

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: data processing software, image analysis software, image reconstruction software, software application, 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/>

License: <https://www.phenix-online.org/license/LICENSE>

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260905T132744+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 11312 mentions in open access literature.

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

Yan L, et al. (2026) The Erlin1/2 complex is a dynamic scaffold for membrane microdomain assembly on the endoplasmic reticulum. *Molecular cell*, 86(7), 1362.

Medina E, et al. (2026) Structural basis for sialoglycan recognition by the immune inhibitory receptor Siglec-10. *Structure (London, England : 1993)*, 34(5), 768.

Huang J, et al. (2026) Cryo-EM structures of antibodies elicited by germline-targeting HIV MPER epitope scaffolds. *Cell reports*, 45(1), 116818.

Deng T, et al. (2026) Structures of ϕ -like phage A8 tail tip bound to OmpC provide insight into receptor recognition. *Structure (London, England : 1993)*, 34(5), 790.

Xue L, et al. (2026) Differential inhibition of Morbillivirus and Henipavirus polymerases by ERDRP-0519 and structure-guided inhibitor optimization. *Cell*, 189(13), 4094.

Bader DLV, et al. (2026) Structural and immunogenetic signatures guide CD4-mimetic HIV vaccine development. *Cell reports*, 45(4), 117180.

Deng M, et al. (2026) Structure of the IgY-FcRY complex and its comparison with IgG-FcRn. *Structure (London, England : 1993)*, 34(6), 893.

Li D, et al. (2026) Cryo-EM structure of soluble VPS13C suggests its regulation by a conformational switch and by calmodulin. *Molecular cell*, 86(14), 2843.

Lupton CJ, et al. (2026) Structure of the lysosomal KICSTOR-GATOR1-SAMTOR nutrient-sensing supercomplex. *Cell*.

Cervantes Rincón T, et al. (2026) Analysis of West Nile disease convalescents identifies human monoclonal antibodies protective against West Nile and related orthoflaviviruses. *Immunity*, 59(7), 2015.

Yang K, et al. (2026) Double-ring assembly of mpox virus I3L reveals an unconventional mechanism for ssDNA engagement. *Cell reports*, 45(7), 117659.

Orkwis JA, et al. (2026) Helminth proteins recapitulate key structural motifs of MIF to facilitate immunomodulation of host receptors. *iScience*, 29(7), 116513.

Kurihara N, et al. (2026) Molecular mechanism of MDA5 nucleation and filament formation by LGP2. *Molecular cell*, 86(4), 707.

Perry TN, et al. (2026) Structural basis of Cas8-independent Cas3 recruitment in Type I-F2 CRISPR-Cas. *Nucleic acids research*, 54(5).

Soma T, et al. (2026) Structure and engineering of the large serine recombinase Bxb1 for gene integration. *Molecular cell*, 86(12), 2247.

Shih RM, et al. (2026) Impacts of DNA methylation on H2A.Z deposition and nucleosome stability. *eLife*, 15.

Ge X, et al. (2026) A receptor-centered approach identifies Lom as a LamB-bound superinfection exclusion factor in bacteriophage ϕ . *Cell reports*, 45(7), 117691.

Gaizauskaite U, et al. (2026) Structural insights into Cas9-mediated prespacer selection in CRISPR-Cas adaptation. *Molecular cell*, 86(5), 791.

Besaw JE, et al. (2026) Structural characterization of the Cu(II)-NTA spin label on α -helices by X-ray crystallography and electron paramagnetic resonance. *Structure (London, England : 1993)*, 34(4), 645.

Li SH, et al. (2026) Childhood immunological imprinting of cross-subtype antibodies targeting the hemagglutinin head domain of influenza viruses. *Cell host & microbe*, 34(5), 873.