

Resource Summary Report

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UEA sRNA toolkit

RRID:SCR_003620

Type: Tool

Proper Citation

UEA sRNA toolkit (RRID:SCR_003620)

Resource Information

URL: <http://srna-tools.cmp.uea.ac.uk/>

Proper Citation: UEA sRNA toolkit (RRID:SCR_003620)

Description: Software tools for the analysis of high-throughput small RNA data.

Abbreviations: UEA sRNA toolkit

Resource Type: software resource

Defining Citation: [PMID:22628521](#)

Resource Name: UEA sRNA toolkit

Resource ID: SCR_003620

Alternate IDs: OMICS_00369

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260912T195600+0000

Ratings and Alerts

No rating or validation information has been found for UEA sRNA toolkit.

No alerts have been found for UEA sRNA toolkit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Gu M, et al. (2026) The RNAi machinery regulates lovastatin biosynthesis via microRNA-like RNAs in industrial *Aspergillus terreus*. *Synthetic and systems biotechnology*, 14, 192.

Zhang Q, et al. (2024) DENV-1 Infection of Macrophages Induces Pyroptosis and Causes Changes in MicroRNA Expression Profiles. *Biomedicines*, 12(12).

Ding Y, et al. (2021) Proteomic and microRNA-omic profiles and potential mechanisms of dysfunction in pancreatic islet cells primed by inflammation. *Experimental and therapeutic medicine*, 21(2), 122.

Deng K, et al. (2021) Genome-wide miRNA expression profiling in potato (*Solanum tuberosum* L.) reveals TOR-dependent post-transcriptional gene regulatory networks in diverse metabolic pathway. *PeerJ*, 9, e10704.

Xie Y, et al. (2021) Differential Expression Pattern of Goat Uterine Fluids Extracellular Vesicles miRNAs during Peri-Implantation. *Cells*, 10(9).

Wang P, et al. (2021) Identification of miRNAs-mediated seed and stone-hardening regulatory networks and their signal pathway of GA-induced seedless berries in grapevine (*V. vinifera* L.). *BMC plant biology*, 21(1), 442.

Xiong J, et al. (2021) An Exploration of Non-Coding RNAs in Extracellular Vesicles Delivered by Swine Anterior Pituitary. *Frontiers in genetics*, 12, 772753.

Cao H, et al. (2020) miRNA expression profiling and zeatin dynamic changes in a new model system of in vivo indirect regeneration of tomato. *PloS one*, 15(12), e0237690.

Feng D, et al. (2020) Integrated analysis of microRNA and mRNA expression profiles in *Crassostrea gigas* to reveal functional miRNA and miRNA-targets regulating shell pigmentation. *Scientific reports*, 10(1), 20238.

Shi W, et al. (2020) Dysregulation of hepatic microRNA expression in C57BL/6 mice affected by excretory-secretory products of *Fasciola gigantica*. *PLoS neglected tropical diseases*, 14(12), e0008951.

Ma L, et al. (2019) Integrated analysis of mRNA-seq and miRNA-seq in calyx abscission zone of Korla fragrant pear involved in calyx persistence. *BMC plant biology*, 19(1), 192.

Martinez Palacios P, et al. (2019) Assessing the Response of Small RNA Populations to Allopolyploidy Using Resynthesized *Brassica napus* Allotetraploids. *Molecular biology and evolution*, 36(4), 709.

Jiu S, et al. (2019) Identification of copper (Cu) stress-responsive grapevine microRNAs and their target genes by high-throughput sequencing. *Royal Society open science*, 6(1), 180735.

Zhang X, et al. (2018) Identification and differential expression of microRNAs in testis and ovary of Amur sturgeon (*Acipenser schrenckii*). *Gene*, 658, 36.

Liu Y, et al. (2018) Integrated miRNA-mRNA analysis reveals regulatory pathways underlying the curly fleece trait in Chinese tan sheep. BMC genomics, 19(1), 360.

Huang J, et al. (2018) Identification and characterization of microRNAs in the liver of rainbow trout in response to heat stress by high-throughput sequencing. Gene, 679, 274.

Ma C, et al. (2018) Comparative analysis of miRNA and mRNA abundance in determinate cucumber by high-throughput sequencing. PloS one, 13(1), e0190691.

Thiebaut F, et al. (2017) Roles of Non-Coding RNA in Sugarcane-Microbe Interaction. Non-coding RNA, 3(4).

Hou M, et al. (2017) Effects of anticholinergic agent on miRNA profiles and transcriptomes in a murine model of allergic rhinitis. Molecular medicine reports, 16(5), 6558.

Bai J, et al. (2015) NGSmirPlant: comprehensive characterization of the small RNA transcriptomes of plants. Protein & cell, 6(6), 397.