Resource Summary Report

Generated by dkNET on Apr 17, 2025

UCLA Diffraction Anisotropy Server

RRID:SCR_018722
Type: Tool

Proper Citation

UCLA Diffraction Anisotropy Server (RRID:SCR_018722)

Resource Information

URL: http://services.mbi.ucla.edu/anisoscale/

Proper Citation: UCLA Diffraction Anisotropy Server (RRID:SCR_018722)

Description: Web server to indicate severity of anisotropy in data set. Degree of anisotropy is indicated by anisotropic delta B statistic.

Resource Type: web service, data access protocol, analysis service resource, production service resource, software resource, service resource

Keywords: Anisotropy, anisotropy severity, anisotropy severity indication, anisotropy degree, anisotropic delta B statistic

Funding:

Availability: Free, Freely available

Resource Name: UCLA Diffraction Anisotropy Server

Resource ID: SCR_018722

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250417T065636+0000

Ratings and Alerts

No rating or validation information has been found for UCLA Diffraction Anisotropy Server.

No alerts have been found for UCLA Diffraction Anisotropy Server.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Eilers G, et al. (2023) Structure of a HIV-1 IN-Allosteric inhibitor complex at 2.93 Å resolution: Routes to inhibitor optimization. PLoS pathogens, 19(3), e1011097.

Fruergaard MU, et al. (2022) The Na+,K+-ATPase in complex with beryllium fluoride mimics an ATPase phosphorylated state. The Journal of biological chemistry, 298(9), 102317.

Young VC, et al. (2022) Structure and function of H+/K+ pump mutants reveal Na+/K+ pump mechanisms. Nature communications, 13(1), 5270.

Ludzia P, et al. (2021) Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. Structure (London, England : 1993), 29(9), 1014.

Abe K, et al. (2021) Gastric proton pump with two occluded K+ engineered with sodium pump-mimetic mutations. Nature communications, 12(1), 5709.

Jiang X, et al. (2020) Structural Basis for Blocking Sugar Uptake into the Malaria Parasite Plasmodium falciparum. Cell, 183(1), 258.

Nakanishi H, et al. (2020) Crystal structure of a human plasma membrane phospholipid flippase. The Journal of biological chemistry, 295(30), 10180.