

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

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: 20260801T190223+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 32 mentions in open access literature.

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

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

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.

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

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.

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.

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.

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.

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

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.

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.

Omidvar V, et al. (2015) Identification of miRNAs with potential roles in regulation of anther development and male-sterility in 7B-1 male-sterile tomato mutant. *BMC genomics*, 16, 878.

Katiyar A, et al. (2015) Identification of novel drought-responsive microRNAs and trans-acting siRNAs from *Sorghum bicolor* (L.) Moench by high-throughput sequencing analysis. *Frontiers in plant science*, 6, 506.