

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

OpenCOR

RRID:SCR_019001

Type: Tool

Proper Citation

OpenCOR (RRID:SCR_019001)

Resource Information

URL: <https://opencor.ws/>

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Description: Open source cross platform modeling environment for reproducible science. Used to organise, edit, simulate and analyse models described in CellML format, using SED-ML and COMBINE archives.

Resource Type: simulation software, software application, software resource

Keywords: Modeling environment, reproducible science, CellML format model, CellML format model analysis, CellML format model simulation

Availability: Free, Available for download, Freely available

Resource Name: OpenCOR

Resource ID: SCR_019001

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260905T132845+0000

Ratings and Alerts

No rating or validation information has been found for OpenCOR.

No alerts have been found for OpenCOR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Maltsev AV, et al. (2023) A novel conceptual model of heart rate autonomic modulation based on a small-world modular structure of the sinoatrial node. *Frontiers in physiology*, 14, 1276023.

Means SA, et al. (2023) Steady-state approximations for Hodgkin-Huxley cell models: Reduction of order for uterine smooth muscle cell model. *PLoS computational biology*, 19(8), e1011359.

Maltsev AV, et al. (2022) Functional Heterogeneity of Cell Populations Increases Robustness of Pacemaker Function in a Numerical Model of the Sinoatrial Node Tissue. *Frontiers in physiology*, 13, 845634.

Yang D, et al. (2021) Ca²⁺ and Membrane Potential Transitions During Action Potentials Are Self-Similar to Each Other and to Variability of AP Firing Intervals Across the Broad Physiologic Range of AP Intervals During Autonomic Receptor Stimulation. *Frontiers in physiology*, 12, 612770.

Shahidi N, et al. (2021) Hierarchical semantic composition of biosimulation models using bond graphs. *PLoS computational biology*, 17(5), e1008859.

Waltemath D, et al. (2020) The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). *Journal of integrative bioinformatics*, 17(2-3).