

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

Electronic Cell Project

RRID:SCR_007381

Type: Tool

Proper Citation

Electronic Cell Project (RRID:SCR_007381)

Resource Information

URL: <http://www.e-cell.org/>

Proper Citation: Electronic Cell Project (RRID:SCR_007381)

Description: Software platform, general technologies and theoretical supports for computational biology with the grand aim to make precise whole cell simulation at the molecular level possible. Technologies include formalisms and techniques, including technologies to predict, obtain or estimate parameters such as reaction rates and concentrations of molecules in the cell. The E-Cell System is a software platform for modeling, simulation and analysis of complex, heterogeneous and multi-scale system like the cell. The E-Cell Project is open to anyone who shares the view with u that development of cell simulation technology, and, even if such ultimate goal might not be within ten years of reach yet, solving various conceptual, computational and experimental problems that will continue to arise in the course of pursuing it, may have a multitude of eminent scientific, medical and engineering impacts on our society.

Synonyms: E-Cell

Resource Type: software application, simulation software, software resource, modeling software

Keywords: gene, protein, ontology, binary executable; software development tool, cell

Resource Name: Electronic Cell Project

Resource ID: SCR_007381

Alternate IDs: nif-0000-00378

Alternate URLs: <https://sources.debian.org/src/ecell/>

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260728T043249+0000

Ratings and Alerts

No rating or validation information has been found for Electronic Cell Project.

No alerts have been found for Electronic Cell Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Tummler K, et al. (2024) Data integration strategies for whole-cell modeling. FEMS yeast research, 24.

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

Kenner B, et al. (2021) Artificial Intelligence and Early Detection of Pancreatic Cancer: 2020 Summative Review. Pancreas, 50(3), 251.

Martinez O, et al. (2018) On an algorithmic definition for the components of the minimal cell. PloS one, 13(6), e0198222.

Alawieh A, et al. (2012) Systems biology, bioinformatics, and biomarkers in neuropsychiatry. Frontiers in neuroscience, 6, 187.

Yachie-Kinoshita A, et al. (2010) A metabolic model of human erythrocytes: practical application of the E-Cell Simulation Environment. Journal of biomedicine & biotechnology, 2010, 642420.

Manninen T, et al. (2010) Postsynaptic signal transduction models for long-term potentiation and depression. Frontiers in computational neuroscience, 4, 152.

Loewe L, et al. (2008) Computational models in systems biology. Genome biology, 9(12), 328.

Selvarajoo K, et al. (2008) Signaling flux redistribution at toll-like receptor pathway junctions. PloS one, 3(10), e3430.

Itoh H, et al. (2007) Simulation of developmental changes in action potentials with ventricular cell models. Systems and synthetic biology, 1(1), 11.

Jiang N, et al. (2007) A kinetic core model of the glucose-stimulated insulin secretion network of pancreatic beta cells. Mammalian genome : official journal of the International Mammalian Genome Society, 18(6-7), 508.

Materi W, et al. (2007) Computational systems biology in cancer: modeling methods and applications. *Gene regulation and systems biology*, 1, 91.

Hu B, et al. (2006) Modeling Hsp70-mediated protein folding. *Biophysical journal*, 91(2), 496.

Nakayama Y, et al. (2005) Dynamic simulation of red blood cell metabolism and its application to the analysis of a pathological condition. *Theoretical biology & medical modelling*, 2, 18.

Nakai K, et al. (2002) Genome informatics for data-driven biology. *Genome biology*, 3(4), REPORTS4010.