Vienna RNA

RRID:SCR_008550
Type: Tool

Proper Citation

Vienna RNA (RRID:SCR_008550)

Resource Information

URL: http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi

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Description: This server provides programs, web services, and databases, related to our work on RNA secondary structures. For general information and other offerings from our group see the main TBI web server. With the 1st of May 2009 we updated our servers to the Vienna RNA package version 1.8.2! The Vienna RNA Servers: * RNAfold server predicts minimum free energy structures and base pair probabilities from single RNA or DNA sequences. * RNAalifold server predicts consensus secondary structures from an alignment of several related RNA or DNA sequences. You need to upload an alignment. * RNAinverse server allows you to design RNA sequences for any desired target secondary structure. * RNAcofold server allows you to predict the secondary structure of a dimer. * RNAup server allows you to predict the accessibility of a target region. * LocARNA server generates structural alignments from a set of sequences. In collaboration with the Bioinformatics Group Freiburg. * barriers server allows you to get insights into RNA folding kinetics. * RNAz server will assist you in detecting thermodynamically stable and evolutionarily conserved RNA secondary structures in multiple sequence alignments. * Structure conservation analysis server will assist you in detecting evolutionarily conserved RNA secondary structures in multiple sequence alignments. * RNAstrand server allows you to predict the reading direction of evolutionarily conserved RNA secondary structures. * RNAxs server assists you in siRNA design. * Bcheck predicts rnpB genes Downloads Get the Source code for: * the Vienna RNA Package, our basic RNA secondary structure analysis software. * The ALIDOT package for finding conserved structure motifs (add-on) * The barriers program for analysis of RNA folding landscapes. Databases * Atlas of conserved Viral RNA Structures found by ALIDOT

Synonyms: Vienna RNA

Resource Type: database, data or information resource, software resource

Defining Citation: [DOI:10.1186/1748-7188-6-26](DOI:10.1186/1748-7188-6-26)

Keywords: bio.tools, FASEB list

Funding:

Resource Name: Vienna RNA

Resource ID: SCR_008550

Alternate IDs: biotools:vienna_rna_package, nif-0000-31411, OMICS_09351

Alternate URLs: https://bio.tools/vienna_rna_package, https://sources.debian.org/src/vienna-rna/

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250412T055302+0000

Ratings and Alerts

No rating or validation information has been found for Vienna RNA.

No alerts have been found for Vienna RNA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 398 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Leong LEX, et al. (2024) Identification of the mechanism for dehalorespiration of monofluoroacetate in the phylum Synergistota. Animal bioscience, 37(2), 396.

Srivastava A, et al. (2024) In silico identification of papaya genome-encoded microRNAs to target begomovirus genes in papaya leaf curl disease. Frontiers in microbiology, 15, 1340275.

Gallagher LT, et al. (2024) Dysregulation of miRNA-mRNA expression in fetal growth restriction in a caloric restricted mouse model. Scientific reports, 14(1), 5579.

Xiong W, et al. (2024) The mitochondrial long non-coding RNA lncMtloop regulates mitochondrial transcription and suppresses Alzheimer's disease. The EMBO journal, 43(23), 6001.

Deng K, et al. (2024) Ythdf2 facilitates precursor miR-378/miR-378-5p maturation to support myogenic differentiation. Cellular and molecular life sciences : CMLS, 81(1), 445.

Chen DY, et al. (2024) Transcriptome profiling of foxtail millet (Setaria italica) pollen and anther. BMC plant biology, 24(1), 1221.

Sirois CL, et al. (2024) CGG repeats in the human FMR1 gene regulate mRNA localization and cellular stress in developing neurons. Cell reports, 43(6), 114330.

Qiao L, et al. (2023) RNA-Seq Reveals the mRNAs, miRNAs, and lncRNAs Expression Profile of Knee Joint Synovial Tissue in Osteoarthritis Patients. Journal of clinical medicine, 12(4).

Lee MA, et al. (2023) Codon Pair Deoptimization (CPD)-Attenuated PRRSV-1 Vaccination Exhibit Immunity to Virulent PRRSV Challenge in Pigs. Vaccines, 11(4).

Bush K, et al. (2023) Utilizing directed evolution to interrogate and optimize CRISPR/Cas guide RNA scaffolds. Cell chemical biology, 30(8), 879.

Athira PP, et al. (2022) A hepatic antimicrobial peptide, hepcidin from Indian major carp, Catla catla: molecular identification and functional characterization. Journal, genetic engineering & biotechnology, 20(1), 49.

Wells KM, et al. (2022) Brucella activates the host RIDD pathway to subvert BLOS1-directed immune defense. eLife, 11.

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.

Kou X, et al. (2022) PbrROP1/2-elicited imbalance of cellulose deposition is mediated by a CrRLK1L-ROPGEF module in the pollen tube of Pyrus. Horticulture research, 9.

Millard RS, et al. (2022) Resistance to white spot syndrome virus in the European shore crab is associated with suppressed virion trafficking and heightened immune responses. Frontiers in immunology, 13, 1057421.

Parreira JR, et al. (2021) MicroRNAs expression dynamics reveal post-transcriptional mechanisms regulating seed development in Phaseolus vulgaris L. Horticulture research, 8(1), 18.

Singh J, et al. (2021) Identification of homologous human miRNAs as antivirals towards COVID-19 genome. Advances in cell and gene therapy, 4(4), e114.

Yan Q, et al. (2021) The Regulatory Mechanism of Feeding a Diet High in Rice Grain on the Growth and microRNA Expression Profiles of the Spleen, Taking Goats as an Artiodactyl Model. Biology, 10(9).

Felletti M, et al. (2021) A nascent polypeptide sequence modulates DnaA translation elongation in response to nutrient availability. eLife, 10.

Wu B, et al. (2021) Identification of miRNA-mRNA Regulatory Modules Involved in Lipid Metabolism and Seed Development in a Woody Oil Tree (Camellia oleifera). Cells, 11(1).