

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

Phenix

RRID:SCR_014224

Type: Tool

Proper Citation

Phenix (RRID:SCR_014224)

Resource Information

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

Proper Citation: Phenix (RRID:SCR_014224)

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 reconstruction software, data processing software, image analysis 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/>

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

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260804T043525+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 10587 mentions in open access literature.

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

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

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

Samani EK, et al. (2026) Structural basis of product recognition by Mycobacterium tuberculosis fatty acid synthase. Protein science : a publication of the Protein Society, 35(1), e70412.

Ali-Ahmad A, et al. (2026) Structure and dynamics of 2x(CENP-A/H4)2 octasome reveal a possible intermediate in centromeric chromatin. Life science alliance, 9(3).

Stehantsev P, et al. (2026) Investigating the mechanism of aluminum resistance conferred by aluminum resistance protein 1. Protein science : a publication of the Protein Society, 35(1), e70405.

Palte RL, et al. (2026) WRN structural flexibility showcased through fragment-based lead discovery of inhibitors. Nature communications, 17(1), 79.

Li X, et al. (2026) Talin-tensin3 interactions regulate fibrillar adhesion formation and tensin3 phase separation. The Journal of cell biology, 225(1).

Abdelaal MR, et al. (2026) The antigen-presenting molecule MR1 binds host-generated riboflavin catabolites. The Journal of experimental medicine, 223(2).

Garcia V, et al. (2026) Design and characterization of calprotectin tetramerization variants for probing the role of oligomerization in receptor activation. Protein science : a publication of the Protein Society, 35(1), e70399.

Ueda Y, et al. (2026) Substrate recognition mechanisms of γ -glutamate oxidase from Streptomyces sp. and its conversion to γ -tyrosine oxidase. Protein science : a publication of the Protein Society, 35(1), e70432.

Stolz M, et al. (2026) Architectural principles of transporter-chaperone coupling within the native MHC I peptide-loading complex. *Science advances*, 12(1), eaea7735.

Yi G, et al. (2026) Covalently constrained 'Di-Gembodies' enable parallel structure solutions by cryo-EM. *Nature chemical biology*, 22(1), 69.

Ma WH, et al. (2026) Targeting PTPN13 with 11-amino-acid peptides of C-terminal APC prevents immune evasion of colorectal cancer. *Cell research*, 36(1), 72.

Lemaire ON, et al. (2026) Carbon-monoxide-driven bioethanol production operates through a tungsten-dependent catalyst. *Nature chemical biology*, 22(1), 28.

Lourenço FM, et al. (2026) Interaction of *Staphylococcus aureus* di-iron Repair of Iron Centers protein with the iron-sulfur cluster assembly SUF system. *Protein science : a publication of the Protein Society*, 35(1), e70406.

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

Zhang M, et al. (2025) Structures of butyrophilin multimers reveal a plier-like mechanism for V α 9V β 2 T cell receptor activation. *Immunity*, 58(7), 1660.

Segura-Covarrubias G, et al. (2025) Structural basis of GluK2 kainate receptor activation by a partial agonist. *Nature structural & molecular biology*, 32(8), 1456.

Xue J, et al. (2025) Structural mechanisms of PIP2 activation and SEA0400 inhibition in human cardiac sodium-calcium exchanger NCX1. *eLife*, 14.

Feng Z, et al. (2025) Structural and functional insights into the evolution of SARS-CoV-2 KP.3.1.1 spike protein. *Cell reports*, 44(7), 115941.