## **Resource Summary Report**

Generated by <u>dkNET</u> on Apr 30, 2025

# **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 resource, software application

**Defining Citation: PMID:20823302** 

Funding:

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: 20250429T054959+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 <u>dkNET</u>.

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.