

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 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 processing software, data visualization software, software application, 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: 20260903T235136+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](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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.