

Resource Summary Report

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

FlowSim

RRID:SCR_005224

Type: Tool

Proper Citation

FlowSim (RRID:SCR_005224)

Resource Information

URL: <http://biohaskell.org/Applications/FlowSim>

Proper Citation: FlowSim (RRID:SCR_005224)

Description: A suite of tools for simulating the 454 pyrosequencing process. It is based on the characteristics of real 454 data, and attempts to model the known aspects of the process.

Abbreviations: FlowSim

Synonyms: FlowSim - a simulation pipeline for pyrosequencing data

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:20823302](#)

Availability: Acknowledgement requested, GNU General Public License

Resource Name: FlowSim

Resource ID: SCR_005224

Alternate IDs: OMICS_00250

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260810T040413+0000

Ratings and Alerts

No rating or validation information has been found for FlowSim.

No alerts have been found for FlowSim.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

David L, et al. (2020) Targeted domain assembly for fast functional profiling of metagenomic datasets with S3A. Bioinformatics (Oxford, England), 36(13), 3975.

Ugarte A, et al. (2018) A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. Microbiome, 6(1), 149.