

Resource Summary Report

Generated by T1D on Aug 9, 2026

MiRPara

RRID:SCR_005294

Type: Tool

Proper Citation

MiRPara (RRID:SCR_005294)

Resource Information

URL: <https://code.google.com/p/mirpara/>

Proper Citation: MiRPara (RRID:SCR_005294)

Description: A SVM (support vector machine-based software tool for prediction of most probable microRNA coding regions in genome scale sequences.

Abbreviations: miRPara

Synonyms: mirpara - know and novel miRNA prediction software

Resource Type: software resource

Defining Citation: [PMID:21504621](#)

Keywords: microrna, prediction, mirbase, novel, support vector machine, mirna, dicer, ago, coding region, genome sequence, high throughput sequencing

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: MiRPara

Resource ID: SCR_005294

Alternate IDs: OMICS_00380

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260808T185837+0000

Ratings and Alerts

No rating or validation information has been found for MiRPara.

No alerts have been found for MiRPara.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Wang Z, et al. (2023) Systematic Characterization and Regulatory Role of lncRNAs in Asian Honey Bees Responding to Microsporidian Infestation. *International journal of molecular sciences*, 24(6).

Li Y, et al. (2023) Multi-omics data provide insight into the adaptation of the glasshouse plant *Rheum nobile* to the alpine subnival zone. *Communications biology*, 6(1), 906.

Zhao Z, et al. (2022) A cypovirus encoded microRNA negatively regulates the NF- κ B pathway to enhance viral multiplication in Silkworm, *Bombyx mori*. *Developmental and comparative immunology*, 131, 104382.

Zhan S, et al. (2022) Transcriptome analysis reveals long non-coding natural antisense transcripts involved in muscle development in fetal goat (*Capra hircus*). *Genomics*, 114(2), 110284.

Escuin D, et al. (2021) Circulating microRNAs in Early Breast Cancer Patients and Its Association With Lymph Node Metastases. *Frontiers in oncology*, 11, 627811.

Oc?o? E, et al. (2021) miRNA expression profile in chicken ovarian follicles throughout development and miRNA-mediated MMP expression. *Theriogenology*, 160, 116.

Gad A, et al. (2020) Plasma extracellular vesicle miRNAs as potential biomarkers of superstimulatory response in cattle. *Scientific reports*, 10(1), 19130.

Metzger JM, et al. (2020) Effects of Cardiac Sympathetic Neurodegeneration and PPAR γ Activation on Rhesus Macaque Whole Blood miRNA and mRNA Expression Profiles. *BioMed research international*, 2020, 9426204.

Li P, et al. (2019) Physiological and Transcriptome Analyses Reveal Short-Term Responses and Formation of Memory Under Drought Stress in Rice. *Frontiers in genetics*, 10, 55.

Piatek P, et al. (2019) MS CD49d+CD154+ Lymphocytes Reprogram Oligodendrocytes into Immune Reactive Cells Affecting CNS Regeneration. *Cells*, 8(12).

Hanif Q, et al. (2018) In silico identification of conserved miRNAs and their selective target gene prediction in indicine (*Bos indicus*) cattle. *PloS one*, 13(10), e0206154.

Ji K, et al. (2018) Long non-coding RNA expression profile in Cdk5-knockdown mouse skin. *Gene*, 672, 195.

Yan H, et al. (2018) siRNAs regulate DNA methylation and interfere with gene and lncRNA expression in the heterozygous polyploid switchgrass. *Biotechnology for biofuels*, 11, 208.

Rosani U, et al. (2017) Oyster RNA-seq Data Support the Development of Malacoherpesviridae Genomics. *Frontiers in microbiology*, 8, 1515.

Ling Y, et al. (2017) Identification and analysis of differentially expressed long non-coding RNAs between multiparous and uniparous goat (*Capra hircus*) ovaries. *PloS one*, 12(9), e0183163.

Elias KM, et al. (2017) Diagnostic potential for a serum miRNA neural network for detection of ovarian cancer. *eLife*, 6.

Rayner S, et al. (2017) Identification of small RNAs in extracellular vesicles from the commensal yeast *Malassezia sympodialis*. *Scientific reports*, 7, 39742.

Xue B, et al. (2016) Integrated Strategy Improves the Prediction Accuracy of miRNA in Large Dataset. *PloS one*, 11(12), e0168392.

Waters AM, et al. (2016) Single Synonymous Mutations in KRAS Cause Transformed Phenotypes in NIH3T3 Cells. *PloS one*, 11(9), e0163272.

Joshi RK, et al. (2016) Genome Wide Identification and Functional Prediction of Long Non-Coding RNAs Responsive to *Sclerotinia sclerotiorum* Infection in *Brassica napus*. *PloS one*, 11(7), e0158784.