

Resource Summary Report

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Rfam

RRID:SCR_007891

Type: Tool

Proper Citation

Rfam (RRID:SCR_007891)

Resource Information

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

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

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: 20260811T043321+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 4040 mentions in open access literature.

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

Lang X, et al. (2026) FungiSNC: An integrated database for fungi small non-coding RNAs based on high-throughput sequencing. *Journal of advanced research*, 84, 187.

Song LCT, et al. (2026) Identification of proteins influencing CRISPR-associated transposases for enhanced genome editing. *Science advances*, 12(1), eaea1429.

Merchant AT, et al. (2026) Semantic design of functional de novo genes from a genomic language model. *Nature*, 649(8097), 749.

Ge F, et al. (2026) The chromosome-level genome of Chinese indicine cattle breed provides insights into bovine adaptation and immunity. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Tang X, et al. (2026) Chromosome-level genome assembly of the medicinal plant *Ophiorrhiza japonica* Blume. *Scientific data*, 13(1).

Xie X, et al. (2026) Chromosome-level genome assembly of mud snail *Bullacta exarata*. *Scientific data*, 13(1).

Ma X, et al. (2026) The role of lncRNA-associated ceRNA networks in yak *longissimus dorsi* muscle development across feeding systems. *BMC veterinary research*, 22(1).

Ge G, et al. (2026) Isolation, identification and genomic analysis of *Mycobacterium caprae* strain SY-1 from Chinese sika deer (*Cervus nippon*). *BMC genomics*, 27(1), 184.

- Pfeifer M, et al. (2026) High-quality haplotype-resolved genome assembly and annotation of *Malus baccata* 'Jackii'. *Scientific data*, 13(1), 14.
- Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.
- Wuyun B, et al. (2026) A telomere-to-telomere gapless genome assembly of the Tibetan wild ass (*Equus kiang*). *Scientific data*, 13(1), 182.
- Chen K, et al. (2026) HiMBar: A High-Fidelity Metagenomic Barcoding Approach for Transkingdom Species Detection and Interaction Analysis in Aquatic Ecosystems. *Molecular ecology resources*, 26(1), e70092.
- Zhang D, et al. (2026) Integrated analysis of RNA expression profiles and regulatory networks in porcine liver in response to cold stress. *BMC genomics*, 27(1), 175.
- Zhang Y, et al. (2026) Multi-omics and functional analyses in *Aesculus wilsonii* elucidate the biosynthetic pathways of moretane- and oleanane-type triterpenoids. *Plant communications*, 7(4), 101715.
- Gutierrez-Vargas C, et al. (2026) Structures of naked mole-rat, tuco-tuco, and guinea pig ribosomes-is rRNA fragmentation linked to translational fidelity? *Nucleic acids research*, 54(3).
- Claus C, et al. (2026) Extracellular Small RNAs in Human Milk: Molecular Profiles, Stability and Fragment-Specific Responses in Cell-Based Assays. *Non-coding RNA*, 12(1).
- Novo M, et al. (2026) ERGA-BGE Genome of *Ailoscolex lacteospumous* Bouch??, 1969 - the enigmatic milky worm endemic to the Pyrenees. *Open research Europe*, 6, 26.
- Cao C, et al. (2026) Protective effect of cannabinoid type II receptor ligand on bleomycin-induced pulmonary fibrosis in mice. *PloS one*, 21(2), e0331168.
- Li M, et al. (2026) De Novo Chromosome-Level Genome Assembly of 'Qing Zhou Mi' Landrace Peach and Analysis of Late Maturity and Fruit Weight Traits in Peach. *Plants (Basel, Switzerland)*, 15(7).
- Chen YF, et al. (2026) Serum exosomal miR-192-5p as a novel predictive biomarker for immunochemotherapy response in advanced non-small cell lung cancer. *BMC cancer*, 26(1).