

Resource Summary Report

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ATSAS

RRID:SCR_015648

Type: Tool

Proper Citation

ATSAS (RRID:SCR_015648)

Resource Information

URL: <https://www.embl-hamburg.de/biosaxs/software.html>

Proper Citation: ATSAS (RRID:SCR_015648)

Description: Software toolkit for small-angle scattering data analysis from biological macromolecules.

Synonyms: Data Analysis Software ATSAS

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

Defining Citation: [PMID:28808438](#)

Keywords: macromolecule, small-angle scattering, ab initio method, rigid body modeling, pbd oriented tool, mixture, flexible system

Resource Name: ATSAS

Resource ID: SCR_015648

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260804T043612+0000

Ratings and Alerts

No rating or validation information has been found for ATSAS.

No alerts have been found for ATSAS.

Data and Source Information

Usage and Citation Metrics

We found 1326 mentions in open access literature.

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

Ahmed FH, et al. (2026) Disordered N-termini enhance the thermostability of SGNH-hydrolase family polyesters. *Protein science : a publication of the Protein Society*, 35(1), e70402.

Braun M, et al. (2026) Computational enzyme design by catalytic motif scaffolding. *Nature*, 649(8095), 237.

Paissoni C, et al. (2025) A conformational fingerprint for amyloidogenic light chains. *eLife*, 13.

Markusson S, et al. (2025) Nanobodies against the myelin enzyme CNPase as tools for structural and functional studies. *Journal of neurochemistry*, 169(1), e16274.

Inoue R, et al. (2025) Revealing an origin of temperature-dependent structural change in intrinsically disordered proteins. *Biophysical journal*, 124(3), 540.

Martín-González A, et al. (2025) Selective cargo and membrane recognition by SNX17 regulates its interaction with Retriever. *EMBO reports*, 26(2), 470.

Monsen RC, et al. (2025) Early events in G-quadruplex folding captured by time-resolved small-angle X-ray scattering. *Nucleic acids research*, 53(3).

Kopečný DJ, et al. (2025) A monomer-dimer switch modulates the activity of plant adenosine kinase. *Journal of experimental botany*, 76(12), 3457.

Nirwal S, et al. (2025) The structure of the MutL-CTD:processivity-clamp complex provides insight regarding strand discrimination in non-methyl-directed DNA mismatch repair. *Nucleic acids research*, 53(4).

Van Veghel MHW, et al. (2025) Identifying recovery trajectories following primary total shoulder arthroplasty: a cohort study of 3,358 patients from the Dutch Arthroplasty Register. *Acta orthopaedica*, 96, 226.

Pérez Carrillo VH, et al. (2025) Structure and Dynamics of Macrophage Infectivity Potentiator Proteins from Pathogenic Bacteria and Protozoans Bound to Fluorinated Piperidic Acid Inhibitors. *Journal of medicinal chemistry*, 68(5), 5926.

Pesce G, et al. (2025) Dissecting Henipavirus W proteins conformational and fibrillation properties: contribution of their N- and C-terminal constituent domains. *The FEBS journal*, 292(3), 556.

Dayan A , et al. (2025) Characterization of DnaB-DnaG Interaction in M. tuberculosis Using Small-Angle X-ray Scattering-Based Dissociation Assay. *Chembiochem : a*

European journal of chemical biology, 26(14), e202500289.

Petersen AB, et al. (2025) Mode of Action of AlgE1: A Modular Mannuronate C-5 Epimerase. *Biochemistry*, 64(14), 3030.

Yu J, et al. (2025) Molecular determinants of picornavirus 3C protease binding to phosphoinositide-enriched lipid membranes. *The Journal of biological chemistry*, 301(9), 110543.

Godwin ARF, et al. (2025) Collagen VI microfibril structure reveals mechanism for molecular assembly and clustering of inherited pathogenic mutations. *Nature communications*, 16(1), 7549.

Zhang L, et al. (2025) Probing molecular mechanisms of emulsifier-modulated lipid crystallization via ultrasonic phase velocity. *Ultrasonics sonochemistry*, 120, 107442.

Malard F, et al. (2025) Molecular basis for the calcium-dependent activation of the ribonuclease EndoU. *Nature communications*, 16(1), 3110.

Chatziefthymiou SD, et al. (2025) Identification, validation, and characterization of approved and investigational drugs interfering with the SARS-CoV-2 endoribonuclease Nsp15. *Protein science : a publication of the Protein Society*, 34(6), e70156.

Hobbs B, et al. (2025) A low-complexity linker as a driver of intra- and intermolecular interactions in DNAJB chaperones. *Nature communications*, 16(1), 5070.