

Resource Summary Report

Generated by T1D on Jul 31, 2026

Pennsylvania State University Huck Institutes Proteomics and Mass Spectrometry Core Facility

RRID:SCR_024462

Type: Tool

Proper Citation

Pennsylvania State University Huck Institutes Proteomics and Mass Spectrometry Core Facility (RRID:SCR_024462)

Resource Information

URL: <https://www.huck.psu.edu/core-facilities/proteomics-and-mass-spectrometry-core-facility>

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Description: Facility offers highly sensitive and accurate mass spectrometry analysis, including identification and quantitation of proteins by liquid chromatography electrospray ionization tandem mass spectrometry (LC-ESI-MS-MS) or by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-TOF-MS).

Synonyms: Huck Institutes' Proteomics and Mass Spectrometry Core Facility

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

Keywords: ABRF, proteomics, mass spectrometry, post-translational modifications, phosphorylation, accurate mass, TMT, iTRAQ

Resource Name: Pennsylvania State University Huck Institutes Proteomics and Mass Spectrometry Core Facility

Resource ID: SCR_024462

Alternate IDs: ABRF_2454

Alternate URLs: https://coremarketplace.org/RRID:SCR_024462?citation=1,
<https://coremarketplace.org/?FacilityID=2454&citation=1>

Record Creation Time: 20230922T050237+0000

Record Last Update: 20260731T043157+0000

Ratings and Alerts

No rating or validation information has been found for Pennsylvania State University Huck Institutes Proteomics and Mass Spectrometry Core Facility.

No alerts have been found for Pennsylvania State University Huck Institutes Proteomics and Mass Spectrometry Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Kothattil S, et al. (2026) Proteomic insights into Pholiota nameko mycelial response to wood-based substrates. Fungal biology, 130(1), 101714.

Zhang H, et al. (2025) FLEXTAG: A Small and Self-renewable Protein Labeling System for Anti-fading Multicolor Super-resolution Imaging. bioRxiv : the preprint server for biology.

Kulkarni S, et al. (2025) Auxin-induced depletion of human CCR4-NOT subunits reveals opposing functions of CNOT1 and CNOT4 in mRNA metabolism. The Journal of biological chemistry, 301(12), 110862.

Akinniyi OT, et al. (2025) Degradation factor 1, Def1, regulates mRNA translation and decay through Ccr4-Not-dependent ubiquitylation of the ribosome. bioRxiv : the preprint server for biology.

Saha P, et al. (2025) Anti-miR oligo-mediated detection of human salivary microRNAs for mild traumatic brain injury. Biosensors & bioelectronics, 278, 117333.

Fekete FJ, et al. (2025) Identifying bacterial heme sensor protein interacting partners under varying oxygen tensions using proximity labeling. Journal of inorganic biochemistry, 274, 113067.

Akinniyi OT, et al. (2025) The DNA damage response and RNA Polymerase II regulator Def1 has posttranscriptional functions in the cytoplasm. bioRxiv : the preprint server for biology.

Dewing SM, et al. (2025) Probing Enzymatic Acetylation Events in Real Time With NMR Spectroscopy: Insights Into Acyl-Cofactor Dependent p300 Modification of Histone H4. Proteins, 93(10), 1837.

Chu LK, et al. (2025) Hydrophobicity analysis of Chinese Hamster Ovary host cell proteins using analytical hydrophobic interaction chromatography and LC-MS. Journal of chromatography. A, 1763, 466440.

Dewing SM, et al. (2024) Acetylation-Dependent Compaction of the Histone H4 Tail Ensemble. *The journal of physical chemistry. B*, 128(43), 10636.

Kulkarni S, et al. (2024) Human CCR4-NOT globally regulates gene expression and is a novel silencer of retrotransposon activation. *bioRxiv : the preprint server for biology*.