

Resource Summary Report

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

Defining Citation: [DOI:10.1093/bioinformatics/btl485](https://doi.org/10.1093/bioinformatics/btl485)

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

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: 20260801T190500+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 435 mentions in open access literature.

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

Theisen FF, et al. (2025) Proline cis/trans Conformational Selection Controls 14-3-3 Binding. *Journal of the American Chemical Society*, 147(7), 5714.

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

Suhag R, et al. (2025) From Quantity to Reactivity: Advancing Kinetic-Based Antioxidant Testing Methods for Natural Compounds and Food Applications. *Comprehensive reviews in food science and food safety*, 24(4), e70229.

Zauser M, et al. (2025) Differential regulation of calcium-activated plant kinases in *Arabidopsis thaliana*. *The Plant journal : for cell and molecular biology*, 123(5), e70413.

Harwood CR, et al. (2025) Agonist efficacy at the $\alpha 2$ AR is driven by the faster association rate of the Gs protein. *Frontiers in pharmacology*, 16, 1367991.

Hernández-Esquivel L, et al. (2025) Modeling Krebs cycle from liver, heart and hepatoma mitochondria, supported Complex I as target for specific inhibition of cancer cell proliferation. *Frontiers in oncology*, 15, 1557638.

Hoffman SM, et al. (2025) Balancing Doses of EL222 and Light Improves Optogenetic Induction of Protein Production in *Komagataella phaffii*. *Biotechnology and bioengineering*, 122(9), 2478.

Sigg A, et al. (2025) The P134Q Sucrose Phosphorylase: Subtle Changes in the Catalytic Properties Benefit the Production of 2-O- α -Glucosyl Glycerol. *Biotechnology and bioengineering*, 122(9), 2465.

Braunstein H, et al. (2025) Modeling the use of transient ligand binding information by AMPA receptors. *NPJ systems biology and applications*, 11(1), 68.

Kiel C, et al. (2025) Quantitative modeling of rod outer segment phagocytosis and recycling. *Scientific reports*, 15(1), 20946.

Kalra P, et al. (2025) A comparative computational analysis of IFN-alpha pharmacokinetics and its induced cellular response in mice and humans. *PLoS computational biology*, 21(9), e1013509.

Merulla AE, et al. (2025) Computational modeling of ATM signaling: a predictive framework for drug repurposing in ataxia-telangiectasia. *NPJ systems biology and applications*, 11(1), 146.

Safenkova IV, et al. (2025) Advancing Lateral Flow Detection in CRISPR/Cas12a Systems Through Rational Understanding and Design Strategies of Reporter Interactions. *Biosensors*, 15(12).

Redfern-Nichols T, et al. (2025) Loss-of-function G α s rare disease variants exert mutation-specific effects on GPCR signaling. *Science signaling*, 18(887), eado7543.

Kaya HE, et al. (2025) Integrated tumour-immune cell response modelling of luminal a breast cancer details malignant signalling and ST3Gal1 inhibitor-induced reversal. *Glycobiology*, 35(8).

Khandibharad S, et al. (2025) Computational Cellular Mathematical Model Aids Understanding the cGAS-STING in NSCLC Pathogenicity. *Bio-protocol*, 15(5), e5223.

Sternebring O, et al. (2025) A Multi-Scale Mechanistic Model of Ulcerative Colitis to Investigate the Effects of Selective Suppression of IL-6 Trans-Signaling. *Clinical and translational science*, 18(9), e70366.

Masison J, et al. (2025) Mathematical modeling reveals ferritin as the strongest cellular driver of dietary iron transfer block in enterocytes. *PLoS computational biology*, 21(3), e1012374.

Stefan A, et al. (2025) Not only an inhibitor: Trehalose enhances the catalytic action exerted on oxaloacetate by rabbit lactate dehydrogenase. *Protein science : a publication of the Protein Society*, 34(10), e70304.

Bowman G, et al. (2025) Exploring Energy Conservation in Sulphate-Dependent Anaerobic Methane-Oxidising Consortia Through Metabolic Modelling. *Environmental microbiology*, 27(7), e70156.