

# 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/>

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

**Defining Citation:** [PMID:21062808](#)

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

**Funding:** Howard Hughes Medical Institute ;  
University of Manchester; Manchester; United Kingdom ;  
Wellcome Trust WT077044/Z/05/Z

**Resource Name:** Rfam

**Resource ID:** SCR\_007891

**Old URLs:** <http://rfam.sanger.ac.uk/>

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260912T195657+0000

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## Ratings and Alerts

No rating or validation information has been found for Rfam.

No alerts have been found for Rfam.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4040 mentions in open access literature.

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

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

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.

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

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).

Geissler AS, et al. (2026) Exploring the regulatory potential of RNA structures in 202 cyanobacterial genomes. Nucleic acids research, 54(4).

- 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).
- 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.
- 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.
- 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.
- 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.
- 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).
- Liu J, et al. (2026) Molecular basis of the short- and long-term osmoregulation capability in the euryhaline unicellular eukaryote *Paramecium calkinsi*. *mBio*, 17(4), e0303225.
- Wang H, et al. (2026) Zero-shot benchmarking of RNA language models in structural, functional, and evolutionary learning. *Briefings in bioinformatics*, 27(2).
- Zhang X, et al. (2026) A high-quality Chromosome-level genome assembly of *Gynostemma guangxiense* (Cucurbitaceae). *Scientific data*, 13(1).
- Chen R, et al. (2026) Chromosome-scale genome assembly and annotation of *Garuga floribunda* var. *gamblei* (King ex W. W. Sm.) Kalkman. *Scientific data*, 13(1).