Resource Summary Report

Generated by RRID on Apr 28, 2025

EMAN

RRID:SCR_016867
Type: Tool

Proper Citation

EMAN (RRID:SCR_016867)

Resource Information

URL: https://blake.bcm.edu/emanwiki/EMAN2

Proper Citation: EMAN (RRID:SCR_016867)

Description: Software suite for processing data from transmission electron microscopes. Used in supercomputing facilities as a test application for large-scale computing. Used for single particle reconstruction, helical reconstruction, 2-D crystallography and whole-cell tomography.

Abbreviations: EMAN

Synonyms: EMAN1, EMAN2

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

Defining Citation: PMID:16859925

Keywords: image, processing, data, transmission, electron, microscope, single, particle, reconstruction, helical, 2D, whole, cell, tomography, bio.tools

Funding: NIH

Availability: Free, Available for download, Freely available

Resource Name: EMAN

Resource ID: SCR_016867

Alternate IDs: biotools:eman

Alternate URLs: https://bio.tools/eman

Old URLs: https://blake.bcm.edu/emanwiki/EMAN1

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250428T054022+0000

Ratings and Alerts

No rating or validation information has been found for EMAN.

No alerts have been found for EMAN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 107 mentions in open access literature.

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

Kraus F, et al. (2024) Global cellular proteo-lipidomic profiling of diverse lysosomal storage disease mutants using nMOST. bioRxiv : the preprint server for biology.

Duan H, et al. (2024) Long trimer-immunization interval and appropriate adjuvant reduce immune responses to the soluble HIV-1-envelope trimer base. iScience, 27(2), 108877.

Roberts EM, et al. (2024) An alternate route for cellulose microfibril biosynthesis in plants. Science advances, 10(50), eadr5188.

Rajan KS, et al. (2024) Structural and mechanistic insights into the function of Leishmania ribosome lacking a single pseudouridine modification. Cell reports, 43(5), 114203.

Zhang X, et al. (2024) In situ structural determination of cyanobacterial phycobilisome-PSII supercomplex by STAgSPA strategy. Nature communications, 15(1), 7201.

Kong WW, et al. (2024) Cryo-electron tomography reveals the packaging pattern of RuBisCOs in Synechococcus ?-carboxysome. Structure (London, England : 1993), 32(8), 1110.

Cai SW, et al. (2024) POT1 recruits and regulates CST-Pol?/primase at human telomeres.

Cell, 187(14), 3638.

Troman L, et al. (2023) Interaction of the periplasmic chaperone SurA with the inner membrane protein secretion (SEC) machinery. The Biochemical journal, 480(4), 283.

Ahmed T, et al. (2022) Structure of the ancient TRPY1 channel from Saccharomyces cerevisiae reveals mechanisms of modulation by lipids and calcium. Structure (London, England : 1993), 30(1), 139.

Cai S, et al. (2022) In situ architecture of the lipid transport protein VPS13C at ER-lysosome membrane contacts. Proceedings of the National Academy of Sciences of the United States of America, 119(29), e2203769119.

Nicolas WJ, et al. (2022) Cryo-electron tomography of the onion cell wall shows bimodally oriented cellulose fibers and reticulated homogalacturonan networks. Current biology : CB, 32(11), 2375.

Kaldmäe M, et al. (2022) A "spindle and thread" mechanism unblocks p53 translation by modulating N-terminal disorder. Structure (London, England : 1993), 30(5), 733.

Zapletal D, et al. (2022) Structural and functional basis of mammalian microRNA biogenesis by Dicer. Molecular cell, 82(21), 4064.

Mostofian B, et al. (2022) Continuum dynamics and statistical correction of compositional heterogeneity in multivalent IDP oligomers resolved by single-particle EM. Journal of molecular biology, 434(9), 167520.

Maib H, et al. (2022) A mechanism for exocyst-mediated tethering via Arf6 and PIP5K1C-driven phosphoinositide conversion. Current biology : CB, 32(13), 2821.

Seraphim TV, et al. (2022) Assembly principles of the human R2TP chaperone complex reveal the presence of R2T and R2P complexes. Structure (London, England : 1993), 30(1), 156.

Wang Q, et al. (2022) Molecular basis of differential receptor usage for naturally occurring CD55-binding and -nonbinding coxsackievirus B3 strains. Proceedings of the National Academy of Sciences of the United States of America, 119(4).

Tian B, et al. (2022) Cryogenic superresolution correlative light and electron microscopy of vitreous sections. Biophysics reports, 8(4), 193.

Huang QJ, et al. (2022) Quantitative structural analysis of influenza virus by cryo-electron tomography and convolutional neural networks. Structure (London, England : 1993), 30(5), 777.

Kantsadi AL, et al. (2022) Structures of SAS-6 coiled coil hold implications for the polarity of the centriolar cartwheel. Structure (London, England : 1993), 30(5), 671.