

Resource Summary Report

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ToRNADo

RRID:SCR_002706

Type: Tool

Proper Citation

ToRNADo (RRID:SCR_002706)

Resource Information

URL: <https://simtk.org/home/rna-viz-proto>

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Description: A software application for animating and visualising RNA and other macromolecular structures. Users are able to use their intuition to interactively refold RNA structures and produce morphs from one structure to another. It allow researchers to explore and manipulate molecular structures Imported from BiositeMaps registry, to better understand structure:function relationships, folding pathways, and molecular motion.

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

Keywords: duplex, protein, rna, visualization

Funding: NIH ;
NIGMS R01GM107340;
NIGMS U54GM072970

Availability: Free, Available for download, Freely available

Resource Name: ToRNADo

Resource ID: SCR_002706

Alternate IDs: nif-0000-23335

License: MIT License

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260905T132955+0000

Ratings and Alerts

No rating or validation information has been found for ToRNADo.

No alerts have been found for ToRNADo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 105 mentions in open access literature.

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

Testi C, et al. (2026) Stabilized real-time Brillouin microscopy reveals fractal organization of protein condensates in living cells. *Nature communications*, 17(1).

Kolb I, et al. (2026) iGABASnFR2 is an improved genetically encoded protein sensor of GABA. *eLife*, 14.

Padr??o N, et al. (2026) Fasting boosts breast cancer therapy efficacy via glucocorticoid activation. *Nature*, 649(8098), 1013.

Pratap JS, et al. (2026) What does it take to learn the rules of RNA base pairing? A lot less than you may think. *Communications biology*, 9(1).

Grillo G, et al. (2026) Transposable elements shape stemness in normal and leukemic hematopoiesis. *Nature genetics*, 58(5), 1087.

Caughey MC, et al. (2026) Cost-effectiveness of a hypothetical assay to evaluate stored blood quality prior to transfusion. *Vox sanguinis*, 121(2), 142.

Groninga J, et al. (2026) Millimetre-Scale Stratification of Microbial Communities in Hydrothermal Sediments. *Environmental microbiology*, 28(1), e70227.

Zhang Y, et al. (2026) The cost-effectiveness of male-partner treatment to prevent recurrence of bacterial vaginosis. *Scientific reports*, 16(1).

Green N, et al. (2025) Latent tuberculosis infection screening of adult close contacts: a cost-utility analysis. *ERJ open research*, 11(3).

Baigutanova A, et al. (2025) A continuous real-world dataset comprising wearable-based heart rate variability alongside sleep diaries. *Scientific data*, 12(1), 1474.

Cao L, et al. (2025) Chloroplast Z-ring dynamics is governed by conserved core regions of evolutionarily divergent FtsZs. *Frontiers in plant science*, 16, 1622675.

Pera J, et al. (2025) Human iPSCs-based modeling unveils SETBP1 as a driver of chromatin rewiring in GATA2 deficiency. *Nature communications*, 16(1), 10035.

Almohannadi M, et al. (2025) Balloon-Occluded Retrograde Transvenous Obliteration (BRTO) for Gastric Varices: A Single-Center Experience in the Middle East. *Cureus*, 17(5), e83726.

Eickhoff N, et al. (2025) TRIM33 loss reduces androgen receptor transcriptional output and H2BK120 ubiquitination. *Communications biology*, 8(1), 1043.

Faraji F, et al. (2025) YAP-driven malignant reprogramming of oral epithelial stem cells at single cell resolution. *Nature communications*, 16(1), 498.

Hill LA, et al. (2025) The fibroblast epigenome underlies SS18::SSX-mediated transformation in synovial sarcoma. *Nature communications*, 16(1), 10830.

Hunter MV, et al. (2025) Mechanical confinement governs phenotypic plasticity in melanoma. *Nature*, 647(8089), 517.

Pasalari H, et al. (2025) Health risk attributed to consumption of vegetables irrigated with different effluents containing enteric viruses via QMRA and DALY. *Scientific reports*, 15(1), 18370.

Lin H, et al. (2025) Modular organization of enhancer network provides transcriptional robustness in mammalian development. *Nucleic acids research*, 53(2).

Troester S, et al. (2025) Transcriptional and epigenetic rewiring by the NUP98::KDM5A fusion oncoprotein directly activates CDK12. *Nature communications*, 16(1), 4656.