

# INVESTIGATING ONLINE RNA DATABASES

- DNA is static where transcriptome is dynamic.
- Transcriptome, the set of all RNA molecules expressed, varies across different tissue, developmental stages and under different physiological conditions and disease state.
- Its important to study transcriptome since it reflects gene expression and since it can provide insights about genetic disorder

- RNA molecules simply categorized;
  - Coding
  - Non-coding
- All RNA molecules are created by the process of transcribing DNA.
- Coding RNAs; formed when DNA is transcribed into mRNA
- mRNA molecules are then translated into proteins by translation mediated by tRNA and rRNA in addition to proteins.
- Non-coding RNAs; tRNAs, siRNAs, miRNAs, rRNAs
  - Function in various cellular processes without being translated into proteins.

# Rfam

(<http://rfam.xfam.org/>)

- Contains information for RNA families
- Annotations for millions of RNA genes are also available
- Possible to view and download MSA
- Investigate distribution of species in different RNA families

## Rfam 14.2 (April 2020, 3024 families)

The Rfam database is a collection of RNA families, each represented by **multiple sequence alignments**, **consensus secondary structures** and **covariance models (CMs)**. [More...](#)

Examples: [SAM](#), [Homo sapiens](#), [snoRNA](#), [author:"Weinberg"](#)

Browse [Families](#), [Clans](#), [Motifs](#), [Genomes](#), or [Families with 3D structures](#)

### QUICK LINKS YOU CAN FIND DATA IN RFAM IN VARIOUS WAYS...

- SEQUENCE SEARCH** Analyze your RNA sequence for Rfam matches
  - VIEW AN RFAM FAMILY** View Rfam family annotation and alignments
  - VIEW AN RFAM CLAN** View Rfam clan details
  - KEYWORD SEARCH** Query Rfam by keywords
  - TAXONOMY SEARCH** Fetch families or sequences by NCBI taxonomy
  - JUMP TO**     
Enter any type of accession or ID to jump to the page for a Rfam family, sequence or genome
- Or view the [help](#) pages for more information

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# MirBase

(<http://www.mirbase.org>)

- Contains published miRNA sequences and their annotations
- Contains information about the sequence location and sequence of the predicted hairpin portion of the miRNA transcripts searched for.
- It's possible to search a miRNA by its name, its genomic location, its sequence and tissue expression



### Latest miRBase blog posts

#### [MicroRNA Gene Ontology annotations](#)

By [sam](#) (June 7, 2018)

You might have noticed some additional information on the mature miRNA pages in the last few weeks. See for example: [http://mirbase.org/cgi-bin/mature.pl?mature\\_acc=MIMAT0000123](http://mirbase.org/cgi-bin/mature.pl?mature_acc=MIMAT0000123) [http://mirbase.org/cgi-bin/mature.pl?mature\\_acc=MIMAT0000069](http://mirbase.org/cgi-bin/mature.pl?mature_acc=MIMAT0000069) The new section "QuickGO function" contains a set of high quality manual annotations of Gene Ontology terms for mature miRNAs, the vast majority of which come from the work of Rachael Huntley et [...]

#### [miRBase 22 release](#)

By [sam](#) (March 12, 2018)

After repeated and unreasonable delay, miRBase 22 is finally released. As you might expect with such a long gap, the number of sequences in the database has jumped significantly — by over a third. The vast majority of the increase comes from new microRNA annotations in species not previous represented in the database. Indeed, there [...]

miRNA count: 38589 entries

[Release 22.1](#): October 2018

### Search by miRNA name or keyword

### Download published miRNA data

[Download page](#) | [FTP site](#)

## miRBase: the microRNA database

miRBase provides the following services:

- The [miRBase database](#) is a searchable database of published miRNA sequences and annotation. Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for [searching](#) and [browsing](#), and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also [available for download](#).
- The [miRBase Registry](#) provides miRNA gene hunters with unique names for novel miRNA genes prior to publication of results. Visit the [help pages](#) for more information about the naming service.

To receive email notification of data updates and feature changes please subscribe to the [miRBase announcements mailing list](#). Any queries about the website or naming service should be directed at [mirbase@manchester.ac.uk](mailto:mirbase@manchester.ac.uk).

miRBase is managed by the [Griffiths-Jones lab](#) at the [Faculty of Biology, Medicine and Health, University of Manchester](#) with funding from the [BBSRC](#). miRBase was previously hosted and supported by the [Wellcome Trust Sanger Institute](#).

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# GWAS Catalog

(<https://www.ebi.ac.uk/gwas/>)

- Curated collection of human SNPs can be found in the GWAS Central, formerly known as the Human Genome Variation Database
- SNP entries have been subjected to an additional quality check and are completely annotated.
- Biomarkers can only be identified by GWAS
- For diagnostic purpose