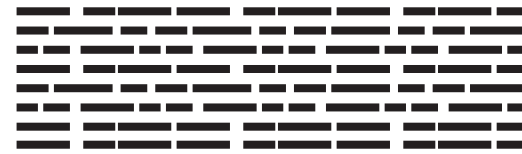Rfam contains 2791 families, each represented by a
- SEED alignment
- covariance model (CM)
- list of annotated hits in Rfamseq database (more than 2 million hits)

If you submit a family to Rfam, these tools become available to the community, allowing it to be annotated in genomes and other datasets.

Rfam also includes community annotation of families (wikipedia), RNA motifs, secondary structure diagrams, alignment statistics, taxonomic information, and sequence search capability.
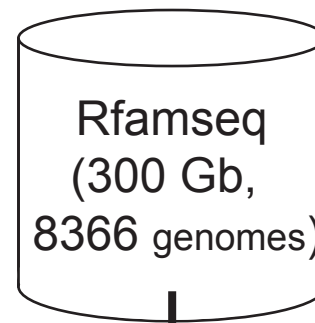
rfam.xfam.org

Rfam SEED alignment including consensus structure annotation

cmbuild, cmcalibrate

covariance model

previously required BLAST pre-filters cmsearch

Rfamseq (300 Gb, 8366 genomes)

"homologs"

Types of RNAs in Rfam

count	type
239	Cis-reg;
28	Cis-reg; frameshift-element;
32	Cis-reg; IRES;
30	Cis-reg; leader;
31	Cis-reg; riboswitch;
10	Cis-reg; thermoregulator;
76	Gene;
29	Gene; antisense;
11	Gene; antitoxin;
64	Gene; CRISPR;
217	Gene; lncRNA;
530	Gene; miRNA;
23	Gene; ribozyme;
15	Gene; rRNA;
3	Gene; snRNA;
463	Gene; snRNA; snoRNA; CD-box;
266	Gene; snRNA; snoRNA; HACA-box;
24	Gene; snRNA; snoRNA; scaRNA;
15	Gene; snRNA; splicing;
471	Gene; sRNA;
2	Gene; tRNA;
9	Intron;