## **Resource Summary Report**

Generated by RRID on Apr 18, 2025

# **maSigPro**

RRID:SCR\_001349

Type: Tool

## **Proper Citation**

maSigPro (RRID:SCR\_001349)

#### **Resource Information**

URL: http://www.bioconductor.org/packages/release/bioc/html/maSigPro.html

**Proper Citation:** maSigPro (RRID:SCR\_001349)

**Description:** A regression based software package to find genes for which there are significant gene expression profile differences between experimental groups in time course microarray experiments.

Abbreviations: maSigPro

Synonyms: Significant Gene Expression Profile Differences in Time Course Microarray Data

Resource Type: software resource

**Defining Citation:** PMID:16481333

Keywords: differential expression, gene expression, time course, microarray

Funding:

Availability: GNU General Public License, v2 or newer

Resource Name: maSigPro

Resource ID: SCR\_001349

Alternate IDs: OMICS\_01990

**Record Creation Time:** 20220129T080207+0000

**Record Last Update:** 20250410T064705+0000

## **Ratings and Alerts**

No rating or validation information has been found for maSigPro.

No alerts have been found for maSigPro.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 197 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID.

Peng Y, et al. (2025) Temporal transcriptome profiling in the response to Salmonella enterica serovar enteritidis infection in chicken cecum. Poultry science, 104(2), 104773.

Fujimori H, et al. (2024) FAXC interacts with ANXA2 and SRC in mitochondria and promotes tumorigenesis in cholangiocarcinoma. Cancer science, 115(6), 1896.

Coschiera A, et al. (2024) Primary cilia promote the differentiation of human neurons through the WNT signaling pathway. BMC biology, 22(1), 48.

Montaldo P, et al. (2024) Whole-Blood Gene Expression Profile After Hypoxic-Ischemic Encephalopathy. JAMA network open, 7(2), e2354433.

O'Leary K, et al. (2024) Metacell-based differential expression analysis identifies cell type specific temporal gene response programs in COVID-19 patient PBMCs. NPJ systems biology and applications, 10(1), 36.

Bertagna MA, et al. (2024) Inferring gene-pathway associations from consolidated transcriptome datasets: an interactive gene network explorer for Tetrahymena thermophila. bioRxiv: the preprint server for biology.

Zhong J, et al. (2024) Heat stress reprograms herbivory-induced defense responses in potato plants. BMC plant biology, 24(1), 677.

Fletcher P, et al. (2024) Pathogenic differences of cynomolgus macaques after Taï Forest virus infection depend on the viral stock propagation. PLoS pathogens, 20(6), e1012290.

Yan Z, et al. (2024) A time-resolved multi-omics atlas of transcriptional regulation in response to high-altitude hypoxia across whole-body tissues. Nature communications, 15(1), 3970.

Zeng M, et al. (2024) Transcriptomic and intervention evidence reveals domestic dogs as a

promising model for anti-inflammatory investigation. Aging cell, 23(5), e14127.

Cheng S, et al. (2024) Dynamic profiles of IncRNAs reveal a functional natural antisense RNA that regulates the development of Schistosoma japonicum. PLoS pathogens, 20(1), e1011949.

Srivastava P, et al. (2024) scMaSigPro: Differential Expression Analysis along Single-Cell Trajectories. Bioinformatics (Oxford, England), 40(7).

Groot Crego C, et al. (2024) CAM evolution is associated with gene family expansion in an explosive bromeliad radiation. The Plant cell, 36(10), 4109.

Fang F, et al. (2024) Quantitative proteomics reveals the dynamic proteome landscape of zebrafish embryos during the maternal-to-zygotic transition. iScience, 27(6), 109944.

Hewitt S, et al. (2024) Transcriptome analysis reveals activation of detoxification and defense mechanisms in smoke-exposed Merlot grape (Vitis vinifera) berries. Scientific reports, 14(1), 21330.

Cea-Sánchez S, et al. (2024) VE-1 regulation of MAPK signaling controls sexual development in Neurospora crassa. mBio, 15(10), e0226424.

Shen L, et al. (2024) Specific plasma microRNA profiles could be potential non-invasive biomarkers for biochemical pregnancy loss following embryo transfer. BMC pregnancy and childbirth, 24(1), 351.

Hasegawa K, et al. (2024) Delta-6 desaturase FADS2 is a tumor-promoting factor in cholangiocarcinoma. Cancer science, 115(10), 3346.

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.

Xu S, et al. (2024) Characteristics of quiescent adult neural stem cells induced by the bFGF/BMP4 combination or BMP4 alone in vitro. Frontiers in cellular neuroscience, 18, 1391556.