Resource Summary Report

Generated by NIF on Apr 19, 2025

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++

Funding:

Availability: GNU General Public License

Resource Name: GSim

Resource ID: SCR_012061

Alternate IDs: OMICS_03390

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250410T070228+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.

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.

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.

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

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.