

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

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: 20260829T182844+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 1377 mentions in open access literature.

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

Kennedy CR, et al. (2026) Covalent fragment screening to inhibit the E3 ligase activity of bacterial NEL enzymes SspH1 and SspH2. *RSC chemical biology*, 7(1), 153.

Dawidziak DM, et al. (2026) Human FASTK preferentially binds single-stranded and G-rich RNA. *The FEBS journal*, 293(3), 729.

Martín-Hurtado A, et al. (2026) The oncogenic CCDC6-RET fusion protein is a dual ATP- and ADP-dependent kinase. *Nature communications*, 17(1).

Singhal A, et al. (2026) Cleavage region organizes the structural architecture of the SINE-derived B2 repressive ribozyme. *Communications biology*, 9(1).

Akanchise T, et al. (2026) Designed Liquid Crystalline Nanoassemblies From Clinically Validated Polyunsaturated Lipids for Combined Antioxidant, Anti-Apoptotic, and Neurotrophic Treatments. *Advanced healthcare materials*, 15(21), e05595.

Gladysheva AV, et al. (2026) Solution Structure of Nucleoprotein Domain 1 from the Emerging Yezo Virus. *International journal of molecular sciences*, 27(12).

Arinkin V, et al. (2026) Dimer asymmetry in signaling of blue light sensor histidine kinases. *Science advances*, 12(27), eaed8943.

Mammen C, et al. (2026) In vitro characterization of the catalytic domain of human histone deacetylase 5. *Scientific reports*, 16(1).

Pignataro MF, et al. (2026) Nanobodies as tools for studying human frataxin biology. *Communications biology*, 9(1), 181.

Raval PK, et al. (2026) Structure determination and dual targeting of a plant TACO1 identifies its ancient role as an organelle translation regulator. *bioRxiv : the preprint server for biology*.

Aljedani SS, et al. (2026) SH3 domains selectively activate the PI3 kinase through non-conventional tertiary contacts. *Communications biology*, 9(1).

Khan SH, et al. (2026) DNA induces non-canonical dimerization of the farnesoid X receptor. *Nucleic acids research*, 54(4).

Capra N, et al. (2026) Structural and oligomeric characterization of substrate- and product-selective nylon hydrolases. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2026) Single-engineered-residue solvation perturbations regulate global protein architecture and function. *Nature communications*, 17(1).

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

Gedeon A, et al. (2026) Structural basis of Mycobacterium Fluoroquinolone Resistance Protein D (MfpD), a versatile pathogeny protein from the mfp conservon of Mycobacterium tuberculosis. *bioRxiv : the preprint server for biology*.

Cavini IA, et al. (2026) Coiled-coil homo-oligomerization and disaggregase Hsp104 act in parallel to stabilize orphan septins. *bioRxiv : the preprint server for biology*.

Rasal TA, et al. (2026) Ligand binding drives proteolysis of the SmcR master transcription factor and controls quorum sensing-state transitions in *Vibrio* species. *mBio*, 17(3), e0344525.

Zúñiga-Domínguez JA, et al. (2026) Hydroxyl radical footprinting modification reveals an intradomain communication pathway in EFL1 disrupted by a Shwachman-Diamond syndrome-associated mutation. *Protein science : a publication of the Protein Society*, 35(4), e70504.

Tan K, et al. (2026) Phylogenetic Analysis and Structural Evaluation of *Staphylococcus aureus* Serine-Aspartate Repeat-Containing Protein D with a Focus on Periprosthetic Joint Infection. *bioRxiv : the preprint server for biology*.