

Resource Summary Report

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Phenix.refine

RRID:SCR_016736

Type: Tool

Proper Citation

Phenix.refine (RRID:SCR_016736)

Resource Information

URL: <https://www.phenix-online.org/documentation/reference/refinement.html>

Proper Citation: Phenix.refine (RRID:SCR_016736)

Description: Software tool for a general purpose crystallographic structure refinement within the PHENIX package. Serves as a critical component in automated model building, final structure refinement, structure validation and deposition to the wwPDB.

Abbreviations: Phenix.refine

Synonyms: Python-based Hierarchical ENvironment for Integrated Xtallography.refine, Phenix.refine, Phenix

Resource Type: software resource, software application, data processing software

Defining Citation: [PMID:22505256](#)

Keywords: crystallographic, structure, refinement, Phenix, model, building, validation

Funding: NIGMS GM063210;
US Department of Energy

Availability: Free, Available for download for non profit, For profit access PHENIX through a Consortium agreement, Tutorial available, Acknowledgement requested

Resource Name: Phenix.refine

Resource ID: SCR_016736

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260731T043003+0000

Ratings and Alerts

No rating or validation information has been found for Phenix.refine.

No alerts have been found for Phenix.refine.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bu W, et al. (2024) Epstein-Barr virus gp42 antibodies reveal sites of vulnerability for receptor binding and fusion to B cells. *Immunity*, 57(3), 559.

McMinimy R, et al. (2024) Reactive oxygen species control protein degradation at the mitochondrial import gate. *Molecular cell*, 84(23), 4612.

Mauxion F, et al. (2023) The human CNOT1-CNOT10-CNOT11 complex forms a structural platform for protein-protein interactions. *Cell reports*, 42(1), 111902.

Yu X, et al. (2023) The evolution and determinants of neutralization of potent head-binding antibodies against Ebola virus. *Cell reports*, 42(11), 113366.

Hattne J, et al. (2023) Electron counting with direct electron detectors in MicroED. *Structure (London, England : 1993)*, 31(12), 1504.

Korenkov M, et al. (2023) Somatic hypermutation introduces bystander mutations that prepare SARS-CoV-2 antibodies for emerging variants. *Immunity*, 56(12), 2803.

Andriianov A, et al. (2023) Phage T3 overcomes the BREX defense through SAM cleavage and inhibition of SAM synthesis by SAM lyase. *Cell reports*, 42(8), 112972.

Inaba K, et al. (2022) Molecular action of larvicidal flavonoids on ecdysteroidogenic glutathione S-transferase Noppera-bo in *Aedes aegypti*. *BMC biology*, 20(1), 43.

Nawarathnage S, et al. (2022) Crystals of TELSAM-target protein fusions that exhibit minimal crystal contacts and lack direct inter-TELSAM contacts. *Open biology*, 12(3), 210271.

Collu G, et al. (2022) Chimeric single α -helical domains as rigid fusion protein connections for protein nanotechnology and structural biology. *Structure (London, England : 1993)*, 30(1), 95.

Nichols AL, et al. (2022) Fluorescence activation mechanism and imaging of drug permeation with new sensors for smoking-cessation ligands. *eLife*, 11.

Milligan JC, et al. (2022) Asymmetric and non-stoichiometric glycoprotein recognition by two distinct antibodies results in broad protection against ebolaviruses. *Cell*, 185(6), 995.

Strong LM, et al. (2021) Structural basis for membrane recruitment of ATG16L1 by WIPI2 in autophagy. *eLife*, 10.

Seydoux E, et al. (2021) Development of a VRC01-class germline targeting immunogen derived from anti-idiotypic antibodies. *Cell reports*, 35(5), 109084.

Patchett S, et al. (2021) A molecular sensor determines the ubiquitin substrate specificity of SARS-CoV-2 papain-like protease. *Cell reports*, 36(13), 109754.

Orth B, et al. (2021) Identification of an atypical interaction site in the BTB domain of the MYC-interacting zinc-finger protein 1. *Structure (London, England : 1993)*, 29(11), 1230.

Landeras-Bueno S, et al. (2021) Cellular mRNA triggers structural transformation of Ebola virus matrix protein VP40 to its essential regulatory form. *Cell reports*, 35(2), 108986.

Guo X, et al. (2021) Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. *eLife*, 10.

Gori I, et al. (2021) Mutations in SKI in Shprintzen-Goldberg syndrome lead to attenuated TGF- β responses through SKI stabilization. *eLife*, 10.

Didychuk AL, et al. (2021) A pentameric protein ring with novel architecture is required for herpesviral packaging. *eLife*, 10.