Resource Summary Report

Generated by NIF on Aug 9, 2026

University of Texas at Austin Biological Mass Spectrometry Proteomics Core Facility

RRID:SCR_021728
Type: Tool

Proper Citation

University of Texas at Austin Biological Mass Spectrometry Proteomics Core Facility (RRID:SCR_021728)

Resource Information

URL: https://research.utexas.edu/cbrs/cores/bms/

Proper Citation: University of Texas at Austin Biological Mass Spectrometry Proteomics Core Facility (RRID:SCR_021728)

Description: Proteomics and Metabolomics services and collaborative efforts are provided at Biological Mass Spectrometry Facility. We use high resolution Orbitrap mass spectrometers with UPLC at high flow for metabolomics and nanoUPLC for proteomics work. We have Bruker Autoflex for self service MALDI. Our proteomics services are protein ID, quantitation, and modification analysis, with fractionation for deeper coverage and de novo sequencing of mAbs available. We collaborate for customized projects. We have untargeted metabolomics for quantitative or qualitative analysis of extracted metabolites using C18 column.

Synonyms: UTA CBRS Biological Mass Spectrometry Facility, The University of Texas at Austin UTA CBRS Biological Mass Spectrometry Facility

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

Keywords: USEDit, ABRF, proteomics service, metabolomics service, mass spectrometry

Resource Name: University of Texas at Austin Biological Mass Spectrometry Proteomics Core Facility

Resource ID: SCR_021728

Alternate IDs: ABRF_1215

Alternate URLs: https://coremarketplace.org/?FacilityID=1215

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260808T190658+0000

Ratings and Alerts

No rating or validation information has been found for University of Texas at Austin Biological Mass Spectrometry Proteomics Core Facility.

No alerts have been found for University of Texas at Austin Biological Mass Spectrometry Proteomics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Keenan Early EM, et al. (2026) Proteomic taxonomic identification can identify cryptic diversity of Squamata in modern and paleontological specimens. Scientific reports, 16(1).

Acharya N, et al. (2026) MEHP exposure damages the basement membrane by suppressing the expression of its constituent proteins in peritubular myoid cells of the rat testis. Toxicological sciences : an official journal of the Society of Toxicology, 209(6).

Biller M, et al. (2026) REV7 associates with ATRIP and inhibits ATR kinase activity. Nucleic acids research, 54(2).

Ruan M, et al. (2026) Cytoplasmic localization of pseudouridine synthase 7 facilitates a pseudouridine-dependent enhancement of cellular stress tolerance. Nature communications, 17(1).

Coughlin C, et al. (2026) Children and adults use distinct neurocognitive mechanisms to support successful memory-based inference. bioRxiv : the preprint server for biology.

Salazar G, et al. (2026) Identification of Novel Interacting Proteins of FUZ and GPR161. Proteomics, e70164.

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. Cell reports, 45(1), 116835.

Halwachs KN, et al. (2026) Tuning scaffold degradation with non-natural peptidomimetics to control human umbilical vein endothelial cell morphology and vessel formation. Acta biomaterialia, 217, 198.

Park J, et al. (2025) Molecular features of the serological IgG repertoire elicited by egg-based, cell-based, or recombinant haemagglutinin-based seasonal influenza vaccines: a comparative, prospective, observational cohort study. The Lancet. Microbe, 6(2), 100935.

Surya A, et al. (2025) Differential impacts of ribosomal protein haploinsufficiency on mitochondrial function. The Journal of cell biology, 224(3).

Parker JK, et al. (2025) Antibacterial microcins are ubiquitous and functionally diverse across bacterial communities. Nature communications, 16(1), 6048.

Tripathy MK, et al. (2025) Modified pea apyrase has altered nuclear functions and enhances the growth of yeast and Arabidopsis. Frontiers in plant science, 16, 1584871.

Ruan M, et al. (2025) Cytoplasmic localization of PUS7 facilitates a pseudouridine-dependent enhancement of cellular stress tolerance. bioRxiv : the preprint server for biology.

Halwachs KN, et al. (2025) Tuning Scaffold Degradation with Non-Natural Peptidomimetics to Control Human Umbilical Vein Endothelial Cell Morphology and Vessel Formation. bioRxiv : the preprint server for biology.

Salazar G, et al. (2025) Identification of novel interacting proteins of FUZ and GPR161. bioRxiv : the preprint server for biology.

Acharya N, et al. (2025) Peritubular myoid cells of the testis produce monocyte chemotactic protein 1 upon direct exposure to Mono-(2-Ethylhexyl) phthalate through the IL-1 signaling pathway. Toxicology, 514, 154118.

Uz-Zaman MH, et al. (2025) Propensity for proto-gene emergence in bacteria. Genome biology, 26(1), 362.

Wang H, et al. (2025) Chromatin-Associated Pea Apyrase psNTP9 Function as a DNA-Binding Regulatory Protein in Yeast and Arabidopsis. Plants (Basel, Switzerland), 14(22).

Pandit S, et al. (2025) Surface-Engineered Nanoparticles Enhance the Peroxidase Activity of Heme-Containing Proteins. ACS nano, 19(7), 7117.

Bryan C, et al. (2025) Human 8-Oxoguanine Glycosylase OGG1 Cleaves Abasic Sites and Covalently Conjugates to 3'-DNA Termini via Cysteine and Histidine Addition. Chembiochem : a European journal of chemical biology, 26(2), e202400705.