

Resource Summary Report

Generated by [NIF](#) on Aug 20, 2026

Stem

RRID:SCR_024499

Type: Tool

Proper Citation

Stem (RRID:SCR_024499)

Resource Information

URL: <https://www.cs.cmu.edu/~jernst/stem/>

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Description: Software tool for analysis of short time series gene expression data. Java program for clustering, comparing, and visualizing short time series gene expression data from microarray experiments. Allows to identify significant temporal expression profiles and genes associated with these profiles and to compare behavior of these genes across multiple conditions. STEM is fully integrated with the Gene Ontology.

Synonyms: Short Time-series Expression Miner

Resource Type: software application, data processing software, software resource, data analysis software

Defining Citation: [PMID:16597342](#)

Keywords: short time series gene expression data analysis, clustering, comparing, visualizing, short time series gene expression data, microarray experiments data, identify temporal expression profiles identify genes associated with expression profiles, compare behavior of genes across multiple conditions,

Availability: Free, Available for download, Freely available

Resource Name: Stem

Resource ID: SCR_024499

Record Creation Time: 20231002T161336+0000

Record Last Update: 20260821T043119+0000

Ratings and Alerts

No rating or validation information has been found for Stem.

No alerts have been found for Stem.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Guo Q, et al. (2025) Epithelial characteristics of ovarian clear cell carcinoma at single-cell resolution. *Communications biology*, 8(1), 1156.

Bak GR, et al. (2025) Changes in the potato rhizosphere microbiota richness and diversity occur in a growth stage-dependent manner. *Scientific reports*, 15(1), 2284.

Guo G, et al. (2024) Genome-wide identification of GA2ox genes family and analysis of PbrGA2ox1-mediated enhanced chlorophyll accumulation by promoting chloroplast development in pear. *BMC plant biology*, 24(1), 166.

Shao L, et al. (2024) Comparative Proteomics and Metabonomics Analysis of Different Diapause Stages Revealed a New Regulation Mechanism of Diapause in *Loxostege sticticalis* (Lepidoptera: Pyralidae). *Molecules* (Basel, Switzerland), 29(15).

Cao QQ, et al. (2021) Transcriptome analysis of molecular mechanisms underlying facial nerve injury repair in rats. *Neural regeneration research*, 16(11), 2316.

Frappier V, et al. (2014) A coarse-grained elastic network atom contact model and its use in the simulation of protein dynamics and the prediction of the effect of mutations. *PLoS computational biology*, 10(4), e1003569.