

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

Flux Simulator

RRID:SCR_005088

Type: Tool

Proper Citation

Flux Simulator (RRID:SCR_005088)

Resource Information

URL: <http://flux.sammeth.net/capacitor.html>

Proper Citation: Flux Simulator (RRID:SCR_005088)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 5, 2023. Software that aims at modeling RNA-Seq experiments in silico: sequencing reads are produced from a reference genome according annotated transcripts. The simulation pipeline models different steps as modules, each with a minimal set of parameters that can be estimated by experimental parameters. The first step is-in fact-a transcriptome simulator. Subsequently, common sources of systematic bias in the abundance and distribution of produced reads are simulated by in silico library preparation and sequencing.

Abbreviations: Flux Simulator

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Flux Simulator

Resource ID: SCR_005088

Alternate IDs: OMICS_01365

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195620+0000

Ratings and Alerts

No rating or validation information has been found for Flux Simulator.

No alerts have been found for Flux Simulator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Sheehan S, et al. (2024) A machine learning approach for quantifying age-related histological changes in the mouse kidney. GeroScience, 46(2), 2571.

Singh D, et al. (2011) FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. Bioinformatics (Oxford, England), 27(19), 2633.