

Resource Summary Report

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SEDPHAT

RRID:SCR_016254

Type: Tool

Proper Citation

SEDPHAT (RRID:SCR_016254)

Resource Information

URL: <http://www.analyticalultracentrifugation.com/sedphat/>

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Description: Software for the global analysis of sedimentation velocity, sedimentation equilibrium, and/or dynamic light scattering experiments. It is a stand-alone sedimentation equilibrium analysis software that also processes isotherms of weight-average sedimentation coefficients, weight-average molar mass values, and other components., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: sedphat

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

Defining Citation: [PMID:17192587](#)

Keywords: sedimentation, isotherm, velocity, molar, mass, isothermal, titration, calorimetry, sedfit

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SEDPHAT

Resource ID: SCR_016254

Alternate URLs: sedfitsedphat.nibib.nih.gov

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260829T182509+0000

Ratings and Alerts

No rating or validation information has been found for SEDPHAT.

No alerts have been found for SEDPHAT.

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](#) .

Campos M, et al. (2025) Orthogonal approaches to AAV vector characterization: Validating quantitative TEM for partially filled particles. *Molecular therapy. Methods & clinical development*, 33(3), 101530.

Bland T, et al. (2024) Optimized PAR-2 RING dimerization mediates cooperative and selective membrane binding for robust cell polarity. *The EMBO journal*, 43(15), 3214.

Batsuli G, et al. (2023) Factor VIII antibody immune complexes modulate the humoral response to factor VIII in an epitope-dependent manner. *Frontiers in immunology*, 14, 1233356.

Rodríguez-Blázquez A, et al. (2023) Crk proteins activate the Rap1 guanine nucleotide exchange factor C3G by segregated adaptor-dependent and -independent mechanisms. *Cell communication and signaling : CCS*, 21(1), 30.

Bou-Nader C, et al. (2022) Rational engineering enables co-crystallization and structural determination of the HIV-1 matrix-tRNA complex. *STAR protocols*, 3(1), 101056.

Al Moussawi K, et al. (2022) Mutant Ras and inflammation-driven skin tumorigenesis is suppressed via a JNK-iASPP-AP1 axis. *Cell reports*, 41(3), 111503.

Bou-Nader C, et al. (2021) HIV-1 matrix-tRNA complex structure reveals basis for host control of Gag localization. *Cell host & microbe*, 29(9), 1421.

Shang J, et al. (2021) Structural mechanism underlying ligand binding and activation of PPAR?. *Structure (London, England : 1993)*, 29(9), 940.

Rudolf AF, et al. (2019) The morphogen Sonic hedgehog inhibits its receptor Patched by a pincer grasp mechanism. *Nature chemical biology*, 15(10), 975.

Li M, et al. (2019) Detection and Characterization of a Mycobacterial L-Arabinofuranose ABC Transporter Identified with a Rapid Lipoproteomics Protocol. *Cell chemical biology*, 26(6), 852.

Gustmann H, et al. (2019) Structure guided fluorescence labeling reveals a two-step binding mechanism of neomycin to its RNA aptamer. *Nucleic acids research*, 47(1), 15.

August A, et al. (2019) Copper and zinc ions govern the trans-directed dimerization of APP family members in multiple ways. *Journal of neurochemistry*, 151(5), 626.

Yoshizawa T, et al. (2018) Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. *Cell*, 173(3), 693.

Li Y, et al. (2018) Limited Cross-Linking of 4-1BB by 4-1BB Ligand and the Agonist Monoclonal Antibody Utomilumab. *Cell reports*, 25(4), 909.

McClintock MA, et al. (2018) RNA-directed activation of cytoplasmic dynein-1 in reconstituted transport RNPs. *eLife*, 7.

Cockburn JJB, et al. (2018) Insights into Kinesin-1 Activation from the Crystal Structure of KLC2 Bound to JIP3. *Structure (London, England : 1993)*, 26(11), 1486.

Zhao H, et al. (2015) SEDPHAT--a platform for global ITC analysis and global multi-method analysis of molecular interactions. *Methods (San Diego, Calif.)*, 76, 137.

Chou CY, et al. (2011) Applications of analytical ultracentrifugation to protein size-and-shape distribution and structure-and-function analyses. *Methods (San Diego, Calif.)*, 54(1), 76.

Nowotny M, et al. (2008) Specific recognition of RNA/DNA hybrid and enhancement of human RNase H1 activity by HBD. *The EMBO journal*, 27(7), 1172.

Nöllmann M, et al. (2005) Behavior of Tn3 resolvase in solution and its interaction with res. *Biophysical journal*, 89(3), 1920.