

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>

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

Defining Citation: [PMID:28250466](#)

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

Funding: NIH R01 GM031627;
NIGMS P01 GM111126

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: 20260728T043519+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 172 mentions in open access literature.

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

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

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

Yagi-Utsumi M, et al. (2025) Microgravity-Assisted Exploration of the Conformational Space of Amyloid ? Affected by Tottori-Type Familial Mutation D7N. *ACS chemical neuroscience*, 16(14), 2682.

Berger C, et al. (2025) In situ and in vitro cryo-EM reveal structures of mycobacterial encapsulin assembly intermediates. *Communications biology*, 8(1), 245.

Fu W, et al. (2025) Mechanisms and engineering of a miniature type V-N CRISPR-Cas12 effector enzyme. *Nature communications*, 16(1), 5667.

Li C, et al. (2025) Structural basis of error-prone DNA synthesis by DNA polymerase ?. *Nature communications*, 16(1), 2063.

Kroh HK, et al. (2025) Mouse monoclonal antibodies against *Clostridioides difficile* toxins TcdA and TcdB target diverse epitopes for neutralization. *Infection and immunity*, 93(10), e0013925.

Blauwkamp JA, et al. (2025) An essential adaptor for apicoplast fission and inheritance in malaria parasites. *Nature communications*, 16(1), 11325.

Alcantara CL, et al. (2025) The subcellular architecture of *Paratrypanosoma confusum* revealed by CryoET: A window into early trypanosome evolution. *Proceedings of the National Academy of Sciences of the United States of America*, 122(50), e2521233122.

Yu Z, et al. (2025) Mechanisms of HSV-1 helicase-primase inhibition and replication fork complex assembly. *Cell*.

Xiao X, et al. (2025) Structural insights into the biotechnologically relevant reversible NADPH-oxidizing NiFe-hydrogenase from *P.furiosus*. *Structure (London, England : 1993)*, 33(9), 1470.

Zhao XT, et al. (2025) The Myo2 adaptor Ldm1 and its receptor Ldo16 mediate actin-dependent lipid droplet motility. *Cell reports*, 44(11), 116475.

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.

Schiøtz OH, et al. (2024) Serial Lift-Out: sampling the molecular anatomy of whole organisms. *Nature methods*, 21(9), 1684.

Jung H, et al. (2024) Structural and Biochemical Characterization of the Nucleosome Containing Variants H3.3 and H2A.Z. *Epigenomes*, 8(2).