

Resource Summary Report

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Refmac

RRID:SCR_014225

Type: Tool

Proper Citation

Refmac (RRID:SCR_014225)

Resource Information

URL: <http://www.ccp4.ac.uk/html/refmac5/description.html>

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Description: A molecular refinement program with two main modes: REVIEW, which checks and updates the input model to establish that the geometric restraints can be properly set up, and REFIN mode, which is the standard mode and documented in keywords. In REVIEW users can: check model coordinates and write an extended output set of coordinates, find disulphide bonds and other covalent links, cis-peptides, output the sequence and REMARK records. In REFIN mode users can carry out rigid body, tls, restrained or unrestrained refinement against Xray data, or idealisation of a macromolecular structure. Also in REFIN mode, Refmac produces an MTZ output file containing weighted coefficients for SigmaA weighted mFo-DFcalc and 2mFo-DFcalc maps. The program is supported by CCP4.

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

Keywords: molecular refinement, data analysis software, sequence analysis software

Resource Name: Refmac

Resource ID: SCR_014225

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260728T043435+0000

Ratings and Alerts

No rating or validation information has been found for Refmac.

No alerts have been found for Refmac.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1978 mentions in open access literature.

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

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

Lourenço FM, et al. (2026) Interaction of Staphylococcus aureus di-iron Repair of Iron Centers protein with the iron-sulfur cluster assembly SUF system. *Protein science : a publication of the Protein Society*, 35(1), e70406.

Gascó R, et al. (2026) Laccases from lactic acid bacteria show cuprous oxidase activity and capture Cu(II) and Ag(I) ions. *Protein science : a publication of the Protein Society*, 35(1), e70385.

Palte RL, et al. (2026) WRN structural flexibility showcased through fragment-based lead discovery of inhibitors. *Nature communications*, 17(1), 79.

Raig ND, et al. (2025) Type II kinase inhibitors that target Parkinson's disease-associated LRRK2. *Science advances*, 11(23), eadt2050.

Hope I, et al. (2025) Crystallographic fragment screening of CDK2-cyclin A: FragLites map sites of protein-protein interaction. *Structure (London, England : 1993)*.

Yu Y, et al. (2025) SignatureFinder enables sequence mining to identify cobalamin-dependent photoreceptor proteins. *The FEBS journal*, 292(3), 635.

Zhu X, et al. (2025) The Aedes aegypti mosquito evolves two types of prophenoloxidasases with diversified functions. *Proceedings of the National Academy of Sciences of the United States of America*, 122(3), e2413131122.

Majocchi S, et al. (2025) NI-3201 Is a Bispecific Antibody Mediating PD-L1-Dependent CD28 Co-stimulation on T Cells for Enhanced Tumor Control. *Cancer immunology research*, 13(3), 365.

Porathoor S, et al. (2025) Mechanism of deamination by mycobacterial deaminase selectively targeting mutagenic bases. *Nucleic acids research*, 53(6).

Gammons MV, et al. (2025) Wnt signalosome assembly is governed by conformational flexibility of Axin and by the AP2 clathrin adaptor. *Nature communications*, 16(1), 4718.

Prakash O, et al. (2025) The post-reactive structures of Leishmania major UDP-sugar pyrophosphorylase provide insights into the product release mechanism. *Microbiology spectrum*, 13(11), e0091125.

Brannigan JA, et al. (2025) Structure and activity of the essential UCH family deubiquitinase DUB16 from *Leishmania donovani*. *The Biochemical journal*, 482(14), 969.

Rowland CE, et al. (2025) Discovery and chemical optimisation of a potent, Bi-cyclic antimicrobial inhibitor of *Escherichia coli* PBP3. *Communications biology*, 8(1), 819.

Burchill L, et al. (2025) Structure, kinetics, and mechanism of *Pseudomonas putida* sulfoquinovose dehydrogenase, the first enzyme in the sulfoglycolytic Entner-Doudoroff pathway. *The Biochemical journal*, 482(2), 57.

Vann KR, et al. (2025) Structure-function relationship of ASH1L and histone H3K36 and H3K4 methylation. *Nature communications*, 16(1), 2235.

Gao T, et al. (2025) Molecular basis of $\alpha 2$ integrin activation by talin unveils subunit-specific mechanisms of integrin signaling. *Cell reports*, 44(5), 115607.

DeWeese DE, et al. (2025) Spectroscopy and crystallography define carotenoid oxygenases as a new subclass of mononuclear non-heme FeII enzymes. *The Journal of biological chemistry*, 301(5), 108444.

Fujita J, et al. (2025) Structural basis for the interaction between the bacterial cell division proteins FtsZ and ZapA. *Nature communications*, 16(1), 5985.

Costa F, et al. (2025) A global survey of intramolecular isopeptide bonds. *Protein science : a publication of the Protein Society*, 34(12), e70342.