

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

Oregon Health and Science University Biophysics Core Facility

RRID:SCR_022744

Type: Tool

Proper Citation

Oregon Health and Science University Biophysics Core Facility (RRID:SCR_022744)

Resource Information

URL: <https://www.ohsu.edu/biophysics-core>

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Description: Core services including ensurance that purified proteins and other biomolecules of interest are uncompromised in terms of their structure and stability. Facilitates analyses of catalytic activities and functional interactions.Examines thermodynamic and kinetic parameters for association between proteins and small molecules.Facilitates hypothesis generation through coalescence of experimental data and computational modeling.Assists in setting up protein crystallization assays.

Synonyms: OHSU Biophysics Core

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

Keywords: USEDit, ABRF, protein structure and stability ensurance service

Availability: Restricted

Resource Name: Oregon Health and Science University Biophysics Core Facility

Resource ID: SCR_022744

Alternate IDs: ABRF_1550

Alternate URLs: <https://coremarketplace.org/?FacilityID=1550&citation=1>

Record Creation Time: 20220915T050143+0000

Record Last Update: 20260731T043134+0000

Ratings and Alerts

No rating or validation information has been found for Oregon Health and Science University Biophysics Core Facility.

No alerts have been found for Oregon Health and Science University Biophysics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Yao W, et al. (2025) Structure of human green cone opsin yields insights into mechanisms underlying the rapid decay of its active, signaling state. Proceedings of the National Academy of Sciences of the United States of America, 122(49), e2516318122.

Oken AC, et al. (2025) A polycyclic scaffold identified by structure-based drug design effectively inhibits the human P2X7 receptor. Nature communications, 16(1), 8283.

Gupta M, et al. (2025) Molecular mechanism of substrate transport by human peroxisomal ABCD3. bioRxiv : the preprint server for biology.

Yao W, et al. (2025) A novel "bio-tag" for cryo-EM studies based on the small, electron-dense protein Csp1. Biophysical journal, 124(9), 1414.