Resource Summary Report

Generated by dkNET on May 19, 2025

SYCAMORE

RRID:SCR_021117
Type: Tool

Proper Citation

SYCAMORE (RRID:SCR_021117)

Resource Information

URL: http://sycamore.h-its.org/sycamore/

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Description: Web browser based application that facilitates construction, simulation and analysis of kinetic models in systems biology. Allows database supported modelling, basic model checking and estimation of unknown kinetic parameters based on protein structures. Integrates different online applications as well as locally installed software. Provides user guidance for sequence of steps associated with model building, model checking, simulation and analysis of results.

Synonyms: SYstems biology Computational Analysis and MOdeling Research Environment

Resource Type: web service, software resource, data access protocol

Defining Citation: PMID:18463116

Keywords: Systems biology computational analysis, modeling research environment, kinetic models analysis, kinetic models construction, kinetic models simulation, systems biology, protein structures, kinetic parameters

Funding: Klaus Tschira Foundation ;
German Ministry of Education and Research

Availability: Free, Freely available

Resource Name: SYCAMORE

Resource ID: SCR_021117

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250519T204234+0000

Ratings and Alerts

No rating or validation information has been found for SYCAMORE.

No alerts have been found for SYCAMORE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Eriksson O, et al. (2022) Combining hypothesis- and data-driven neuroscience modeling in FAIR workflows. eLife, 11.