

# Resource Summary Report

Generated by [dkNET](#) on Aug 23, 2026

## libRoadRunner

RRID:SCR\_014763

Type: Tool

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### Proper Citation

libRoadRunner (RRID:SCR\_014763)

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### 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:** 20260821T194028+0000

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### Ratings and Alerts

No rating or validation information has been found for libRoadRunner.

No alerts have been found for libRoadRunner.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

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.