

Resource Summary Report

Generated by T1D on Aug 2, 2026

UEA sRNA Workbench

RRID:SCR_020947

Type: Tool

Proper Citation

UEA sRNA Workbench (RRID:SCR_020947)

Resource Information

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

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Description: Software package for analysing small RNA data. Software suite of tools for analyzing miRNAs and sRNAs. Performs analysis of single or multiple sample small RNA datasets from both plants and animals.

Synonyms: UEA small RNA Workbench

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

Defining Citation: [PMID:29722807](https://pubmed.ncbi.nlm.nih.gov/29722807/)

Keywords: Analysing small RNA data, analyzing miRNAs, profiling small RNA expression patterns, genetic data, bio.tools, bio.tools, bio.tools

Funding: BBSRC BB/L021269/1

Availability: Free, Available for download, Freely available

Resource Name: UEA sRNA Workbench

Resource ID: SCR_020947

Alternate IDs: biotools:siloco, biotools:mircat

Alternate URLs: https://github.com/sRNAworkbenchuea/UEA_sRNA_Workbench, <https://bio.tools/mircat>, <https://bio.tools/siloco>,

License: MIT

Record Creation Time: 20220129T080353+0000

Ratings and Alerts

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

No alerts have been found for UEA sRNA Workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Santoro DF, et al. (2025) Polyploidization-driven transcriptomic dynamics in Medicago sativa neotetraploids: mRNA, smRNA and allele-specific gene expression. BMC plant biology, 25(1), 108.

Chen J, et al. (2023) Multiomics studies with co-transformation reveal microRNAs via miRNA-TF-mRNA network participating in wood formation in Hevea brasiliensis. Frontiers in plant science, 14, 1068796.

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. Functional & integrative genomics, 23(1), 33.

Yang L, et al. (2023) From single- to multi-omics: future research trends in medicinal plants. Briefings in bioinformatics, 24(1).

Lizamore D, et al. (2021) Elevated transcription of transposable elements is accompanied by het-siRNA-driven de novo DNA methylation in grapevine embryogenic callus. BMC genomics, 22(1), 676.

Nath A, et al. (2021) Comprehensive Analysis of microRNAs in Human Adult Erythropoiesis. Cells, 10(11).

Beckers M, et al. (2017) Comprehensive processing of high-throughput small RNA sequencing data including quality checking, normalization, and differential expression analysis using the UEA sRNA Workbench. RNA (New York, N.Y.), 23(6), 823.