

Rfam 15: RNA families database in 2025

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Abstract

The Rfam database, a widely-used repository of non-coding RNA (ncRNA) families, has undergone significant updates in release 15.0. This paper introduces major improvements, including the expansion of Rfamseq to 26,106 genomes, a 76% increase, incorporating the latest UniProt reference proteomes and additional viral genomes. Sixty-five RNA families were enhanced using experimentally determined 3D structures, improving the accuracy of consensus secondary structures and annotations. R-scape covariation analysis was used to refine structural predictions in 26 families. Gene Ontology and Sequence Ontology annotations were comprehensively updated, increasing GO term coverage to 75% of families. The release adds 14 new Hepatitis C Virus RNA families and completes microRNA family synchronisation with miRBase, resulting in 1,603 microRNA families. New data types, including FULL alignments, have been implemented. Integration with APICURON for improved curator attribution and multiple website enhancements further improve user experience. These updates significantly expand Rfam's coverage and improve annotation quality, reinforcing its critical role in RNA research, genome annotation, and the development of machine learning models. Rfam is freely available at <https://rfam.org>.

Introduction

The Rfam database was established in 2002 (1) in order to provide a central repository of non-coding RNA (ncRNA) families for genomic annotations. Each family is represented by three key components: (i) a multiple sequence alignment called the SEED alignment that contains aligned sequences of homologous RNA sequences that share a consensus secondary structure, (ii) a covariance model (CM) built using the Infernal software (2) that was trained on the SEED alignment, and (iii) a set of matches that were found using the covariance model, called the set of FULL hits. The families are built manually by Rfam curators using scientific literature or alignments submitted by the community.

For each model the curators search for homologs in a sequence database, Rfamseq, and select a bit score threshold, called the gathering threshold, that separates homologous sequences from unrelated or more distantly related sequences, taking into account phylogenetic distribution of hits. The cutoff can be used by Infernal to report only sequences that score higher than this threshold when annotating genomes or searching in sequence databases.

Each major release of the Rfam database, such as 14.0 or 15.0, corresponds to a new version of Rfamseq. Prior to Rfam 13.0, Rfamseq was based on a set of sequences from the ENA database (3). However, due to the explosive growth in ENA, in Rfam 13.0 Rfamseq transitioned to a representative and reduced redundancy set of genomes produced by the UniProt team (4) for the Reference Proteomes dataset (5). The representative proteomes from UniProt are mapped to their corresponding genomes and the genomic sequence is analysed by Rfam (5). This provides users with a representative collection of genomes which have comprehensive ncRNA and protein annotations.

Rfam has been widely adopted by various scientific communities, with uses ranging from the annotation of small non-coding RNAs (ncRNAs) in genomic resources like Ensembl (6), to serving as a dataset for training machine learning models such as AlphaFold 3 (7). Additionally, Rfam is frequently used as a key reference for known non-coding RNAs. To ensure it remains current and valuable to the scientific community, we continuously review, update, and enhance the Rfam families.

In release 15.0 we have updated and expanded Rfamseq, improved families using 3D structures and R-scape (8), improved Gene Ontology (9) and Sequence Ontology (10) annotations and completed the synchronisation of miRBase (11) microRNAs into Rfam.

New Rfamseq database

Rfam 15 is based on the 2024_03 release of UniProt reference proteomes that includes 23,158 genomes (see Figure 1 showing the taxonomic distribution). We attempted to download all components of the genomes used to build the proteome set. In some cases, the specified genome was replaced by a newer version, which was used instead. In a very few cases, less than 50, all versions of the genome were either outdated or removed. In those cases we did not fetch any genome.

In addition to the genomes in the UniProt set, we also fetched all viral genomes from the protein information resource (12) at 75% percent identity for an additional 2,985 viral genomes. This set was added because during our viral work, described below, we found that the UniProt reference proteome work under reports the diversity of viral genomes. This has led to some viral Rfam families having very few or no FULL hits. Rfam would prefer that all families have at least one match outside of the SEED sequences. While using an additional set of viral genomes leads to a large increase in the number of genomes, the total size of Rfamseq is dominated by cellular organisms as <1% of the nucleotides come from a viral genome. Table 1 shows the comparison of Rfamseq in the last major release Rfam 14.0 vs Rfam 15.0.

Table 1. The number of genomes in Rfamseq corresponding to release 14.0 and 15.0. The size on disk is the uncompressed size of all sequences in Rfamseq.

Kingdom	Rfamseq v14	Rfamseq v15
Total sequence length	3.68e11	1.46e12
Number of species	14,774	26,106
Eukaryotes	1,057	2,613
Archaea	418	370
Bacteria	7,808	9,601
Viruses	5,491	13,552
Number of Rfam hits	2,897,296	10,736,534
Size on disk	170 GB	772 GB

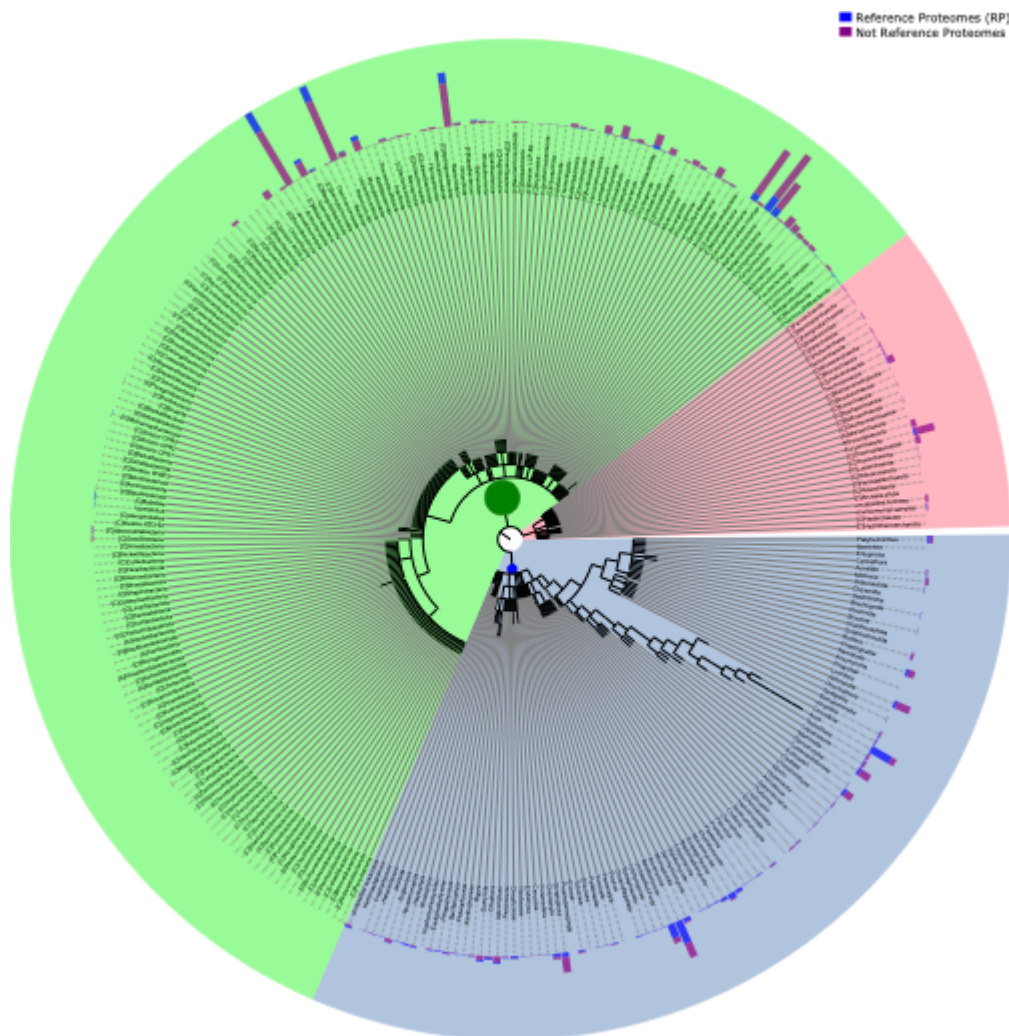


Figure 1. The taxonomic distribution of cellular organisms in Rfamseq 15 organised by the phylogenetic kingdom. Shown on the outside is the number of reference and non-reference proteomes in each lineage. Each coloured section indicates the kingdom with bacteria (green), archaea (pink) and eukaryotes (blue).

Once Rfamseq was updated all families were searched against the updated database and the matches were collected. Many older or larger families have not been rescanned in years due to technical pipeline limitations, for example, the 5S rRNA (RF00001) has not had its matches updated since 2014.

Once all families were updated, we compared the matches of families in 14.3, which was the last published version, and 15.0 to determine how Rfam has changed. Of the 3,431 families in common between 14.3 and 15.0, 98 had no FULL hits in 14.3 and when moving to 15.0, 23 of these families gained at least one hit while 21 lost all hits, leading to 96 families in 15.0 without FULL hits. Families without FULL hits occur because either the curator-selected gathering threshold of the family is too high, or if Rfamseq does not contain any similar sequences. Future work will look to see if these families require updating the threshold or if additional genomes need to be added to Rfamseq.

Of the 3,302 families with hits in both releases, the average family grew by 166%, with 2,335 gaining at least one hit, 547 losing hits and 420 with no change in the number of hits.

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3 Examining the families with an increase shows that there are 26 families with a greater than
4 10x growth. These families are primarily microRNA families matching to plant genomes. While,
5 as described below, these families have been synchronised with miRBase, we are revisiting
6 these families to see if they need additional future updates in the light of these additional hits,
7 or if the genomes are poorly assembled and should be excluded from Rfamseq.
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10 Overall the update to Rfamseq has led to a considerable change in all Rfam families. This will
11 provide the community with a consistent and up-to-date dataset to reuse. Future updates to
12 Rfamseq will seek to maximise the coverage of known organisms.
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15 16 Improving existing Rfam families

17 18 19 Using RNA 3D structures to revise Rfam secondary structures

20 Rfam families are based on multiple sequence alignments annotated with consensus
21 secondary structures that indicate base pairing. The accuracy and completeness of the
22 consensus secondary structure is of critical importance as it guides the SEED alignment,
23 informs the Infernal CM, and is used for training and benchmarking of software for RNA 2D
24 and 3D structure prediction, including AlphaFold 3 (7) and R-scape (8).
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29 Most of the Rfam families with known 3D structure were created prior to the 3D structure
30 determination using less accurate, predicted secondary structures. For example, while the
31 FMN riboswitch family (RF00050) correctly captured 5 helices of the FMN riboswitch, it did not
32 include 1 helix, 2 pseudoknots, and several key base pairings (Figure 2B). As such, one major
33 goal of this project was to include the pseudoknots which are observed in 3D structures into
34 the Rfam families.
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37 To aid the Rfam curators with updating Rfam alignments an automated pipeline was
38 developed to map RNA sequences and secondary structures of experimentally determined
39 RNA 3D structures to Rfam SEED alignments. Every week Rfam families are mapped to the
40 latest set of RNA chains from PDB (13) using the Infernal *cmscan* program. For each Rfam
41 family with one or more matching structures, the sequences and secondary structures are
42 iteratively added to the alignment in the Stockholm format using Infernal's *cmalign* program.
43 The base pairing information, as determined by FR3D (14), is also included in the alignment
44 as an additional GR annotation line (one per 3D structure). The pipeline is automatically
45 executed weekly and the Rfam curators receive notifications of newly mapped structures
46 (Figure 2A).
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50 The resulting alignments undergo manual review to determine whether the family consensus
51 secondary structure is consistent with the base pair information from PDB structures. The
52 structure and annotated based pairs are always kept in the alignment, even in cases where
53 the structure is not used to update the consensus secondary structure, e.g. low resolution
54 structure or non-canonical base pairs. Additional annotations are also included in the
55 Stockholm files, such as RNA structural elements. For example P1, P2, and P3 domains are
56 included in the Pistol ribozyme RF02679, while the SAM riboswitch (RF00162) now includes
57 a kink-turn annotation.
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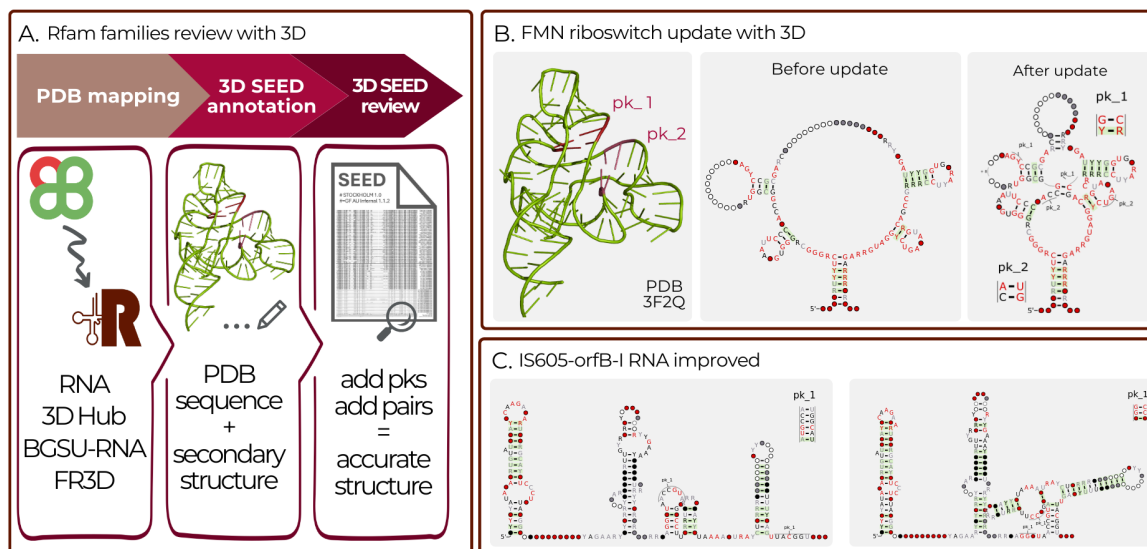


Figure 2. A) Pipeline for reviewing Rfam families using experimentally determined RNA 3D structures from PDB. B) Example of the FMN riboswitch (RF00050) before and after improvements with a 3D structure. Improvements included adding 2 pseudoknots and creating a missing helices. C) A summary of how the IS605-orfB-I RNA (RF03065) family was reviewed and improved using R-scape.

Our pipeline detects 143 Rfam families which match at least one 3D structure. We began updating families with 3D structures in release 14.5 and since then Rfam has updated 65 families, with 298 chains from 3D structures. This includes well known families such as the SAM riboswitch (RF00162), the FMN riboswitch (RF00050) and microRNA 16 precursor (RF00254). The updates included the addition of pseudoknots (PK) in 42 of the 65 families, of which 6 had 2 PK, and 1 had 3. These features include ligand binding sites for riboswitches (28 annotations), locations of well known motifs such kink-turns (8 annotations), and structural regions such as helices and domains (60 annotations). A detailed table showing which families were updated with which 3D structures and can also be found online at <https://rfam.org/3d>. Rfam curators work to keep families as up-to-date with the latest structures as possible, which has led to 11 families being updated more than once since release 14.5.

The review of structures is part of the ongoing curation process, and additional families will be improved in future releases. The pipeline is implemented in Python and is available at <https://github.com/Rfam/rfam-3d-seed-alignments> and the weekly updates are found in the file `pdb_full_region.txt.gz` located in the preview section of the FTP archive (<http://ftp.ebi.ac.uk/pub/databases/Rfam/preview/>).

Using R-scape to improve Rfam consensus secondary structures

Since version 13.0 (5) the Rfam website included the results of the R-scape analysis (8) to help users evaluate consensus secondary structures for each Rfam family, as well as alternative secondary structures generated using the R-scape CaCoFold algorithm. CaCoFold evaluates all possible consensus secondary structures that are consistent with multiple

sequence alignment and can propose a structure maximising the number of base pairs with statistically significant covariation (15).

In release 14.9, the R-scape software was used to systematically review all Rfam families and identify those that could be enhanced using R-scape CaCoFold structures. We examined all families with an increased number of covarying base pairs and selected 26 families for updates. These families are listed in Table 2. Shown in Figure 2C is an example of a family, IS605-orfB-I, before and after improvement.

Table 2: Summary of the R-scape based improvements. This shows the families which were improved by using R-scape CaCoFold structures.

Family	Additional Covarying Basepairs
RF02033 (HEARO)	24
RF03065 (IS605-orfB-I)	14
RF03068 (RT-3)	8
RF03072 (raiA)	5
RF02969 (DUF3800-I)	4
RF01688 (Actino-pnp)	3
RF02004 (group-II-D1D4-5)	3
RF02005 (group-II-D1D4-6)	3
RF02913 (pemK)	3
RF03077 (RT-2)	3
RF03135 (L4-Archaeoglobi)	3
RF03144 (eL15-Euryarchaeota)	3
RF00062 (HgcC)	2
RF01731 (TwoAYGGAY)	2
RF01794 (sok)	2
RF02221 (sRNA-Xcc1)	2
RF02947 (cow-rumen-2)	2
RF03000 (LOOT)	2
RF03158 (L31-Actinobacteria)	2
RF01864 (plasmodium_snoR21)	1
RF01867 (CC2171)	1
RF02944 (c4-2)	1
RF02968 (DUF3800-IX)	1

RF02987 (GA-cis)	1
RF03019 (RT-16)	1
RF03046 (Pseudomonadales-1)	1

Gene and Sequence Ontology annotations

Rfam is commonly used as a source of functional information for non-coding RNAs. This takes several forms, from users reading our curated descriptions and Wikipedia articles to understand the role of an ncRNA, to using the Gene Ontology (GO) and Sequence Ontology (SO) annotations that Rfam curators provide to understand the role of an ncRNA. Rfam is the largest source of GO annotations with over 10 million sequences having an Rfam based GO annotation. In addition to providing information to human users, Rfam is also used in training Large Language Models (LLM). LLMs such as ChatGPT and Claude have clearly been trained on Rfam data and are able to output entries in the formats, Stockholm and DESC, that Rfam uses. Thus providing a completely new way for scientists to access the information found in Rfam.

The Gene Ontology is a resource to classify and provide functional information for biomolecules using structured annotations and ontologies (9). Similarly the Sequence Ontology provides an ontology and structured annotations for the types of biomolecules (10). Both resources are continuously updated to better reflect scientific knowledge. For example, since the last publication of Rfam the SO gained several terms specific to the location of rRNA, e.g. cytosolic_rRNA (SO:0002343) and obsoleted the more generic rRNA terms.

Rfam provides GO and SO annotations for families, however, these annotations are not regularly reviewed to stay up-to-date with the latest changes in the ontologies. As an example, prior to 15.0 the rRNA families used obsoleted SO terms. For 15.0 we manually reviewed all annotations and updated them to better reflect changes in the GO and SO, as well as improved the specificity of annotations where possible.

We ensured that all families had at least one up-to-date SO term and the annotation was as specific as possible. For GO terms, we ensured the terms were up-to-date and added related terms where possible. A few examples of the changes we made were to 1) ensure all snoRNAs had a snoRNA specific SO term and included an RNA processing GO term; 2) add the sodium ion binding term to the NA⁺ riboswitch; and 3) updated families with the generic mature_transcript SO term to the more specific ncRNA SO term. Of the 3,431 common families between 14.3 and 15.0 2,084 had a GO term in 14.3 while 2,426 did in 15.0. For all families in 15.0 we now have at least one GO term for 3,157, which covers 75% of all families, an increase from 60% in 14.3. These changes increased the total number of GO terms from 3,752 to 4,446. As these updates propagate through the community, we expect these changes to lead to millions more sequences annotated with functional information.

Viral RNAs

Starting with Rfam 14.3 we collaborated with the Marz group to develop a new workflow for viral RNA families (16). This workflow is based upon whole genome alignments of viruses and led to the creation of *Flaviviridae* and *Coronaviridae* families as described previously (16). Since the last publication we have continued to use this workflow and have added *Hepatitis C Virus* (HCV) (17) families. We included 14 new families and removed 4 outdated families. A schematic of the new families can be seen in Figure 3. These families include structures found in both the non-coding and coding regions of the viral alignments. All viral families organised by viral clade can be seen at <https://rfam.org/viruses>. We plan to continue to use the viral pipeline and improve the representation of viral families in Rfam and expect to focus on HDV and pestivirus families in the near future.

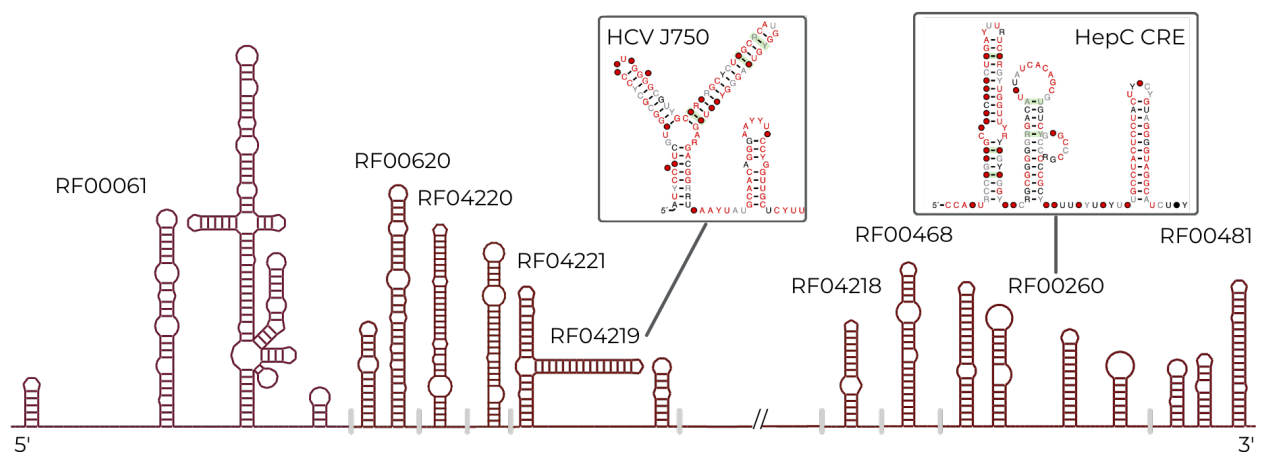


Figure 3: A schematic of the HCV viral families Rfam now contains. These families were built from whole genome alignments, as described in (17). The figure shows their relative locations in the HCV genomic alignment and shown in the inset are two of the new HCV families.

MicroRNAs

MicroRNAs are an important class of ncRNA that regulate gene expression in animals and plants, with many microRNAs being implicated in disease. For example, the mir-17~92 cluster (18) and mir-155 (19) are amongst a number of microRNAs which act as oncogenes. Understanding the evolutionary and family relationships of microRNAs across species allows the transfer of annotation, for example from model organisms to humans and vice versa.

Since early releases, Rfam has included microRNA families, e.g let-7 (20) was deposited in 2002 for Rfam 1.1. However, they were not subject to regular review and were not coordinated with miRBase (11), an authoritative resource for microRNA annotation that assigns identifiers for microRNA genes and sequences. As of Rfam 13.0, out of 1,983 microRNA families found in miRBase v21, only 28% matched one or more of the 529 Rfam microRNA families.

Starting in Rfam 14, we began systematically reviewing microRNA families with the goal to synchronise Rfam microRNA families with miRBase. To this end, we worked to ensure that

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3 the SEED alignments of all microRNA families in Rfam were built from microRNA sequences
4 that are tracked in the miRBase database. Multiple sequence alignments of microRNA
5 sequences were extracted from miRBase and mapped to Rfam accessions. Each sequence
6 was assigned a RNAcentral Unique RNA Sequence (URS) (21) identifier to remove sequence
7 redundancy and represent only distinct sequences for each species. For each alignment a
8 covariance model was built using Infernal and used to search the Rfamseq database. Bit score
9 thresholds for each model (known as gathering thresholds (16)) were manually curated. These
10 thresholds enable automatic and accurate genome annotation using Rfam microRNA families
11 with Infernal.
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15 Pre-existing Rfam microRNA families were reviewed and replaced with miRBase-derived
16 SEED alignments where possible. New families were created when Rfam did not already
17 represent the microRNA sequences. MicroRNA families found in Rfam that did not match
18 miRBase were reviewed and updated or deleted. In cases where the miRBase alignment
19 matched several Rfam families we manually inspected the alignment and families and split
20 and merged families and built clans of families as appropriate.
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24 Rfam release 15.0 marks the completion of the synchronisation process, as we have
25 processed all microRNA alignments from miRBase. For roughly 200 miRBase-derived
26 alignments, we determined that the family was not suitable for inclusion into Rfam. In most
27 cases this was because there was a single unique sequence in the miRBase alignment. A
28 small fraction of the alignments which have not been added may be removed from miRBase
29 in the future. Table 3 shows the summary of changes since release 14.3, and a list of all
30 microRNA families is found in Supplementary information in Table S1. All miRBase microRNA
31 sequences that are not represented in updated Rfam families will be periodically and
32 systematically reviewed in a cycle of improvements and curation of both Rfam and miRBase.
33 Rfam and miRBase will continue to synchronise our resources as new microRNAs and new
34 microRNA alignments are available, with miRBase acting as the repository of microRNA
35 sequences, and Rfam as the authority on the grouping of those sequences into families. Rfam
36 microRNA family classifications will be available through both resources.
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41 Table 3: A summary of the changes in Rfam microRNA families since last publication (16) with
42 release 14.3.

	Changes for Rfam 15.0
Total number of microRNA families	1,603
New families	722
Updated families	881
Deleted families	8

54 55 New families

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57 While the primary focus of Rfam has been to complete the microRNA project, and improve
58 existing families with 3D structures, we have continued to create new families. Since Rfam
59 14.3 (16), Rfam has created 16 new non-microRNA or viral RNA families. The families cover
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a range of phylogenetic and functional types. A few examples include Bacteroidales small SRP (RF04183), the signal recognition particle RNA of Bacteroidetes (22), Hairpin-meta1, a virus-like ribozyme reported in RNA satellites of plant viruses (RF04190) (23), Hovlinc ribozyme (RF04188) (24), a newly discovered type of self-cleaving ribozymes found in human and other hominids and RF04222 PLRV xrRNA, a exoribonuclease-resistant RNA detected in Flavivirus Potato virus (25), RF04247 bZIP family which is a non canonical Hac1/Xbp1 intron found in *Metazoa* (26). Shown in Figure 4 are the secondary structures of selected families.

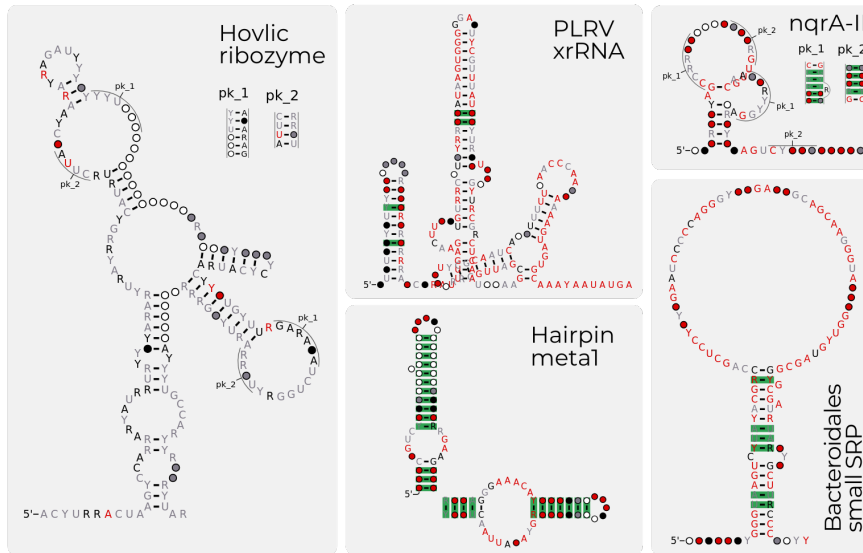


Figure 4: A selection of the new families for Rfam 15.0. The five families shown Hovlinc ribozyme (RF04188), the PLRV xrRNA (RF04222), the hairpin meta ribozyme (RF04190), nqrA-II ncRNA motif (RF04310) and Bacteroidales small SRP (RF04183) are several of the new families created for Rfam 15.0.

These families are curated through a combination of literature reviews and community submissions. We actively encourage groups with candidate RNAs to contribute their alignments and secondary structure data to Rfam. However, it is important to note that Rfam requires all sequences in SEED alignments to be traceable to public databases such as GenBank (27) or RNAcentral (21). With the increasing ease of sequencing, many laboratories maintain private sequence databases for constructing alignments. As a result, many of these new alignments cannot be incorporated into Rfam due to the lack of traceable public records. We strongly recommend that the scientific community submit their sequences to publicly accessible databases, ensuring they are available for reuse and analysis by the broader research community. Furthermore, when publishing alignments, using public accessions will facilitate faster and more efficient integration into resources like Rfam.

Other improvements

Updating FULL alignments

Rfam provides several data types for interested users to download from our FTP site. These include the SEED alignments, CMs and FULL sequences. Older versions of Rfam included

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3 FULL alignments, which are an alignment of all matching sequences to the CM. Previously,
4 these were no longer produced because of technical limitations, however, with improvements
5 to infernal and growth in available compute power it is now possible to create these alignments
6 again. We now produce full alignments for all Rfam families. These are available for each
7 model in the 'full_alignments' section on the FTP site
8 (https://ftp.ebi.ac.uk/pub/databases/Rfam/CURRENT/full_alignments).
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11 APICURON integration

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13 APICURON (<https://apicuron.org/>) is a database to track and credit biocurators for the work
14 they do (28). The database allows for databases to credit curators for each activity they
15 perform and provides overall statistics for each database including Rfam. In Rfam, it is
16 common for a curator to perform many small updates and fixes to families to produce a
17 release. Currently, this work goes unacknowledged except during publication, which are
18 generally separated by several years. By integrating with APICURON we are able to display
19 all the changes curators perform as part of their duties on a more regular schedule.
20 Additionally, APICURON updates ORCID records (<https://orcid.org/>) to help credit curators for
21 their activities. We update our APICURON records with each release and our APICURON
22 page is available at: <https://apicuron.org/databases/rfam>. APICURON requires that each
23 resource track the activities of each curator, unfortunately some historical Rfam activity does
24 not have the required specificity, leading to some older curators lacking attributions. This is
25 being worked on and we hope to properly credit all curators for their contributions to Rfam.
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31 Website improvements

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33 The Rfam website (<http://rfam.org>) has undergone continuous development since our last
34 publication. We have added several new features, such as dedicated landing pages for each
35 project, e.g. viral families can easily be browsed at <http://rfam.org/viruses>. These pages make
36 it simpler for users interested in a particular project, e.g. the 3D structure alignments, to see
37 our progress and fetch all data related to the project.
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41 We have recently updated some terminology used for riboswitch families in Rfam. We have
42 found that some users are confused that Rfam riboswitch families generally include just the
43 aptamer domains. This is because aptamers align well, while it is difficult to build an alignment
44 of a whole riboswitch. We have added a short note to the header of each Rfam riboswitch
45 page to indicate that this family is only the aptamer domain and a short explanation of what
46 that means. Additionally, the descriptions of families now include the term 'aptamer' to clarify
47 this point. We have not updated the identifiers or accessions of any families.
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51 Finally, we have integrated the RNAcentral LitScan widget from RNAcentral. RNAcentral has
52 developed a pipeline, LitScan, which identifies and extracts mentions of any non-coding RNA
53 in all open access literature (29). The result of this pipeline can be reused by embedding a
54 simple HTML widget. The widget allows users to browse and search the related literature in a
55 convenient way. We have embedded this widget on all Rfam family pages under the new
56 'Publications' tab. The results are updated with each RNAcentral release, roughly every 4
57 months. An example of the widget for the Glutamine riboswitch family page is shown in Figure
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The screenshot shows the 'Family: *glnA* (RF01739)' page. The description is 'Glutamine riboswitch'. The widget includes a sidebar with navigation options: Summary, Sequences, Alignment, Secondary structure, Species, Trees, Structures, Motif matches, Database references, Curation, and Publications. The main content area is titled 'Open Access Publications 1136 total'. It features a search bar with 'Sort by score - default', 'Text search within results', 'Filter', and 'Clear' buttons. Below the search bar are three article cards. The first card is titled 'Inactivation of Glutamine Synthetase-Coding Gene *glnA* Increases Susceptibility to Quinolones Through Increasing Outer Membrane Protein F in *Salmonella enterica* Serovar Typhi' by Millanao, Ana R. et al., Frontiers in Microbiology, 2020. The second card is 'Genotypic and Lipid Analyses of Strains From the Archaeal Genus *Halorubrum* Reveal Insights Into Their Taxonomy, Divergence, and Population Structure' by de la Haba, Rafael R. et al., Frontiers in Microbiology, 2018. The third card is 'A Novel *Campylobacter jejuni* Sequence Type from a Culture-Negative Patient in The Gambia' by Morris, Gerard A. J. et al., PLoS ONE, 2008. The sidebar also includes filters for 'Keyword' (glnA, RF01739), 'Article type' (Research article, Review article, Brief report, Case report, Other, Letter, Rapid communication), 'Paper section' (Title, Abstract, Main text), and 'Mentioned Organism' (cellular organisms, Bacteria, Eukaryota, Opisthokonta, Metazoa, Eumetazoa, Bilateria).

Figure 5: The LitScan widget embedded in the Glutamine riboswitch family page. This widget shows users which open access articles mention the family. Families are searched using their Rfam ID and Rfam accession in all open access literature. It allows users to search the matched articles by several types of metadata such as the article type (research, review, report, etc), the section of the paper which mentions the family and organisms mentioned in the paper. Additionally, users can perform a text search within the sentences which mention the Rfam family.

Conclusions

After more than 20 years of work (1), Rfam has grown to over 4,000 families and continues to be a key resource in RNA science. We continue to provide a large centralised collection of ncRNA families, which are used in many ways. Rfam was originally created to annotate genomes, but we have grown far beyond that use case. We would like to take this opportunity to thank everyone who has worked on or collaborated with Rfam over the past 20 years. Anyone interested in learning about the history and changes in Rfam since its inception are encouraged to visit <https://rfam.org/rfam20> to find interviews with many former and current staff and users.

Since our last publication we have focused on completing our synchronisation with miRBase and improving existing families using R-scape and 3D structures. This has led to a large increase in the number and quality of families. Rfam plans to stay synchronised with miRBase and complete the 3D structure improvements by connecting each family to at least one

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3 structure where possible. Outside of those projects, we will continue to import viral RNAs and
4 return to capturing more novel families discovered by the community. Finally, we will explore
5 ways to expand Rfamseq to better improve our coverage of the phylogenetic space.
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8 It is essential to note that there has been a major shift in bioinformatics with the publication of
9 AlphaFold and its effect on protein structure prediction. We expect that as the field of RNA
10 structure prediction matures, Rfam will continue to play a key role as a source of ground truth.
11 In order to best serve this new use case, we will begin exploring ways to grow faster than
12 before, while maintaining the high standards the community has come to expect of Rfam
13 alignments. This will be essential to providing the test and training sets required for deep
14 learning based approaches.
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17 Finally, we encourage any interested community members to reach out for collaboration or to
18 provide data. As discussed here, much of our major work is carried out with interested
19 community members and can lead to new directions for the resource. We invite new data
20 submissions and feedback at <https://docs.rfam.org/page/contact-us.html>.
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24 Data availability

25 All Rfam data are released under the Creative Commons Zero (CC0) licence at
26 <https://rfam.org>. The data can be accessed via an API, a public MySQL database, and the
27 FTP archive. The Rfam documentation (<https://docs.rfam.org>) and (30) contain detailed
28 instructions. All code is available on GitHub under the Apache 2.0 licence at
29 <https://github.com/Rfam>.
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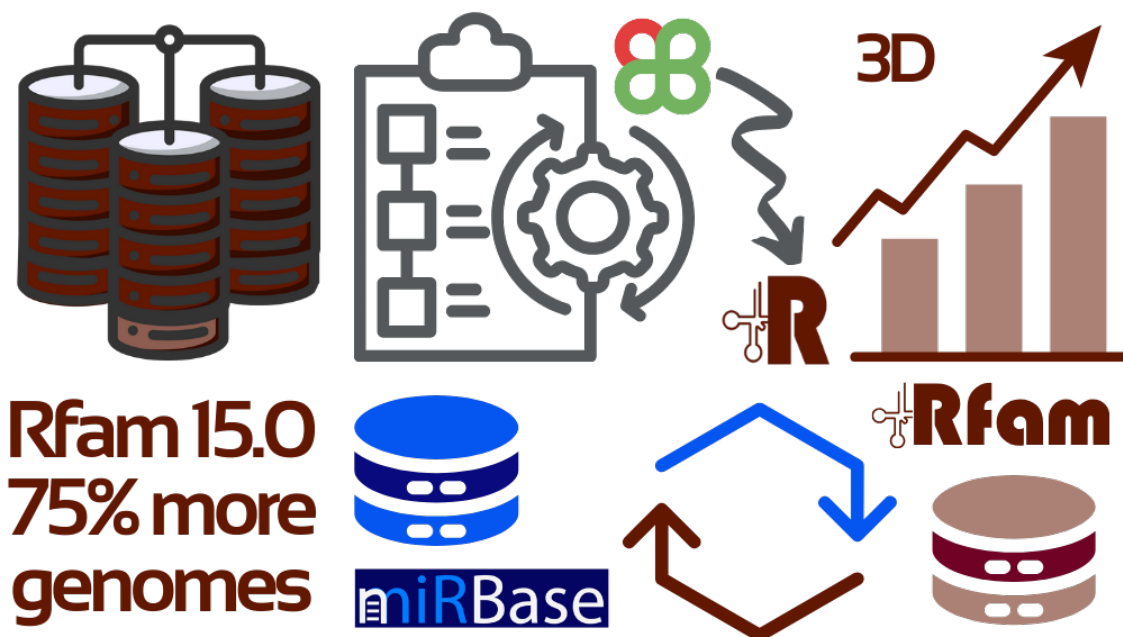
44 Conflict of interest

45 AB is a member of the Nucleic Acids Research Editorial Board.
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53 their contributions, including providing alignments and feedback for families. In particular we
54 thank Lars Barquist, Fei Qi, Christina Weinberg, Zasha Weinberg and Quentin Vincens who
55 kindly shared their data with us and worked with us in the creation of new families.
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Graphical Abstract



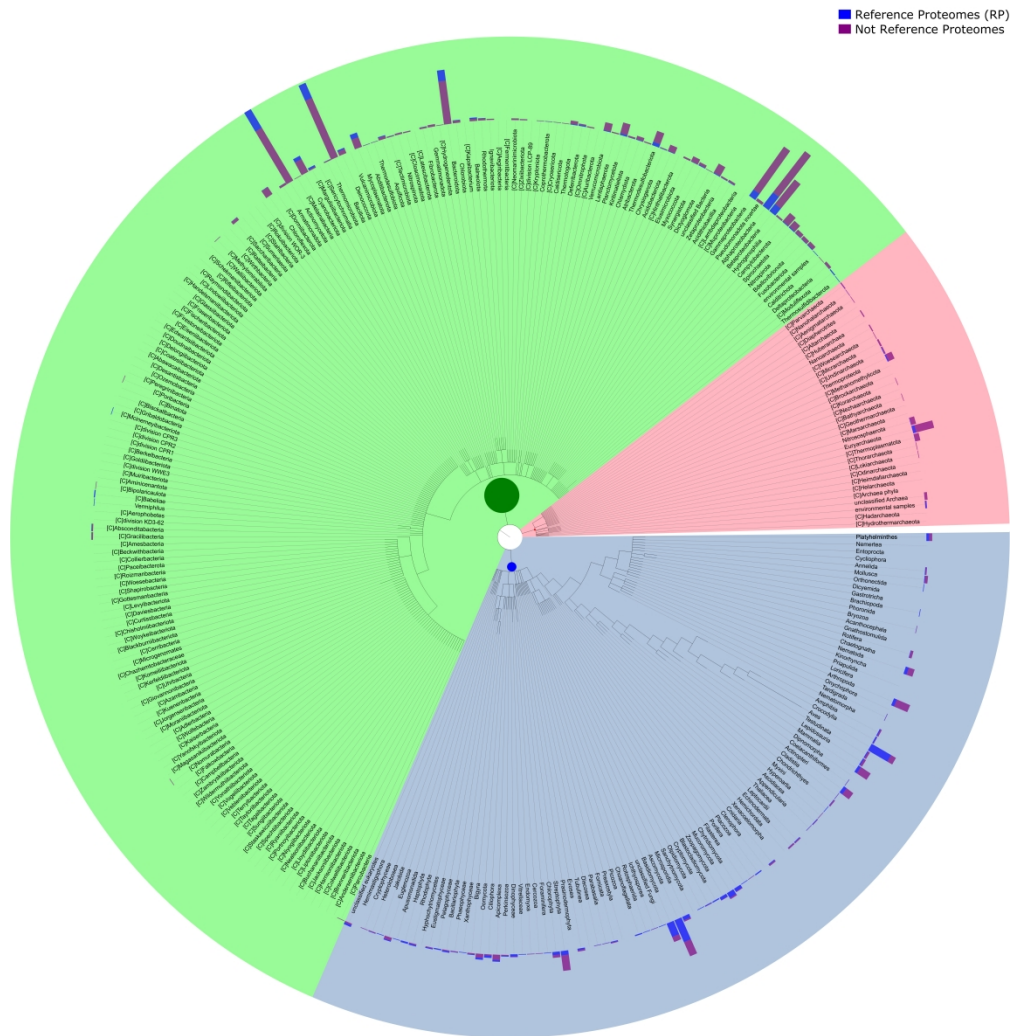
Rfam has undergone a major update with the release of 15.0. We have increased the number of genomes in our sequence database Rfamseq by 75%, completed the synchronisation with miRBase and improved 65 families using 3D structures.

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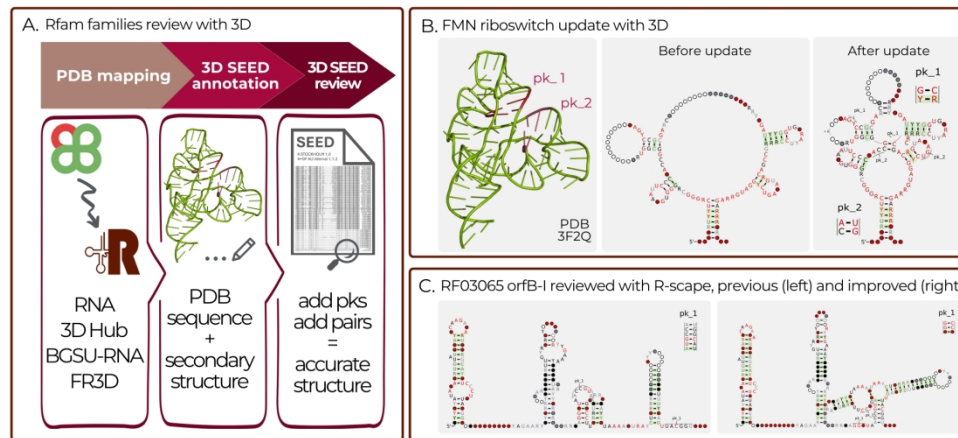
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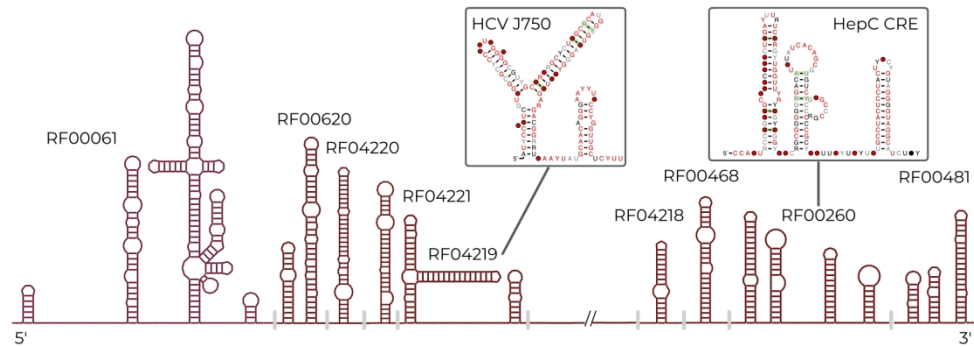
The taxonomic distribution of cellular organisms in Rfamseq 15 organised by the phylogenetic kingdom. Shown on the outside is the number of reference and non-reference proteomes in each lineage. Each coloured section indicates the kingdom with bacteria (green), archaea (pink) and eukaryotes (blue).

1291x1329mm (118 x 118 DPI)



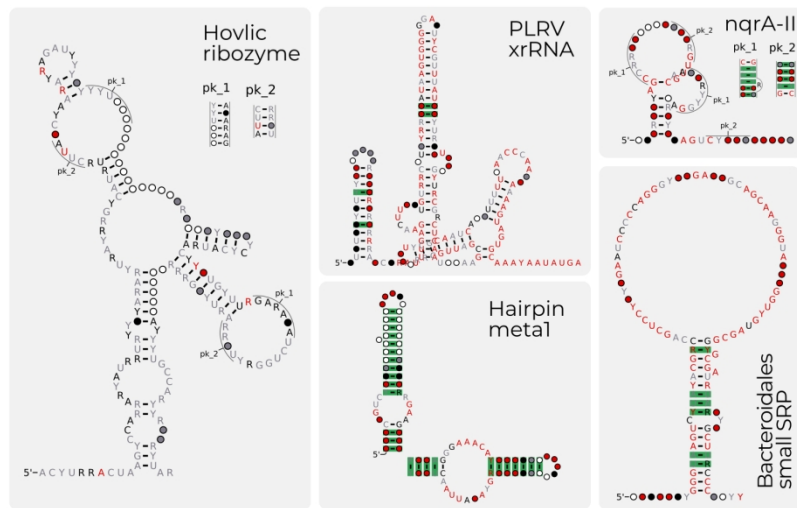
25 A) Pipeline for reviewing Rfam families using experimentally determined RNA 3D structures from PDB. B)
26 Example of the FMN riboswitch (RF00050) before and after improvements with a 3D structure.
27 Improvements included adding 2 pseudoknots and creating a missing helices. C) A summary of how the
28 IS605-orfB-I RNA (RF03065) family was reviewed and improved using R-scape.

29 1283x721mm (38 x 38 DPI)



25 A schematic of the HCV viral families Rfam now contains. These families were built from whole genome
26 alignments, as described in (17). The figure shows their relative locations in the HCV genomic alignment and
27 shown in the inset are two of the new HCV families.

28 1283x721mm (38 x 38 DPI)



A selection of the new families for Rfam 15.0. The five families shown Hovlic ribozyme (RF04188), the PLRV xrRNA (RF04222), the hairpin meta ribozyme (RF04190), nqrA-II ncRNA motif (RF04310) and Bacteroidales small SRP (RF04183) are several of the new families created for Rfam 15.0.

1283x721mm (38 x 38 DPI)

Family: *glnA* (RF01739)
Description: *Glutamine riboswitch*

1712 sequences 87 species 0 structures

Summary
Sequences
Alignment
Secondary structure
Species
Trees
Structures
Motif matches
Database references
Curation
Publications

Open Access Publications 1136 total

Sort by score - default Text search within results Filter Clear

Keyword

- glnA* (1125)
- RF01739 (11)

Article type

- Research article (1010)
- Review article (91)
- Brief report (19)
- Case report (5)
- Other (5)
- Letter (4)
- Rapid communication (1)

Paper section

- Title (7)
- Abstract (60)
- Main text (1135)

Mentioned Organism

- cellular organisms (507)
- Bacteria (491)
- Eukaryota (480)
- Opisthokonta (453)
- Metazoa (438)
- Eumetazoa (437)
- Bilateria (436)

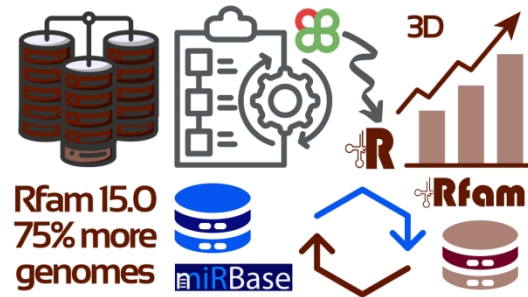
Inactivation of Glutamine Synthetase-Coding Gene *glnA* Increases Susceptibility to Quinolones Through Increasing Outer Membrane Protein F in *Salmonella enterica* Serovar Typhi
Millanao, Ana R. et al., *Frontiers in Microbiology*, 2020. [Europe PMC]
*Our findings indicate that **glnA** inactivation promotes ompF expression, that translates into increased OmpF protein, facilitating the entry of ciprofloxacin, thus increasing susceptibility to ciprofloxacin through 2 possible mechanisms.* [Abstract](#)
- View abstract

Genotypic and Lipid Analyses of Strains From the Archaeal Genus *Halorubrum* Reveal Insights Into Their Taxonomy, Divergence, and Population Structure
de la Haba, Rafael R. et al., *Frontiers in Microbiology*, 2018. Cited by 8 articles. [Europe PMC]
*Reanalysis that excluded comparison of the two type strains with Fb21 demonstrated a rise in the correlation coefficient for all genes or genomes: 0.60 for 16S rRNA gene, 0.60 for *ppsA*, 0.69 for *atpB*, 0.70 for *rpoB*, 0.80 for ***glnA***, 0.83 for *EF-2*, and 0.77 and 0.73 for the concatenated sequences and the ANI values, respectively.* [Main text](#)
- View abstract

A Novel *Campylobacter jejuni* Sequence Type from a Culture-Negative Patient in The Gambia
Morris, Gerard A. J. et al., *PLoS ONE*, 2008. Cited by 4 articles. [PubMed] [Europe PMC]
*The novel ST was designated ST-2928: With an allele profile code; 24, 2, 2, 15, 294, 3, 12, for *aspA*, ***glnA***, *uncA*, *glyA*, *pgm*, *tkt*, and *gltA* respectively.* [Main text](#)
- View abstract

The LitScan widget embedded in the Glutamine riboswitch family page. This widget shows users which open access articles mention the family. Families are searched using their Rfam ID and Rfam accession in all open access literature. It allows users to search the matched articles by several types of metadata such as the article type (research, review, report, etc), the section of the paper which mentions the family and organisms mentioned in the paper. Additionally, users can perform a text search within the sentences which mention the Rfam family.

424x318mm (72 x 72 DPI)



Rfam has undergone a major update with the release of 15.0. We have increased the number of genomes in our sequence database Rfamseq by 75%, completed the synchronisation with miRBase and improved 65 families using 3D structures.

1283x721mm (38 x 38 DPI)

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Kingdom	Rfamseq v14	Rfamseq v15
Total sequence length	3.68e11	1.46e12
Number of species	14,774	26,106
Eukaryotes	1,057	2,613
Archaea	418	370
Bacteria	7,808	9,601
Viruses	5,491	13,552
Number of Rfam hits	2,897,296	10,736,534
Size on disk	170 GB	772 GB

Family	Additional Covarying Basepairs
RF02033 (HEARO)	24
RF03065 (IS605-orfB-I)	14
RF03068 (RT-3)	8
RF03072 (raiA)	5
RF02969 (DUF3800-I)	4
RF01688 (Actino-pnp)	3
RF02004 (group-II-D1D4-5)	3
RF02005 (group-II-D1D4-6)	3
RF02913 (pemK)	3
RF03077 (RT-2)	3
RF03135 (L4-Archaeoglobi)	3
RF03144 (eL15-Euryarchaeota)	3
RF00062 (HgcC)	2
RF01731 (TwoAYGGAY)	2
RF01794 (sok)	2
RF02221 (sRNA-Xcc1)	2
RF02947 (cow-rumen-2)	2
RF03000 (LOOT)	2
RF03158 (L31-Actinobacteria)	2
RF01864 (plasmodium_snoR21)	1
RF01867 (CC2171)	1
RF02944 (c4-2)	1
RF02968 (DUF3800-IX)	1
RF02987 (GA-cis)	1
RF03019 (RT-16)	1
RF03046 (Pseudomonadales-1)	1

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	Changes for Rfam 15.0
Total number of microRNA families	1,603
New families	722
Updated families	881
Deleted families	8

Rfam Accession	Rfam ID	miRBase Family Accession
RF00027	let-7	MIPF0000002
RF00047	mir-2	MIPF0000049
RF00051	mir-17	MIPF0000001
RF00052	lin-4	MIPF0000303
RF00053	mir-7	MIPF0000022
RF00073	mir-156	MIPF0000008
RF00074	mir-29	MIPF0000009
RF00075	mir-166	MIPF0000004
RF00076	mir-181	MIPF0000007
RF00103	mir-1	MIPF0000038
RF00104	mir-10	MIPF0000033
RF00104	mir-10	MIPF0000025
RF00104	mir-10	MIPF0000268
RF00104	mir-10	MIPF0000271
RF00129	mir-103	MIPF0000024
RF00130	mir-192	MIPF0000063
RF00131	mir-30	MIPF0000005
RF00143	mir-6	MIPF0000119
RF00144	mir-199	MIPF0000040
RF00237	mir-9	MIPF0000014
RF00239	mir-124	MIPF0000021
RF00241	mir-8	MIPF0000019
RF00244	mir-26	MIPF0000043
RF00245	mir-19	MIPF0000011
RF00246	mir-135	MIPF0000028
RF00247	mir-160	MIPF0000032
RF00251	mir-219	MIPF0000044
RF00253	mir-101	MIPF0000046
RF00254	mir-16	MIPF0000006
RF00255	mir-218	MIPF0000026
RF00256	mir-196	MIPF0000031

RF00257	mir-194	MIPF0000055
RF00258	mir-130	MIPF0000034
RF00363	mir-BART1	MIPF0000325
RF00365	mir-BHRF1-1	MIPF0000331
RF00366	mir-BHRF1-2	MIPF0000332
RF00446	mir-133	MIPF0000029
RF00455	mir-15	MIPF0000006
RF00637	mir-276	MIPF0000124
RF00638	MIR159	MIPF0000010
RF00639	mir-515	MIPF0000020
RF00640	MIR167	MIPF0000023
RF00641	mir-154	MIPF0000018
RF00642	mir-23	MIPF0000027
RF00643	MIR171_1	MIPF0000030
RF00644	mir-27	MIPF0000036
RF00645	MIR169_2	MIPF0000037
RF00646	mir-204	MIPF0000042
RF00647	MIR164	MIPF0001794
RF00648	MIR396	MIPF0000047
RF00649	mir-128	MIPF0000048
RF00650	mir-153	MIPF0000050
RF00651	mir-221	MIPF0000051
RF00652	MIR478	MIPF0000052
RF00653	mir-22	MIPF0000053
RF00654	mir-216	MIPF0000054
RF00655	mir-28	MIPF0000057
RF00656	mir-205	MIPF0000058
RF00657	mir-184	MIPF0000059
RF00658	mir-21	MIPF0000060
RF00659	mir-365	MIPF0000061
RF00660	mir-214	MIPF0000062
RF00661	mir-31	MIPF0000064
RF00662	mir-132	MIPF0000065

RF00663	mir-183	MIPF0000066
RF00664	mir-223	MIPF0000067
RF00665	mir-290	MIPF0000068
RF00666	mir-32	MIPF0000069
RF00667	mir-33	MIPF0000070
RF00668	mir-302	MIPF0000071
RF00669	mir-96	MIPF0000072
RF00670	mir-105	MIPF0000074
RF00671	mir-138	MIPF0000075
RF00672	mir-190	MIPF0000076
RF00673	mir-217	MIPF0000077
RF00674	mir-187	MIPF0000078
RF00675	mir-145	MIPF0000079
RF00676	mir-127	MIPF0000080
RF00677	MIR168	MIPF0000081
RF00678	mir-140	MIPF0000085
RF00679	mir-210	MIPF0000086
RF00680	mir-224	MIPF0000088
RF00681	mir-198	MIPF0000090
RF00682	mir-144	MIPF0000093
RF00683	mir-143	MIPF0000094
RF00684	mir-122	MIPF0000095
RF00685	mir-36	MIPF0000096
RF00686	mir-338	MIPF0000097
RF00687	mir-136	MIPF0000099
RF00688	MIR394	MIPF0000100
RF00689	MIR390	MIPF0000101
RF00690	MIR408	MIPF0000102
RF00691	mir-146	MIPF0000103
RF00692	MIR171_2	MIPF0000104
RF00693	mir-147	MIPF0000105
RF00694	mir-137	MIPF0000106
RF00695	MIR398	MIPF0000107

RF00696	mir-203	MIPF0000108
RF00697	mir-186	MIPF0000109
RF00698	mir-489	MIPF0000111
RF00699	mir-134	MIPF0000112
RF00700	mir-375	MIPF0000114
RF00701	mir-126	MIPF0000115
RF00702	mir-182	MIPF0000116
RF00703	mir-139	MIPF0000117
RF00704	MIR397	MIPF0000120
RF00705	mir-202	MIPF0000121
RF00706	mir-263	MIPF0000122
RF00707	mir-197	MIPF0000123
RF00708	mir-450	MIPF0000128
RF00709	mir-455	MIPF0000129
RF00710	mir-44	MIPF0000132
RF00711	mir-449	MIPF0000133
RF00712	mir-460	MIPF0000134
RF00713	mir-239	MIPF0000135
RF00714	MIR535	MIPF0000136
RF00715	mir-383	MIPF0000137
RF00716	mir-3	MIPF0000140
RF00717	mir-315	MIPF0000141
RF00718	mir-431	MIPF0000142
RF00719	mir-326	MIPF0000143
RF00720	mir-317	MIPF0000144
RF00721	MIR475	MIPF0000145
RF00722	mir-451	MIPF0000148
RF00723	mir-448	MIPF0000149
RF00724	mir-282	MIPF0000150
RF00725	mir-iab-4	MIPF0000151
RF00726	mir-87	MIPF0000152
RF00727	bantam	MIPF0000153
RF00728	mir-81	MIPF0000154

RF00729	mir-278	MIPF0000155
RF00730	mir-277	MIPF0000156
RF00731	mir-155	MIPF0000157
RF00732	mir-305	MIPF0000158
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RF00760	mir-342	MIPF0000190
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RF00774	mir-360	MIPF0000210
RF00775	mir-432	MIPF0000211
RF00776	mir-540	MIPF0000212
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RF00780	MIR477	MIPF0000216
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RF00838	mir-252	MIPF0000285
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RF00843	mir-228	MIPF0000292
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RF00846	mir-64	MIPF0000295
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RF00879	mir-615	MIPF0000342
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RF00890	mir-668	MIPF0000357
RF00891	mir-671	MIPF0000358
RF00892	mir-551	MIPF0000360
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RF00895	mir-786	MIPF0000363
RF00896	mir-787	MIPF0000364
RF00897	mir-675	MIPF0000365
RF00898	mir-242	MIPF0000366
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RF00973	mir-597	MIPF0000479
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RF01002	mir-936	MIPF0000517
RF01003	mir-563	MIPF0000519
RF01004	mir-557	MIPF0000520
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RF01007	mir-624	MIPF0000523
RF01008	mir-636	MIPF0000524
RF01009	mir-M7	MIPF0000526

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RF01022	mir-611	MIPF0000539
RF01023	mir-940	MIPF0000540
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RF01028	mir-633	MIPF0000546
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RF01030	mir-422	MIPF0000548
RF01031	mir-639	MIPF0000549
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RF01034	mir-618	MIPF0000553
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RF01039	mir-937	MIPF0000560
RF01040	mir-573	MIPF0000561
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RF02022	mir-1275	MIPF0000674
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RF03857	mir-3129	MIPF0001458
RF03858	mir-1991	MIPF0000732
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RF03873	mir-3192	MIPF0001597
RF03874	mir-8834	MIPF0002099
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RF03876	mir-7132	MIPF0002098
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RF03890	mir-B8	MIPF0002021
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RF03892	mir-4860	MIPF0001765
RF03893	mir-4879	MIPF0001780
RF03894	mir-5736	MIPF0001480
RF03895	MIR2679	MIPF0000892
RF03896	MIR2275	MIPF0000797
RF03897	mir-4077	MIPF0000905
RF03898	mir-7616	MIPF0001718
RF03899	mir-5912	MIPF0001497
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RF03903	mir-679	MIPF0001564
RF03904	MIR7991	MIPF0001701
RF03905	MIR6149	MIPF0001580
RF03906	mir-3199	MIPF0001026
RF03907	mir-4428	MIPF0001630
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RF03909	mir-3804	MIPF0001255
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RF03922	MIR2119	MIPF0000762
RF03923	mir-964	MIPF0000949
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RF03925	mir-1011	MIPF0000969
RF03926	MIR1435	MIPF0000760
RF03927	MIR538	MIPF0000161
RF03929	mir-6579	MIPF0001492
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RF03932	mir-1597	MIPF0000764
RF03933	MIR6445	MIPF0001621
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RF03958	mir-959	MIPF0000910
RF03959	mir-303	MIPF0001013
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RF03961	mir-9033	MIPF0002087
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RF03963	mir-2996	MIPF0001023
RF03964	mir-H1	MIPF0000738
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RF03966	mir-76	MIPF0000902
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RF03969	mir-622	MIPF0000619
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RF03972	mir-3150	MIPF0001102
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RF03977	mir-976	MIPF0000916
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RF03982	mir-4865	MIPF0001750
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RF03984	MIR2933	MIPF0001072

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RF03992	mir-6302	MIPF0001398
RF03993	mir-8536	MIPF0002030
RF03994	mir-7558	MIPF0001716
RF03995	mir-7957	MIPF0001668
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RF03997	mir-8510	MIPF0001886
RF03998	mir-2160	MIPF0000769
RF03999	mir-7883	MIPF0001849
RF04000	MIR8139	MIPF0001665
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RF04005	mir-4599	MIPF0001252
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RF04010	mir-3003	MIPF0000818
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RF04024	mir-9571	MIPF0002068
RF04025	mir-7964	MIPF0001749
RF04026	mir-8499	MIPF0002029
RF04027	mir-1422	MIPF0000565
RF04028	mir-7948	MIPF0001695
RF04029	mir-8521	MIPF0001871
RF04030	mir-6096	MIPF0001436
RF04031	mir-2686	MIPF0000927
RF04032	MIR2912	MIPF0000778
RF04033	mir-8512	MIPF0002076
RF04035	mir-7910	MIPF0001840
RF04036	mir-2076	MIPF0001795
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RF04038	mir-5985	MIPF0001491
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RF04043	mir-2062	MIPF0001753
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RF04046	mir-2154	MIPF0000781
RF04047	mir-9228	MIPF0001876
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RF04068	mir-3927	MIPF0001462
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RF04070	MIR6440	MIPF0001406
RF04071	MIR2863	MIPF0000925
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RF04074	mir-1199	MIPF0001659
RF04075	mir-1545	MIPF0001711
RF04076	mir-H11	MIPF0000833
RF04077	mir-1245	MIPF0000620
RF04078	mir-1905	MIPF0000753
RF04079	MIR161	MIPF0000455
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RF04082	mir-54	MIPF0000874
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RF04096	mir-4433	MIPF0001826
RF04097	MIR2630	MIPF0000814
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RF04099	MIR837	MIPF0001155
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RF04101	mir-8864	MIPF0001919
RF04102	MIR6457	MIPF0001534
RF04103	mir-8356	MIPF0001997
RF04104	MIR918	MIPF0000374
RF04105	mir-3165	MIPF0001635
RF04106	mir-1303	MIPF0000608
RF04107	mir-5391	MIPF0001944
RF04108	mir-2513	MIPF0000980
RF04109	mir-1305	MIPF0000965
RF04110	MIR5084	MIPF0002026
RF04111	MIR6274	MIPF0001706
RF04112	MIR5512	MIPF0001478
RF04113	MIR1523	MIPF0001327
RF04114	MIR4374	MIPF0001152
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RF04116	MIR9672	MIPF0001942
RF04117	MIR5200	MIPF0001904
RF04118	MIR9481	MIPF0002096
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RF04120	MIR5998	MIPF0001613
RF04121	mir-1289	MIPF0000626
RF04122	mir-1204	MIPF0000671
RF04123	mir-3127	MIPF0001439
RF04124	MIR8565	MIPF0001889
RF04125	MIR9408	MIPF0002027
RF04126	mir-9198	MIPF0001887
RF04127	MIR8007	MIPF0001839
RF04128	MIR8562	MIPF0001861
RF04129	MIR4240	MIPF0001198
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RF04132	mir-4436	MIPF0001236
RF04133	MIR2646	MIPF0001010
RF04134	MIR7504	MIPF0001798
RF04135	MIR5062	MIPF0001922
RF04136	MIR1862	MIPF0000580
RF04137	MIR834	MIPF0001183
RF04138	mir-9243	MIPF0001926
RF04139	MIR841	MIPF0001112
RF04140	mir-3118	MIPF0001928
RF04141	MIR8622	MIPF0001931
RF04142	mir-1299	MIPF0000625
RF04143	MIR869	MIPF0001167
RF04144	MIR9783	MIPF0001947
RF04145	MIR8706	MIPF0001953
RF04146	mir-4742	MIPF0001552
RF04147	MIR6224	MIPF0001435
RF04148	MIR844	MIPF0001197
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RF04150	MIR2655	MIPF0000813
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RF04152	mir-3618	MIPF0001710

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RF04155	mir-9236	MIPF0001905
RF04156	MIR2670	MIPF0000855
RF04157	MIR9486	MIPF0002054
RF04158	mir-568	MIPF0000408
RF04159	MIR1437	MIPF0001762
RF04160	MIR868	MIPF0001173
RF04161	mir-3688	MIPF0001263
RF04162	MIR9662	MIPF0002119
RF04163	mir-8364	MIPF0001877
RF04164	MIR1507	MIPF0000699
RF04165	mir-2483	MIPF0001532
RF04166	mir-2278	MIPF0001522
RF04167	mir-1972	MIPF0001025
RF04168	MIR839	MIPF0001143
RF04169	mir-2235	MIPF0000825
RF04170	MIR7723	MIPF0001739
RF04171	MIR1509	MIPF0000771
RF04172	MIR8675	MIPF0002106
RF04173	MIR847	MIPF0001171
RF04174	MIR4208	MIPF0001108
RF04175	mir-1260b	MIPF0001381
RF04176	mir-3149	MIPF0001935
RF04185	MIR2118_2	MIPF0001409
RF04186	mir-278_2	MIPF0000728
RF04187	MIR862	MIPF0001145
RF04193	mir-51	MIPF0000268
RF04194	mir-57	MIPF0000271
RF04195	MIR6217	MIPF0001550
RF04196	MIR5638	MIPF0001350
RF04197	mir-9457	MIPF0002122
RF04198	MIR8670	MIPF0002041

RF04199	MIR6027	MIPF0001424
RF04200	mir-9437	MIPF0001943
RF04201	MIR7510	MIPF0001684
RF04202	MIR5380	MIPF0001331
RF04203	MIR1144	MIPF0000432
RF04204	mir-3473	MIPF0001230
RF04205	MIR2606	MIPF0000888
RF04206	MIR9555	MIPF0002081
RF04207	MIR5048	MIPF0001453
RF04208	MIR8742	MIPF0002016
RF04209	MIR7533	MIPF0001834
RF04210	MIR8643	MIPF0002008
RF04211	MIR5185	MIPF0001246
RF04212	mir-8904	MIPF0001977
RF04213	MIR7807	MIPF0002091
RF04214	MIR7526	MIPF0001651
RF04215	mir-9214	MIPF0002108
RF04216	mir-509	MIPF0000130
RF04217	mir-297	MIPF0000204
RF04223	MIR2619	MIPF0001294
RF04224	mir-9229	MIPF0001875
RF04225	MIR7502	MIPF0001869
RF04226	mir-9186	MIPF0001868
RF04227	mir-9215	MIPF0001893
RF04228	MIR6140	MIPF0001666
RF04229	mir-9279	MIPF0001911
RF04230	mir-9261	MIPF0001938
RF04231	mir-9191	MIPF0001987
RF04232	mir-9318	MIPF0002056
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RF04234	mir-1421	MIPF0000564
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RF04237	mir-1490	MIPF0000525
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RF04239	mir-4679	MIPF0001228
RF04240	mir-4716	MIPF0001476
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RF04244	MIR169_6	MIPF0001058
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RF04248	MIR7486	MIPF0001682
RF04249	mir-310	MIPF0000566
RF04250	mir-236	MIPF0000232
RF04251	MIR5070	MIPF0002013
RF04252	mir-8186	MIPF0002035
RF04254	mir-1677	MIPF0000849
RF04255	MIR8001	MIPF0001852
RF04257	mir-9230	MIPF0002035
RF04258	mir-994	MIPF0001045
RF04259	mir-2003	MIPF0002049
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RF04261	MIR1861	MIPF0000567
RF04262	MIR1319	MIPF0001448
RF04263	MIR2593	MIPF0000733
RF04264	mir-5408	MIPF0001313
RF04265	mir-4650	MIPF00001234
RF04266	mir-9412	MIPF0001891
RF04267	mir-362	MIPF0000209
RF04268	mir-512	MIPF0000518
RF04269	mir-373	MIPF0000500
RF04270	mir-743	MIPF0000386
RF04271	mir-1244	MIPF0000569
RF04272	mir-8908	MIPF0001890

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RF04275	mir-2733	MIPF0000766
RF04276	MIR4371	MIPF0001141
RF04277	mir-1268	MIPF0000946
RF04278	MIR4372	MIPF0001257
RF04279	mir-H20	MIPF0001760
RF04280	mir-890	MIPF0000386
RF04281	mir-8791	MIPF0001882
RF04282	mir-507	MIPF0000130
RF04283	mir-3135	MIPF0001219
RF04284	mir-532	MIPF0000113
RF04285	mir-660	MIPF0000113
RF04286	mir-513	MIPF0000130
RF04287	mir-9195	MIPF0001939
RF04288	mir-9201	MIPF0001898
RF04289	mir-3596	MIPF0001194
RF04290	mir-1197	MIPF0000126
RF04291	mir-368	MIPF0000091
RF04292	mir-379	MIPF0000126
RF04293	mir-889	MIPF0000514
RF04294	mir-3578	MIPF0001166
RF04295	mir-329	MIPF0000110
RF04296	mir-485	MIPF0000201
RF04297	mir-35_2	MIPF0001648
RF04298	mir-36_2	MIPF0001664
RF04299	MIR814	MIPF0000351
RF04300	mir-39	MIPF0000304
RF04301	mir-200	MIPF0000491
RF04302	mir-506	MIPF0000130
RF04303	MIR162_2	MIPF0000169

Table S1: The mapping between Rfam accessions, ids and miRBase family accessions.