

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: software resource, software application, simulation software, data analysis software, standalone software, data processing 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: 20260808T190029+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 445 mentions in open access literature.

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

Manias DM, et al. (2026) Mechanistic Understanding of Pandemic Dynamics: A Multiscale Algorithmic Framework. *Life* (Basel, Switzerland), 16(6).

Pang H, et al. (2026) Evidence for hydroperoxide formation through atmospheric aqueous photochemistry of α -keto acids. *Science advances*, 12(2), eadx4527.

Goswami S, et al. (2026) miRNA-Mediated Signaling Networks in Non-Small Cell Lung Cancer: Linking Tumor Progression to Sarcopenia. *International journal of molecular sciences*, 27(11).

Rodríguez-Correa E, et al. (2026) A kinetics-based model of haematopoiesis reveals extrinsic regulation of skewed lineage output from stem cells. *Nature cell biology*, 28(6), 1127.

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).

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.

Akopyan K, et al. (2025) Preparation for mitosis requires gradual CDK1 activation. *iScience*, 28(5), 112292.

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.

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.

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

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

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

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.

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.

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

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

Peñas-Defrutos MN, et al. (2025) Opposite Effects of Added AsPh₃ Reveal a Drastic Mechanistic Switch in RhI/AuI Transmetalations via Rh-Au Bonded Intermediates. *Inorganic chemistry*, 64(27), 13729.

Holló G, et al. (2025) A tool for modeling gene regulatory networks (GRN_modeler) and its applications to synthetic biology. *Molecular systems biology*, 21(11), 1618.