

Resource Summary Report

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RELION

RRID:SCR_016274

Type: Tool

Proper Citation

RELION (RRID:SCR_016274)

Resource Information

URL: <http://www2.mrc-lmb.cam.ac.uk/relion>

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Description: Software for determination of cryo-EM structures. It employs an empirical Bayesian approach to refinement of (multiple) 3D reconstructions or 2D class averages in electron cryo-microscopy.

Synonyms: RELION, REgularised Likelihood Optimisation, RELION-3

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

Defining Citation: [PMID:23000701](#)

Keywords: cryo, cryogenic, cryo em, determination, analysis, bayesian, statistic, map, maximum a posteriori, electron, cryomicroscopy

Funding: UK Medical Research Council

Availability: Free, Available for download, Tutorial available

Resource Name: RELION

Resource ID: SCR_016274

Alternate IDs: OMICS_15597

Alternate URLs: <https://sources.debian.org/src/relion-bin+mpi+gui/>

License: GPLv2 License

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260803T040716+0000

Ratings and Alerts

No rating or validation information has been found for RELION.

No alerts have been found for RELION.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 408 mentions in open access literature.

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

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*.

Ishida H, et al. (2025) Cryo-EM structures of the zinc transporters ZnT3 and ZnT4 provide insights into their transport mechanisms. *FEBS letters*, 599(1), 41.

Balch S, et al. (2025) Cryo-EM structure of human telomerase dimer reveals H/ACA RNP-mediated dimerization. *Science (New York, N.Y.)*, 389(6756), eadr5817.

An Nguyen B, et al. (2025) Structural variability of apolipoprotein A-I amyloid fibrils across organs, mutations, and clinical presentations, revealed by cryo-EM. *bioRxiv : the preprint server for biology*.

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

An J, et al. (2025) Dimerization of GAS2 mediates crosslinking of microtubules and F-actin. *The EMBO journal*, 44(10), 2997.

Shi J, et al. (2025) Structural insights into transcription regulation of the global OmpR/PhoB family regulator PhoP from *Mycobacterium tuberculosis*. *Nature communications*, 16(1), 1573.

Qiu X, et al. (2025) Structural insights into toxicant export mediated by ABCC2 in *Arabidopsis thaliana*. *Nature communications*, 16(1), 11554.

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

Casiraghi M, et al. (2025) Structure and dynamics determine G protein coupling specificity at a class A GPCR. *Science advances*, 11(12), eadq3971.

Coleman B, et al. (2025) Lecithin:cholesterol acyltransferase binds a discontinuous binding site on adjacent apolipoprotein A-I belts in HDL. *Journal of lipid research*, 66(5), 100786.

Carver A, et al. (2025) Molecular basis of FIGNL1 in dissociating RAD51 from DNA and chromatin. *Science (New York, N.Y.)*, 387(6732), 426.

Butryn A, et al. (2025) Unidirectional MCM translocation away from ORC drives origin licensing. *Nature communications*, 16(1), 782.

Issa KHB, et al. (2025) Molecular basis for the activation of outer dynein arms in cilia. *Nature structural & molecular biology*, 32(12), 2454.

Zheng F, et al. (2025) Metabolic environment-driven remodeling of mitochondrial ribosomes regulates translation and biogenesis. *Molecular cell*, 85(23), 4437.

Weissman JD, et al. (2025) Structure of Photosystem I-FCP from giant kelp uncovers drivers of antenna evolution across the red lineage. *bioRxiv : the preprint server for biology*.

Mueller AU, et al. (2025) Real-time capture of ??N transcription initiation intermediates reveals mechanism of ATPase-driven activation by limited unfolding. *bioRxiv : the preprint server for biology*.

Hickman AB, et al. (2025) Activity of the mammalian DNA transposon piggyBat from *Myotis lucifugus* is restricted by its own transposon ends. *Nature communications*, 16(1), 458.

Zhou J, et al. (2025) In situ structures of the contractile nanomachine myophage Mu in both its extended and contracted states. *Journal of virology*, 99(3), e0205624.