# **Resource Summary Report**

Generated by RRID on May 22, 2025

## **SYCAMORE**

RRID:SCR\_021117

Type: Tool

### **Proper Citation**

SYCAMORE (RRID:SCR\_021117)

#### **Resource Information**

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

**Proper Citation:** SYCAMORE (RRID:SCR\_021117)

**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:** 20250522T061249+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 RRID.

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