

Resource Summary Report

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FoXS

RRID:SCR_017269

Type: Tool

Proper Citation

FoXS (RRID:SCR_017269)

Resource Information

URL: <https://modbase.compbio.ucsf.edu/foxs/>

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Description: Web server for computing theoretical scattering profile of structure and fitting of experimental profile. Computes SAXS profile of given atomistic model and fits it to experimental profile. Used for structural modeling applications with small angle X-ray scattering data.

Synonyms: Fast X-Ray Scattering

Resource Type: analysis service resource, data access protocol, production service resource, service resource, software resource, web service

Defining Citation: [PMID:23972848](#), [PMID:27151198](#)

Keywords: computing, theoretical, scattering, profile, structure, fitting, small, angle, X ray, data

Funding: Lawrence Berkeley National Lab IDAT program ;
NCRR U54 RR022220;
NIGMS P41 GM109824;
NIGMS R01 GM083960;
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Weizmann Institute Advancing Women in Science

Availability: Free, Available for download, Freely available

Resource Name: FoXS

Resource ID: SCR_017269

Record Creation Time: 20220129T080334+0000

Ratings and Alerts

No rating or validation information has been found for FoXS.

No alerts have been found for FoXS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

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.

De'Ath C, et al. (2026) YdbL directly modulates YdbH-YnbE bridge formation to maintain *Escherichia coli* outer membrane homeostasis. *bioRxiv : the preprint server for biology*.

Inaba-Inoue S, et al. (2025) Plasticity and Co-Factor-Dependent Structural Changes in the RecA Nucleoprotein Filament Studied by Small-Angle X-Ray Scattering (SAXS) Measurements and Molecular Modeling. *Molecules (Basel, Switzerland)*, 30(8).

Saharan K, et al. (2025) Structure-function studies of a nucleoplasmin isoform from *Plasmodium falciparum*. *The Journal of biological chemistry*, 301(4), 108379.

Almeida-Juarez AG, et al. (2025) Investigating the quaternary structure of a homomultimeric catechol 1,2-dioxygenase: An integrative structural biology study. *PloS one*, 20(5), e0315992.

Khmelinskaia A, et al. (2025) Local structural flexibility drives oligomorphism in computationally designed protein assemblies. *Nature structural & molecular biology*, 32(6), 1050.

Trewhella J, et al. (2024) Benchmarking predictive methods for small-angle X-ray scattering from atomic coordinates of proteins using maximum likelihood consensus data. *IUCrJ*, 11(Pt 5), 762.

Burchert JP, et al. (2023) A small-angle X-ray scattering study of red blood cells in continuous flow. *Journal of synchrotron radiation*, 30(Pt 3), 582.

Mielecki M, et al. (2022) Structure-Activity Relationship of the Dimeric and Oligomeric Forms of a Cytotoxic Biotherapeutic Based on Diphtheria Toxin. *Biomolecules*, 12(8).

Bermeo S, et al. (2022) De novo design of obligate ABC-type heterotrimeric proteins. *Nature structural & molecular biology*, 29(12), 1266.

Trewhella J, et al. (2022) A round-robin approach provides a detailed assessment of biomolecular small-angle scattering data reproducibility and yields consensus curves for benchmarking. *Acta crystallographica. Section D, Structural biology*, 78(Pt 11), 1315.

Xia C, et al. (2021) Molecular mechanism of interactions between ACAD9 and binding partners in mitochondrial respiratory complex I assembly. *iScience*, 24(10), 103153.

Alam J, et al. (2021) Expression and analysis of the SAM-dependent RNA methyltransferase Rsm22 from *Saccharomyces cerevisiae*. *Acta crystallographica. Section D, Structural biology*, 77(Pt 6), 840.

Chesterman C, et al. (2021) Co-crystallization with diabodies: A case study for the introduction of synthetic symmetry. *Structure (London, England : 1993)*, 29(6), 598.

Garcia-Rodriguez G, et al. (2021) Alternative dimerization is required for activity and inhibition of the HEPN ribonuclease RnIA. *Nucleic acids research*, 49(12), 7164.

Wei KY, et al. (2020) Computational design of closely related proteins that adopt two well-defined but structurally divergent folds. *Proceedings of the National Academy of Sciences of the United States of America*, 117(13), 7208.

Azmi L, et al. (2020) High-resolution structure of the alcohol dehydrogenase domain of the bifunctional bacterial enzyme AdhE. *Acta crystallographica. Section F, Structural biology communications*, 76(Pt 9), 414.

Niazi M, et al. (2020) Biophysical analysis of *Pseudomonas*-phage PaP3 small terminase suggests a mechanism for sequence-specific DNA-binding by lateral interdigitation. *Nucleic acids research*, 48(20), 11721.

Bochel AJ, et al. (2020) Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains 7-11??Uncovers the Mannose 6-Phosphate Binding Site of Domain 9. *Structure (London, England : 1993)*, 28(12), 1300.

Gabrielsen M, et al. (2019) Identification and Characterization of Mutations in Ubiquitin Required for Non-covalent Dimer Formation. *Structure (London, England : 1993)*, 27(9), 1452.