Resource Summary Report

Generated by NIF on Apr 26, 2025

Rfam

RRID:SCR_007891
Type: Tool

Proper Citation

Rfam (RRID:SCR_007891)

Resource Information

URL: http://rfam.xfam.org/

Proper Citation: Rfam (RRID:SCR_007891)

Description: The Rfam database is a collection of RNA families, each represented by multiple sequence alignments, consensus secondary structures and covariance models (CMs). The families in Rfam break down into three broad functional classes: Non-coding RNA genes, structured cis-regulatory elements and self-splicing RNAs. Typically these functional RNAs often have a conserved secondary structure which may be better preserved than the RNA sequence. The CMs used to describe each family are a slightly more complicated relative of the profile hidden Markov models (HMMs) used by Pfam. CMs can simultaneously model RNA sequence and the structure in an elegant and accurate fashion. Rfam is also available via FTP. You can find data in Rfam in various ways... * Analyze your RNA sequence for Rfam matches * View Rfam family annotation and alignments * View Rfam clan details * Query Rfam by keywords * Fetch families or sequences by NCBI taxonomy * Enter any type of accession or ID to jump to the page for a Rfam family, sequence or genome

Abbreviations: Rfam, RFAM

Synonyms: RFAM, Rfam database

Resource Type: service resource, data analysis service, data or information resource, database, production service resource, analysis service resource

Defining Citation: PMID:21062808

Keywords: family, genome, clan, structure, non-coding rna, FASEB list

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Resource Name: Rfam

Resource ID: SCR_007891

Old URLs: http://rfam.sanger.ac.uk/

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250426T060007+0000

Ratings and Alerts

No rating or validation information has been found for Rfam.

No alerts have been found for Rfam.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3266 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Willemsen A, et al. (2025) Novel High-Quality Amoeba Genomes Reveal Widespread Codon Usage Mismatch Between Giant Viruses and Their Hosts. Genome biology and evolution, 17(1).

Seifert-Dávila W, et al. (2025) Structural and kinetic insights into tRNA promoter engagement by yeast general transcription factor TFIIIC. Nucleic acids research, 53(1).

Lee YT, et al. (2025) The conformational space of RNase P RNA in solution. Nature, 637(8048), 1244.

Zhang W, et al. (2025) Chromosome-level genome assembly of tetraploid Chinese cherry (Prunus pseudocerasus). Scientific data, 12(1), 136.

Liu J, et al. (2025) Chromosome-level genome assembly of the seasonally polyphenic scorpionfly (Panorpa liui). Scientific data, 12(1), 22.

Li L, et al. (2025) A Chromosomal-level genome assembly and annotation of fat greenling (Hexagrammos otakii). Scientific data, 12(1), 78.

Ma L, et al. (2025) lncRNA, miRNA, and mRNA of plasma and tumor-derived exosomes of cardiac myxoma-related ischaemic stroke. Scientific data, 12(1), 91.

Yang Y, et al. (2025) A Chromosome-Scale Genome of Trametes versicolor and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene Biosynthesis. Journal of fungi (Basel, Switzerland), 11(1).

Qu Z, et al. (2025) Selective utilization of medicinal polysaccharides by human gut Bacteroides and Parabacteroides species. Nature communications, 16(1), 638.

Wang MY, et al. (2025) Chromosome-level genome assembly, annotation, and population genomic resource of argali (Ovis ammon). Scientific data, 12(1), 57.

Xie MQ, et al. (2025) Regulatory networks of mRNAs and miRNAs involved in the immune response of diamondback moth, Plutella xylostella to fungal infection. BMC genomics, 26(1), 15.

Gong X, et al. (2025) Chromosome-level genome assembly of Iodes seguinii and its metabonomic implications for rheumatoid arthritis treatment. The plant genome, 18(1), e20534.

Zhang L, et al. (2025) Chromosome-level genome assembly and annotation of the gynogenetic large-scale loach (Paramisgurnus dabryanus). Scientific data, 12(1), 155.

Morey-Yagi SR, et al. (2025) Expression of spider silk protein in tobacco improves drought tolerance with minimal effects on its mechanotype. The Plant journal : for cell and molecular biology, 121(2), e17213.

Wu J, et al. (2025) A chromosome-level genome assembly of the cabbage aphid Brevicoryne brassicae. Scientific data, 12(1), 167.

Ding R, et al. (2025) Chromosome-Level Genome Assembly and Whole-Genome Resequencing Revealed Contrasting Population Genetic Differentiation of Black Bream (Megalobrama skolkovii) (Teleostei: Cyprinidae) Allopatric and Sympatric to Its Kin Species. Ecology and evolution, 15(1), e70874.

Qiu X, et al. (2025) Robust RNA secondary structure prediction with a mixture of deep learning and physics-based experts. Biology methods & protocols, 10(1), bpae097.

Putumbaka S, et al. (2025) Tungsten is utilized for lactate consumption and SCFA production by a dominant human gut microbe Eubacterium limosum. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2411809121.

Yang G, et al. (2025) Chromosome-level genome assembly of Megachile sculpturalis Smith (Hymenoptera, Apoidea, Megachilidae). Scientific data, 12(1), 46.

Santoro DF, et al. (2025) Polyploidization-driven transcriptomic dynamics in Medicago sativa neotetraploids: mRNA, smRNA and allele-specific gene expression. BMC plant biology, 25(1), 108.