

# Resource Summary Report

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

## VisSR

RRID:SCR\_012024

Type: Tool

### Proper Citation

VisSR (RRID:SCR\_012024)

### Resource Information

**URL:** <http://srna-workbench.cmp.uea.ac.uk/tools/visualisation-tools/vissr/>

**Proper Citation:** VisSR (RRID:SCR\_012024)

**Description:** Software to generate a visual representation of sRNAs and user-imported genomic features. The tool may be run on its own or from other tools, e.g. miRCat.

**Abbreviations:** VisSR

**Synonyms:** Visualisation of sRNAs

**Resource Type:** data visualization software, software application, data processing software, software resource

**Resource Name:** VisSR

**Resource ID:** SCR\_012024

**Alternate IDs:** OMICS\_02107, biotools:vissr

**Alternate URLs:** <https://bio.tools/vissr>

**Record Creation Time:** 20220129T080308+0000

**Record Last Update:** 20260801T190432+0000

### Ratings and Alerts

No rating or validation information has been found for VisSR.

No alerts have been found for VisSR.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Wang Y, et al. (2025) Transcriptome, miRNA, and degradome sequencing reveal the leaf stripe (*Pyrenophora graminea*) resistance genes in Tibetan hulless barley. *BMC plant biology*, 25(1), 71.

Asha S, et al. (2017) The sRNAome mining revealed existence of unique signature small RNAs derived from 5.8SrRNA from *Piper nigrum* and other plant lineages. *Scientific reports*, 7, 41052.

Wu J, et al. (2016) Comparative Analysis of miRNAs and Their Target Transcripts between a Spontaneous Late-Ripening Sweet Orange Mutant and Its Wild-Type Using Small RNA and Degradome Sequencing. *Frontiers in plant science*, 7, 1416.