Resource Summary Report

Generated by NIF on Apr 21, 2025

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

Defining Citation: PMID:19461840

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

Funding:

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: 20250421T053953+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 2398 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

Loyau J, et al. (2025) Biparatopic binding of ISB 1442 to CD38 in trans enables increased cell antibody density and increased avidity. mAbs, 17(1), 2457471.

Huang XX, et al. (2025) Effects of RAR? ligand binding domain mutations on breast fibroepithelial tumor function and signaling. NPJ breast cancer, 11(1), 1.

Ríos Carrasco M, et al. (2025) The Q226L mutation can convert a highly pathogenic H5 2.3.4.4e virus to bind human-type receptors. bioRxiv : the preprint server for biology.

Markusson S, et al. (2025) Nanobodies against the myelin enzyme CNPase as tools for structural and functional studies. Journal of neurochemistry, 169(1), e16274.

Jiao M, et al. (2025) Molybdate uptake interplay with ROS tolerance modulates bacterial pathogenesis. Science advances, 11(3), eadq9686.

Czyzyk D, et al. (2025) Structural insights into isoform-specific RAS-PI3K? interactions and the role of RAS in PI3K? activation. Nature communications, 16(1), 525.

Tandhavanant S, et al. (2025) Genetic variation of hemolysin co-regulated protein 1 affects the immunogenicity and pathogenicity of Burkholderia pseudomallei. PLoS neglected tropical diseases, 19(1), e0012758.

Yazaki S, et al. (2025) Crystal Structures of Antigen-Binding Fragment of Anti-Osteocalcin Antibody KTM219. International journal of molecular sciences, 26(2).

Lotz R, et al. (2025) Alternative splicing in the DBD linker region of p63 modulates binding to DNA and iASPP in vitro. Cell death & disease, 16(1), 4.

Litschko C, et al. (2025) Transition transferases prime bacterial capsule polymerization. Nature chemical biology, 21(1), 120.

Wang X, et al. (2025) Characterizing Y224 conformational flexibility in FtmOx1-catalysis using 19F NMR spectroscopy. Catalysis science & technology, 15(2), 386.

Miranda-Zaragoza B, et al. (2025) Structure-Function Relationship of the ?-Hairpin of Thermus thermophilus HB27 Laccase. International journal of molecular sciences, 26(2).

Ding Q, et al. (2024) The evolutionary origin of naturally occurring intermolecular Diels-Alderases from Morus alba. Nature communications, 15(1), 2492.

Ma Y, et al. (2024) Molecular mechanism of human ISG20L2 for the ITS1 cleavage in the processing of 18S precursor ribosomal RNA. Nucleic acids research, 52(4), 1878.

Hadži S, et al. (2024) Fuzzy recognition by the prokaryotic transcription factor HigA2 from Vibrio cholerae. Nature communications, 15(1), 3105.

Yan Y, et al. (2024) Substrate recruitment via eIF2? enhances catalytic efficiency of a holophosphatase that terminates the integrated stress response. Proceedings of the National Academy of Sciences of the United States of America, 121(14), e2320013121.

Shen J, et al. (2024) Chloroflexus aurantiacus acetyl-CoA carboxylase evolves fused biotin carboxylase and biotin carboxyl carrier protein to complete carboxylation activity. mBio, 15(5), e0341423.

Nemchinova M, et al. (2024) Exploring the Ligand Binding and Conformational Dynamics of the Substrate-Binding Domain 1 of the ABC Transporter GlnPQ. The journal of physical chemistry. B, 128(32), 7822.

Kind L, et al. (2024) Molecular mechanism of HNF-1A-mediated HNF4A gene regulation and promoter-driven HNF4A-MODY diabetes. JCI insight, 9(11).