

Resource Summary Report

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UltraScan

RRID:SCR_018126

Type: Tool

Proper Citation

UltraScan (RRID:SCR_018126)

Resource Information

URL: <http://ultrascan.aucsolutions.com/>

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Description: Software package for hydrodynamic data from analytical ultracentrifugation experiments. Features integrated data editing and analysis environment with portable graphical user interface. Provides resolution for sedimentation velocity experiments using high-performance computing modules for 2-dimensional spectrum analysis, genetic algorithm, and for Monte Carlo analysis.

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

Keywords: Hydrodynamic data, analytical ultracentrifugation experiment, data editing, analysis, sedimentation velocity experiment, spectrum analysis, genetic algorithm, Monte Carlo analysis

Funding: Howard Hughes Medical Institute ;
NCRR RR 022200 03S1;
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NSF ACI 1339649;
NSF ANI 228927;
NSF DBI 9724273;
NSF DBI 9974819;
NSF OCI 1032742;
NSF TG-MCB 060019T;
NSF TG-MCB 070038;
NSF TG-MCB 070039;
NSF TG-MCB 070040;
Robert J. Kleberg Jr. and Helen C. Kleberg Foundation ;
San Antonio Life Science Institute

Availability: Free, Available for download, Freely available

Resource Name: UltraScan

Resource ID: SCR_018126

License: GNU Lesser General Public License version 3

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260912T195858+0000

Ratings and Alerts

No rating or validation information has been found for UltraScan.

No alerts have been found for UltraScan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Wood DM, et al. (2025) Mechanism of NanR transcriptional activation of sialic acid metabolism in *Streptococcus pneumoniae*. *bioRxiv : the preprint server for biology*.

Currie MJ, et al. (2024) Structural and biophysical analysis of a *Haemophilus influenzae* tripartite ATP-independent periplasmic (TRAP) transporter. *eLife*, 12.

Shearer HL, et al. (2024) Hypothiocyanous acid reductase is critical for host colonization and infection by *Streptococcus pneumoniae*. *The Journal of biological chemistry*, 300(5), 107282.

Waszkiewicz R, et al. (2023) DNA supercoiling-induced shapes alter minicircle hydrodynamic properties. *bioRxiv : the preprint server for biology*.

Waszkiewicz R, et al. (2023) DNA supercoiling-induced shapes alter minicircle hydrodynamic properties. *Nucleic acids research*, 51(8), 4027.

Luijten G, et al. (2023) 3D surgical instrument collection for computer vision and extended reality. *Scientific data*, 10(1), 796.

Horne CR, et al. (2021) Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. *Nature communications*, 12(1), 1988.

- Peskin AV, et al. (2021) Modifying the resolving cysteine affects the structure and hydrogen peroxide reactivity of peroxiredoxin 2. *The Journal of biological chemistry*, 296, 100494.
- Turk LS, et al. (2021) The structure-function relationship of a signaling-competent, dimeric Reelin fragment. *Structure (London, England : 1993)*, 29(10), 1156.
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- Savelyev A, et al. (2020) Moving analytical ultracentrifugation software to a good manufacturing practices (GMP) environment. *PLoS computational biology*, 16(6), e1007942.
- Edwards GB, et al. (2020) Analytical Ultracentrifugation (AUC): An Overview of the Application of Fluorescence and Absorbance AUC to the Study of Biological Macromolecules. *Current protocols in molecular biology*, 133(1), e131.
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- Yarawsky AE, et al. (2020) The biofilm adhesion protein Aap from *Staphylococcus epidermidis* forms zinc-dependent amyloid fibers. *The Journal of biological chemistry*, 295(14), 4411.
- Xiong X, et al. (2011) Structural insights into quinolone antibiotic resistance mediated by pentapeptide repeat proteins: conserved surface loops direct the activity of a Qnr protein from a gram-negative bacterium. *Nucleic acids research*, 39(9), 3917.
- Catanese DJ, et al. (2011) Disconnected Interacting Protein 1 binds with high affinity to pre-tRNA and ADAT. *Biochemical and biophysical research communications*, 414(3), 506.
- Fajardo-Sanchez E, et al. (2008) Computer design of obligate heterodimer meganucleases allows efficient cutting of custom DNA sequences. *Nucleic acids research*, 36(7), 2163.
- Schuermann JP, et al. (2008) Structure of the Hsp110:Hsc70 nucleotide exchange machine. *Molecular cell*, 31(2), 232.