Resource Summary Report

Generated by dkNET on May 21, 2025

iMosflm

RRID:SCR_014217
Type: Tool

Proper Citation

iMosflm (RRID:SCR_014217)

Resource Information

URL: http://www.mrc-lmb.cam.ac.uk/harry/imosflm/ver721/introduction.html

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Description: Software which processes diffraction data/images and produces an MTZ file of reflection indices with their intensities, standard deviations, and other parameters. The MTZ file is passed onto other programs of the CCP4 program suite for further data reduction. iMosflm processes data from CCD and pixel detectors. It is available for Windows, Mac OSX and Linux platforms. Tutorials are available at the website.

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

Keywords: image processing software, diffraction image, mtz file

Funding:

Resource Name: iMosflm

Resource ID: SCR_014217

Record Creation Time: 20220129T080319+0000

Record Last Update: 20250521T061527+0000

Ratings and Alerts

No rating or validation information has been found for iMosflm .

No alerts have been found for iMosflm .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 316 mentions in open access literature.

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

Shin OS, et al. (2024) Crimean-Congo hemorrhagic fever survivors elicit protective non-neutralizing antibodies that target 11 overlapping regions on glycoprotein GP38. Cell reports, 43(7), 114502.

Shahri MA, et al. (2024) Deciphering the structure of a multi-drug resistant Acinetobacter baumannii short-chain dehydrogenase reductase. PloS one, 19(2), e0297751.

Wachino J-i, et al. (2024) Hydroxyhexylitaconic acids as potent IMP-type metallo-?-lactamase inhibitors for controlling carbapenem resistance in Enterobacterales. Microbiology spectrum, 12(3), e0234423.

Pijning T, et al. (2024) Structural and time-resolved mechanistic investigations of protein hydrolysis by the acidic proline-specific endoprotease from Aspergillus niger. Protein science : a publication of the Protein Society, 33(1), e4856.

Ghafoori SM, et al. (2024) RNA Binding Properties of SOX Family Members. Cells, 13(14).

Edgar RCS, et al. (2024) On-target, dual aminopeptidase inhibition provides cross-species antimalarial activity. mBio, 15(6), e0096624.

Cross EM, et al. (2024) A functional and structural comparative analysis of large tumor antigens reveals evolution of different importin ?-dependent nuclear localization signals. Protein science : a publication of the Protein Society, 33(2), e4876.

Chen X, et al. (2024) The presence of broadly neutralizing anti-SARS-CoV-2 RBD antibodies elicited by primary series and booster dose of COVID-19 vaccine. PLoS pathogens, 20(6), e1012246.

Nguyen MC, et al. (2024) Molecular insight into interactions between the Taf14, Yng1 and Sas3 subunits of the NuA3 complex. Nature communications, 15(1), 5335.

May AJ, et al. (2024) Structural and antigenic characterization of novel and diverse Henipavirus glycoproteins. bioRxiv : the preprint server for biology.

Nguy AKL, et al. (2024) Non-Canonical Cytochrome P450 Enzymes in Nature. bioRxiv : the

preprint server for biology.

Kato Y, et al. (2024) Functional and structural analyses of IMP-27 metallo-?-lactamase: evolution of IMP-type enzymes to overcome Zn(II) deprivation. Microbiology spectrum, 12(12), e0039124.

Ke Z, et al. (2024) N terminus of SARS-CoV-2 nonstructural protein 3 interrupts RNA-driven phase separation of N protein by displacing RNA. The Journal of biological chemistry, 300(11), 107828.

Pous J, et al. (2023) Structural basis of a redox-dependent conformational switch that regulates the stress kinase p38?. Nature communications, 14(1), 7920.

Qin T, et al. (2023) Structural Insight into Polymerase Mechanism via a Chiral Center Generated with a Single Selenium Atom. International journal of molecular sciences, 24(21).

Sun Z, et al. (2023) Klebsiella pneumoniae carbapenemase variant 44 acquires ceftazidime-avibactam resistance by altering the conformation of active-site loops. The Journal of biological chemistry, 300(1), 105493.

Lu S, et al. (2023) Mutagenesis and structural analysis reveal the CTX-M ?-lactamase active site is optimized for cephalosporin catalysis and drug resistance. The Journal of biological chemistry, 299(5), 104630.

Micelli C, et al. (2023) A conserved zinc-binding site in Acinetobacter baumannii PBP2 required for elongasome-directed bacterial cell shape. Proceedings of the National Academy of Sciences of the United States of America, 120(8), e2215237120.

Luo Y, et al. (2023) Discovery of the SHP2 allosteric inhibitor 2-((3R,4R)-4-amino-3-methyl-2-oxa-8-azaspiro[4.5]decan-8-yl)-5-(2,3-dichlorophenyl)-3-methylpyrrolo[2,1-f][1,2,4] triazin-4(3H)-one. Journal of enzyme inhibition and medicinal chemistry, 38(1), 398.

Nguyen HTV, et al. (2023) Structure of the heterotrimeric membrane protein complex FtsB-FtsL-FtsQ of the bacterial divisome. Nature communications, 14(1), 1903.