Module 9: RNA Family

Objective

- The objective of this module is to:
  - To determine if the nucleotide sequence under investigation has characteristics to define it as a an non-coding RNA.

Rfam

- The Rfam database is similar to Pfam in that multi-sequence alignments are used to build families.

- Rfam uses models built on conserved sequences and secondary structures to search through an unknown sequence for non-coding RNA genes (e.g. rRNAs, tRNAs, and other small RNAs), regulatory motifs within the transcribed regions of protein-coding genes (e.g., riboswitches), and motifs associated with self-splicing RNAs.

- This module should be run on the nucleotide sequence of hypothetical genes if no other hits have been found in modules to this point.

- If you have good evidence that your gene encodes a functional or highly conserved (even if hypothetical) protein from other module results, this module will likely not offer any additional information.

Procedures

- Navigate to Rfam at http://xfam.org.
- Enter the **nucleotide sequence** of the gene being annotated.

Rfam 14.1 (January 2019, 3016 families)

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

Try the **new Rfam search** and <u>let us know</u> if you have any feedback

| Search Rfam | 🔍 **Search** |

Examples: <u>*SAM*</u>, <u>*Homo sapiens*</u>, <u>*snoRNA*</u>, <u>*author:"Weinberg"*</u>

Browse <u>*Families*</u>, <u>*Clans*</u>, <u>*Motifs*</u>, New <u>*Genomes*</u>, *or* <u>*Families with 3D structures*</u>

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 accession or ID [Go] [Example]

Enter any type of accession or ID to jump to the page for a Rfam family, sequence or genome

Or view the <u>help</u> pages for more information

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QUICK LINKS

SEQUENCE SEARCH

VIEW AN RFAM FAMILY

VIEW AN RFAM CLAN

KEYWORD SEARCH

TAXONOMY SEARCH

JUMP TO

ANALYZE YOUR RNA SEQUENCE FOR RFAM MATCHES

Paste your RNA sequence here to find matching Rfam families.

	Go
	Example

Annotate a sequence with Rfam families using <u>Infernal *cmscan*</u>.

Try the **new Rfam search** and <u>let us know</u> if you have any feedback

Search Rfam	🔍 **Search**

Examples: <u>*SAM*</u>, <u>*Homo sapiens*</u>, <u>*snoRNA*</u>, <u>*author:"Weinberg"*</u>

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QUICK LINKS

SEQUENCE SEARCH

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JUMP TO

ANALYZE YOUR RNA SEQUENCE FOR RFAM MATCHES

Paste your RNA sequence here to find matching Rfam families.

```
>16S ribosomal RNA [Kytococcus sedentarius DSM 20547: NC_013169] (+)strand
TTCTACGGAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTT
AACACATGCAAGTCGAACGGTGAAGCGAGTGCTTGCACTCGTGGATCAGT
GGCGAACGGGTGAGTAACACGTGAGTAACCTGCCCTCCACTCTGGGATAA
GCGCTGGAAACGGCGTCTAATACTGGATACGACCGACCCTCGCATGGGGT
GTTGGTGGAAAGATTTATCGGTGGTGGATGGACTCGCGGCCTATCAGCTT
GTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGA
GGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG
GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC
CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAG
AAGCTTTTGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTACGTGCCA
GCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCG
TAAAGAGCTTGTAGGCGGTTTGTCGCGTCTGCTGTGAAAATTCAGGGCTT
AACCCTGGACGTGCAGTGGGTACGGGCAGACTAGAGTATGGTAGGGGAGA
CTGGAATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACC
GATGGCGAAGGCAGGTCTCTGGGCCATTACTGACGCTGAGAAGCGAAAGC
ATGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCATGCCGTAAACGTT
GGGCGCTAGGCGTGGGTCTCATTCCACGAGATCCGTGTCGCAGCTAACGC
ATTAAGCGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGA
ATTGACGGGGGCCCGCACAAGCGGCGGAGCATGCTGATTAATTCGATGCA
ACGCGAAGAACCTTACCAAGGCTTGACATGCACTGGATCGCCTCAGAGAT
GGGGTTTCCCTTTGGGCTGGTGCACAGGTGGTGCATGGTTGTCGTCAGCT
CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTC
TATGTTGCCAGCACGTAATGGTGGGGACTCATAGGAGACTGCCGGGGTCA
ACTCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGTCTT
```

[Go] [Example]

Annotate a sequence with Rfam families using <u>Infernal *cmscan*</u>.

- The results will show if any families of RNA were found, the position of the hit along with the score, and the alignment of the sequence to the family.
- Report the score and record the alignment in the Lab Notebook.

Rfam matches

Download your results as: JSON T*

Id	Accession	Start	End	Bits score	E-value	Strand	Show/hide alignment
SSU_rRNA_archaea	RF01959	7	1523	1060.4	0	+	Show
SSU_rRNA_bacteria	RF00177	2	1525	1593.2	0	+	Show
SSU_rRNA_microsporidia	RF02542	7	1520	715.8	9.9e-218	+	Show
SSU_rRNA_eukarya	RF01960	7	1520	702.1	8.4e-211	+	Show

Rfam is part of the ELIXIR infrastructure
Rfam is an Elixir service Read more

Family: *SSU_rRNA_bacteria* (RF00177)
Description: *Bacterial small subunit ribosomal RNA*

22047 sequences   6962 species   750 structures

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

Summary

Clan

This family is a member of clan (CL00111), which contains the following 5 members:

SSU_rRNA_archaea   SSU_rRNA_bacteria   SSU_rRNA_eukarya   SSU_rRNA_microsporidia SSU_trypano_mito

Wikipedia annotation   Edit Wikipedia article

The Rfam group coordinates the annotation of Rfam families in Wikipedia. This family is described by a Wikipedia entry Ribosomal RNA. **More...**

Ribosomal ribonucleic acid (**rRNA**) is the RNA component of the ribosome, and is essential for protein synthesis in all living organisms. It constitutes the predominant material within the ribosome, which is approximately 60% rRNA and 40% protein by weight, or 3/5 of ribosome mass. Ribosomes contain two major rRNAs and 50 or more proteins. The ribosomal RNAs form two subunits, the large subunit (LSU) and small subunit (SSU). The LSU rRNA acts as a ribozyme, catalyzing peptide bond formation. The SSU and LSU rRNA sequences are widely used for working out evolutionary relationships among organisms, since they are of ancient origin and are found in all known forms of life.

Structure

The ribosomal RNAs complex with proteins to form two subunits, the large subunit (LSU) and small subunit (SSU). During translation, mRNA is sandwiched between the small and large subunits, and the ribosome catalyzes the formation of a peptide bond between the two amino acids that are contained in the rRNA.

A ribosome also has three binding sites called A, P, and E.

- The A site in the ribosome binds to an aminoacyl-tRNA (a tRNA bound to an amino acid).
- The amino (NH_2) group of the aminoacyl-tRNA, which contains the new amino acid, attacks the ester linkage of peptidyl-tRNA (contained within the P site), which contains the last amino acid of the growing chain, forming a new peptide bond. This reaction is catalyzed by peptidyl transferase.
- The tRNA that was holding onto the last amino acid is moved to the E site, and what used to be the aminoacyl-tRNA is the peptidyl-tRNA.

A single mRNA can be translated simultaneously by multiple ribosomes.

Subunits and ribosomal RNA genes
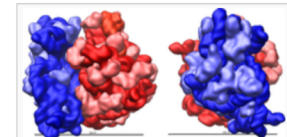
Three-dimensional views of the ribosome, showing rRNA in dark blue (small subunit) and dark red (large subunit). Lighter colors represent ribosomal proteins.

RNA Module

Rfam

go to http://rfam.sanger.ac.uk

Rfam number (RF#####)

```
 save for annotation report
```

Rfam name

```
 save for annotation report
```

Score

```
score
```

E-value

```
e-value
```

Pairwise Alignment

```
alignment
```

Be sure to save this document after completing the RNA module!