

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Refmac

RRID:SCR_014225

Type: Tool

Proper Citation

Refmac (RRID:SCR_014225)

Resource Information

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

Proper Citation: Refmac (RRID:SCR_014225)

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

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

Resource Name: Refmac

Resource ID: SCR_014225

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260905T132744+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 2011 mentions in open access literature.

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

Gunning V, et al. (2026) Mechanistic design of cell-penetrating disruptors for phospho-dependent TACC3-CHC interaction. *Structure (London, England : 1993)*, 34(6), 915.

Lesire L, et al. (2026) Enhancing antitumour response to proteasome inhibitors with inhibitors of insulin-degrading enzyme, a new molecular vulnerability in multiple myeloma. *British journal of pharmacology*, 183(12), 3355.

Orkwis JA, et al. (2026) Helminth proteins recapitulate key structural motifs of MIF to facilitate immunomodulation of host receptors. *iScience*, 29(7), 116513.

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

Frederick A, et al. (2026) Altering chemotaxis as a strategy to enhance the foraging range of motility-restricted bacteria. *Communications biology*, 9(1), 197.

Luk CYM, et al. (2026) Csep1P protein from *Campylobacter concisus* induces a chemokine-dominant inflammatory state in macrophages and enhances proinflammatory response to gut bacteria. *PLoS pathogens*, 22(2), e1013951.

Kavaš V, et al. (2026) Structure-Activity Relationship and Crystallographic Study of New Monobactams. *Journal of medicinal chemistry*, 69(4), 3887.

Desveaux JM, et al. (2026) Neutralizing human monoclonal antibodies that target the PcrV component of the type III secretion system of *Pseudomonas aeruginosa* act through distinct mechanisms. *eLife*, 14.

Xiao Q, et al. (2026) Structural basis for sequence-specific DNA recognition by a group IId WRKY transcription factor GhWRKY17 in cotton. *The Biochemical journal*, 483(2), 149.

Sundman AK, et al. (2026) Spider venom phospholipase D toxin structure: Interfacial binding site, mechanism, activation, and head group preference. *Proceedings of the National Academy of Sciences of the United States of America*, 123(15), e2513997123.

Leiva Martel HN, et al. (2026) Roles of acidic residues in SpeG acetyltransferases-insights into importance for kinetic activity and polyamine binding in allosteric and acceptor sites. *The Biochemical journal*, 483(6), 1075.

Han X, et al. (2026) Ribosomal RNA cleavage by the previously unidentified RelS-RelI toxin-antitoxin system controls growth of *Mycobacterium tuberculosis*. *Nucleic acids research*, 54(12).

Shamsabadi A, et al. (2026) Utilizing Constrained Bicyclic Peptides for In Vitro Diagnostics. *ACS nano*, 20(7), 5928.

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.

Guo Y, et al. (2026) Analysis of the heterogenous structural states of the hexameric ATPase PilU of the type IV pili from *Vibrio cholerae*. *Protein science : a publication of the Protein Society*, 35(6), e70609.

Verma S, et al. (2026) Structural insights into PFAS- γ -lactoglobulin binding mechanism mediating PFAS toxicity. *bioRxiv : the preprint server for biology*.

Giner-Llorca M, et al. (2026) Engineering *Penicillium expansum* antifungal proteins unveils new clues about their mode of action. *Applied microbiology and biotechnology*, 110(1).

de Lange EMF, et al. (2026) Competition between binding partners of yeast Pex3 affects peroxisome biology. *The FEBS journal*, 293(1), 175.

Guo Y, et al. (2026) Analysis of the heterogenous structural states of the hexameric ATPase PilU of the Type IV pili from *Vibrio cholerae*. *bioRxiv : the preprint server for biology*.

Gimenis GHB, et al. (2026) Conformational gating mechanism for processive catalysis of ? (1,3)-glucans. *Nature communications*, 17(1).