Resource Summary Report

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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/

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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: access service resource, service resource, core facility

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: 20260729T044531+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 50 mentions in open access literature.

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

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

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.

Ishida S, et al. (2025) Directed Evolution of a SelB Variant that Does Not Require a Selenocysteine Insertion Sequence Element for Function. ACS synthetic biology, 14(7), 2681.

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.

Lancaster EB, et al. (2025) Conversion of Inactive Non-Pro1 Tautomerase Superfamily Members into Active Tautomerases: Analysis of the Pro1 Mutants. Biochemistry, 64(4), 812.

Park J, et al. (2025) Broadly neutralizing antibodies targeting pandemic GII.4 variants or seven GII genotypes of human norovirus. Science translational medicine, 17(788), eads8214.

Maeda GP, et al. (2025) A secreted endosymbiont protein essential for colonizing host cells. bioRxiv : the preprint server for biology.

Lee S, et al. (2025) Label-Free Quantification of DNA Loading on Centrifugation-Resistant Spherical Nucleic Acids. Analytical chemistry, 97(23), 12267.

Smisek T, et al. (2025) Characterization of Lipidated New Delhi Metallo-?-lactamase Using Synthetic Nanodiscs. Biochemistry, 64(12), 2679.

Lin M, et al. (2025) Mass spectrometry imaging reveals alterations in protein and N-glycan molecular signatures in endometriosis tissues. Analytical and bioanalytical chemistry, 417(18), 4133.

Melkonian TR, et al. (2025) Beyond the ?-?-? Fold: Characterization of a SnoaL Domain in the Tautomerase Superfamily. Biochemistry, 64(9), 1950.

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

Halwachs KN, et al. (2025) Effects of Stiffness and Degradability on Cardiac Fibroblast Contractility and Extracellular Matrix Secretion in Three-Dimensional Hydrogel Scaffolds. ACS biomaterials science & engineering, 11(11), 6521.