

Resource Summary Report

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miRDeep

RRID:SCR_010829

Type: Tool

Proper Citation

miRDeep (RRID:SCR_010829)

Resource Information

URL: [https://www.mdc-](https://www.mdc-berlin.de/8551903/en/research/research_teams/systems_biology_of_gene_regulatory_elements/pro)

[berlin.de/8551903/en/research/research_teams/systems_biology_of_gene_regulatory_elements/pro](https://www.mdc-berlin.de/8551903/en/research/research_teams/systems_biology_of_gene_regulatory_elements/pro)

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Description: Software tool to identify known and novel miRNA genes in seven animal clades by analyzing sequenced RNAs. Used for discovering known and novel miRNAs from small RNA sequencing data.

Abbreviations: miRDeep2

Resource Type: data processing software, data analysis software, software resource, sequence analysis software, software application

Defining Citation: [PMID:18392026](#), [PMID:21911355](#)

Keywords: miRNA, gene, animal, clade, analysis, sequence, RNA, data

Funding: Helmholtz-Alliance on Systems Biology ;
Helmholtz Association ;
German Ministry of Education and Research ;
Senate of Berlin ;
China Scholarship Council ;
Max Delbrück Centrum Systems Biology Network

Availability: Free, Available for download, Freely available

Resource Name: miRDeep

Resource ID: SCR_010829

Alternate IDs: OMICS_00373

Alternate URLs: <https://github.com/rajewsky-lab/mirdeep2>

License: GNU GPL v3

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260805T044247+0000

Ratings and Alerts

No rating or validation information has been found for miRDeep.

No alerts have been found for miRDeep.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 163 mentions in open access literature.

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

Campbell AM, et al. (2025) Profiling miRNA changes in Epstein-Barr virus lytic infection identifies a function for BZLF1 in upregulating miRNAs from the DLK1-DIO3 locus. PLoS pathogens, 21(7), e1013347.

Lin X, et al. (2025) Integrating gonadal RNA-seq and small RNA-seq to analyze mRNA and miRNA changes in medaka sex differentiation. Scientific data, 12(1), 778.

Chen Y, et al. (2025) Overexpression of miR-516a-5p Promotes Erosive Oral Lichen Planus: In Vitro Study Based on Bioinformatics Analyses. Clinical and experimental dental research, 11(6), e70270.

Wei Y, et al. (2025) A panel of six immune-related mRNAs as biomarkers for tuberculosis diagnosis. Frontiers in genetics, 16, 1544007.

Kolanchi P, et al. (2025) Genomic exploration of Bemisia tabaci microRNAs using predictive modeling and confirmation through experimental evidence. Scientific reports, 15(1), 34006.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Javaid N, et al. (2025) SFTSV NSs interacts with AGO2 to regulate the RNAi pathway for viral replication. Journal of virology, 99(4), e0220524.

de la Cruz-Ojeda P, et al. (2025) In silico analysis of lncRNA-miRNA-mRNA signatures related to Sorafenib effectiveness in liver cancer cells. World journal of gastroenterology, 31(3), 95207.

Wang M, et al. (2025) MicroRNA-mediated regulatory mechanisms in cow's ileum and ileum lymph node in response to *Mycobacterium avium* subspecies paratuberculosis infection. *Scientific reports*, 15(1), 43030.

Wang J, et al. (2025) Integrative and comparative analysis of whole-transcriptome sequencing in circCOL1A1-knockdown and circCOL1A1-overexpressing goat hair follicle stem cells. *Animal bioscience*, 38(6), 1116.

Zeng L, et al. (2025) miR-32533 Reduces Cognitive Impairment and Amyloid- β Overload by Targeting CREB5-Mediated Signaling Pathways in Alzheimer's Disease. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(10), e2409986.

Vattathil SM, et al. (2025) Mapping the microRNA landscape in the older adult brain and its genetic contribution to neuropsychiatric conditions. *Nature aging*, 5(2), 306.

Liu Q, et al. (2025) Whole transcriptome analysis in oviduct provides insight into microRNAs and ceRNA regulative networks that targeted reproduction of goat (*Capra hircus*). *BMC genomics*, 26(1), 250.

Mai W, et al. (2025) Expression regulation network in papillae of sea cucumbers: Whole-transcriptome and DNA methylation datasets. *Scientific data*, 12(1), 1231.

Yu T, et al. (2025) Evolution of KoRV-A transcriptional silencing in wild koalas. *Cell*, 188(8), 2081.

Hwang N, et al. (2024) Carbon monoxide-induced autophagy enhances human mesenchymal stromal cell function via paracrine actions in murine polymicrobial sepsis. *Molecular therapy : the journal of the American Society of Gene Therapy*, 32(7), 2232.

Todorov H, et al. (2024) Stage-specific expression patterns and co-targeting relationships among miRNAs in the developing mouse cerebral cortex. *Communications biology*, 7(1), 1366.

He W, et al. (2024) Overexpression of Let-7a mitigates diploidization in mouse androgenetic haploid embryonic stem cells. *iScience*, 27(5), 109769.

Wang Z, et al. (2024) A novel and ubiquitous miRNA-involved regulatory module ensures precise phosphorylation of RNA polymerase II and proper transcription. *PLoS pathogens*, 20(4), e1012138.

de Oliveira AC, et al. (2024) MicroRNA Transcriptomes Reveal Prevalence of Rare and Species-Specific Arm Switching Events During Zebrafish Ontogenesis. *Evolutionary bioinformatics online*, 20, 11769343241263230.