

Resource Summary Report

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GUSSI

RRID:SCR_014962

Type: Tool

Proper Citation

GUSSI (RRID:SCR_014962)

Resource Information

URL: <http://biophysics.swmed.edu/MBR/software.html>

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Description: Software program that can illustrate the output of SEDFIT and SEDPHAT programs and can perform simple calculations with the data. It is designed to work with sedimentation velocity, sedimentation equilibrium, ITC, DLS, and isotherm data.

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

Defining Citation: [PMID:26412649](https://pubmed.ncbi.nlm.nih.gov/26412649/)

Keywords: data visualization software, sedimentation, sedimentation velocity, sedimentation equilibrium, isotherm

Availability: Available for download, Free

Resource Name: GUSSI

Resource ID: SCR_014962

License URLs: <http://biophysics.swmed.edu/MBR/README.txt>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260803T040705+0000

Ratings and Alerts

No rating or validation information has been found for GUSSI.

No alerts have been found for GUSSI.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 221 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Kopečný DJ, et al. (2025) A monomer-dimer switch modulates the activity of plant adenosine kinase. *Journal of experimental botany*, 76(12), 3457.

Wright MM, et al. (2025) Stabilization of a miniprotein fold by an unpuckered proline surrogate. *Communications chemistry*, 8(1), 76.

Pareek G, et al. (2025) ASPL couples the assembly of stress granules with their VCP-mediated disassembly. *Science advances*, 11(41), eady3735.

Ayinuola O, et al. (2025) Hydrophobic residues in the D-domain of a plasminogen-binding M-protein modulate α -helicity, oligomerization, and surface anchoring in *Streptococcus pyogenes*. *Protein science : a publication of the Protein Society*, 34(10), e70287.

Deka RK, et al. (2025) Biophysical and biochemical evidence for the role of acetate kinases (AckAs) in an acetogenic pathway in pathogenic spirochetes. *PloS one*, 20(1), e0312642.

Fung HYJ, et al. (2025) Nap1 and Kap114 co-chaperone H2A-H2B and facilitate targeted histone release in the nucleus. *The Journal of cell biology*, 224(1).

Rodenstein C, et al. (2025) Identification of relevant analytical methods for adeno-associated virus stability assessment during formulation development. *Microbiology spectrum*, 13(8), e0180624.

Nguyen E, et al. (2025) A small periplasmic protein governs broad physiological adaptations in *Vibrio cholerae* via regulation of the DbfRS two-component system. *bioRxiv : the preprint server for biology*.

Pevec M, et al. (2025) Structural basis of G-quadruplex recognition by a camelid antibody fragment. *Nucleic acids research*, 53(10).

Fung HYJ, et al. (2025) Phosphate-dependent nuclear export via a non-classical NES class recognized by exportin Msn5. *Nature communications*, 16(1), 2580.

Saharan K, et al. (2025) Structure-function studies of a nucleoplasmin isoform from *Plasmodium falciparum*. *The Journal of biological chemistry*, 301(4), 108379.

Ferraz MVF, et al. (2025) Design of nanobody targeting SARS-CoV-2 spike glycoprotein using CDR-grafting assisted by molecular simulation and machine learning. *PLoS computational biology*, 21(4), e1012921.

Reddington CJ, et al. (2025) Unconventional structure and function of PHD domains from additional sex combs-like proteins. *The FEBS journal*, 292(24), 6626.

Duncalf L, et al. (2025) PNUTS:PP1 recruitment to Tox4 regulates chromosomal dispersal in *Drosophila* germline development. *Cell reports*, 44(5), 115693.

Wydorski PM, et al. (2025) DnaJB1 chaperone inhibits tau aggregation by recognizing its N-terminus. *bioRxiv : the preprint server for biology*.

Mao T, et al. (2025) Stabilizing effect of amino acids on protein and colloidal dispersions. *Nature*, 645(8082), 915.

Hirohata K, et al. (2025) Use of cesium chloride density gradient ultracentrifugation for the purification and characterization of recombinant adeno-associated virus. *European biophysics journal : EBJ*, 54(6), 415.

Martin F, et al. (2025) Structure of the nucleosome-bound human BCL7A. *Nucleic acids research*, 53(7).

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.

Lotz R, et al. (2025) Alternative splicing in the DBD linker region of p63 modulates binding to DNA and iASPP in vitro. *Cell death & disease*, 16(1), 4.