## **Resource Summary Report**

Generated by NIF on Apr 29, 2025

# VARNA

RRID:SCR\_024373 Type: Tool

**Proper Citation** 

VARNA (RRID:SCR\_024373)

### **Resource Information**

URL: http://varna.lri.fr/

Proper Citation: VARNA (RRID:SCR\_024373)

**Description:** Software tool for automated drawing, visualization and annotation of secondary structure of RNA, designed as companion software for web servers and databases. Allows manual modification and structural annotation of resulting drawing using either interactive point and click approach, within web server or through command-line arguments.

Synonyms: , Visualization Applet for RNA, varna

Resource Type: software resource, software toolkit

Defining Citation: PMID:19398448

**Keywords:** Java, secondary structure of RNA drawing, secondary structure of RNA visualization, secondary structure of RNA annotation,

#### Funding:

Availability: Free, Available for download, Freely available,

**Resource Name: VARNA** 

Resource ID: SCR\_024373

Alternate IDs: OMICS\_04455

Alternate URLs: https://sources.debian.org/src/varna/

Record Creation Time: 20230830T050217+0000

Record Last Update: 20250429T060339+0000

## **Ratings and Alerts**

No rating or validation information has been found for VARNA.

No alerts have been found for VARNA.

## Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Tsishevskaya AA, et al. (2024) Untranslated Regions of a Segmented Kindia Tick Virus Genome Are Highly Conserved and Contain Multiple Regulatory Elements for Viral Replication. Microorganisms, 12(2).

Hu YJ, et al. (2024) Comparative mitogenome research revealed the phylogenetics and evolution of the superfamily Tenebrionoidea (Coleoptera: Polyphage). Ecology and evolution, 14(6), e11520.

Park D, et al. (2024) Deciphering the evolutionary landscape of severe fever with thrombocytopenia syndrome virus across East Asia. Virus evolution, 10(1), veae054.

Yu G, et al. (2023) Genome-wide probing of eukaryotic nascent RNA structure elucidates cotranscriptional folding and its antimutagenic effect. Nature communications, 14(1), 5853.

Yang Y, et al. (2023) Beyond a PPR-RNA recognition code: Many aspects matter for the multi-targeting properties of RNA editing factor PPR56. PLoS genetics, 19(8), e1010733.