

Resource Summary Report

Generated by [NIF](#) on Aug 2, 2026

ASTRA

RRID:SCR_016255

Type: Tool

Proper Citation

ASTRA (RRID:SCR_016255)

Resource Information

URL: <https://www.wyatt.com/products/software/astra.html>

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Description: Software for the characterization of macromolecules and nanoparticles via multi-angle and dynamic light scattering. It simplifies MALS and DLS analysis for assessment of molar mass, size, conformation, conjugation, and other essential physical parameters.

Synonyms: ASTRA6, Wyatt Technologies ASTRA, ASTRA Software

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

Keywords: macromolecule, nanoparticle, light, scattering, mals, dls, hplc, sequence, processing

Resource Name: ASTRA

Resource ID: SCR_016255

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260801T190532+0000

Ratings and Alerts

No rating or validation information has been found for ASTRA.

No alerts have been found for ASTRA.

Data and Source Information

Usage and Citation Metrics

We found 88 mentions in open access literature.

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

Oda K, et al. (2025) Molecular basis of IFN- γ -induced STAT3 phosphorylation stimulated by Sendai virus C protein. The Journal of biological chemistry, 301(11), 110744.

Ozkan E, et al. (2025) Analytical validation of total mucin concentration assay using SEC MALLS dRI for diagnosing and monitoring mucoobstructive lung diseases. Scientific reports, 15(1), 15024.

Azhieh A, et al. (2025) Rapidly evolving orphan immunity genes protect human gut bacteria from intoxication by the type VI secretion system. bioRxiv : the preprint server for biology.

Kumari J, et al. (2025) Distinct filament morphology and membrane tethering features of the dual FtsZ paralogs in Odinarchaeota. The EMBO journal, 44(21), 5940.

Sachar K, et al. (2025) A conserved chaperone protein is required for the formation of a noncanonical type VI secretion system spike tip complex. The Journal of biological chemistry, 301(3), 108242.

Jang GJ, et al. (2025) Modular in vivo assembly of Arabidopsis FCA oligomers into condensates competent for RNA 3' processing. The EMBO journal, 44(7), 2056.

Qerqez AN, et al. (2025) Selective decoupling of IgG1 binding to viral Fc receptors restores antibody-mediated NK cell activation against HCMV. Cell reports, 44(12), 116593.

Petrova ZO, et al. (2025) The role of kinase domain dimerization in EGFR activation. Structure (London, England : 1993).

Song X, et al. (2024) The structure of TRAF7 coiled-coil trimer provides insight into its function in zebrafish embryonic development. Journal of molecular cell biology, 16(1).

Zhang L, et al. (2024) Structure basis for recognition of plant Rpn10 by phytoplasma SAP05 in ubiquitin-independent protein degradation. iScience, 27(2), 108892.

Sirirungruang S, et al. (2024) Structural and biochemical basis for regiospecificity of the flavonoid glycosyltransferase UGT95A1. The Journal of biological chemistry, 300(9), 107602.

Agarwal A, et al. (2024) Mycobacterium smegmatis putative Holliday junction resolvases RuvC and RuvX play complementary roles in the processing of branched DNA structures. The Journal of biological chemistry, 300(10), 107732.

Rezazadeh H, et al. (2024) Optimization of the fermentation media, mathematical modeling, and enhancement of paclitaxel production by *Alternaria alternata* after elicitation with pectin. *Scientific reports*, 14(1), 12980.

Wang WW, et al. (2024) The structure of the archaeal nuclease RecJ2 implicates its catalytic mechanism and inability to interact with GINS. *The Journal of biological chemistry*, 300(6), 107379.

Quinodoz M, et al. (2024) De novo variants in LRRC8C resulting in constitutive channel activation cause a human multisystem disorder. *The EMBO journal*.

Barra ALC, et al. (2024) Structure and dynamics of the staphylococcal pyridoxal 5-phosphate synthase complex reveal transient interactions at the enzyme interface. *The Journal of biological chemistry*, 300(6), 107404.

Smalakyte D, et al. (2024) Filament formation activates protease and ring nuclease activities of CRISPR Lon-SAVED. *Molecular cell*, 84(21), 4239.

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

Yu J, et al. (2024) A replisome-associated histone H3-H4 chaperone required for epigenetic inheritance. *Cell*, 187(18), 5010.

Kim DY, et al. (2023) Sequence tolerance of immunoglobulin variable domain framework regions to noncanonical intradomain disulfide linkages. *The Journal of biological chemistry*, 299(11), 105278.