

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

[autoPROC](#)

RRID:SCR_015748

Type: Tool

Proper Citation

autoPROC (RRID:SCR_015748)

Resource Information

URL: <https://www.globalphasing.com/autoproc/>

Proper Citation: autoPROC (RRID:SCR_015748)

Description: Data processing software for X-ray diffraction data. autoPROC is a set of tools and programs to automate steps involved in data processing, such as image analysis, integration, indexing, and determination.

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

Defining Citation: [PMID:21460447](#)

Keywords: xray, diffraction, data processing, crystallography

Funding: European Commission LSHG-CT-2003-503420

Availability: Free for academic use, Available for download

Resource Name: autoPROC

Resource ID: SCR_015748

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260821T194047+0000

Ratings and Alerts

No rating or validation information has been found for autoPROC.

No alerts have been found for autoPROC.

Data and Source Information

Usage and Citation Metrics

We found 330 mentions in open access literature.

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

Gao A, et al. (2026) Structural basis of QueC-family protein function in qatABCD anti-phage defense. Nature communications, 17(1).

Lemaire ON, et al. (2026) Carbon-monoxide-driven bioethanol production operates through a tungsten-dependent catalyst. Nature chemical biology, 22(1), 28.

Yang R, et al. (2026) The molecular mechanisms of the ShosTA system in mediating anti-phage defense. Nucleic acids research, 54(5).

Bencze G, et al. (2026) Identification and Validation of an Inhibitor of the Protein Kinases PIM and DYRK. Journal of medicinal chemistry, 69(7), 7920.

Lourenço FM, et al. (2026) Interaction of Staphylococcus aureus di-iron Repair of Iron Centers protein with the iron-sulfur cluster assembly SUF system. Protein science : a publication of the Protein Society, 35(1), e70406.

Chambers LR, et al. (2026) A DNA damage-activated kinase controls bacterial immune pathway expression. bioRxiv : the preprint server for biology.

Shabbir K, et al. (2026) A truncated CDC14A retains catalytic structure and phosphatase activity preserving male fertility but causes nonsyndromic deafness. The Journal of biological chemistry, 302(1), 110982.

Palte RL, et al. (2026) WRN structural flexibility showcased through fragment-based lead discovery of inhibitors. Nature communications, 17(1), 79.

Sánchez-Alba L, et al. (2026) Structural basis for transcriptional regulation by the cell division regulator MraZ in Mycoplasma genitalium. Nature communications, 17(1).

Shirakawa KT, et al. (2026) The clinical missense variant E282K in PPP3CA/calcineurin shifts substrate dephosphorylation by altering active site recruitment. Nature communications, 17(1).

Banna HA, et al. (2026) Structures of the eIF4G-binding RNA domains among picornaviral IRES types are topologically conserved. Nature communications, 17(1).

Greschik H, et al. (2026) Development of High-Affinity CHD1 Chromodomain Inhibitors. Journal of medicinal chemistry, 69(10), 12020.

Xiao Q, et al. (2026) Structural basis for sequence-specific DNA recognition by a group IId WRKY transcription factor GhWRKY17 in cotton. The Biochemical journal, 483(2), 149.

Cooper A, et al. (2026) The Crystal Structure of Human Transport and Golgi Organization 2 Homolog (TANGO2) Protein Reveals an $\alpha\beta\gamma\delta$ -Fold Arrangement. *Proteins*, 94(2), 515.

Milburn AE, et al. (2026) Molecular architecture of meiotic pro-crossover factor HEI10 reveals coupling of higher-order assembly and ubiquitin chain formation. *bioRxiv : the preprint server for biology*.

Nikolopoulos N, et al. (2026) Crystal structure of HERV-K envelope glycoprotein surface subunit. *Journal of virology*, 100(6), e0019526.

Liu L, et al. (2026) Structural Analysis and Inhibitor Modeling of Bacterioferritin From *Brucella abortus*. *Proteins*, 94(6), 1170.

Manser BP, et al. (2026) Catalytic pKa Attenuation in a Hydrolytic Metalloenzyme by Genetic Code Expansion. *Biochemistry*, 65(5), 559.

Woloszyn K, et al. (2026) Blunt-force assembly of programmable DNA architectures using π - π stacking. *Nature communications*, 17(1).

Michail C, et al. (2026) The SETD2 L1609P mutation found in leukemia disrupts methyltransferase activity and reduces histone H3K36 trimethylation. *The Journal of biological chemistry*, 302(3), 111259.