

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 analysis service, data or information resource, database, service resource, 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: 20260801T190341+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 3693 mentions in open access literature.

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

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

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Chen J, et al. (2026) Genomic and transcriptomic analysis of yield enhancement mechanism of lipopeptide iturin W by tryptone supplementation. *Microbiology spectrum*, 14(1), e0324725.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia* ?? *blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

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.

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

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

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.

Guo Y, et al. (2025) Chromosome-level genome assembly of the intertidal lucinid clam *Indoaustriella scarlatoi*. *Scientific data*, 12(1), 275.

Liang Z, et al. (2025) A chromosomal-scale reference genome for *Rosa hugonis*. *Scientific data*, 12(1), 272.

Jin Y, et al. (2025) Delivering miR-23b-3p by small extracellular vesicles to promote cell senescence and aberrant lipid metabolism. *BMC biology*, 23(1), 41.

Hiew JY, et al. (2025) Integrated transcriptomic profiling reveals a STING-mediated Type II Interferon signature in SOD1-mutant amyotrophic lateral sclerosis models. *Communications biology*, 8(1), 347.