Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

OHSU Proteomics Shared Resource Core Facility

RRID:SCR_009991
Type: Tool

Proper Citation

OHSU Proteomics Shared Resource Core Facility (RRID:SCR_009991)

Resource Information

URL: https://www.ohsu.edu/proteomics-shared-resource

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Description: Core facility that provides the following services: Protein identification and partial sequencing, Determination of whole protein mass, Targeted SRM analysis of known proteins, Protein quantitation assay, Gel electrophoresis. The OHSU Protemics Shared Resource facility was established to make state-of-the-art mass spectrometry based protein analysis analytical capabilities available to the biomedical research community at OHSU.

Synonyms: OHSU Proteomics Shared Resource Core Laboratory

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

Keywords: ABRF, USEDit, partial protein sequencing, protein identification, protein mass determination by mass spectrometry, multiple reaction monitoring, protein quantitation assay, electrophoresis

Resource Name: OHSU Proteomics Shared Resource Core Facility

Resource ID: SCR_009991

Alternate IDs: nlx_156459

Old URLs: http://ohsu.eagle-i.net/i/0000012a-24ff-d2af-d994-629180000000

Record Creation Time: 20220129T080256+0000

Record Last Update: 20260905T133339+0000

Ratings and Alerts

No rating or validation information has been found for OHSU Proteomics Shared Resource Core Facility.

No alerts have been found for OHSU Proteomics Shared Resource Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Heo D, et al. (2026) All-in-one, Cas13d-based cell-specific gene knockdown system for zebrafish. bioRxiv : the preprint server for biology.

Holden P, et al. (2026) Isobaric quantitative proteomics reveals altered extracellular matrix, cytoskeletal, and degradation pathways in glaucomatous trabecular meshwork cells. Scientific reports, 16(1).

Valdes Angues R, et al. (2026) The Nodding syndrome cerebrospinal fluid proteome: a lens into neurodevelopmental failure consistent with environmentally triggered MECP2 dysregulation? Frontiers in molecular neuroscience, 19, 1717920.

Wang J, et al. (2026) Cyclic di-GMP suppresses cancer metastasis by targeting proteasome 26S subunit non-ATPase 3 independently of STING. Signal transduction and targeted therapy, 11(1), 44.

Park J, et al. (2026) Efficient and rapid isolation of native AMPA receptor complexes for cryo-EM. Protein science : a publication of the Protein Society, 35(2), e70483.

Coombs AM, et al. (2026) PIEZOs regulate oligodendrocyte sheath formation, expansion, and myelination potential. bioRxiv : the preprint server for biology.

Fang C, et al. (2026) Native AMPA receptor architecture reveals SynDIG4 engagement and auxiliary subunit heterogeneity. Science advances, 12(24), eaee7973.

Warren J, et al. (2026) Identification of clofibric acid as a SYVN1 ligand for PROTAC development. bioRxiv : the preprint server for biology.

Jozi?? A, et al. (2026) In vivo endosomal escape assay identifies mechanisms for efficient hepatic LNP delivery. Nature biotechnology.

Warren J, et al. (2026) Identification of Clofibric Acid as a Synoviolin (SYVN1) Ligand for Proteolysis-Targeting Chimera (PROTAC) Development. ACS medicinal chemistry letters, 17(7), 1430.

Yang Y, et al. (2025) GNL3 SUMOylation is essential for DNA double-strand break repair by homologous recombination. bioRxiv : the preprint server for biology.

Collins HY, et al. (2025) FBXW7 regulates MYRF levels to control myelin capacity and homeostasis in the adult central nervous system. Nature communications, 16(1), 7822.