Resource Summary Report

Generated by NIF on Apr 20, 2025

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

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: 20250420T014709+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 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.

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

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

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

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).

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

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

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

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.

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.

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

Linares R, et al. (2025) About bacteriophage tail terminator and tail completion proteins: structure of the proximal extremity of siphophage T5 tail. Journal of virology, 99(1), e0137624.

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

Ocampo RF, et al. (2025) DNA targeting by compact Cas9d and its resurrected ancestor. Nature communications, 16(1), 457.

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.

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.

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.