

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: 20260912T195524+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 236 mentions in open access literature.

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

Yang X, et al. (2026) RFLNA mitigates heat stress-impaired chondrocyte proliferation and vertebral development through cytoskeletal regulation in pigs. *Journal of animal science and biotechnology*, 17(1).

Tomaszewski E, et al. (2026) At the breaking point: developmental and molecular insights into *Physalis grisea* fruit abscission. *Frontiers in plant science*, 17, 1733427.

Doratt BM, et al. (2026) Transcriptional signatures of rapid protection from Sudan virus infection by a single dose of a vesicular stomatitis virus-based vaccine. *PLoS pathogens*, 22(4), e1014143.

Marapana DS, et al. (2026) GID/CTLH E3 ligase complex control cell fate programs for sexual development of *Plasmodium falciparum*. *Nature communications*, 17(1).

Ye X, et al. (2026) Integrated multi-omics profiling identifies genetic loci of African swine fever resistance in pigs. *GigaScience*, 15.

Ando K, et al. (2026) Intestinal transcriptomic analysis and prediction of biomarkers associated with mucosal healing following vedolizumab treatment in ulcerative colitis using machine learning. *BMC gastroenterology*, 26(1), 117.

Powers MJ, et al. (2026) Transcriptomic Adjustment to Decreasing Oxygen Reveals Novel Functional Strategies for Extreme Hypoxia Tolerance in the Copepod *Tigriopus californicus*. *Genome biology and evolution*, 18(2).

Xiong K, et al. (2026) Visinin-like protein 1 disrupts calcium homeostasis and promotes atrial fibrillation in human and rodent models. *Signal transduction and targeted therapy*, 11(1).

Broderick CM, et al. (2026) Influenza coinfection inhibits control of mycobacterial infection in a human challenge model. *Nature communications*, 17(1).

Haraldsson EB, et al. (2026) A chromosome-scale genome assembly of *Hordeum erectifolium*: genomic, transcriptomic and anatomical adaptations to drought in a wild barley relative. *The New phytologist*, 250(4), 2652.

Morihara N, et al. (2026) Functional Annotation Workflow for Fungal Transcriptomes. *Journal of fungi* (Basel, Switzerland), 12(2).

Dunican C, et al. (2026) Predicting trajectories of illness using RNA velocity of whole blood. *Nature communications*, 17(1).

Marti-Garcia D, et al. (2026) Endometrial cortisol level and its relationship with psychological stress, molecular tissue changes, and clinical outcomes in infertile women. *Scientific reports*, 16(1).

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

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.

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.

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.

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.

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.