

Resource Summary Report

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MIREAP

RRID:SCR_013025

Type: Tool

Proper Citation

MIREAP (RRID:SCR_013025)

Resource Information

URL: <http://sourceforge.net/projects/mireap/>

Proper Citation: MIREAP (RRID:SCR_013025)

Description: A software tool which can be used to identify both known and novel microRNAs from small RNA libraries deeply sequenced by Solexa/454/Solid technology.

Abbreviations: MIREAP

Resource Type: software resource

Availability: GNU General Public License, v2

Resource Name: MIREAP

Resource ID: SCR_013025

Alternate IDs: OMICS_00376

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260905T132731+0000

Ratings and Alerts

No rating or validation information has been found for MIREAP.

No alerts have been found for MIREAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 389 mentions in open access literature.

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

Zhang K, et al. (2026) Novel_circ_002651 regulates the immune defense of eastern honeybee larvae against fungal invasion through sponging miR-6001-y. *Virulence*, 17(1), 2656530.

Yao B, et al. (2026) Cascaded regulatory network composed of small RNAs involves in the symbiosis of *Panax notoginseng* and fungus *Acremonium* sp. D212. *Scientific reports*, 16(1).

Hu L, et al. (2026) Identification and analysis of microRNAs responsible for brown planthopper resistance in BPH14 and BPH15 pyramiding rice. *BMC plant biology*, 26(1).

Miranda-Rodríguez JR, et al. (2025) The chromosome-level genome assembly of the slug *Deroceras laeve* facilitates its use as a comparative model of regeneration. *G3* (Bethesda, Md.), 15(10).

Zhao Z, et al. (2025) Transcriptome analysis of liver and ileum reveals potential regulation of long non-coding RNA in pigs with divergent feed efficiency. *Animal bioscience*, 38(4), 588.

Yang S, et al. (2025) Integrated analysis of the expression profiles of the lncRNA-miRNA-mRNA ceRNA network in CSMCs under hypoxia and normoxia conditions in yak heart. *Scientific reports*, 15(1), 9165.

Zhang J, et al. (2025) The infection of mycovirus down regulates Aa-miR13 to weaken the pathogenicity of the *Alternaria alternata* f. sp. mali. *Frontiers in plant science*, 16, 1598183.

Li SY, et al. (2025) Comprehensive circRNA expression profile and hub genes screening during human liver development. *Annals of medicine*, 57(1), 2497111.

Cheng S, et al. (2025) Identification and characterization of microRNAs in the liver of yak (*Bos grunniens*) associated with energy deficiency at high-altitude. *Animal bioscience*, 38(7), 1372.

Hu S, et al. (2025) Cancer Cell-Secreted miR-33a Reduces Stress Granule Formation by Targeting Polyamine Metabolism in Stroma to Promote Tumourigenesis. *Journal of extracellular vesicles*, 14(9), e70153.

Ding D, et al. (2024) Whole-transcriptome sequencing revealed the role of noncoding RNAs in susceptibility and resistance of Pekin ducks to DHAV-3. *Poultry science*, 103(3), 103416.

Zhong S, et al. (2024) Distinct small RNAs are expressed at different stages of *Phytophthora capsici* and play important roles in development and pathogenesis. *Frontiers in genetics*, 15, 1296533.

Zhang W, et al. (2024) Profile of miRNAs induced during sheep fat tail development and roles of four key miRNAs in proliferation and differentiation of sheep preadipocytes. *Frontiers in veterinary science*, 11, 1491160.

Hu Q, et al. (2024) Astrocyte-neuron crosstalk through extracellular vesicle-shuttled miRNA-382-5p promotes traumatic brain injury. *Experimental & molecular medicine*, 56(12), 2642.

Jin Q, et al. (2024) mRNA-miRNA analyses reveal the involvement of CsbHLH1 and miR1446a in the regulation of caffeine biosynthesis in *Camellia sinensis*. *Horticulture research*, 11(2), uhad282.

Zhang S, et al. (2024) Whole-Transcriptome Sequencing Reveals the Global Molecular Responses and NAC Transcription Factors Involved in Drought Stress in *Dendrobium catenatum*. *Antioxidants (Basel, Switzerland)*, 13(1).

Yang Y, et al. (2024) RNA-Seq Analysis Revealed circRNAs and Genes Associated with Abdominal Fat Deposition in Ducks. *Animals : an open access journal from MDPI*, 14(2).

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.

Saroha M, et al. (2024) Genome-wide expression analysis of novel heat-responsive microRNAs and their targets in contrasting wheat genotypes at reproductive stage under terminal heat stress. *Frontiers in plant science*, 15, 1328114.

Shi H, et al. (2024) CircRNA profiling reveals the regulatory role of circPAN3 in Hezuo boars Sertoli cell growth. *BMC genomics*, 25(1), 1258.