Resource Summary Report

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XDSME

RRID:SCR_016943
Type: Tool

Proper Citation

XDSME (RRID:SCR_016943)

Resource Information

URL: https://github.com/legrandp/xdsme

Proper Citation: XDSME (RRID:SCR_016943)

Description: Software package of python scripts made to simplify the processing of crystal diffraction images.

Abbreviations: xdsme

Synonyms: XDSME, X-ray Detector Software Made Easier, XDS Made Easier

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

Keywords: simplify, processing, crystal, diffraction, image, data, XDS

Funding:

Availability: Free, Available for download, Freely available

Resource Name: XDSME

Resource ID: SCR_016943

License: BSD License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250509T060224+0000

Ratings and Alerts

No rating or validation information has been found for XDSME.

No alerts have been found for XDSME.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lublin V, et al. (2024) Does Acinetobacter calcoaceticus glucose dehydrogenase produce self-damaging H2O2? Bioscience reports, 44(5).

Zinke M, et al. (2024) Ton motor conformational switch and peptidoglycan role in bacterial nutrient uptake. Nature communications, 15(1), 331.

Brier L, et al. (2023) Novel dithiocarbamates selectively inhibit 3CL protease of SARS-CoV-2 and other coronaviruses. European journal of medicinal chemistry, 250, 115186.

Madru C, et al. (2023) DNA-binding mechanism and evolution of replication protein A. Nature communications, 14(1), 2326.

Zinke M, et al. (2023) Ton Motor Conformational Switch and Peptidoglycan Role in Bacterial Nutrient Uptake. bioRxiv : the preprint server for biology.

Seif-El-Dahan M, et al. (2023) PAXX binding to the NHEJ machinery explains functional redundancy with XLF. Science advances, 9(22), eadg2834.

Fyfe CD, et al. (2022) Crystallographic snapshots of a B12-dependent radical SAM methyltransferase. Nature, 602(7896), 336.

Damke PP, et al. (2022) ComFC mediates transport and handling of single-stranded DNA during natural transformation. Nature communications, 13(1), 1961.

Chavas LMG, et al. (2021) PROXIMA-1 beamline for macromolecular crystallography measurements at Synchrotron SOLEIL. Journal of synchrotron radiation, 28(Pt 3), 970.

Marsin S, et al. (2021) Study of the DnaB:DciA interplay reveals insights into the primary mode of loading of the bacterial replicative helicase. Nucleic acids research, 49(11), 6569.

Ciccone L, et al. (2020) Monoaryl derivatives as transthyretin fibril formation inhibitors:

Design, synthesis, biological evaluation and structural analysis. Bioorganic & medicinal chemistry, 28(18), 115673.

Maveyraud L, et al. (2020) Protein X-ray Crystallography and Drug Discovery. Molecules (Basel, Switzerland), 25(5).

Veyron S, et al. (2019) A Ca2+-regulated deAMPylation switch in human and bacterial FIC proteins. Nature communications, 10(1), 1142.

Campanacci V, et al. (2019) Selection and Characterization of Artificial Proteins Targeting the Tubulin ? Subunit. Structure (London, England : 1993), 27(3), 497.