

Resource Summary Report

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Coot

RRID:SCR_014222

Type: Tool

Proper Citation

Coot (RRID:SCR_014222)

Resource Information

URL: <http://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/>

Proper Citation: Coot (RRID:SCR_014222)

Description: Software for macromolecular model building, model completion and validation, and protein modelling using X-ray data. Coot displays maps and models and allows model manipulations such as idealization, rigid-body fitting, ligand search, Ramachandran plots, non-crystallographic symmetry and more. Source code is available.

Abbreviations: COOT

Synonyms: Crystallographic Object-Oriented Toolkit

Resource Type: model, software toolkit, software application, simulation software, data or information resource, software resource

Defining Citation: [PMID:15572765](#)

Keywords: software toolkit, simulation software, model manipulation, protein modeling, bio.tools

Availability: Available for download, Acknowledgement requested

Resource Name: Coot

Resource ID: SCR_014222

Alternate IDs: biotools:coot

Alternate URLs: <http://strucbio.biologie.uni-konstanz.de/ccp4wiki/index.php/Coot>,
<https://bio.tools/coot>

License: GPL v3, GLP v2, LGPL v3

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260804T043533+0000

Ratings and Alerts

No rating or validation information has been found for Coot.

No alerts have been found for Coot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14789 mentions in open access literature.

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

Parnandi VA, et al. (2026) A small Candida glabrata protein promotes hyphal growth in C. albicans during mixed-species invasive candidiasis. Current biology : CB, 36(1), 1.

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

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

Samani EK, et al. (2026) Structural basis of product recognition by Mycobacterium tuberculosis fatty acid synthase. Protein science : a publication of the Protein Society, 35(1), e70412.

Zhang Y, et al. (2026) Schisandrin B Targets PXR to Enhance Bile Acid Metabolism and Alleviate ANIT-Induced Cholestatic Liver Injury via Dual Pathways. International journal of biological sciences, 22(1), 387.

Allport T, et al. (2026) Uncovering the structural impact of KatG Ser315 mutations in Mycobacterium tuberculosis via cryo-EM. Protein science : a publication of the Protein Society, 35(1), e70409.

Schütt I, et al. (2026) Inhibitors of GapN-dependent NADPH supply as potential lead compounds for novel therapeutics against Streptococcus pyogenes. Virulence, 17(1), 2609393.

Ali-Ahmad A, et al. (2026) Structure and dynamics of 2x(CENP-A/H4)2 octasome reveal a possible intermediate in centromeric chromatin. Life science alliance, 9(3).

Chen S, et al. (2026) Human FcRL5 is an Fc receptor that simultaneously engages two IgGs. Science advances, 12(1), eaeb8865.

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

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.

Abdelaal MR, et al. (2026) The antigen-presenting molecule MR1 binds host-generated riboflavin catabolites. *The Journal of experimental medicine*, 223(2).

Garcia V, et al. (2026) Design and characterization of calprotectin tetramerization variants for probing the role of oligomerization in receptor activation. *Protein science : a publication of the Protein Society*, 35(1), e70399.

Ueda Y, et al. (2026) Substrate recognition mechanisms of γ -glutamate oxidase from *Streptomyces* sp. and its conversion to γ -tyrosine oxidase. *Protein science : a publication of the Protein Society*, 35(1), e70432.

Stolz M, et al. (2026) Architectural principles of transporter-chaperone coupling within the native MHC I peptide-loading complex. *Science advances*, 12(1), eaea7735.

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.

Lee E, et al. (2026) *Streptococcus pneumoniae* HtrA is a dynamic and monomeric virulence factor capable of forming larger oligomeric complexes. *Protein science : a publication of the Protein Society*, 35(1), e70411.

Bista S, et al. (2026) Targeting of interaction between BB0323-BB0238 informs new paradigms in Lyme disease therapeutics. *PLoS pathogens*, 22(1), e1013805.

Lyu Y, et al. (2026) An open axial channel of the AAA ClpXP protease enhances degradation of specific classes of protein substrates. *Protein science : a publication of the Protein Society*, 35(1), e70372.

Penning S, et al. (2026) Structural and functional specialization of *Bordetella pertussis* DsbA for pertussis toxin folding. *Protein science : a publication of the Protein Society*, 35(1), e70421.