

# Resource Summary Report

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## 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:** access service resource, core facility, 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/RRID:SCR_024462?citation=1),  
<https://coremarketplace.org/?FacilityID=2454&citation=1>

**Record Creation Time:** 20230922T050237+0000

**Record Last Update:** 20260905T133438+0000

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## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 19 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Akinniyi OT, et al. (2026) Degradation factor 1, Def1, regulates mRNA translation and decay through Ccr4-Not-dependent ubiquitylation of the ribosome. RNA (New York, N.Y.), 32(6), 930.

Hewa Inaththappulige SIN, et al. (2026) Enabling Fluoroalkyl-Sulfonylalkylation and Fluoroalkyl-Halogenation of Alkenes and Alkynes via Photoredox Catalysis. Journal of the American Chemical Society, 148(16), 16882.

Zhang H, et al. (2026) FLEXTAG: a small and self-renewable protein labeling system for anti-fading multi-color super-resolution imaging. Nature communications, 17(1).

Joshi MP, et al. (2026) Increasing the Compositional Heterogeneity of Single-Chain Amphiphile Membranes Supported by Coacervate Cores Alters Stability and Properties of the Hybrid Protocells. Langmuir : the ACS journal of surfaces and colloids, 42(19), 13582.

Chen AP, et al. (2026) Oxidative stress impairs processive motility of the axonal transport motor KIF1A. The Journal of biological chemistry, 302(6), 111471.

Fraser OA, et al. (2026) PAX3-FOXO1 Contacts BRD4 through Its Acetylated Intrinsically Disordered Region. Biochemistry, 65(13), 2066.

Akinniyi OT, et al. (2026) Gene expression analysis and proximity labeling reveal post-transcriptional functions of the yeast RNA polymerase II regulator Def1. The Journal of biological chemistry, 302(2), 111003.

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

Chong PG, et al. (2026) Kinetically Divergent Dimanganese-Tyrosyl Radical Cofactor Assembly in Listeria monocytogenes Class I Ribonucleotide Reductase. Biochemistry, 65(15), 2387.

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.

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.

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*.

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*.