

Resource Summary Report

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University of Nebraska Lincoln Nebraska Center for Biotechnology Proteomics and Metabolomics Core Facility

RRID:SCR_021314

Type: Tool

Proper Citation

University of Nebraska Lincoln Nebraska Center for Biotechnology Proteomics and Metabolomics Core Facility (RRID:SCR_021314)

Resource Information

URL: <https://biotech.unl.edu/proteomics-and-metabolomics#tab1>

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Description: Provides services using mass spectrometry, including identification and relative quantification of proteins and several advanced methods for profiling and quantitation of small molecules. Provides outreach and education program including workshops, seminars and courses. Proteomics services include Bottom-up 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 techniques with microscale subfractionation to increase coverage; Post Translational Modification Characterization especially phosphopeptide enrichment from whole organism digests, but also ubiquitylation, acetylation, etc. Metabolomics services include Untargeted Quantification of small molecules; Primary metabolism using GC-MS and NIST/Fiehn Libraries; Secondary metabolism using LC-MS and Progenesis QI, NIST Library, mzCloud; Targeted Quantification using HPLC or LCMS.

Abbreviations: PMF

Synonyms: UNL Proteomics and Metabolomics Facility

Resource Type: access service resource, core facility, service resource

Keywords: USEDit, ABRF, mass spectrometry, protein identification, protein relative quantification, small molecules, proteomics, metabolomics

Availability: open

Resource Name: University of Nebraska Lincoln Nebraska Center for Biotechnology Proteomics and Metabolomics Core Facility

Resource ID: SCR_021314

Alternate IDs: ABRF_1189

Alternate URLs: <https://coremarketplace.org/?FacilityID=1189>

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194153+0000

Ratings and Alerts

No rating or validation information has been found for University of Nebraska Lincoln Nebraska Center for Biotechnology Proteomics and Metabolomics Core Facility.

No alerts have been found for University of Nebraska Lincoln Nebraska Center for Biotechnology Proteomics and Metabolomics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 60 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#).

Roy P, et al. (2026) A stress-induced PI3P complex controls autophagy in erythroid precursors. *iScience*, 29(4), 115182.

Tejero-Rivas MC, et al. (2026) Phytochemical Profile and Bioactive Potential of *Hampea rovirosae* Standl.: Antioxidant, Antimicrobial, and Carbohydrate-Hydrolyzing Enzyme Inhibitory Activities. *Current issues in molecular biology*, 48(3).

Niyorukundo J, et al. (2026) Breeding colored sweet corn for improved micronutrient content. *Frontiers in plant science*, 17, 1813937.

Moen KE, et al. (2026) A protein disulfide isomerase coordinates redox homeostasis and ER calcium regulation for optimal lytic cycle progression in *Toxoplasma gondii*. *mBio*, 17(5), e0312425.

Bertolini MS, et al. (2026) Composition and role of the vacuolar transporter chaperone complex in polyphosphate synthesis and infectivity in *Trypanosoma cruzi*. *mBio*, 17(6), e0037226.

Sazon LAR, et al. (2026) Stem nitrogen accumulation through vegetative storage proteins and mobilization to seeds supports high-yielding soybean. *Journal of experimental botany*, 77(10), 2998.

LaBrant EW, et al. (2026) Lipid metabolism and contact site homologs are present at the chloroplast envelope-thylakoid interface. *Nature communications*, 17(1).

Verma K, et al. (2026) Sorghum ferulate-5-hydroxylase overexpression enhances aphid proliferation and weakens brown midrib12-linked resistance. *Journal of experimental botany*.

Baierna B, et al. (2026) Evolutionary remodeling of ubiquinone biosynthesis in *Toxoplasma gondii* reveals an essential bi-functional monooxygenase. *Nature communications*, 17(1).

Lam C, et al. (2026) PAMD-Ch17, a Polymeric Analog of Plerixafor, Induces Mitochondrial Dysfunction in T-ALL Cells Independent of CXCR4. *Molecular cancer therapeutics*, 25(8), 1369.

Baierna B, et al. (2026) Evolutionary Remodeling of Ubiquinone Biosynthesis in *Toxoplasma gondii* Reveals an Essential Bi-functional Monooxygenase. *bioRxiv : the preprint server for biology*.

Qian P, et al. (2025) Evolutionarily convergent mechanism of formin regulation coordinates actin polymerization in apicomplexan parasites. *Science advances*, 11(50), eaea2136.

Van Haute MJ, et al. (2025) Comparative genomic and phenotypic analysis of potential beneficial properties of *Bifidobacterium adolescentis*. *mSphere*, 10(11), e0067325.

Doran MH, et al. (2025) Evolutionary adaptations of doublet microtubules in trypanosomatid parasites. *Science (New York, N.Y.)*, 387(6739), eadr5507.

Wallin S, et al. (2025) Surveying the Proteome-Wide Landscape of Mitoxantrone and Examining Drug Sensitivity in BRCA1-Deficient Ovarian Cancer Using Quantitative Proteomics. *Proteomes*, 13(4).

Liu B, et al. (2025) Identification of novel protein biomarkers of macrophage polarization using comparative proteomic analyses of murine primary macrophages. *Journal of immunology (Baltimore, Md. : 1950)*.

Sarkar P, et al. (2025) Early tolerance mechanisms in citrus: transcriptome and hormone profiling of NPR1-mediated responses to *Candidatus Liberibacter asiaticus*. *Frontiers in plant science*, 16, 1719694.

Kathol M, et al. (2025) High enzyme promiscuity in lignin degradation mechanisms in *Rhodopseudomonas palustris* CGA009. *Applied and environmental microbiology*, 91(8), e0057325.

Mallareddy JR, et al. (2025) Fluorescence based live cell imaging identifies exon 14 skipped hepatocyte growth factor receptor (MET) degraders. *RSC advances*, 15(13), 10419.

Hernandez JB, et al. (2025) Microbiome and metabolome association network analysis identifies *Clostridium_sensu_stricto_1* as a stronger keystone genus candidate than *Bifidobacterium* in the gut of common marmosets. *mSystems*, 10(8), e0021425.