

Resource Summary Report

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Virtual Cell at the National Resource for Cell Analysis and Modeling

RRID:SCR_007421

Type: Tool

Proper Citation

Virtual Cell at the National Resource for Cell Analysis and Modeling (RRID:SCR_007421)

Resource Information

URL: <http://vcell.org/>

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Description: V-Cell is a remote user modeling and simulation environment utilizing Java's Remote Method Invocation (RMI). The biologically oriented user interface allows experimentalists to create models, define cellular geometry, specify simulations and analyze the simulation results. The results are run and stored on a remote server and can be reviewed in the software and/or exported in a variety of popular formats. The design of the biological to mathematical mapping allows for separate use of biological and math components, and includes automatic mathematical simplification using pseudo-steady approximations and mass conservation relationships. This allows for direct specification of mathematical problems, performing simulations and analysis on those systems. The stand alone mathematics user interface is also a powerful tool for modeling reaction-diffusion systems. A transparent general purpose solver is used to translate the initial biological description into a set of concise mathematical problems. The solver is transparent to the average user, but is accessible to the theorist as the Math Editor component. The software is composed of three main components: 1. The modeling framework represents the physiological models of the Virtual Cell and allows for persistence and database support. 2. The mathematics framework transparently solves an important class of mathematical problems encountered in the cellular modeling. 3. The WWW accessible graphical user interface provides access to the technology mentioned above. The user interface has been developed using Java 2 Applets.

Abbreviations: V-Cell, VCell

Synonyms: VCell - The Virtual Cell, Virtual Cell

Resource Type: simulation software, software application, software resource

Keywords: cell modeling, model cell, virtual cell, virtual cell, FASEB list

Resource Name: Virtual Cell at the National Resource for Cell Analysis and Modeling

Resource ID: SCR_007421

Alternate IDs: nif-0000-00529

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260821T193816+0000

Ratings and Alerts

No rating or validation information has been found for Virtual Cell at the National Resource for Cell Analysis and Modeling.

No alerts have been found for Virtual Cell at the National Resource for Cell Analysis and Modeling.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 79 mentions in open access literature.

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

Bener MB, et al. (2026) Protocol to evaluate a lineage marking system in the Drosophila testis. STAR protocols, 7(2), 104479.

Kannan M, et al. (2025) Leveraging public AI tools to explore systems biology resources in mathematical modeling. NPJ systems biology and applications, 11(1), 15.

Al Ghafari M, et al. (2025) Key genes altered in glioblastoma based on bioinformatics (Review). Oncology letters, 29(5), 243.

Wan Y, et al. (2025) Protein interactions, calcium, phosphorylation, and cholesterol modulate CFTR cluster formation on membranes. Proceedings of the National Academy of Sciences of the United States of America, 122(11), e2424470122.

Bener MB, et al. (2025) Detection of dedifferentiated stem cells in Drosophila testis. bioRxiv : the preprint server for biology.

Khan S, et al. (2025) Resistance and germination of spores of Bacillus species lacking members of a spore integral inner membrane protein family and locations of these proteins in spores. Journal of bacteriology, 207(10), e0021725.

Bener MB, et al. (2025) Detection of dedifferentiated stem cells in the Drosophila testis. *iScience*, 28(10), 113564.

Zhou X, et al. (2024) A noncanonical GTPase signaling mechanism controls exit from mitosis in budding yeast. *bioRxiv : the preprint server for biology*.

Norman CA, et al. (2023) The release of inhibition model reproduces kinetics and plasticity of neurotransmitter release in central synapses. *Research square*.

Loconte V, et al. (2023) Soft X-ray tomograms provide a structural basis for whole-cell modeling. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 37(1), e22681.

Mendes P, et al. (2023) Reproducibility and FAIR principles: the case of a segment polarity network model. *Frontiers in cell and developmental biology*, 11, 1201673.

Mendes P, et al. (2023) Reproducibility and FAIR Principles: The Case of a Segment Polarity Network Model. *ArXiv*.

Danielsson BE, et al. (2023) Nuclear lamina strain states revealed by intermolecular force biosensor. *Nature communications*, 14(1), 3867.

Ruiter FAA, et al. (2023) Optimization of Media Change Intervals through Hydrogels Using Mathematical Models. *Biomacromolecules*, 24(2), 604.

Karagöz Z, et al. (2023) Computational evidence for multi-layer crosstalk between the cadherin-11 and PDGFR pathways. *Scientific reports*, 13(1), 15804.

Nosbisch JL, et al. (2022) A kinetic model of phospholipase C- α 1 linking structure-based insights to dynamics of enzyme autoinhibition and activation. *The Journal of biological chemistry*, 298(5), 101886.

Sinner EK, et al. (2022) Purification and characterization of sequential cobalamin-dependent radical SAM methylases ThnK and TokK in carbapenem β -lactam antibiotic biosynthesis. *Methods in enzymology*, 669, 29.

Jayasinghe MK, et al. (2022) The Role of in silico Research in Developing Nanoparticle-Based Therapeutics. *Frontiers in digital health*, 4, 838590.

Liu F, et al. (2022) Hybrid modelling of biological systems: current progress and future prospects. *Briefings in bioinformatics*, 23(3).

Paes D, et al. (2022) Computational investigation of the dynamic control of cAMP signaling by PDE4 isoform types. *Biophysical journal*, 121(14), 2693.