

Resource Summary Report

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MotionCor2

RRID:SCR_016499

Type: Tool

Proper Citation

MotionCor2 (RRID:SCR_016499)

Resource Information

URL: <https://emcore.ucsf.edu/cryoem-software>

Proper Citation: MotionCor2 (RRID:SCR_016499)

Description: Software tool for anisotropic correction of beam-induced motion for improved cryo-electron microscopy. Used to describe the sample motion as a local deformation that varies smoothly throughout the exposure. A program running on Linux.

Synonyms: MotionCor

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

Defining Citation: [PMID:28250466](#)

Keywords: anisotropic, correction, beam, induced, motion, cryo, electron, microscopy, exposure, data

Funding: NIGMS P01 GM111126;
NIH R01 GM031627

Availability: Restricted

Resource Name: MotionCor2

Resource ID: SCR_016499

Old URLs: <http://msg.ucsf.edu/em/software/motioncor2.html>

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260905T132809+0000

Ratings and Alerts

No rating or validation information has been found for MotionCor2.

No alerts have been found for MotionCor2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 186 mentions in open access literature.

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

Wu L, et al. (2026) CLCC1 governs ER bilayer equilibration to maintain lipid homeostasis. Nature, 652(8109), 471.

Rasouli S, et al. (2026) Archaeal and eukaryotic MCM rings sequentially melt DNA for replication initiation. Nature communications, 17(1).

Lu MA, et al. (2026) Molecular mechanisms of flotillin complexes in organizing membrane microdomains. Nature communications, 17(1).

Huffine CA, et al. (2026) [CO₂] Alters Cyanobacterial Carboxysome Encapsulation and Redox State. Research square.

Ettema TW, et al. (2026) Shared structural mechanisms of alternating access between the secondary peptide transporter SbmA and ABC transporters. Nature communications, 17(1).

Pinto CS, et al. (2026) Actin arginylation alters myosin engagement and F-actin patterning despite structural conservation. The Journal of cell biology, 225(1).

Mishra P, et al. (2026) Miniprotein inhibitors of the Staphylococcus aureus efflux transporter NorA. bioRxiv : the preprint server for biology.

Aggarwal P, et al. (2026) Recognition and remodelling of nucleosomes and hexasomes by the human INO80 complex. 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.

Duan J, et al. (2026) Structural basis for the extended-spectrum antimicrobial activity of Garvieacin Q. Applied and environmental microbiology, 92(2), e0177325.

Lupton CJ, et al. (2026) Structure of the lysosomal KICSTOR-GATOR1-SAMTOR nutrient-sensing supercomplex. Cell.

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.

Yan L, et al. (2026) The Erlin1/2 complex is a dynamic scaffold for membrane microdomain assembly on the endoplasmic reticulum. *Molecular cell*, 86(7), 1362.

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

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

Xie P, et al. (2025) A fiducial-assisted strategy compatible with resolving small MFS transporter structures in multiple conformations using cryo-EM. *Nature communications*, 16(1), 7.

Jiang J, et al. (2025) Molecular landscape of the fungal plasma membrane and implications for antifungal action. *Nature communications*, 16(1), 9125.

Notti RQ, et al. (2025) The resting and ligand-bound states of the membrane-embedded human T-cell receptor-CD3 complex. *Nature communications*, 16(1), 10996.

Xue J, et al. (2025) Structural mechanisms of PIP2 activation and SEA0400 inhibition in human cardiac sodium-calcium exchanger NCX1. *eLife*, 14.