

Resource Summary Report

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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 toolkit, software resource

Defining Citation: [PMID:19398448](#)

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

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: 20260729T044609+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 8 mentions in open access literature.

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

Li C, et al. (2025) DDX3 Regulates the Cap-Independent Translation of the Japanese Encephalitis Virus via Its Interactions with PABP1 and the Untranslated Regions of the Viral Genome. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(27), e2502493.

Tangudu CS, et al. (2025) Exchanging the stem-loop A promoter of Zika virus with the corresponding region of tick-borne encephalitis virus generates a chimeric virus that replicates in vertebrate and mosquito cells. *Archives of virology*, 170(12), 236.

Shah K, et al. (2025) LncRNA SLNCR phenocopies the E2F1 DNA binding site to promote melanoma progression. *Cell reports*, 44(5), 115608.

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).

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

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.

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.