

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 [dkNET](#) .

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.

Cooper A, et al. (2026) The Crystal Structure of Human Transport and Golgi Organization 2 Homolog (TANGO2) Protein Reveals an α -Fold Arrangement. Proteins, 94(2), 515.

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

Hauser D, et al. (2026) Rieske Iron-Sulfur Cluster Proteins From an Anaerobic Ammonium Oxidizer Suggest Unusual Energetics in Their Parent Rieske/Cytochrome b Complexes. Proteins, 94(4), 905.

Hoque NJ, et al. (2026) Cooperative ligand binding in a bacterial heme-based oxygen sensor. The Journal of biological chemistry, 302(2), 111025.

Wang H-Q, et al. (2026) Structural and functional insights into Uly1040, an ulvan lyase from polysaccharide lyase family 40. Applied and environmental microbiology, 92(2),

e0210125.

Frederick A, et al. (2026) Altering chemotaxis as a strategy to enhance the foraging range of motility-restricted bacteria. *Communications biology*, 9(1), 197.

Pinheiro F, et al. (2026) Mass spectrometry footprinting reveals how kinetic stabilizers counteract transthyretin dynamics altered by pathogenic mutations. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519908122.

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.

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

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.

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.

Parker KL, et al. (2026) Crystal structure of *Schistosoma mansoni* cathepsin D1 in complex with a nanobody reveals the conformation of the propeptide-bound state. *Acta crystallographica. Section D, Structural biology*, 82(Pt 2), 140.

Ma C, et al. (2026) Zinc-finger transcription factor Fzf1 binds to its target DNA in a non-canonical manner. *Nucleic acids research*, 54(3).

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).

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.