

Resource Summary Report

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STARANISO

RRID:SCR_018362

Type: Tool

Proper Citation

STARANISO (RRID:SCR_018362)

Resource Information

URL: <http://staraniso.globalphasing.org/cgi-bin/staraniso.cgi>

Proper Citation: STARANISO (RRID:SCR_018362)

Description: Web server for anisotropy of diffraction limit and Bayesian estimation of structure amplitudes by Global Phasing Limited. Server uses DEBYE and STARANISO software to perform anisotropic cut off of merged intensity data, to perform Bayesian estimation of structure amplitudes and to apply anisotropic correction to data.

Synonyms: The STARANISO Server, STARANISO Server, STARANISO server

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

Keywords: Anisotropy, diffraction limit, Bayesian estimation, structure amplitude, Global Phasing Limited, anisotropic cut off, data, anisotropic correction data

Funding: Global Phasing Consortium

Availability: Free, Freely available

Resource Name: STARANISO

Resource ID: SCR_018362

License URLs: http://staraniso.globalphasing.org/staraniso_conditions.html

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260729T044444+0000

Ratings and Alerts

No rating or validation information has been found for STARANISO.

No alerts have been found for STARANISO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 70 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

Tangpeerachaikul A, et al. (2025) Zidesamtinib Selective Targeting of Diverse ROS1 Drug-Resistant Mutations. *Molecular cancer therapeutics*, 24(7), 1005.

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

Heiringhoff RS, et al. (2025) Structure of the human nonmuscle myosin 2A motor domain: Insights into isoform-specific mechanochemistry. *The Journal of biological chemistry*, 301(10), 110691.

Zakharova K, et al. (2025) Crystal structures of *Salmonella enterica* FraB deglycase reveal a conformational heterodimer with remarkable structural plasticity at the active site. *Protein science : a publication of the Protein Society*, 34(9), e70260.

Velcicky J, et al. (2025) Discovery of selective low molecular weight interleukin-36 receptor antagonists by encoded library technologies. *Nature communications*, 16(1), 1669.

Esler MA, et al. (2025) Structural basis for varying drug resistance of SARS-CoV-2 Mpro E166 variants. *mBio*, 16(7), e0262424.

Li Y, et al. (2024) Cystine-knot peptide inhibitors of HTRA1 bind to a cryptic pocket within the active site region. *Nature communications*, 15(1), 4359.

Sun D, et al. (2024) The discovery and structural basis of two distinct state-dependent inhibitors of BamA. *Nature communications*, 15(1), 8718.

Gr??schow S, et al. (2024) CRISPR antiphage defence mediated by the cyclic nucleotide-binding membrane protein Csx23. *Nucleic acids research*, 52(6), 2761.

Markusson S, et al. (2024) Nanobodies against the myelin enzyme CNPase as tools for structural and functional studies. *bioRxiv : the preprint server for biology*.

Stoll GA, et al. (2024) Crystal structure and biochemical activity of the macrodomain from rubella virus p150. *Journal of virology*, 98(2), e0177723.

Michel MA, et al. (2024) Secondary interactions in ubiquitin-binding domains achieve linkage or substrate specificity. *Cell reports*, 43(8), 114545.

Nishio S, et al. (2024) ZP2 cleavage blocks polyspermy by modulating the architecture of the egg coat. *Cell*, 187(6), 1440.

Kottur J, et al. (2023) Structures of SARS-CoV-2 N7-methyltransferase with DOT1L and PRMT7 inhibitors provide a platform for new antivirals. *PLoS pathogens*, 19(7), e1011546.

Donath T, et al. (2023) EIGER2 hybrid-photon-counting X-ray detectors for advanced synchrotron diffraction experiments. *Journal of synchrotron radiation*, 30(Pt 4), 723.

Lannes L, et al. (2023) Zinc-finger BED domains drive the formation of the active Hermes transpososome by asymmetric DNA binding. *Nature communications*, 14(1), 4470.

Engrola F, et al. (2023) Arsenite oxidase in complex with antimonite and arsenite oxyanions: Insights into the catalytic mechanism. *The Journal of biological chemistry*, 299(8), 105036.

Abdullayev S, et al. (2023) Selectively Modified Lactose and N-Acetyllactosamine Analogs at Three Key Positions to Afford Effective Galectin-3 Ligands. *International journal of molecular sciences*, 24(4).

Yin L, et al. (2023) Structural basis of sequence-specific cytosine deamination by double-stranded DNA deaminase toxin DddA. *Nature structural & molecular biology*, 30(8), 1153.