

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

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: 20260912T195900+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 78 mentions in open access literature.

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

Korban SA, et al. (2026) Structural Basis of pppGpp Binding to the N-Terminal Domain of the Bifunctional RelA/SpoT Homolog RelSeq: Crystal Structure and MD Analysis. International journal of molecular sciences, 27(12).

Makarova MO, et al. (2026) The interaction between the RNA aptamer Dap1 and DasR mirrors DNA operator site recognition in GntR repressors. Nucleic acids research, 54(10).

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

Yu M, et al. (2026) Regulation of BCL11A DNA binding and expression in human erythrocyte precursor HUDEP-2 cells. bioRxiv : the preprint server for biology.

Peirano E, et al. (2026) Trio analysis in dystonia identifies de novo KLC1 variants in a kinesinopathy with distinct motor and neurodevelopmental features. EBioMedicine, 129, 106358.

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.

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

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.

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

Kanai R, et al. (2025) How palytoxin transforms the Na⁺,K⁺ pump into a cation channel. Proceedings of the National Academy of Sciences of the United States of America, 122(38), e2506450122.

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.

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

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*.

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.

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.