

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

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

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: 20260808T190029+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 15682 mentions in open access literature.

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

Deng T, et al. (2026) Structures of ϕ -like phage A8 tail tip bound to OmpC provide insight into receptor recognition. Structure (London, England : 1993), 34(5), 790.

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.

Xue L, et al. (2026) Differential inhibition of Morbillivirus and Henipavirus polymerases by ERDRP-0519 and structure-guided inhibitor optimization. Cell, 189(13), 4094.

Bader DLV, et al. (2026) Structural and immunogenetic signatures guide CD4-mimetic HIV vaccine development. Cell reports, 45(4), 117180.

Deng M, et al. (2026) Structure of the IgY-FcRY complex and its comparison with IgG-FcRn. Structure (London, England : 1993), 34(6), 893.

Peirano E, et al. (2026) Trio analysis in dystonia identifies de novo KLC1 variants in a kinesinopathy with distinct motor and neurodevelopmental features. EBioMedicine, 129, 106358.

Li D, et al. (2026) Cryo-EM structure of soluble VPS13C suggests its regulation by a conformational switch and by calmodulin. Molecular cell, 86(14), 2843.

Yan L, et al. (2026) The Erlin1/2 complex is a dynamic scaffold for membrane microdomain assembly on the endoplasmic reticulum. Molecular cell, 86(7), 1362.

Niu B, et al. (2026) Oligomerization-Dependent Regulation of LrhA Controls Bacterial Flagellar Biosynthesis. Journal of molecular biology, 438(7), 169682.

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*.

Wilcox XE, et al. (2026) Structural repertoire of HCV broadly neutralizing antibodies targeting the E2 front layer supersite. *Structure (London, England : 1993)*, 34(4), 572.

Cervantes Rincón T, et al. (2026) Analysis of West Nile disease convalescents identifies human monoclonal antibodies protective against West Nile and related orthoflaviviruses. *Immunity*, 59(7), 2015.

Yang K, et al. (2026) Double-ring assembly of mpox virus I3L reveals an unconventional mechanism for ssDNA engagement. *Cell reports*, 45(7), 117659.

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).

Soma T, et al. (2026) Structure and engineering of the large serine recombinase Bxb1 for gene integration. *Molecular cell*, 86(12), 2247.

Perry TN, et al. (2026) Structural basis of Cas8-independent Cas3 recruitment in Type I-F2 CRISPR-Cas. *Nucleic acids research*, 54(5).

Xie X, et al. (2026) Nucleosome spacing regulates linker methylation by DNMT3A2/3B3. *Molecular cell*, 86(5), 834.

Kurihara N, et al. (2026) Molecular mechanism of MDA5 nucleation and filament formation by LGP2. *Molecular cell*, 86(4), 707.