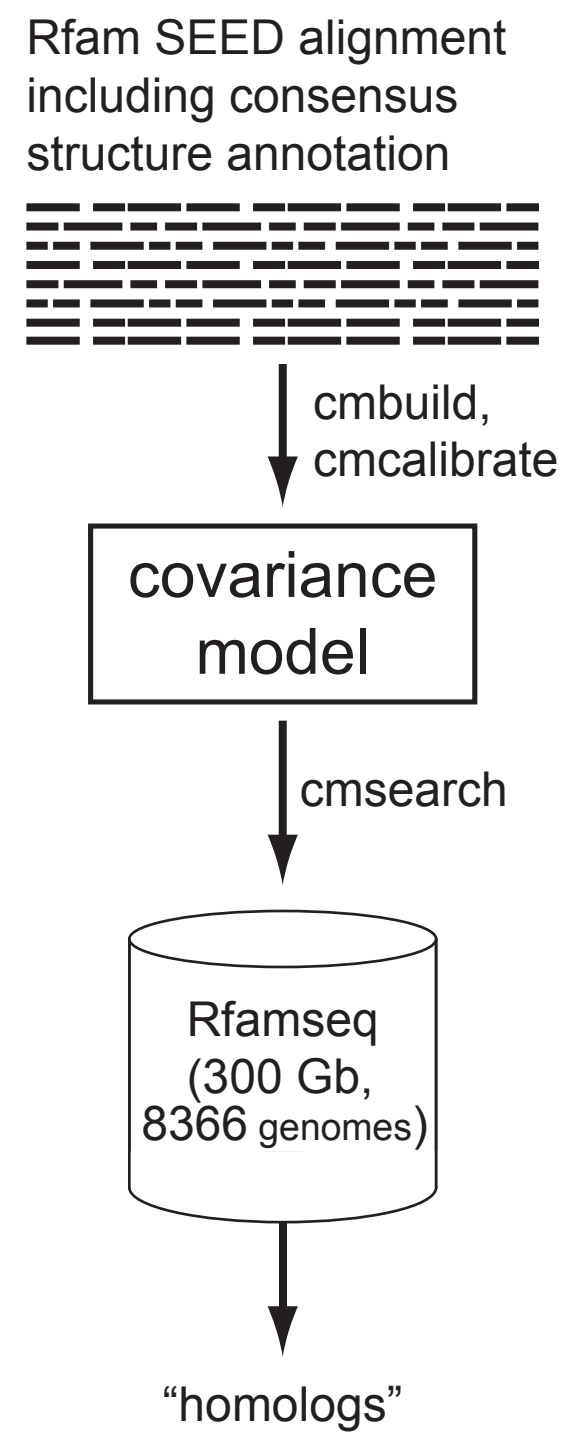Rfam contains 2686 families, each represented by a
 - SEED alignment
 - covariance model (CM)
 - list of annotated hits in Rfamseq database (2,272,100 total hits)

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

cmsearch

Rfamseq (300 Gb, 8366 genomes)

"homologs"

Types of RNAs in Rfam

#fams all	#fams viral	#hits viral	type
241	114	757	Cis-reg;
28	21	116	Cis-reg; frameshift-element;
32	10	127	Cis-reg; IRES;
30	2	3	Cis-reg; leader;
33	1	18	Cis-reg; riboswitch;
31	1	19	Cis-reg; thermoregulator;
74	7	155	Gene;
38	2	46	Gene; antisense;
11	0	-	Gene; antitoxin;
64	0	-	Gene; CRISPR;
219	0	-	Gene; lncRNA;
529	15	52	Gene; miRNA;
30	4	60	Gene; ribozyme;
14	0	-	Gene; rRNA;
3	1	4	Gene; snRNA;
470	1	3	Gene; snRNA; snoRNA; CD-box;
269	0	-	Gene; snRNA; snoRNA; HACA-box;
29	0	-	Gene; snRNA; snoRNA; scaRNA;
15	0	-	Gene; snRNA; splicing;
513	3	6	Gene; sRNA;
2	1	5330	Gene; tRNA;
9	1	141	Intron;
2686	184	6837	

Rfam