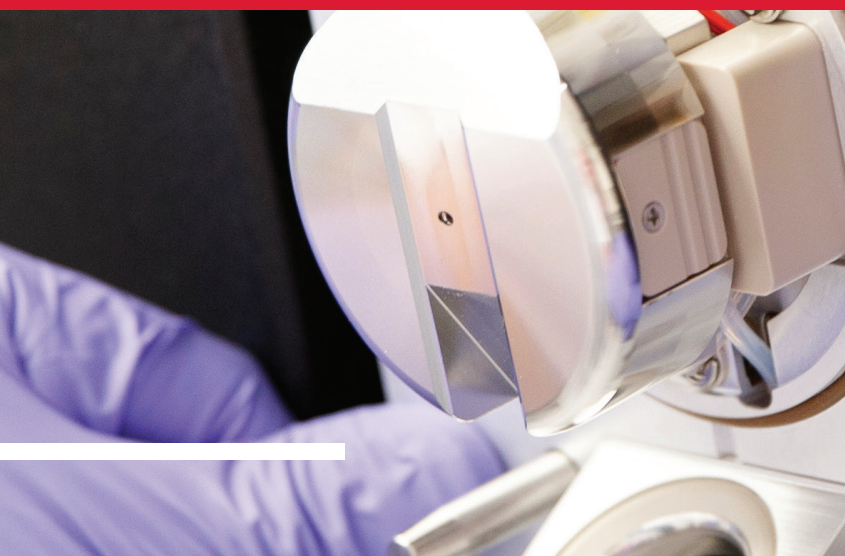
N CENTER FOR BIOTECHNOLOGY



**PROTEOMICS AND
METABOLOMICS
CORE FACILITY**

PROTEOMICS SERVICES

- Proteomics of whole organisms, organs, organelles, tissues, cell pellets, pulldowns, complex or single protein mixes from solutions or gels
- Quantification by label-free or multiplexed labeling (e.g., TMT-10/16plex) techniques with microscale sub-fractionation to increase coverage
- Post-translational modification characterization
- High resolution/high mass accuracy data for intact mass protein analysis
- Phosphoproteomics using TiO₂ phosphopeptide enrichment
- Technological platforms supported by bioinformatics tools to process data and report results, e.g., Mascot 2.7, Proteome Discoverer 2.4, Scaffold 4.8.9, Peaks 8, MaxQuant



METABOLOMICS SERVICES

Targeted Metabolomics Platform

Targeted quantification using HPLC, GC-MS or LC-MS includes:

- Primary metabolite assays - free sugars, amino acids, glycolysis/TCA Cycle/pentose phosphate pathway, polyamines, pyrimidine pathway, SCFA, FAME
- Secondary metabolite assays - non-mevalonate pathway, bile acids, TCA and TCHA (hemp and cannabis), phytohormones, gibberellins, flavonoids and phenolic acids, carotenoids, beta and alpha acids (hops)
- Hydrolyzed amino acids for protein content

See our website for a full list of compounds in each assay.

Untargeted Metabolomics Platform

Untargeted quantification of a wide range of small molecules, including:

- Volatiles and carbon metabolism using GC-MS and NIST14/ public libraries
- Primary and secondary metabolism using RP and HILIC-MS platform and NIST17, mzCloud, public libraries



SELF-SERVICE PLATFORM

The PMF connects with a range of scientists to complete consultations, projects and self-service tasks. We provide:

- Consultation to determine project feasibility
- One-on-one training
- Access to self-service instruments, including the Sciex QTRAP 6500+, Agilent GC-MS 5977 and Agilent 1290 Infinity II UPLC

