

Resource Summary Report

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CCP4

RRID:SCR_007255

Type: Tool

Proper Citation

CCP4 (RRID:SCR_007255)

Resource Information

URL: <http://www.ccp4.ac.uk/>

Proper Citation: CCP4 (RRID:SCR_007255)

Description: Portal for Macromolecular X-Ray Crystallography to produce and support an integrated suite of programs that allows researchers to determine macromolecular structures by X-ray crystallography, and other biophysical techniques. Used in the education and training of scientists in experimental structural biology for determination and analysis of protein structure.

Abbreviations: CCP4

Synonyms: The Collaborative Computational Project Number 4 in Protein Crystallography, Collaborative Computational Project Number 4

Resource Type: data analysis software, data or information resource, data processing software, portal, service resource, simulation software, software application, software resource

Keywords: macromolecular, x-ray, crystallography, biophysical, technique, structural, biology, analysis, protein, Research Complex at Harwell, computational, collaborative, project

Funding: Science and Technology Facilities Council

Availability: Free, Available for download, Freely available, Tutorial available

Resource Name: CCP4

Resource ID: SCR_007255

Alternate IDs: SCR_016709, nif-0000-30238

Record Creation Time: 20220129T080240+0000

Ratings and Alerts

No rating or validation information has been found for CCP4.

No alerts have been found for CCP4.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4896 mentions in open access literature.

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

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

Besaw JE, et al. (2026) Structural characterization of the Cu(II)-NTA spin label on α -helices by X-ray crystallography and electron paramagnetic resonance. Structure (London, England : 1993), 34(4), 645.

Hijazi S, et al. (2026) Two birds with one stone: An antibiotic hit blocking Staphylococcus aureus heme uptake with serendipitous hemoglobin left-shifting activity. iScience, 29(5), 115625.

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.

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

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

Shen R, et al. (2026) EEPD1 evolved a unique DNA clamping dimer protecting reversed replication forks. Nucleic acids research, 54(5).

De'Ath C, et al. (2026) YdbL directly modulates YdbH-YnbE bridge formation to maintain Escherichia coli outer membrane homeostasis. bioRxiv : the preprint server for biology.

Gedeon A, et al. (2026) Structural basis of Mycobacterium Fluoroquinolone Resistance Protein D (MfpD), a versatile pathogeny protein from the mfp conservon of Mycobacterium tuberculosis. bioRxiv : the preprint server for biology.

Troisi R, et al. (2026) The Binding of 3-O-Methylfluorescein Phosphate to the Catalytic Domain of the Human CDC25B Phosphatase: A Structural Investigation. Chembiochem :

a European journal of chemical biology, 27(7), e202600010.

Chen HA, et al. (2026) Structure and catalytic activity of the SAM-utilizing ribozyme SAMURI. *Nature chemical biology*, 22(6), 938.

Cooper A, et al. (2026) The Crystal Structure of Human Transport and Golgi Organization 2 Homolog (TANGO2) Protein Reveals an $\alpha\beta\gamma\delta$ -Fold Arrangement. *Proteins*, 94(2), 515.

Ueda Y, et al. (2026) Structure of chloramphenicol-bound MexB reveals residues in the distal binding pocket that are critical for substrate recognition. *Journal of biochemistry*, 179(6), 403.

Zhang R, et al. (2026) Covalent modification of a glutamic acid inspired by HaloTag technology. *Nature communications*, 17(1), 1257.

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.

Nomura A, et al. (2026) Crystal structure of human INPP5K with an allosteric inhibitor reveals the structural basis for species specific potency. *Scientific reports*, 16(1).

Huang EY, et al. (2026) Structural basis of allosteric activation of *Mycobacterium tuberculosis* isocitrate lyase 2. *Communications biology*, 9(1).

Williams HM, et al. (2026) Phosphorylation of inner core heptose is a major determinant of bacterial surface lipopolysaccharide recognition by the innate immune protein hSP-D. *The Journal of biological chemistry*, 302(4), 111307.

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.

Nath BK, et al. (2026) Structural insights into the nuclear import of ovine gammaherpesvirus 2 ORF73 LANA homologue. *The Journal of general virology*, 107(4).