

Resource Summary Report

Generated by RRID on Aug 12, 2026

mitochondria simulator

RRID:SCR_023430

Type: Tool

Proper Citation

mitochondria simulator (RRID:SCR_023430)

Resource Information

URL: <https://github.com/lufuhao/mitochondria-simulator>

Proper Citation: mitochondria simulator (RRID:SCR_023430)

Description: Software repository for mtDNA assembly project.

Synonyms: mitochondria-simulator

Resource Type: software application, software resource

Keywords: mitochondria, assembly, de bruijn graph, data mining, mtDNA assembly project,

Availability: Free, Available for download, Freely available

Resource Name: mitochondria simulator

Resource ID: SCR_023430

License: GNU General Public License v3.0

Record Creation Time: 20230404T050219+0000

Record Last Update: 20260810T040836+0000

Ratings and Alerts

No rating or validation information has been found for mitochondria simulator.

No alerts have been found for mitochondria simulator.

Data and Source Information

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Vega NM, et al. (2017) Stochastic assembly produces heterogeneous communities in the *Caenorhabditis elegans* intestine. *PLoS biology*, 15(3), e2000633.

Evans BD, et al. (2016) PyRhO: A Multiscale Optogenetics Simulation Platform. *Frontiers in neuroinformatics*, 10, 8.

Christensen CD, et al. (2015) Tracing regulatory routes in metabolism using generalised supply-demand analysis. *BMC systems biology*, 9, 89.

Mashamaite LN, et al. (2015) The glutaredoxin mono- and di-thiol mechanisms for deglutathionylation are functionally equivalent: implications for redox systems biology. *Bioscience reports*, 35(1).

Leroux AE, et al. (2013) Dissecting the catalytic mechanism of *Trypanosoma brucei* trypanothione synthetase by kinetic analysis and computational modeling. *The Journal of biological chemistry*, 288(33), 23751.

Khandelwal RA, et al. (2013) Community flux balance analysis for microbial consortia at balanced growth. *PloS one*, 8(5), e64567.

Eicher JJ, et al. (2012) Determining enzyme kinetics for systems biology with nuclear magnetic resonance spectroscopy. *Metabolites*, 2(4), 818.

Pillay CS, et al. (2011) The logic of kinetic regulation in the thioredoxin system. *BMC systems biology*, 5, 15.