

Resource Summary Report

Generated by NIF on Apr 30, 2025

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

Defining Citation: [PMID:15572765](#)

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

Funding:

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: 20250430T055924+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 13250 mentions in open access literature.

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

Bal?kç? E, et al. (2025) Structure of the Nipah virus polymerase complex. *The EMBO journal*, 44(2), 563.

Feng Z, et al. (2025) Mechanism of activation of contact-dependent growth inhibition tRNase toxin by the amino acid biogenesis factor CysK in the bacterial competition system. *Nucleic acids research*, 53(1).

Górniak I, et al. (2025) Structural insights into translocation and tailored synthesis of hyaluronan. *Nature structural & molecular biology*, 32(1), 161.

Petrychenko V, et al. (2025) Structural basis for translational control by the human 48S initiation complex. *Nature structural & molecular biology*, 32(1), 62.

Tian Y, et al. (2025) Structural insight into Okazaki fragment maturation mediated by PCNA-bound FEN1 and RNaseH2. *The EMBO journal*, 44(2), 484.

Markusson S, et al. (2025) Nanobodies against the myelin enzyme CNPase as tools for structural and functional studies. *Journal of neurochemistry*, 169(1), e16274.

Wiechert F, et al. (2025) Visualizing the modification landscape of the human 60S ribosomal subunit at close to atomic resolution. *Nucleic acids research*, 53(1).

Hoque M, et al. (2025) Structural characterization of two ?? TCR/CD3 complexes. *Nature communications*, 16(1), 318.

Jiao M, et al. (2025) Molybdate uptake interplay with ROS tolerance modulates bacterial pathogenesis. *Science advances*, 11(3), eadq9686.

Li HZ, et al. (2025) Transport and inhibition of the sphingosine-1-phosphate exporter SPNS2. *Nature communications*, 16(1), 721.

Awad W, et al. (2025) Cigarette smoke components modulate the MR1-MAIT axis. *The Journal of experimental medicine*, 222(2).

Trasviña-Arenas CH, et al. (2025) Crystal structure of MutYX: A novel clusterless adenine DNA glycosylase with a distinct C-terminal domain and 8-Oxoguanine recognition sphere. *bioRxiv : the preprint server for biology*.

Malik D, et al. (2025) Mechanisms of chromatin remodeling by an Snf2-type ATPase. *bioRxiv : the preprint server for biology*.

Kaley NE, et al. (2025) Bioisosteric replacement of pyridoxal-5'-phosphate to pyridoxal-5'-tetrazole targeting *Bacillus subtilis* GabR. *Protein science : a publication of the Protein Society*, 34(1), e70014.

Czyzyk D, et al. (2025) Structural insights into isoform-specific RAS-PI3K? interactions and the role of RAS in PI3K? activation. *Nature communications*, 16(1), 525.

Linares R, et al. (2025) About bacteriophage tail terminator and tail completion proteins: structure of the proximal extremity of siphophage T5 tail. *Journal of virology*, 99(1), e0137624.

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.

Yan H, et al. (2025) The characterization and structural basis of a human broadly binding antibody to HBV core protein. *Journal of virology*, 99(1), e0169424.

O'Brien JH, et al. (2025) Cryo-EM Structure of Recombinantly Expressed hUGDH Unveils a Hidden, Alternative Allosteric Inhibitor. *Biochemistry*, 64(1), 92.

Choi SH, et al. (2025) Crystal structure of ?-carbonic anhydrase from the polyextremophilic bacterium *Aeribacillus pallidus*. *Molecules and cells*, 48(1), 100165.