

Resource Summary Report

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

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: 20260912T195837+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 92 mentions in open access literature.

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

Srivastava DK, et al. (2026) The chromatin reader ZMYND8 recruits the NuRD component GATAD2A through its MYND domain to regulate MAPT213 long noncoding RNA transcription. *The Journal of biological chemistry*, 302(6), 111463.

Gallego-Del-Sol F, et al. (2026) Phages communicate across species to shape microbial ecosystems. *Cell*, 189(10), 3025.

Furukawa K, et al. (2026) Mitochondrial fission during mitophagy requires both inner and outer mitofissins. *EMBO reports*, 27(4), 853.

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*.

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.

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.

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.

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

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.

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

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).

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

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.

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.

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.

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

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.

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