Resource Summary Report

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Phenix

RRID:SCR_014224
Type: Tool

Proper Citation

Phenix (RRID:SCR_014224)

Resource Information

URL: https://www.phenix-online.org/

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Description: A Python-based software suite for the automated determination of molecular structures using X-ray crystallography and other methods. Phenix includes programs for assessing data quality, experimental phasing, molecular replacement, model building, structure refinement, and validation. It also includes tools for reflection data and creating maps and models. Phenix can also be used for neutron crystallography. Tutorials and examples are available in the documentation tab.

Synonyms: Python-based Hierarchical ENvironment for Integrated Xtallography

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

Keywords: automation, molecular structure, xray crystallography, neutron crystallography, image reconstruction software

Funding: NIGMS

Availability: Available for download, Free for nonprofit work, Acknowledgement requested, For profit groups may access PHENIX through a Consortium agreement

Resource Name: Phenix

Resource ID: SCR_014224

Alternate URLs: https://www.phenix-online.org/documentation/

Record Creation Time: 20220129T080319+0000

Record Last Update: 20250402T061142+0000

Ratings and Alerts

No rating or validation information has been found for Phenix.

No alerts have been found for Phenix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9373 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

Tian Y, et al. (2025) Structural insight into Okazaki fragment maturation mediated by PCNA-bound FEN1 and RNaseH2. The EMBO journal, 44(2), 484.

Park SK, et al. (2025) Structural basis for the evolution of a domesticated group II intron-like reverse transcriptase to function in host cell DNA repair. bioRxiv : the preprint server for biology.

Jabbari K, et al. (2025) The Structural, Biophysical, and Antigenic Characterization of the Goose Parvovirus Capsid. Microorganisms, 13(1).

Jaiswal R, et al. (2025) Cryo-EM structure of AAV2 Rep68 bound to integration site AAVS1: insights into the mechanism of DNA melting. Nucleic acids research, 53(3).

Petrychenko V, et al. (2025) Structural basis for translational control by the human 48S initiation complex. Nature structural & molecular biology, 32(1), 62.

Yan H, et al. (2025) The characterization and structural basis of a human broadly binding antibody to HBV core protein. Journal of virology, 99(1), e0169424.

Górniak I, et al. (2025) Structural insights into translocation and tailored synthesis of hyaluronan. Nature structural & molecular biology, 32(1), 161.

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

Wiechert F, et al. (2025) Visualizing the modification landscape of the human 60S ribosomal subunit at close to atomic resolution. Nucleic acids research, 53(1).

Awad W, et al. (2025) Cigarette smoke components modulate the MR1-MAIT axis. The Journal of experimental medicine, 222(2).

Shi H, et al. (2025) Human P2X4 receptor gating is modulated by a stable cytoplasmic cap and a unique allosteric pocket. Science advances, 11(3), eadr3315.

Shikha S, et al. (2025) Numerous rRNA molecules form the apicomplexan mitoribosome via repurposed protein and RNA elements. Nature communications, 16(1), 817.

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

Yue Y, et al. (2025) Structural insights into the regulation of monomeric and dimeric apelin receptor. Nature communications, 16(1), 310.

Shah SZ, et al. (2025) Structural insights into distinct mechanisms of RNA polymerase II and III recruitment to snRNA promoters. Nature communications, 16(1), 141.

Hoque M, et al. (2025) Structural characterization of two ?? TCR/CD3 complexes. Nature communications, 16(1), 318.

Rhein-Knudsen N, et al. (2025) Identification and Characterization of a New Thermophilic ?-Carrageenan Sulfatase. Journal of agricultural and food chemistry, 73(3), 2044.

Trasviña-Arenas CH, et al. (2025) Crystal structure of MutYX: A novel clusterless adenine DNA glycosylase with a distinct C-terminal domain and 8-Oxoguanine recognition sphere. bioRxiv : the preprint server for biology.

Malik D, et al. (2025) Mechanisms of chromatin remodeling by an Snf2-type ATPase. bioRxiv : the preprint server for biology.