

Resource Summary Report

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cisTEM

RRID:SCR_016502

Type: Tool

Proper Citation

cisTEM (RRID:SCR_016502)

Resource Information

URL: <https://cistem.org/>

Proper Citation: cisTEM (RRID:SCR_016502)

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 application, software resource

Defining Citation: [DOI:10.7554/eLife.35383](https://doi.org/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

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 67 mentions in open access literature.

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

Kong L, et al. (2026) Unbend, correction of local beam-induced sample motion in cryo-EM images using a 3D spline model. eLife, 14.

Qian C, et al. (2025) Multi-epitope transplantation enables cross-type neutralization of phylogenetically distant HPV11/6/53 in mice. iScience, 28(10), 113477.

Smith AM, et al. (2025) The HIV-1 nuclear export complex reveals the role of RNA in CRM1 cargo recognition. Molecular cell, 85(16), 3108.

Qerqez AN, et al. (2025) Selective decoupling of IgG1 binding to viral Fc receptors restores antibody-mediated NK cell activation against HCMV. Cell reports, 44(12), 116593.

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.

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

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

Westphall MS, et al. (2022) Three-dimensional structure determination of protein complexes using matrix-landing mass spectrometry. Nature communications, 13(1), 2276.

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.

- 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.
- Koester DC, et al. (2022) Discovery of Novel Quinoline-Based Proteasome Inhibitors for Human African Trypanosomiasis (HAT). Journal of medicinal chemistry, 65(17), 11776.
- 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.
- Yu J, et al. (2021) Mechanism of gating and partial agonist action in the glycine receptor. Cell, 184(4), 957.
- Kumar N, et al. (2021) Structure of the human secretory immunoglobulin M core. Structure (London, England : 1993), 29(6), 564.
- 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.
- Myasnikov A, et al. (2021) Structural analysis of the full-length human LRRK2. Cell, 184(13), 3519.