

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

libRoadRunner

RRID:SCR_014763

Type: Tool

Proper Citation

libRoadRunner (RRID:SCR_014763)

Resource Information

URL: <http://libroadrunner.org/>

Proper Citation: libRoadRunner (RRID:SCR_014763)

Description: Simulation engine for systems and synthetic biology to be used with other software applications. It retains the original functionality of RoadRunner but has changes in performance, back-end design, event handling, new C++ API, and stochastic simulation support.

Resource Type: simulation software, software application, software resource

Defining Citation: [DOI:10.1093/bioinformatics/btv363](https://doi.org/10.1093/bioinformatics/btv363)

Keywords: simulation engine, simulation software, road runner, roadrunner, systems biology, synthetic biology

Funding: NIGMS GM081070

Availability: Open source, Available for download

Resource Name: libRoadRunner

Resource ID: SCR_014763

Alternate IDs: OMICS_09368

Old URLs: <https://sources.debian.org/src/libroadrunner-dev/>

License: Apache License version 2.0

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260919T195302+0000

Ratings and Alerts

No rating or validation information has been found for libRoadRunner.

No alerts have been found for libRoadRunner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Lázaro J, et al. (2025) Enhancing genome-scale metabolic models with kinetic data: resolving growth and citramalate production trade-offs in Escherichia coli. Bioinformatics advances, 5(1), vbaf166.

Matzko RO, et al. (2024) BioNexusSentinel: a visual tool for bioregulatory network and cytohistological RNA-seq genetic expression profiling within the context of multicellular simulation research using ChatGPT-augmented software engineering. Bioinformatics advances, 4(1), vbae046.

Wu J, et al. (2023) BioNetGMMFit: estimating parameters of a BioNetGen model from time-stamped snapshots of single cells. NPJ systems biology and applications, 9(1), 46.

Mendes P, et al. (2023) Reproducibility and FAIR principles: the case of a segment polarity network model. Frontiers in cell and developmental biology, 11, 1201673.

Mendes P, et al. (2023) Reproducibility and FAIR Principles: The Case of a Segment Polarity Network Model. ArXiv.

Arsène S, et al. (2022) Modeling the disruption of respiratory disease clinical trials by non-pharmaceutical COVID-19 interventions. Nature communications, 13(1), 1980.

Karagöz Z, et al. (2021) Win, Lose, or Tie: Mathematical Modeling of Ligand Competition at the Cell-Extracellular Matrix Interface. Frontiers in bioengineering and biotechnology, 9, 657244.

Porubsky VL, et al. (2020) Best Practices for Making Reproducible Biochemical Models. Cell systems, 11(2), 109.

Smith RW, et al. (2018) DMPy: a Python package for automated mathematical model construction of large-scale metabolic systems. BMC systems biology, 12(1), 72.

Zelezniak A, et al. (2018) Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. Cell systems, 7(3), 269.

Katz Y, et al. (2016) Probabilistic adaptation in changing microbial environments. PeerJ, 4, e2716.