

Resource Summary Report

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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/>

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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: software resource, data processing software, software application

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: 20260803T040407+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 81 mentions in open access literature.

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

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

Xiao B, et al. (2025) Single-cell RNA sequencing reveals hemocyte heterogeneity, differentiation trajectories, and viral tropism in shrimp (*Macrobrachium rosenbergii*) infected with decapodiridovirus litopenaeus1. *Journal of virology*, 99(8), e0079025.

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.

Bao H, et al. (2024) Alteration of Gene Expression After Entecavir and Pegylated Interferon Therapy in HBV-Infected Chimeric Mouse Liver. *Viruses*, 16(11).

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.

Luo L, et al. (2024) Effects of Different Salinity Stress on the Transcriptomic Responses of Freshwater Crayfish (*Procambarus clarkii*, Girard, 1852). *Biology*, 13(7).

- Li K, et al. (2024) Growth hormone promotes the reconstruction of injured axons in the hypothalamo-neurohypophyseal system. *Neural regeneration research*, 19(10), 2249.
- 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.
- 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).
- 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 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.
- Bai S, et al. (2023) Regulation of hormone pathways in wheat infested by *Blumeria graminis* f. sp. *tritici*. *BMC plant biology*, 23(1), 554.
- Wang Y, et al. (2023) Liver Transcriptome Analysis of the Black Porgy (*Acanthopagrus schlegelii*) under Acute Low-Temperature Stress. *Life (Basel, Switzerland)*, 13(3).
- 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.
- Lin JQ, et al. (2022) Newly discovered molecules associated with trimetazidine on improvement of skeletal muscle function in aging: evidence from myoblasts and mice. *Experimental gerontology*, 161, 111733.
- Chen F, et al. (2021) The identification of neutrophils-mediated mechanisms and potential therapeutic targets for the management of sepsis-induced acute immunosuppression using bioinformatics. *Medicine*, 100(12), e24669.
- Luo H, et al. (2021) Comprehensive Analysis of circRNA Expression Profiles During Cervical Carcinogenesis. *Frontiers in oncology*, 11, 676609.
- Cheng K, et al. (2021) Integrated Transcriptomic and Bioinformatics Analyses Reveal the Molecular Mechanisms for the Differences in Seed Oil and Starch Content Between *Glycine max* and *Cicer arietinum*. *Frontiers in plant science*, 12, 743680.