## **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

# **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

**Proper Citation:** UEA sRNA Workbench (RRID:SCR\_020947)

**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, data processing software, software resource,

software application

**Defining Citation:** PMID: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

**Record Last Update:** 20250429T060042+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 dkNET.

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.