Resource Summary Report

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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 throughputut sequencing

Funding:

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: 20250410T065242+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 FDI Lab - SciCrunch.org.

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.

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.

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

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? 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).

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

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.

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.

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

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

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.