

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: software application, software resource, data processing software, data acquisition 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: 20260729T044432+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 213 mentions in open access literature.

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

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

Khandelwal NK, et al. (2025) Structure and inhibition mechanisms of Mycobacterium tuberculosis essential transporter efflux protein A. *Nature communications*, 16(1), 3139.

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

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

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.

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

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.

Duong L, et al. (2025) Bactericidal activity of mammalian histones is caused by large membrane pore formation. *Cell reports*, 44(5), 115658.

Yamaguchi T, et al. (2025) Structural insights into heterohexameric assembly of epilepsy-related ligand-receptor complex LGI1-ADAM22. *eLife*, 14.

Bunbury F, et al. (2025) Cyanobacteria and Chloroflexota cooperate to structure light-responsive biofilms. *Proceedings of the National Academy of Sciences of the United States of America*, 122(5), e2423574122.

Zhang J, et al. (2025) Structural basis for the interaction between the Drosophila RTK Sevenless (dROS1) and the GPCR BOSS. *Nature communications*, 16(1), 808.

Moser D, et al. (2025) The slit diaphragm in Drosophila exhibits a bilayered, fishnet architecture. *Nature communications*, 16(1), 8741.

Wang Y, et al. (2025) Rational design of flavivirus E protein vaccine optimizes immunogenicity and mitigates antibody dependent enhancement risk. *Nature communications*, 16(1), 11558.

França CT, et al. (2025) Yeast Display Reveals Plentiful Mutations That Improve Fusion Peptide Vaccine-Elicited Antibodies Beyond 59% HIV-1 Neutralization Breadth. *Vaccines*, 13(11).

Musalgaonkar S, et al. (2025) The assembly factor Reh1 is released from the ribosome during its initial round of translation. *Nature communications*, 16(1), 1278.

Castel J, et al. (2025) Deciphering molecular determinants of GPBAR1-Gs protein interactions by HDX-MS and cryo-EM. *Scientific reports*, 15(1), 31517.

Wang X, et al. (2025) De Novo Design of Integrin $\alpha 5 \beta 1$ Modulating Proteins to Enhance Biomaterial Properties. *Advanced materials* (Deerfield Beach, Fla.), 37(34), e2500872.

Pinner MT, et al. (2025) Programmable DNA shell scaffolds for directional membrane budding. *Nature communications*, 16(1), 8972.

Maiwald SA, et al. (2025) TRIP12 structures reveal HECT E3 formation of K29 linkages and branched ubiquitin chains. *Nature structural & molecular biology*, 32(9), 1766.