

Resource Summary Report

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SEDFIT

RRID:SCR_018365

Type: Tool

Proper Citation

SEDFIT (RRID:SCR_018365)

Resource Information

URL: <https://sedfitsedphat.nibib.nih.gov/software/default.aspx>

Proper Citation: SEDFIT (RRID:SCR_018365)

Description: Software tool for analytical ultracentrifugation developed by Dynamics of Macromolecular Assembly group of Laboratory of Cellular Imaging and Macromolecular Biophysics, National Institute of Biomedical Imaging and Bioengineering, NIH. Used for biophysical analysis of macromolecular assembly.

Synonyms: SEDFIT version 14.7g

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

Keywords: Analytical ultracentrifugation, biophysical analysis, macromolecular assembly, data, analysis, National Institute of Biomedical Imaging and Bioengineering

Funding: NIH

Availability: Free, Available for download, Freely available

Resource Name: SEDFIT

Resource ID: SCR_018365

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260821T194131+0000

Ratings and Alerts

No rating or validation information has been found for SEDFIT.

No alerts have been found for SEDFIT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Chen C, et al. (2026) Drug screening to identify compounds to eliminate Burkholderia pseudomallei through Hcp protein. iScience, 29(4), 115367.

Corchado JC, et al. (2026) Pathway-specific canalization and plasticity of gene expression during C. elegans dauer development. iScience, 29(4), 115058.

Li M, et al. (2025) Human Schlafen 14 Cleavage of Short Double-Stranded RNAs Underpins its Antiviral Activity. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(37), e01727.

Moussa R, et al. (2025) Fine-tuning the yeast GAL10 promoter and growth conditions for efficient recombinant membrane protein production and purification. Protein science : a publication of the Protein Society, 34(5), e70125.

Zhao H, et al. (2025) Evolution of a fuzzy ribonucleoprotein complex in viral assembly. eLife, 14.

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

Liu R, et al. (2024) Structural basis for difunctional mechanism of m-AMSA against African swine fever virus pP1192R. Nucleic acids research, 52(18), 11301.

Liu Y, et al. (2024) Demonstration of Physicochemical and Functional Similarity of the Biosimilar BAT1806/BIIB800 to Reference Tocilizumab. BioDrugs : clinical immunotherapeutics, biopharmaceuticals and gene therapy, 38(4), 571.

Nguyen A, et al. (2024) Modulation of biophysical properties of nucleocapsid protein in the mutant spectrum of SARS-CoV-2. eLife, 13.

Huang B, et al. (2023) Accurate and efficient protein sequence design through learning concise local environment of residues. Bioinformatics (Oxford, England), 39(3).

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.

Campos Y, et al. (2022) Biophysical and functional study of CRL5Ozz, a muscle specific ubiquitin ligase complex. Scientific reports, 12(1), 7820.

Gullett JM, et al. (2022) Identification of structural transitions in bacterial fatty acid binding proteins that permit ligand entry and exit at membranes. *The Journal of biological chemistry*, 298(3), 101676.

Wang M, et al. (2022) Discovery of a New Microbial Origin Cold-Active Neopullulanase Capable for Effective Conversion of Pullulan to Panose. *International journal of molecular sciences*, 23(13).

Radka CD, et al. (2022) Biochemical characterization of the first step in sulfonolipid biosynthesis in *Alistipes finegoldii*. *The Journal of biological chemistry*, 298(8), 102195.

Seraphim TV, et al. (2022) Assembly principles of the human R2TP chaperone complex reveal the presence of R2T and R2P complexes. *Structure (London, England : 1993)*, 30(1), 156.

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.

Szefczyk M, et al. (2022) Controlling the conformational stability of coiled-coil peptides with a single stereogenic center of a peripheral γ -amino acid residue. *RSC advances*, 12(8), 4640.

Martin EW, et al. (2021) Interplay of folded domains and the disordered low-complexity domain in mediating hnRNPA1 phase separation. *Nucleic acids research*, 49(5), 2931.

Ko CY, et al. (2021) Effects of γ -Lipoic Acid on Phagocytosis of Oligomeric Beta-Amyloid1-42 in BV-2 Mouse Microglial Cells. *Frontiers in aging neuroscience*, 13, 788723.