Resource Summary Report

Generated by dkNET on May 20, 2025

COPASI

RRID:SCR_014260
Type: Tool

Proper Citation

COPASI (RRID:SCR_014260)

Resource Information

URL: http://copasi.org/

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Description: Software application for simulation and analysis of biochemical network models and their dynamics. COPASI supports models in the SBML standard and can simulate their behavior using ODEs or Gillespies stochastic simulation algorithm. Arbitrary discrete events can be included in such simulations. Models in COPASI are based on reactions that convert a set of species into another set of species. Simulation can be performed either with stochastic kinetics or with differential equations. COPASI also includes various methods of analysis and data visualization.

Abbreviations: COPASI

Synonyms: COPASI: Biochemical System Simulator

Resource Type: software application, data analysis software, data processing software, software resource, standalone software, simulation software

Defining Citation: DOI:10.1093/bioinformatics/btl485

Keywords: standalone software, simulation software, data analysis, biochemical system simulator, biochemical network model, biochemical network dynamics, bio.tools

Funding:

Availability: Free, Available for download, Acknowledgement requested

Resource Name: COPASI

Resource ID: SCR_014260

Alternate IDs: biotools:copasi

Alternate URLs: https://bio.tools/copasi

License: Artistic License 2.0

Record Creation Time: 20220129T080319+0000

Record Last Update: 20250519T203825+0000

Ratings and Alerts

No rating or validation information has been found for COPASI.

No alerts have been found for COPASI.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 405 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Dong J, et al. (2025) ZNF143 binds DNA and stimulates transcription initiation to activate and repress direct target genes. Nucleic acids research, 53(2).

Lang PF, et al. (2024) Reusable rule-based cell cycle model explains compartment-resolved dynamics of 16 observables in RPE-1 cells. PLoS computational biology, 20(1), e1011151.

Riepl D, et al. (2024) Long-range charge transfer mechanism of the III2IV2 mycobacterial supercomplex. Nature communications, 15(1), 5276.

Domínguez-Romero E, et al. (2024) Making PBPK models more reproducible in practice. Briefings in bioinformatics, 25(6).

Pilhál F, et al. (2024) Kinetic, thermodynamic, and ab initio insights of AsnGly isomerisation as a ticking time bomb for protein integrity. Communications chemistry, 7(1), 303.

Xu J, et al. (2024) Curating models from BioModels: Developing a workflow for creating OMEX files. bioRxiv : the preprint server for biology.

Yabut KCB, et al. (2024) Drugs Form Ternary Complexes with Human Liver Fatty Acid Binding Protein 1 (FABP1) and FABP1 Binding Alters Drug Metabolism. Molecular pharmacology, 105(6), 395.

Yabut KCB, et al. (2024) CYP2C9, CYP3A and CYP2C19 metabolize ?9-tetrahydrocannabinol to multiple metabolites but metabolism is affected by human liver fatty acid binding protein (FABP1). Biochemical pharmacology, 228, 116191.

Kampourakis T, et al. (2024) Cardiac myosin binding protein-C phosphorylation as a function of multiple protein kinase and phosphatase activities. Nature communications, 15(1), 5111.

Steiner MR, et al. (2024) Using the phospha-Michael reaction for making phosphonium phenolate zwitterions. Beilstein journal of organic chemistry, 20, 41.

Ramsey K, et al. (2024) The dynamic hypoosmotic response of Vibrio cholerae relies on the mechanosensitive channel MscS. iScience, 27(6), 110001.

Bálint D, et al. (2024) Reversible covalent c-Jun N-terminal kinase inhibitors targeting a specific cysteine by precision-guided Michael-acceptor warheads. Nature communications, 15(1), 8606.

Venkatachalapathy H, et al. (2024) Inertial effect of cell state velocity on the quiescence-proliferation fate decision. NPJ systems biology and applications, 10(1), 111.

Yabut KCB, et al. (2024) Drugs Form Ternary Complexes with Human Liver Fatty Acid Binding Protein (FABP1) and FABP1 Binding Alters Drug Metabolism. bioRxiv : the preprint server for biology.

Castaño-Cerezo S, et al. (2024) Combining systems and synthetic biology for in vivo enzymology. The EMBO journal, 43(21), 5169.

Khanijou JK, et al. (2024) Systems biology approach for enhancing limonene yield by re-engineering Escherichia coli. NPJ systems biology and applications, 10(1), 109.

Jallet D, et al. (2024) Integrative in vivo analysis of the ethanolamine utilization bacterial microcompartment in Escherichia coli. mSystems, 9(8), e0075024.

Lambreva MD, et al. (2024) Redesign of the Chlamydomonas reinhardtii QB binding niche reveals photosynthesis works in the absence of a driving force for QA-QB electron transfer. Physiologia plantarum, 176(6), e70008.

Peterson KJ, et al. (2024) Bridging molecular to cellular scales for models of membrane receptor signaling. bioRxiv : the preprint server for biology.

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.