

Resource Summary Report

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Phaser

RRID:SCR_014219

Type: Tool

Proper Citation

Phaser (RRID:SCR_014219)

Resource Information

URL: <https://www.phenix-online.org/documentation/reference/phaser.html>

Proper Citation: Phaser (RRID:SCR_014219)

Description: Crystallographic software which solves structures using algorithms and automated rapid search calculations to perform molecular replacement and experimental phasing methods.

Resource Type: image analysis software, image reconstruction software, data acquisition software, software application, software resource, data processing software

Defining Citation: [PMID:19461840](#)

Keywords: crystallographic software, molecular replacement, experimental phasing method, data acquisition software, image analysis software, image reconstruction software

Availability: Available through Phenix, Available through CCP4, Acknowledgement requested

Resource Name: Phaser

Resource ID: SCR_014219

Alternate URLs:

http://www.phaser.cimr.cam.ac.uk/index.php/Phaser_Crystallographic_Software

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260801T190509+0000

Ratings and Alerts

No rating or validation information has been found for Phaser.

No alerts have been found for Phaser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2572 mentions in open access literature.

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

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

Yudenko A, et al. (2025) Structural basis of signaling complex inhibition by IL-6 domain-swapped dimers. Structure (London, England : 1993), 33(1), 171.

Kaplan E, et al. (2025) APH Inhibitors that Reverse Aminoglycoside Resistance in Enterococcus casseliflavus. ChemMedChem, 20(8), e202400842.

Walla B, et al. (2025) Application of a Rational Crystal Contact Engineering Strategy on a Poly(ethylene terephthalate)-Degrading Cutinase. Bioengineering (Basel, Switzerland), 12(6).

Choi SB, et al. (2025) Structural Insights into the ADCC Mechanism and Resistance of Mogamulizumab, a First-in-Class Anti-CCR4 Therapy for Cutaneous T Cell Lymphoma. International journal of molecular sciences, 26(12).

Kuge M, et al. (2025) Structural Insights into Broad-Range Polyphosphate Kinase 2-II Enzymes Applicable for Pyrimidine Nucleoside Diphosphate Synthesis. Chembiochem : a European journal of chemical biology, 26(5), e202400970.

Youle RL, et al. (2025) Structural and functional characterization of the extended-diKH domain from the antiviral endoribonuclease KHNYN. The Journal of biological chemistry, 301(4), 108336.

Li Y, et al. (2025) Structural insights into calcium-dependent CIB2-TMC1 interaction in hair cell mechanotransduction. Communications biology, 8(1), 306.

Wang DP, et al. (2025) Structural insights into polymerase-catalyzed FAD capping of hepatitis C virus RNA. Nature communications, 16(1), 7298.

Anraku Y, et al. (2025) Structural and virological identification of neutralizing antibody footprint provides insights into therapeutic antibody design against SARS-CoV-2 variants. Communications biology, 8(1), 483.

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.

Ahmed SF, et al. (2025) The structural basis of substrate selectivity of the acinetobactin biosynthetic adenylation domain, BasE. *The Journal of biological chemistry*, 301(4), 108413.

Hoffpauir ZA, et al. (2025) Identification of the phosphatase essential for riboflavin biosynthesis in *Aquifex aeolicus*. *The Journal of biological chemistry*, 301(5), 108443.

Ferraro G, et al. (2025) Cytotoxicity and Binding to DNA, Lysozyme, Ribonuclease A, and Human Serum Albumin of the Diiodido Analog of Picoplatin. *Inorganic chemistry*, 64(18), 8895.

Esakova OA, et al. (2025) Structural basis for catalysis by human lipoyl synthase. *Nature communications*, 16(1), 6355.

Yin H, et al. (2025) Multi-dimensional annotation of porcine variants using genomic and epigenomic features in pigs. *BMC biology*, 23(1), 188.

Rolfe N, et al. (2025) Sal is a proteobacterial bile acid aldolase that repurposes key thiolase catalytic residues for retroaldol cleavage of C5 steroid side chains. *The Journal of biological chemistry*, 301(8), 110439.

Venskutonyt? R, et al. (2025) MHC I of the Great Reed Warbler Promotes a Flat Peptide Binding Mode. *Immunology*, 176(4), 508.

Welland JWJ, et al. (2025) Conformational dynamics and membrane insertion mechanism of B4GALNT1 in ganglioside synthesis. *Nature communications*, 16(1), 5442.

Peng YH, et al. (2025) Structure-Based Design of Potent and Selective MerTK Inhibitors by Modulating the Conformation of ?C Helix. *Journal of medicinal chemistry*, 68(11), 10877.