Resource Summary Report

Generated by dkNET on May 19, 2025

AIMLESS

RRID:SCR_015747
Type: Tool

Proper Citation

AIMLESS (RRID:SCR_015747)

Resource Information

URL: http://www.ccp4.ac.uk/html/aimless.html

Proper Citation: AIMLESS (RRID:SCR_015747)

Description: Data processing software for x-ray diffraction data. AIMLESS scales together multiple observations of reflections, and merges multiple observations into an average intensity.

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

Defining Citation: PMID:23793146

Keywords: xray, differentiation, observation, reflection, scaling, scale

Funding:

Availability: Free, Available for download

Resource Name: AIMLESS

Resource ID: SCR_015747

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250519T204534+0000

Ratings and Alerts

No rating or validation information has been found for AIMLESS.

No alerts have been found for AIMLESS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 495 mentions in open access literature.

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

Vascon F, et al. (2025) Snapshots of Pseudomonas aeruginosa SOS response reveal structural requisites for LexA autoproteolysis. iScience, 28(2), 111726.

Pramono H, et al. (2025) Crystal structure of a novel heterooligomeric aminotransferase from Serratia sp. ATCC 39006 provides insights into function. FEBS letters, 599(1), 74.

Clough SE, et al. (2025) A metal-trap tests and refines blueprints to engineer cellular protein metalation with different elements. Nature communications, 16(1), 810.

Zhang L, et al. (2024) Structure basis for recognition of plant Rpn10 by phytoplasma SAP05 in ubiquitin-independent protein degradation. iScience, 27(2), 108892.

Pomowski A, et al. (2024) Revisiting the metal sites of nitrous oxide reductase in a low-dose structure from Marinobacter nauticus. Journal of biological inorganic chemistry : JBIC : a publication of the Society of Biological Inorganic Chemistry, 29(3), 279.

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

Tomar R, et al. (2024) DNA Replication across ?-l-(3'-2')-Threofuranosyl Nucleotides Mediated by Human DNA Polymerase ?. Biochemistry, 63(19), 2425.

Valerie NCK, et al. (2024) Coupling cellular drug-target engagement to downstream pharmacology with CeTEAM. Nature communications, 15(1), 10347.

Peng W, et al. (2024) Reverse-engineering the anti-MUC1 antibody 139H2 by mass spectrometry-based de novo sequencing. Life science alliance, 7(6).

Sridhar S, et al. (2024) Structural enzymology studies with the substrate 3S-hydroxybutanoyl-CoA: bifunctional MFE1 is a less efficient dehydrogenase than monofunctional HAD. FEBS open bio, 14(4), 655.

Barnsby-Greer L, et al. (2024) UBE2A and UBE2B are recruited by an atypical E3 ligase module in UBR4. Nature structural & molecular biology, 31(2), 351.

Peluso-Iltis C, et al. (2024) 4-Hydroxy-1?,25-Dihydroxyvitamin D3: Synthesis and Structure-Function Study. Biomolecules, 14(5).

Ray J, et al. (2024) Drug-resistant menin variants retain high binding affinity and interactions with MLL1. The Journal of biological chemistry, 300(10), 107777.

Yu J, et al. (2024) Structural basis of ?-opioid receptor targeting by a nanobody antagonist. Nature communications, 15(1), 8687.

Harrison TE, et al. (2024) Rational structure-guided design of a blood stage malaria vaccine immunogen presenting a single epitope from PfRH5. EMBO molecular medicine, 16(10), 2539.

Kremer M, et al. (2024) Bacteria employ lysine acetylation of transcriptional regulators to adapt gene expression to cellular metabolism. Nature communications, 15(1), 1674.

Albanese KI, et al. (2024) Rationally seeded computational protein design of ?-helical barrels. Nature chemical biology, 20(8), 991.

Qin C, et al. (2024) Acetyl-CoA synthetase activity is enzymatically regulated by lysine acetylation using acetyl-CoA or acetyl-phosphate as donor molecule. Nature communications, 15(1), 6002.

Rehman S, et al. (2024) The Legionella collagen-like protein employs a distinct binding mechanism for the recognition of host glycosaminoglycans. Nature communications, 15(1), 4912.

Soukarieh F, et al. (2024) Design, Synthesis, and Evaluation of New 1H-Benzo[d]imidazole Based PqsR Inhibitors as Adjuvant Therapy for Pseudomonas aeruginosa Infections. Journal of medicinal chemistry, 67(2), 1008.