Resource Summary Report

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Penn State Hershey College of Medicine cryo-EM Core Facility

RRID:SCR_021178
Type: Tool

Proper Citation

Penn State Hershey College of Medicine cryo-EM Core Facility (RRID:SCR_021178)

Resource Information

URL: https://pennstatehealthnews.org/topics/cryo-em/

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Description: Cryo-electron microscopy (cryo-EM) facility providesTitan Krios cryo-transmission electron microscope that is fully equipped for high-throughput data collection of the utmost quality possible. It has the ability to determine the atomic structure of a single protein or view molecules interacting in their cellular context. Provides guidance, training or data collection for researchers at the College of Medicine.Equipment includes Zeiss LSM 980 Cryo-Confocal Microscope,300 kV Krios Cryo-TEM for SPA and tomography, Equipped with Volta phase plates, bioquantum energy filter and K3 direct electron detector,200 kV thermionic JEOL 2100 for cryo-imaging, cryo-tomography, and standard imaging of stained grids.

Synonyms: Penn State COM Cryo-EM, Penn State College of Medicine cryo-EM facility

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

Keywords: ABRF, cryo electron microscopy services,

Availability: Restricted

Resource Name: Penn State Hershey College of Medicine cryo-EM Core Facility

Resource ID: SCR_021178

Alternate IDs: ABRF_1167

Alternate URLs: https://coremarketplace.org/?FacilityID=1167

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194151+0000

Ratings and Alerts

No rating or validation information has been found for Penn State Hershey College of Medicine cryo-EM Core Facility.

No alerts have been found for Penn State Hershey College of Medicine cryo-EM Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Purnell C, et al. (2025) Training Generalized Segmentation Networks with Real and Synthetic Cryo-ET data. bioRxiv : the preprint server for biology.

Kumar A, et al. (2025) Cryo-EM structure of the brine shrimp mitochondrial ATP synthase suggests an inactivation mechanism for the ATP synthase leak channel. Cell death and differentiation, 32(8), 1518.

Pujhari S, et al. (2025) In situ architecture of the endosymbiont Wolbachia pipientis. bioRxiv : the preprint server for biology.

Bianchini EN, et al. (2025) Cryo-EM structures of HBV capsids from human cells at near-atomic resolution. Structure (London, England : 1993).

Tsvetkova IB, et al. (2025) Genetically Engineered, Multichromophore Virus-Like Nanoparticles with Ultranarrow Distribution of Emission Intensity. ACS nano, 19(1), 479.

Minamide LS, et al. (2023) Visualizing Cofilin-Actin Filaments by Immunofluorescence and CryoEM: Essential Steps for Observing Cofilactin in Cells. Methods in molecular biology (Clifton, N.J.), 2593, 265.

Jentink N, et al. (2023) Cryoelectron tomography reveals the multiplex anatomy of condensed native chromatin and its unfolding by histone citrullination. Molecular cell, 83(18), 3236.

Kim C, et al. (2023) Structure of the Hepatitis B virus capsid quasi-6-fold with a??trapped C-terminal domain reveals capsid movements associated with domain exit. The Journal of biological chemistry, 299(9), 105104.

Purnell C, et al. (2023) Rapid Synthesis of Cryo-ET Data for Training Deep Learning Models. bioRxiv : the preprint server for biology.

Ren SC, et al. (2022) Mutations at the Alphavirus E1'-E2 Interdimer Interface Have Host-Specific Phenotypes. Journal of virology, 96(5), e0214921.

Heebner JE, et al. (2022) Deep Learning-Based Segmentation of Cryo-Electron Tomograms. Journal of visualized experiments : JoVE(189).

Liu H, et al. (2022) Cryo-EM structures of human hepatitis B and woodchuck hepatitis virus small spherical subviral particles. Science advances, 8(31), eabo4184.

Hylton RK, et al. (2022) Cofilactin filaments regulate filopodial structure and dynamics in neuronal growth cones. Nature communications, 13(1), 2439.

Tillinghast J, et al. (2021) Structural mechanisms for gating and ion selectivity of the human polyamine transporter ATP13A2. Molecular cell, 81(22), 4650.

Wang JC, et al. (2021) Publisher Correction: Structural basis for the structural dynamics of human mitochondrial chaperonin mHsp60. Scientific reports, 11(1), 17372.

Wang JC, et al. (2021) Structural basis for the structural dynamics of human mitochondrial chaperonin mHsp60. Scientific reports, 11(1), 14809.