

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 reconstruction software, data processing software, software application, image analysis software, data acquisition software, software resource

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: 20260810T040622+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 2664 mentions in open access literature.

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

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.

Goel R, et al. (2026) A versatile nanobody platform for live and super-resolution imaging of synaptic vesicle dynamics and plasticity in rodent and human neurons. *Journal of nanobiotechnology*, 24(1).

Willsey GG, et al. (2026) Broadly conserved protective epitopes on the lyme disease vaccine antigen, OspA. *PLoS pathogens*, 22(4), e1013740.

Shibata S, et al. (2026) Structural analysis of a motor with increased mechanical output reveals new transitions in kinesin microtubule motility. *Scientific reports*, 16(1), 487.

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

Aschenwald S, et al. (2026) Dual function of ERH in primary miRNA biogenesis. *Nucleic acids research*, 54(12).

Murphy NP, et al. (2026) Engineering and Application of a Thermostable MHETase for PET Depolymerization. *ACS sustainable chemistry & engineering*, 14(24), 10981.

Jang H, et al. (2026) Structural Insights into MltC from *Acinetobacter baumannii*: Conservation of the Catalytic Residue and Flexibility in Substrate Recognition. *Journal of microbiology and biotechnology*, 36, e2511019.

Gérard SF, et al. (2026) Structural basis for carbohydrate recognition by the Gal/GalNAc lectin of *Entamoeba histolytica* involved in host cell adhesion. *PLoS pathogens*, 22(2), e1013948.

Chen SY, et al. (2026) Binding of 14-3-3 stabilises recombinant AMPK γ 2-containing complexes. *The Biochemical journal*, 483(5), 621.

Capra N, et al. (2026) Structural and oligomeric characterization of substrate- and product-selective nylon hydrolases. *bioRxiv : the preprint server for biology*.

Wang W, et al. (2026) The conserved human astrovirus-receptor interface reveals a targetable vulnerability for antiviral development. *Nature communications*, 17(1).

Vacilotto MM, et al. (2026) Enzymatic Production of Prebiotic Xylooligosaccharides Using a *Bacillus pumilus* GH30_8 Glucuronoxylanase: Structural Basis of Glucuronoxylan Recognition and Hydrolysis. *Journal of agricultural and food chemistry*, 74(6), 5417.

Sundberg B, et al. (2026) Bidirectional allosteric ligand regulation in a central glycolytic enzyme. *bioRxiv : the preprint server for biology*.

San Martin F, et al. (2026) Core-sheath coupling controls flagellar curvature and motility in *Leptospira*. *bioRxiv : the preprint server for biology*.

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.

Pietrzyk-Brzezinska AJ, et al. (2026) Molecular basis of antibiotic sensing by the TetR family regulator CecR - a structural perspective. *The FEBS journal*, 293(6), 1801.

Liu L, et al. (2026) Structural Analysis and Inhibitor Modeling of Bacterioferritin From *Brucella abortus*. *Proteins*, 94(6), 1170.

Ye F, et al. (2026) Dynamic control of bacterial antiphage defense through the CdnG-Cap5 cyclic oligonucleotide-based antiphage pathway in *Vibrio cholerae*. *The Journal of biological chemistry*, 302(1), 111021.

Wu F, et al. (2026) Development of VP30-targeted nanoparticles using DPS4 fusion peptides for the inhibition of Ebola virus. *Journal of nanobiotechnology*, 24(1).