

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

Short Time-series Expression Miner (STEM)

RRID:SCR_005016

Type: Tool

Proper Citation

Short Time-series Expression Miner (STEM) (RRID:SCR_005016)

Resource Information

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

Proper Citation: Short Time-series Expression Miner (STEM) (RRID:SCR_005016)

Description: The Short Time-series Expression Miner (STEM) is a Java program for clustering, comparing, and visualizing short time series gene expression data from microarray experiments (~8 time points or fewer). STEM allows researchers to identify significant temporal expression profiles and the genes associated with these profiles and to compare the behavior of these genes across multiple conditions. STEM is fully integrated with the Gene Ontology (GO) database supporting GO category gene enrichment analyses for sets of genes having the same temporal expression pattern. STEM also supports the ability to easily determine and visualize the behavior of genes belonging to a given GO category or user defined gene set, identifying which temporal expression profiles were enriched for these genes. (Note: While STEM is designed primarily to analyze data from short time course experiments it can be used to analyze data from any small set of experiments which can naturally be ordered sequentially including dose response experiments.) Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: STEM

Synonyms: Short Time-series Expression Miner

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

Defining Citation: [PMID:16597342](#), [PMID:15961453](#)

Keywords: statistical analysis, term enrichment, visualization, cluster, compare, short time series, gene expression, microarray, expression profile, gene, gene ontology, gene enrichment analyses, FASEB list

Funding: NIAID NO1 AI-5001;
NSF 0448453

Availability: Open unspecified license - Free for academic use

Resource Name: Short Time-series Expression Miner (STEM)

Resource ID: SCR_005016

Alternate IDs: nlx_97053

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260821T193730+0000

Ratings and Alerts

No rating or validation information has been found for Short Time-series Expression Miner (STEM).

No alerts have been found for Short Time-series Expression Miner (STEM).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Tian Y, et al. (2026) Cytokinin Oxidase/Dehydrogenase 1 (FvCKX1) Coordinates Receptacle Growth and Achene Maturation in Strawberry. *Plants* (Basel, Switzerland), 15(8).

Kohsar A, et al. (2026) Comprehensive analysis of spinal cord inflammatory factors in HIV Tat-induced neuropathy in mice. *Neuroscience*, 595, 205.

Chen Y, et al. (2025) MicroRNA expression dynamics in mouse liver at different stages of *Echinococcus multilocularis* infection. *BMC genomics*, 26(1), 941.

Wang M, et al. (2025) Unraveling the interaction between the phageome and bacteriome in the rumen and its role in influencing metabolome dynamics in dairy cows at different lactation stages. *Microbiome*, 13(1), 257.

Xiao B, et al. (2025) Single-cell RNA sequencing reveals hemocyte heterogeneity, differentiation trajectories, and viral tropism in shrimp (*Macrobrachium rosenbergii*) infected with decapodiridovirus *litopenaeus*1. *Journal of virology*, 99(8), e0079025.

Li K, et al. (2024) Growth hormone promotes the reconstruction of injured axons in the hypothalamo-neurohypophyseal system. *Neural regeneration research*, 19(10), 2249.

- Zhu K, et al. (2024) Metabolome and Transcriptome Analyses Reveal Metabolomic Variations and Key Transcription Factors Involved in Lipid Biosynthesis During Seed Development in *Carya illinoensis*. *International journal of molecular sciences*, 25(21).
- Bao H, et al. (2024) Alteration of Gene Expression After Entecavir and Pegylated Interferon Therapy in HBV-Infected Chimeric Mouse Liver. *Viruses*, 16(11).
- Luo L, et al. (2024) Effects of Different Salinity Stress on the Transcriptomic Responses of Freshwater Crayfish (*Procambarus clarkii*, Girard, 1852). *Biology*, 13(7).
- Zhao Y, et al. (2024) Exploring Alashan Ground Squirrel (*Spermophilus alashanicus*) Diversity: Metagenomic and Transcriptomic Datasets from the Helan Mountains. *Scientific data*, 11(1), 517.
- Wang Y, et al. (2023) Proteomic profiles and the function of RBP4 in endometrium during embryo implantation phases in pigs. *BMC genomics*, 24(1), 200.
- He L, et al. (2023) HMMR alleviates endoplasmic reticulum stress by promoting autophagolysosomal activity during endoplasmic reticulum stress-driven hepatocellular carcinoma progression. *Cancer communications (London, England)*, 43(9), 981.
- Wang Y, et al. (2023) Liver Transcriptome Analysis of the Black Porgy (*Acanthopagrus schlegelii*) under Acute Low-Temperature Stress. *Life (Basel, Switzerland)*, 13(3).
- Wu B, et al. (2023) A chemically defined system supports two distinct types of stem cell from a single blastocyst and their self-assembly to generate blastoid. *Cell proliferation*, 56(6), e13396.
- Sun Q, et al. (2023) Transcriptome Analysis Reveals the Response Mechanism of *Digitaria sanguinalis*, *Arabidopsis thaliana* and *Poa annua* under 4,8-Dihydroxy-1-tetralone Treatment. *Plants (Basel, Switzerland)*, 12(14).
- Sun B, et al. (2023) Dynamic observation of circRNA and mRNA profiles in a rat model of deep vein thrombosis. *Experimental and therapeutic medicine*, 26(4), 467.
- Ren ZW, et al. (2023) Nutrient accumulation and transcriptome patterns during grain development in rice. *Journal of experimental botany*, 74(3), 909.
- Huang W, et al. (2023) Differentially expression analyses in fruit of cultivated and wild species of grape and peach. *Scientific reports*, 13(1), 1997.
- Liu YS, et al. (2023) A comparison of the impact on neuronal transcriptome and cognition of rAAV5 transduction with three different doses in the mouse hippocampus. *Frontiers in molecular neuroscience*, 16, 1195327.
- Bai S, et al. (2023) Regulation of hormone pathways in wheat infested by *Blumeria graminis* f. sp. *tritici*. *BMC plant biology*, 23(1), 554.