

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 REFINE 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 REFINEMENT mode users can carry out rigid body, tls, restrained or unrestrained refinement against Xray data, or idealisation of a macromolecular structure. Also in REFINEMENT 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: software application, data analysis software, data processing software, sequence analysis software, software resource

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

Funding:

Resource Name: Refmac

Resource ID: SCR_014225

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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 1884 mentions in open access literature.

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

Lotz R, et al. (2025) Alternative splicing in the DBD linker region of p63 modulates binding to DNA and iASPP in vitro. *Cell death & disease*, 16(1), 4.

Koning HJ, et al. (2025) Structural plasticity of the coiled-coil interactions in human SFPQ. *Nucleic acids research*, 53(2).

Tandhavanant S, et al. (2025) Genetic variation of hemolysin co-regulated protein 1 affects the immunogenicity and pathogenicity of *Burkholderia pseudomallei*. *PLoS neglected tropical diseases*, 19(1), e0012758.

Yazaki S, et al. (2025) Crystal Structures of Antigen-Binding Fragment of Anti-Osteocalcin Antibody KTM219. *International journal of molecular sciences*, 26(2).

Mahana Y, et al. (2024) Structural evidence for protein-protein interaction between the non-canonical methyl-CpG-binding domain of SETDB proteins and C11orf46. *Structure (London, England : 1993)*, 32(3), 304.

Manakova E, et al. (2024) The missing part: the *Archaeoglobus fulgidus* Argonaute forms a functional heterodimer with an N-L1-L2 domain protein. *Nucleic acids research*, 52(5), 2530.

Stojan J, et al. (2024) Disentangling the formation, mechanism, and evolvement of the covalent methanesulfonyl fluoride acetylcholinesterase adduct: Insights into an aged-like inactive complex susceptible to reactivation by a combination of nucleophiles. *Protein science : a publication of the Protein Society*, 33(5), e4977.

Li H, et al. (2024) Crystallographic and Computational Insights into Isoform-Selective Dynamics in Nitric Oxide Synthase. *Biochemistry*, 63(6), 788.

Ferens FG, et al. (2024) Deficiency in PHD2-mediated hydroxylation of HIF2 α underlies Pacak-Zhuang syndrome. *Communications biology*, 7(1), 240.

Spiwoková P, et al. (2024) Nature-Inspired Gallinamides Are Potent Antischistosomal Agents: Inhibition of the Cathepsin B1 Protease Target and Binding Mode Analysis. *ACS infectious diseases*, 10(6), 1935.

Chikunova A, et al. (2024) Conserved proline residues prevent dimerization and aggregation in the β -lactamase BlaC. *Protein science : a publication of the Protein Society*, 33(4), e4972.

Loh TJ, et al. (2024) The molecular basis underlying T cell specificity towards citrullinated epitopes presented by HLA-DR4. *Nature communications*, 15(1), 6201.

Gusach A, et al. (2024) Molecular recognition of an odorant by the murine trace amine-associated receptor TAAR7f. *Nature communications*, 15(1), 7555.

Arrowsmith TJ, et al. (2024) Inducible auto-phosphorylation regulates a widespread family of nucleotidyltransferase toxins. *Nature communications*, 15(1), 7719.

Wojciechowski M, et al. (2024) Cytosine analogues as DNA methyltransferase substrates. *Nucleic acids research*, 52(15), 9267.

Dutkiewicz Z, et al. (2024) Bioinformatic, Enzymatic, and Structural Characterization of *Trichuris suis* Hexosaminidase HEX-2. *Biochemistry*, 63(15), 1941.

Gerninghaus J, et al. (2024) Back-pocket optimization of 2-aminopyrimidine-based macrocycles leads to potent dual EPHA2/GAK kinase inhibitors with antiviral activity. *bioRxiv : the preprint server for biology*.

Koller TO, et al. (2024) Paenilamicins from the honey bee pathogen *Paenibacillus* larvae are context-specific translocation inhibitors of protein synthesis. *bioRxiv : the preprint server for biology*.

Gurriaran-Rodriguez U, et al. (2024) Identification of the Wnt signal peptide that directs secretion on extracellular vesicles. *Science advances*, 10(50), eado5914.

Daniel-Ivad P, et al. (2024) Structure of methyltransferase RedM that forms the dimethylpyrrolinium of the bisindole reductasporine. *The Journal of biological chemistry*, 300(1), 105520.