

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

## UCLA Diffraction Anisotropy Server

RRID:SCR\_018722

Type: Tool

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### Proper Citation

UCLA Diffraction Anisotropy Server (RRID:SCR\_018722)

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### 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:** analysis service resource, data access protocol, production service resource, service resource, software resource, web service

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

**Availability:** Free, Freely available

**Resource Name:** UCLA Diffraction Anisotropy Server

**Resource ID:** SCR\_018722

**Record Creation Time:** 20220129T080341+0000

**Record Last Update:** 20260905T133010+0000

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### 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.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in Mycobacterium tuberculosis constitutively generates subpopulations with distinct clinical phenotypes. iScience, 29(5), 115045.

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

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

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

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<sup>+</sup> 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.