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: 20250513T061812+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 38 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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.

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

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

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.

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

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.

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.

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.

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.

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

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-? 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.

Huang B, et al. (2021) Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. Structure (London, England : 1993), 29(8), 804.