

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

Defining Citation: [PMID: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: 20260821T194031+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 237 mentions in open access literature.

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

Shirakawa KT, et al. (2026) The clinical missense variant E282K in PPP3CA/calcineurin shifts substrate dephosphorylation by altering active site recruitment. *Nature communications*, 17(1).

Audibert A, et al. (2026) Subunit-specific isotope labelling of heteromeric complexes using cell-free protein expression: application to the 760 kDa ClpXP molecular machine. *RSC chemical biology*, 7(2), 260.

Want K, et al. (2026) Cross-regulation of [2Fe-2S] cluster synthesis by ferredoxin-2 and frataxin. *Nature*, 649(8097), 721.

Ye JS, et al. (2026) Bacterial ubiquitin ligase engineered for small molecule and protein target identification. *The EMBO journal*, 45(3), 1024.

Irvin SC, et al. (2026) The role of large immune complexes in anti-drug antibody development: a case study of anti-SARS-CoV-2 antibody therapeutics and co-administered mRNA vaccine. *Frontiers in immunology*, 17, 1769163.

Allouche A, et al. (2026) Aging alters the vulnerability pattern to amyloid-beta oligomers in wild-type mice: a behavioral and neurobiological study. *Alzheimer's research & therapy*, 18(1).

Melicher F, et al. (2026) Structural and functional characterization of the newly identified *Photorhabdus laumondii* tumor necrosis factor-like lectin. *The FEBS journal*, 293(4), 1168.

Yu X, et al. (2026) Quantification of Glycan in Glycoproteins via AUCAgent-Enhanced Analytical Ultracentrifugation. *Pharmaceuticals (Basel, Switzerland)*, 19(2).

Komarek J, et al. (2026) Selective targeting of cortactin tandem repeat acetylation by human lysine deacetylases. *The FEBS journal*, 293(12), 3528.

Nam Y, et al. (2026) A remote surface loop modulates core structure and cold activity in phosphopantetheine adenylyltransferase. *PLoS one*, 21(3), e0342296.

Tsarenko E, et al. (2026) POx-Lipids as an Alternative to PEG-Lipids? Multimethod Assessment of Chemistry and Structure. *Analytical chemistry*, 98(11), 8277.

Woods RA, et al. (2026) *Staphylococcus aureus* adapts to the host nutritional environment by coordinating the activity of central metabolic enzymes. *PLoS pathogens*, 22(5), e1014183.

Genova R, et al. (2026) Chemotaxis to plant defense compounds in phytopathogens. PLoS pathogens, 22(5), e1014240.

Tucholski FT, et al. (2025) Tracking reduction-induced molecular changes in pathological free light chains by SV-AUC. European biophysics journal : EBJ, 54(6), 365.

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

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.

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.

Spiewla T, et al. (2025) An MST-based assay reveals new binding preferences of IFIT1 for canonically and noncanonically capped RNAs. RNA (New York, N.Y.), 31(2), 181.

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