

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/>

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

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 4740 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

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

Le Bas A, et al. (2025) Structure of WzxE the lipid III flippase for Enterobacterial Common Antigen polysaccharide. Open biology, 15(1), 240310.

Hope I, et al. (2025) Crystallographic fragment screening of CDK2-cyclin A: FragLites map sites of protein-protein interaction. Structure (London, England : 1993).

Benjamin JS, et al. (2025) 23ME-01473, an Fc Effector-Enhanced Anti-ULBP6/2/5 Antibody, Restores NK Cell-Mediated Antitumor Immunity through NKG2D and FcγRIIIa Activation. Cancer research communications, 5(3), 476.

Hou P, et al. (2025) Cryo-EM structure of cyanopodophage Pan3 reveals a modular tail architecture for host recognition. Structure (London, England : 1993).

Mockler NM, et al. (2025) N-Terminal Protein Binding and Disorder-to-Order Transition by a Synthetic Receptor. Biochemistry, 64(5), 1092.

Zhang L, et al. (2025) Antagonist Targeting the Species-Specific Fatty Acid Dehydrogenase/Isomerase FabX for Anti-H. pylori Infection. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2414844.

Fischer K, et al. (2025) Rapid discovery of monoclonal antibodies by microfluidics-enabled FACS of single pathogen-specific antibody-secreting cells. Nature biotechnology, 43(6), 960.

Asahi K, et al. (2025) Cryo-EM structure of the bacterial intramembrane metalloprotease RseP in the substrate-bound state. Science advances, 11(9), eadu0925.

Figueras-Novoa C, et al. (2025) Caspase cleavage of influenza A virus M2 disrupts M2-LC3 interaction and regulates virion production. *EMBO reports*, 26(7), 1768.

Wang J, et al. (2025) Cryo-EM meets crystallography: A model-independent view of the heteronuclear Mn₄Ca cluster structure of photosystem II. *Proceedings of the National Academy of Sciences of the United States of America*, 122(10), e2423012122.

Nesa ML, et al. (2025) Crystal structure of ferric recombinant horseradish peroxidase. *Journal of biological inorganic chemistry : JBIC : a publication of the Society of Biological Inorganic Chemistry*, 30(3), 221.

Pramono H, et al. (2025) Crystal structure of a novel heterooligomeric aminotransferase from *Serratia* sp. ATCC 39006 provides insights into function. *FEBS letters*, 599(1), 74.

Schwartz TA, et al. (2025) Molecular Basis of Interchain Disulfide Bond Formation in BMP-9 and BMP-10. *Journal of molecular biology*, 437(4), 168935.

Ujiie K, et al. (2025) Specific recognition mechanism of an antibody to sulfated tyrosine and its potential use in biological research. *The Journal of biological chemistry*, 301(2), 108176.

Cheung YWS, et al. (2025) Structure of the human autophagy factor EPG5 and the molecular basis of its conserved mode of interaction with Atg8-family proteins. *Autophagy*, 21(6), 1173.

Polidori N, et al. (2025) Structure, Oligomerization, and Thermal Stability of a Recently Discovered Old Yellow Enzyme. *Proteins*, 93(6), 1181.

Zak KM, et al. (2025) Discovery of Small Molecules that Bind to Son of Sevenless 2 (SOS2). *Journal of medicinal chemistry*, 68(3), 2680.

Wei K, et al. (2025) Humanized Candida and NanoBiT Assays Expedite Discovery of Bdf1 Bromodomain Inhibitors With Antifungal Potential. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(10), e2404260.