

# Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

## NSR Physiome Project

RRID:SCR\_007379

Type: Tool

### Proper Citation

NSR Physiome Project (RRID:SCR\_007379)

### Resource Information

**URL:** <http://nsr.bioeng.washington.edu/>

**Proper Citation:** NSR Physiome Project (RRID:SCR\_007379)

**Description:** Database of physiological, pharmacological, and pathological information on humans and other organisms and integration through computational modeling. Models include everything from diagrammatic schema, suggesting relationships among elements composing a system, to fully quantitative, computational models describing the behavior of physiological systems and an organism's response to environmental change. Each mathematical model is an internally self-consistent summary of available information, and thereby defines a working hypothesis about how a system operates. Predictions from such models are subject to test, with new results leading to new models. A Tool developed for the NSR Physiome project is JSim, an open source, free software. JSim is a Java-based simulation system for building quantitative numeric models and analyzing them with respect to experimental reference data. JSim's primary focus is in physiology and biomedicine, however its computational engine is quite general and applicable to a wide range of scientific domains. JSim models may intermix ODEs, PDEs, implicit equations, integrals, summations, discrete events and procedural code as appropriate. JSim's model compiler can automatically insert conversion factors for compatible physical units as well as detect and reject unit unbalanced equations. JSim also imports the SBML and CellML model archival formats. All JSim models are open source. Goals of the Physiome Project: - To develop and database observations of physiological phenomenon and interpret these in terms of mechanism (a fundamentally reductionist goal). - To integrate experimental information into quantitative descriptions of the functioning of humans and other organisms (modern integrative biology glued together via modeling). - To disseminate experimental data and integrative models for teaching and research. - To foster collaboration amongst investigators worldwide, to speed up the discovery of how biological systems work. - To determine the most effective targets (molecules or systems) for therapy, either pharmaceutical or genomic. - To provide information for the design of tissue-engineered, biocompatible implants.

**Abbreviations:** NSR Physiome Project

**Synonyms:** National Simulation Resource Physiome Project

**Resource Type:** data or information resource, software resource, training resource, software application, topical portal, simulation software, professional program, portal

**Keywords:** physiome, computational modeling, cell, organ, organism, human, model, physiological, pharmacological, pathological, model repository, sbml, cellml, biophysics, biochemistry, database, proteome, jsim simulation analysis system, data analysis tool, parameter optimization tool, integrating biological system

**Funding:** NSF BE08407;  
NHLBI T15 HL88516-01;  
NSF BES-0506477;  
NHLBI R01HL073598;  
NIBIB R01EB001973

**Resource Name:** NSR Physiome Project

**Resource ID:** SCR\_007379

**Alternate IDs:** nif-0000-00532

**Record Creation Time:** 20220129T080241+0000

**Record Last Update:** 20260808T185907+0000

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## Ratings and Alerts

No rating or validation information has been found for NSR Physiome Project.

No alerts have been found for NSR Physiome Project.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Morton EL, et al. (2019) Transcriptional Circuit Fragility Influences HIV Proviral Fate. Cell reports, 27(1), 154.

Munro PD, et al. (2016) Aspects of protein-DNA interactions: a review of quantitative thermodynamic theory for modelling synthetic circuits utilising LacI and CI repressors, IPTG and the reporter gene lacZ. Biophysical reviews, 8(4), 331.

Vinnakota K, et al. (2006) Dynamics of muscle glycogenolysis modeled with pH time course computation and pH-dependent reaction equilibria and enzyme kinetics.

Biophysical journal, 91(4), 1264.