

Resource Summary Report

Generated by [T1D](#) on Sep 5, 2026

QmRLFS-finder

RRID:SCR_014584

Type: Tool

Proper Citation

QmRLFS-finder (RRID:SCR_014584)

Resource Information

URL: <http://rloop.bii.a-star.edu.sg/?pg=qmrlfs-finder>

Proper Citation: QmRLFS-finder (RRID:SCR_014584)

Description: A software which predicts R-loop Forming Sequences (RLFSs) in nucleic acid sequences based on the experimentally supported structural models of RLFSs. The tool identifies and visualizes RLFS coordinates from natural or artificial DNA or RNA input sequences and creates standard-compliant output files for later annotation and analysis.

Synonyms: QmRLFS finder

Resource Type: data analytics software, software application, software resource

Defining Citation: [PMID:26400173](#), [PMID:25883153](#)

Keywords: r-loop, r loop, rlf, rlfs, dna, rna, input sequences, output files, annotation, analysis, bio.tools

Funding: Singapore Agency for Science Technology and Research

Availability: Open Source

Resource Name: QmRLFS-finder

Resource ID: SCR_014584

Alternate IDs: biotools:qmrlfs-finder

Alternate URLs: <https://omictools.com/qmrlfs-finder-tool>, <https://bio.tools/qmrlfs-finder>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260904T000429+0000

Ratings and Alerts

No rating or validation information has been found for QmRLFS-finder.

No alerts have been found for QmRLFS-finder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Adala JD, et al. (2026) In silico mapping of non-canonical DNA structures across the human ribosomal DNA locus. *G3* (Bethesda, Md.), 16(2).

Tsai BS, et al. (2026) DNA-DETR: sequence representation matters in object detection for functional genomic elements. *Briefings in bioinformatics*, 27(4).

Vanhaeren T, et al. (2025) Enhancing R-loop prediction with high-throughput sequencing data. *NAR genomics and bioinformatics*, 7(2), lqaf077.

Rao Z, et al. (2025) Cancer driver topologically associated domains identify oncogenic and tumor-suppressive lncRNAs. *Genome research*, 35(8), 1842.

D'Ignazio L, et al. (2025) A hexamer tandem repeat RNA embedded within an SVA retrotransposon drives R-loop formation and neurodegeneration. *Cell reports*, 44(7), 115812.

Bhatt U, et al. (2024) Preferential formation of Z-RNA over intercalated motifs in long noncoding RNA. *Genome research*, 34(2), 217.

Hu J, et al. (2024) Deep learning-enhanced R-loop prediction provides mechanistic implications for repeat expansion diseases. *iScience*, 27(8), 110584.

Luo H, et al. (2022) HOTTIP-dependent R-loop formation regulates CTCF boundary activity and TAD integrity in leukemia. *Molecular cell*, 82(4), 833.

Talotta R, et al. (2022) Sequence complementarity between human noncoding RNAs and SARS-CoV-2 genes: What are the implications for human health? *Biochimica et biophysica acta. Molecular basis of disease*, 1868(2), 166291.

Shi X, et al. (2022) An updated overview of experimental and computational approaches to identify non-canonical DNA/RNA structures with emphasis on G-quadruplexes and R-loops. *Briefings in bioinformatics*, 23(6).

Wongsurawat T, et al. (2020) R-loop-forming Sequences Analysis in Thousands of Viral Genomes Identify A New Common Element in Herpesviruses. *Scientific reports*, 10(1), 6389.

Kuznetsov VA, et al. (2018) Toward predictive R-loop computational biology: genome-scale prediction of R-loops reveals their association with complex promoter structures, G-quadruplexes and transcriptionally active enhancers. *Nucleic acids research*, 46(15), 7566.

Briggs E, et al. (2018) Genome-wide mapping reveals conserved and diverged R-loop activities in the unusual genetic landscape of the African trypanosome genome. *Nucleic acids research*, 46(22), 11789.

Jenjaroenpun P, et al. (2017) R-loopDB: a database for R-loop forming sequences (RLFS) and R-loops. *Nucleic acids research*, 45(D1), D119.

Heinonen M, et al. (2016) Transcription-coupled genetic instability marks acute lymphoblastic leukemia structural variation hotspots. *eLife*, 5.

Jenjaroenpun P, et al. (2015) QmRLFS-finder: a model, web server and stand-alone tool for prediction and analysis of R-loop forming sequences. *Nucleic acids research*, 43(W1), W527.