

Resource Summary Report

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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

Availability: Free, Available for download

Resource Name: AIMLESS

Resource ID: SCR_015747

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T190833+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 541 mentions in open access literature.

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

Lee E, et al. (2026) Streptococcus pneumoniae HtrA is a dynamic and monomeric virulence factor capable of forming larger oligomeric complexes. Protein science : a publication of the Protein Society, 35(1), e70411.

Galindo JL, et al. (2025) Functional and structural characterization of AtAbf43C: an exo-1,5-?-L-arabinofuranosidase from Acetivibrio thermocellus DSM1313. The Biochemical journal, 482(16), 1181.

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.

Osika KR, et al. (2025) Crystal Structure and Catalytic Mechanism of Drimenol Synthase, a Bifunctional Terpene Cyclase-Phosphatase. bioRxiv : the preprint server for biology.

Gregory KS, et al. (2025) Molecular basis of human angiotensin-1 converting enzyme inhibition by a series of diprolyl-derived compounds. The FEBS journal, 292(5), 1141.

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.

Deschenes NM, et al. (2025) Functional and Structural Characterization of Treatment-Emergent Nirmatrelvir Resistance Mutations at Low Frequencies in the Main Protease (Mpro) Reveals a Unique Evolutionary Route for SARS-CoV-2 to Gain Resistance. The Journal of infectious diseases, 232(5), e789.

Bekkhoshin Z, et al. (2025) Atg23 Interacts With Both the N- and C-termini of Atg9 Via a Hydrophobic Binding Pocket. bioRxiv : the preprint server for biology.

Esdar C, et al. (2025) M4205 (IDRX-42) Is a Highly Selective and Potent Inhibitor of Relevant Oncogenic Driver and Resistance Variants of KIT in Cancer. Molecular cancer therapeutics, 24(7), 1040.

Das T, et al. (2025) Efficient coordination between the winged helix domain and the aromatic-rich loop restructures the ATPase domain and facilitates DNA unwinding by human RECQ1. Nucleic acids research, 53(11).

Antón-Plágaro C, et al. (2025) Mapping of endosomal proximity proteomes reveals Retromer as a hub for RAB GTPase regulation. Nature communications, 16(1), 6990.

Mehboob J, et al. (2025) Itaconate utilisation by the human pathogen Pseudomonas aeruginosa requires uptake via the IctPQM TRAP transporter. The Biochemical journal, 482(17), 1277.

Scaletti Hutchinson E, et al. (2025) The anabolic steroid stanozolol is a potent inhibitor of human MutT homolog 1. FEBS letters, 599(19), 2790.

Subach OM, et al. (2025) Next-generation orange-to-far-red photoconvertible fluorescent protein for single-molecule microscopy and protein dynamic tracking. *Scientific reports*, 15(1), 40166.

Trenker R, et al. (2025) Structure-Guided Stapling of Dimeric Conformations and Linker Engineering Enhance Thermostability and Fine-Tune Activity of Bispecific VHH Cytokine Agonists. *Antibodies (Basel, Switzerland)*, 14(3).

Rohilla R, et al. (2025) The *yxiD* gene from *Bacillus subtilis* 6633 encodes a polymorphic toxin with tRNase activity and is neutralized by the cognate immunity protein YxxD. *Nucleic acids research*, 53(22).

McDowell MA, et al. (2025) Structural characterisation of the fungal Pmt4 homodimer. *Nature communications*, 16(1), 11134.

Tjo H, et al. (2025) Structural insights into xyloglucan recognition by an ABC transporter from a Gram-positive, thermophilic bacterium. *bioRxiv : the preprint server for biology*.

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

Diaz-Palacios K, et al. (2025) Phospho-regulated tethering of focal adhesion kinase to vinculin links force transduction to focal adhesion signaling. *Cell communication and signaling : CCS*, 23(1), 190.