Resource Summary Report

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SerialEM

RRID:SCR_017293
Type: Tool

Proper Citation

SerialEM (RRID:SCR_017293)

Resource Information

URL: http://bio3d.colorado.edu/SerialEM/

Proper Citation: SerialEM (RRID:SCR_017293)

Description: Software tool for automated EM data acquisition. Used for efficient tilt series acquisition and interface for image capture, display, and storage and for control of some aspects of microscope function.

Resource Type: data acquisition software, software resource, software application, data processing software

Defining Citation: PMID:16182563

Keywords: automated, data, acquisition, tilt, image, capture, display, storage, microscope

Funding: NCRR RR00592;
NIGMS P01 GM61306

Availability: Restricted

Resource Name: SerialEM

Resource ID: SCR_017293

License: MIT license

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260808T190107+0000

Ratings and Alerts

No rating or validation information has been found for SerialEM.

No alerts have been found for SerialEM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 228 mentions in open access literature.

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

Perry TN, et al. (2026) Structural basis of Cas8-independent Cas3 recruitment in Type I-F2 CRISPR-Cas. Nucleic acids research, 54(5).

Afonso AC, et al. (2026) Ultrastructure Analysis by Cryo-Electron Tomography Revealed Mesosomes in the Gram-negative Delftia Acidovorans. Microbial ecology, 89(1), 48.

Ma Q, et al. (2026) Insights into the structure and modulation of human TWIK-2. Nature communications, 17(1).

Zhang W, et al. (2026) Structures of the human glucose-6-phosphate transporter provide insights into its transport cycle and substrate recognition. PLoS biology, 24(3), e3003731.

Kutchuashvili A, et al. (2026) Anticodon loop remodeling and D-stem shape drive the specific recognition of ANN-decoding tRNAs for t6A modification. Nucleic acids research, 54(11).

Karasmanis EP, et al. (2026) The molecular architecture of tunneling nanotubes. bioRxiv : the preprint server for biology.

Bellofatto K, et al. (2026) Implantable vascularized endocrine constructs for clinically scalable insulin delivery. Trends in biotechnology.

Do TT, et al. (2026) A correlative workflow for synaptic imaging by cryo-electron tomography. Structure (London, England : 1993), 34(5), 839.

Yang K, et al. (2026) Double-ring assembly of mpox virus I3L reveals an unconventional mechanism for ssDNA engagement. Cell reports, 45(7), 117659.

Morgan CJ, et al. (2026) The phage nucleus synergizes with an anti-defense protein to resist bacterial immunity. Cell reports, 45(4), 117219.

Li D, et al. (2026) Cryo-EM structure of soluble VPS13C suggests its regulation by a conformational switch and by calmodulin. Molecular cell, 86(14), 2843.

Liao Z, et al. (2026) Faf1 accelerates p97-mediated protein unfolding by promoting ubiquitin engagement. Cell reports, 45(6), 117393.

Bai Z, et al. (2026) Dynamic dimer-of-dimers architecture defines Mg2+ transport in human CNNM4. Cell.

Ay S, et al. (2025) In vivo HIV-1 nuclear condensates safeguard against cGAS and license reverse transcription. The EMBO journal, 44(1), 166.

Chen S, et al. (2025) Cryo-electron tomography reveals the microtubule-bound form of inactive LRRK2. eLife, 13.

Xin Y, et al. (2025) Direct trapping of the transport-segment DNA by the central domain of type IIA topoisomerases. Science advances, 11(51), eadw2839.

Mohan HM, et al. (2025) Endogenous retrovirus-like proteins recruit UBQLN2 to stress granules and shape their functional biology. Science advances, 11(29), eadu6354.

Hibshman GN, et al. (2025) Structural basis of a dual-function type II-B CRISPR-Cas9. Nucleic acids research, 53(12).

Schenck S, et al. (2025) Structures of native SV2A reveal the binding mode for tetanus neurotoxin and anti-epileptic racetams. Nature communications, 16(1), 4172.

Hu S, et al. (2025) Structural and functional analysis of the Nipah virus polymerase complex. Cell, 188(3), 688.