

Resource Summary Report

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[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

Availability: Free, Available for download, Freely available

Resource Name: maSigPro

Resource ID: SCR_001349

Alternate IDs: OMICS_01990

License: GNU General Public License, v2 or newer

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260801T190149+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 222 mentions in open access literature.

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

Bjune JI, et al. (2025) IRX3 controls a SUMOylation-dependent differentiation switch in adipocyte precursor cells. *Nature communications*, 16(1), 7248.

Campos SE, et al. (2025) Wnt signaling restores evolutionary loss of regenerative potential in Hydra. *bioRxiv : the preprint server for biology*.

Liu Q, et al. (2025) Association of human-specific expanded short tandem repeats with neuron-specific regulatory features. *Science advances*, 11(22), eadp9707.

Gao Y, et al. (2025) Transcriptomic profiling of gastrointestinal tracts in dairy cattle during lactation reveals molecular adaptations for milk synthesis. *Journal of advanced research*, 71, 67.

Xie Y, et al. (2025) Transcriptomic exploration yields novel perspectives on the regulatory network underlying trichome initiation in *Gossypium arboreum* hypocotyl. *Frontiers in plant science*, 16, 1604186.

Xiao C, et al. (2025) Oncogenic roles of young human de novo genes and their potential as neoantigens in cancer immunotherapy. *Cell genomics*, 5(9), 100928.

Yang J, et al. (2025) Genome-wide profiling and functional characterization of circular RNAs in neural development and injury: insights from a rat model research. *Cellular and molecular life sciences : CMLS*, 82(1), 135.

Serdar LD, et al. (2025) mRNA stability fine-tunes gene expression in the developing cortex to control neurogenesis. *PLoS biology*, 23(2), e3003031.

Asano H, et al. (2025) Ropinirole Functions Through a Dopamine Receptor D2-Independent Mechanism to Ameliorate Amyotrophic Lateral Sclerosis Phenotypes in TARDBP-Mutant iPSC-Derived Motor Neurons. *Journal of neurochemistry*, 169(8), e70183.

Thompson L, et al. (2025) The Maternal Blood Transcriptome Reflects Changes in Fetal Growth and Is an Accurate Predictor of Birth Weight in Cattle. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(21), e71201.

- Li X, et al. (2025) Comparative transcriptome analysis reveals involvement of FOXL2 in regulation of ovulation cycle in chicken. *Poultry science*, 104(10), 105461.
- He J, et al. (2025) Comparative transcriptomics of two petal variants reveals key functional genes underlying petal shape development in lotus (*Nelumbo*). *Frontiers in plant science*, 16, 1596925.
- Tan J, et al. (2025) Alternative promoter usage during organ development. *PLoS genetics*, 21(3), e1011635.
- Wang Y, et al. (2025) Transcriptomic landscape and chromatin accessibility uncover pivotal regulators driving programmed larval-larval molting in the domesticated silkworm. *PLoS genetics*, 21(8), e1011837.
- Boschiero C, et al. (2025) Time-dependent RNA transcriptional profiling of abomasal mucosa in cattle infected with *Ostertagia ostertagi*. *Scientific data*, 12(1), 315.
- Li K, et al. (2025) The methylation signature of hepatocellular carcinoma trajectory based on pseudotime and chronological time for predicting precancerous patients. *The oncologist*, 30(8).
- Lee JY, et al. (2025) Imp/IGF2BP and Syp/SYNCRIP temporal RNA interactomes uncover combinatorial networks of regulators of *Drosophila* brain development. *Science advances*, 11(6), eadr6682.
- Serrano-Quintanilla J, et al. (2025) Transcriptional memory dampens heat shock responses in yeast: functional role of Mip6 and its interaction with Rpd3. *G3 (Bethesda, Md.)*, 15(8).
- Sheikh SI, et al. (2025) A shared gene but distinct dynamics regulate mimicry polymorphisms in closely related species. *bioRxiv : the preprint server for biology*.
- 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.