

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

GSim

RRID:SCR_012061

Type: Tool

Proper Citation

GSim (RRID:SCR_012061)

Resource Information

URL: <http://sourceforge.net/projects/gsim/>

Proper Citation: GSim (RRID:SCR_012061)

Description: Free software tool for visualisation and processing of experimental and simulated nuclear magnetic resonance (NMR) spectra.

Resource Type: software resource

Keywords: standalone software, c++

Availability: GNU General Public License

Resource Name: GSim

Resource ID: SCR_012061

Alternate IDs: OMICS_03390

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260808T185939+0000

Ratings and Alerts

No rating or validation information has been found for GSim.

No alerts have been found for GSim.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Dennis T, et al. (2024) ZMIX: estimating ancestry proportions using GWAS association Z-scores. *Bioinformatics advances*, 4(1), vbae128.

Zarei M, et al. (2024) A global multi catchment and multi dataset synthesis for water fluxes and storage changes on land. *Scientific data*, 11(1), 1333.

do Nascimento TVM, et al. (2024) EStreams: An integrated dataset and catalogue of streamflow, hydro-climatic and landscape variables for Europe. *Scientific data*, 11(1), 879.

Kudelin AI, et al. (2021) Microwave-Assisted Synthesis, Characterization and Modeling of CPO-27-Mg Metal-Organic Framework for Drug Delivery. *Molecules* (Basel, Switzerland), 26(2).

Yan C, et al. (2019) DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. *BMC bioinformatics*, 20(Suppl 15), 538.

Martínez-Sanz M, et al. (2014) Characterization of polyhydroxyalkanoates synthesized from microbial mixed cultures and of their nanobiocomposites with bacterial cellulose nanowhiskers. *New biotechnology*, 31(4), 364.

Amar D, et al. (2014) Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. *BMC plant biology*, 14, 329.