

Resource Summary Report

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TM4 Microarray Software Suite - TIGR MultiExperiment Viewer

RRID:SCR_001915

Type: Tool

Proper Citation

TM4 Microarray Software Suite - TIGR MultiExperiment Viewer (RRID:SCR_001915)

Resource Information

URL: <http://www.tm4.org/mev.html>

Proper Citation: TM4 Microarray Software Suite - TIGR MultiExperiment Viewer (RRID:SCR_001915)

Description: A desktop application for the analysis, visualization and data-mining of large-scale genomic data. It is a versatile microarray tool, incorporating sophisticated algorithms for clustering, visualization, classification, statistical analysis and biological theme discovery. MeV generates informative and interrelated displays of expression and annotation data from single or multiple experiments. A huge array of algorithms are included in MeV modules, and are available at a button-click, such as K-means clustering, Hierarchical clustering, t-Tests, Significance Analysis of Microarrays, Gene Set Enrichment Analysis, and EASE. Extensive documentation is available for helping new users get started with MeV. A Quickstart Guide provides the tutorial a brand new person will need to get their first dataset loaded and displayed in the program. Returning MEV users will want to check out the release notes to see what new features are available in the latest versions of the program. Tutorials have been written about several of its more involved features.

Abbreviations: MeV

Synonyms: MultiExperiment Viewer, MultiExperiment Viewer (MeV), TM4 TIGR MeV

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

Defining Citation: [PMID:16939790](#), [PMID:12613259](#)

Keywords: gene expression, analysis, annotation, classification, microarray, visualization, statistical analysis, clustering, biological theme, graphic, annotation, data mining

Funding: NCRR 5P20RR015578-07

Availability: Open unspecified license, Free for academic use

Resource Name: TM4 Microarray Software Suite - TIGR MultiExperiment Viewer

Resource ID: SCR_001915

Alternate IDs: SCR_005576, OMICS_00781

License: Artistic License v2

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260903T234508+0000

Ratings and Alerts

No rating or validation information has been found for TM4 Microarray Software Suite - TIGR MultiExperiment Viewer.

No alerts have been found for TM4 Microarray Software Suite - TIGR MultiExperiment Viewer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 487 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kumar V, et al. (2026) Host-Induced Silencing of Rhizoctonia Solani 5-Enolpyruvylshikimate-3-Phosphate Synthase Impairs Its Virulence in Rice. Plant biotechnology journal, 24(6), 3573.

Veitia RA, et al. (2025) Deciphering the Impact of AKT1 Pathogenic Variants in Juvenile Granulosa Cell Tumors Using a Drosophila Model. Molecular & cellular proteomics : MCP, 24(12), 101466.

Sato S, et al. (2025) Effects of female hormone withdrawal and ulipristal acetate on MED12 mutation positive and negative uterine leiomyomas using a xenograft model. Scientific reports, 15(1), 40028.

Degrelle SA, et al. (2024) Understanding bovine embryo elongation: a transcriptomic study of trophoblastic vesicles. Frontiers in physiology, 15, 1331098.

Shi J, et al. (2024) Early 2-Factor Transcription Factors Associated with Progression and Recurrence in Bevacizumab-Responsive Subtypes of Glioblastoma. Cancers, 16(14).

- Chaubal R, et al. (2024) Surgical Tumor Resection Deregulates Hallmarks of Cancer in Resected Tissue and the Surrounding Microenvironment. *Molecular cancer research : MCR*, 22(6), 572.
- Selvaraj S, et al. (2023) Diclofenac Disrupts the Circadian Clock and through Complex Cross-Talks Aggravates Immune-Mediated Liver Injury-A Repeated Dose Study in Minipigs for 28 Days. *International journal of molecular sciences*, 24(2).
- Lin W, et al. (2023) IGFBP5 is an ROR1 ligand promoting glioblastoma invasion via ROR1/HER2-CREB signaling axis. *Nature communications*, 14(1), 1578.
- Kwon H, et al. (2023) Extracellular Vesicles Released by *Lactobacillus paracasei* Mitigate Stress-induced Transcriptional Changes and Depression-like Behavior in Mice. *Experimental neurobiology*, 32(5), 328.
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- Dong X, et al. (2023) Characterization of Genes That Exhibit Genotype-Dependent Allele-Specific Expression and Its Implications for the Development of Maize Kernel. *International journal of molecular sciences*, 24(5).
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- Bychkov I, et al. (2023) Regulation of VEGFR2 and AKT signaling by Musashi-2 in lung cancer. *bioRxiv : the preprint server for biology*.
- Miguel-Quesada C, et al. (2023) Astrocytes adjust the dynamic range of cortical network activity to control modality-specific sensory information processing. *Cell reports*, 42(8), 112950.
- Pieri V, et al. (2023) Aberrant L-Fucose Accumulation and Increased Core Fucosylation Are Metabolic Liabilities in Mesenchymal Glioblastoma. *Cancer research*, 83(2), 195.
- Ueno M, et al. (2022) Long-term impact of maternal dietary intervention on metabolic homeostasis in male offspring in mice. *The Journal of nutritional biochemistry*, 104, 108971.
- Lakhwani D, et al. (2022) Genome wide identification of MADS box gene family in *Musa balbisiana* and their divergence during evolution. *Gene*, 836, 146666.
- Periselneris J, et al. (2022) Pneumolysin suppresses the initial macrophage pro-inflammatory response to *Streptococcus pneumoniae*. *Immunology*, 167(3), 413.
- Pérez-Sánchez R, et al. (2022) A proteomics informed by transcriptomics insight into the proteome of *Ornithodoros erraticus* adult tick saliva. *Parasites & vectors*, 15(1), 1.
- Shi J, et al. (2022) Machine learning and bioinformatics approaches for classification and clinical detection of bevacizumab responsive glioblastoma subtypes based on miRNA expression. *Scientific reports*, 12(1), 8685.