

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: 20260725T190504+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 [nidm-terms](#) .

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.

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

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.

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.

Boschiero C, et al. (2025) Time-dependent RNA transcriptional profiling of abomasal mucosa in cattle infected with *Ostertagia ostertagi*. *Scientific data*, 12(1), 315.

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.

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).

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.

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.

Li X, et al. (2025) Comparative transcriptome analysis reveals involvement of FOXL2 in regulation of ovulation cycle in chicken. *Poultry science*, 104(10), 105461.

Tan J, et al. (2025) Alternative promoter usage during organ development. *PLoS genetics*, 21(3), e1011635.

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.