

# Resource Summary Report

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## AIMLESS

RRID:SCR\_015747

Type: Tool

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### Proper Citation

AIMLESS (RRID:SCR\_015747)

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### 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

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### Ratings and Alerts

No rating or validation information has been found for AIMLESS.

No alerts have been found for AIMLESS.

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### 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 [ASWG](#) .

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.

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.

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.

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.

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.

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.

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.

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.

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.

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).

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).

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.

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.

Gieselmann L, et al. (2025) Profiling of HIV-1 elite neutralizer cohort reveals a CD4bs bnAb for HIV-1 prevention and therapy. *Nature immunology*, 26(11), 2016.