Resource Summary Report

Generated by NIF on Apr 27, 2025

cisTEM

RRID:SCR_016502
Type: Tool

Proper Citation

cisTEM (RRID:SCR_016502)

Resource Information

URL: https://cistem.org/

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Description: Software to process cryo-EM images of macromolecular complexes and obtain high-resolution 3D reconstructions from them.

Abbreviations: cisTEM

Synonyms: computational imaging system for Transmission Electron Microscopy

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

Defining Citation: DOI:10.7554/eLife.35383

Keywords: data, processing, high, resolution, electron, cryo, macroscopy, single, particle, averaging, image, macromolecule, high, resolution, 3D, bio.tools

Funding: Howard Hughes Medical Institute

Availability: Open source, Trial available

Resource Name: cisTEM

Resource ID: SCR_016502

Alternate IDs: biotools:cistem

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

License: the Janelia Research Campus Software License

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250426T060549+0000

Ratings and Alerts

No rating or validation information has been found for cisTEM.

No alerts have been found for cisTEM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Remesh SG, et al. (2023) Computational pipeline provides mechanistic understanding of Omicron variant of concern neutralizing engineered ACE2 receptor traps. Structure (London, England : 1993), 31(3), 253.

Lucas BA, et al. (2023) Baited reconstruction with 2D template matching for high-resolution structure determination in vitro and in vivo without template bias. eLife, 12.

Silva RP, et al. (2023) Identification of a conserved S2 epitope present on spike proteins from all highly pathogenic coronaviruses. eLife, 12.

Yu X, et al. (2023) The evolution and determinants of neutralization of potent head-binding antibodies against Ebola virus. Cell reports, 42(11), 113366.

Eren E, et al. (2022) Structural characterization of the Myxococcus xanthus encapsulin and ferritin-like cargo system gives insight into its iron storage mechanism. Structure (London, England : 1993), 30(4), 551.

Koester DC, et al. (2022) Discovery of Novel Quinoline-Based Proteasome Inhibitors for Human African Trypanosomiasis (HAT). Journal of medicinal chemistry, 65(17), 11776.

Zhang K, et al. (2022) A step-by-step protocol for capturing conformational snapshots of ligand gated ion channels by single-particle cryo-EM. STAR protocols, 3(4), 101732.

Rabuck-Gibbons JN, et al. (2022) Quantitative mining of compositional heterogeneity in cryo-

EM datasets of ribosome assembly intermediates. Structure (London, England : 1993), 30(4), 498.

Milligan JC, et al. (2022) Asymmetric and non-stoichiometric glycoprotein recognition by two distinct antibodies results in broad protection against ebolaviruses. Cell, 185(6), 995.

Kumar N, et al. (2021) Structure of the human secretory immunoglobulin M core. Structure (London, England : 1993), 29(6), 564.

Yu J, et al. (2021) Mechanism of gating and partial agonist action in the glycine receptor. Cell, 184(4), 957.

Jiang D, et al. (2021) Open-state structure and pore gating mechanism of the cardiac sodium channel. Cell, 184(20), 5151.

Rong Y, et al. (2021) TMEM120A contains a specific coenzyme A-binding site and might not mediate poking- or stretch-induced channel activities in cells. eLife, 10.

Lucas BA, et al. (2021) Locating macromolecular assemblies in cells by 2D template matching with cisTEM. eLife, 10.

Hsieh CL, et al. (2021) Stabilized coronavirus spike stem elicits a broadly protective antibody. Cell reports, 37(5), 109929.

Joyce MG, et al. (2021) SARS-CoV-2 ferritin nanoparticle vaccines elicit broad SARS coronavirus immunogenicity. Cell reports, 37(12), 110143.

Myasnikov A, et al. (2021) Structural analysis of the full-length human LRRK2. Cell, 184(13), 3519.

Travis BA, et al. (2021) Structural Basis for Virulence Activation of Francisella tularensis. Molecular cell, 81(1), 139.

Wisedchaisri G, et al. (2021) Structural Basis for High-Affinity Trapping of the NaV1.7 Channel in Its Resting State by Tarantula Toxin. Molecular cell, 81(1), 38.

Kschonsak M, et al. (2021) Structures of HCMV Trimer reveal the basis for receptor recognition and cell entry. Cell, 184(5), 1232.