# Resource Summary Report

Generated by NIF on May 8, 2025

# RNase P Database

RRID:SCR_006680
Type: Tool

## Proper Citation

RNase P Database (RRID:SCR_006680)

## Resource Information

**URL:** http://www.mbio.ncsu.edu/RNaseP/home.html

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**Description:** Ribonuclease P is responsible for the 5''-maturation of tRNA precursors. Ribonuclease P is a ribonucleoprotein, and in bacteria (and some Archaea) the RNA subunit alone is catalytically active in vitro, i.e. it is a ribozyme. The Ribonuclease P Database is a compilation of ribonuclease P sequences, sequence alignments, secondary structures, three-dimensional models and accessory information. The database contains information on bacterial, archaeal, and eukaryotic RNase P. The RNase P and protein sequences are available from phylogentically-arranged lists, individual sequences, or aligned in GenBank format. The database also provides secondary structures and 3D models, as well as movies, still images, and other accessory information.

**Abbreviations:** RNase P Database

**Synonyms:** The RNase P Database, Ribonuclease P Database

**Resource Type:** data or information resource, database

**Defining Citation:** PMID:9847214

**Keywords:** ribonuclease p, ribonucleoprotein, ribozyme, sequence, sequence alignment, secondary structure, 3-d model, rnase p rna

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**Resource Name:** RNase P Database

**Resource ID:** SCR_006680

**Alternate IDs:** nif-0000-03403

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20250507T060439+0000

## Ratings and Alerts

No rating or validation information has been found for RNase P Database.

No alerts have been found for RNase P Database.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Khan AL, et al. (2022) Genome structure and evolutionary history of frankincense producing Boswellia sacra. iScience, 25(7), 104574.

Chiu JK, et al. (2012) Conformational features of topologically classified RNA secondary structures. PloS one, 7(7), e39907.

Marvin MC, et al. (2009) Broadening the mission of an RNA enzyme. Journal of cellular biochemistry, 108(6), 1244.

Hammann C, et al. (2007) Searching genomes for ribozymes and riboswitches. Genome biology, 8(4), 210.

Luo C, et al. (2006) Rapid evolution of a recently retroposed transcription factor YY2 in mammalian genomes. Genomics, 87(3), 348.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Gardner PP, et al. (2004) A comprehensive comparison of comparative RNA structure prediction approaches. BMC bioinformatics, 5, 140.

Törö I, et al. (2001) RNA binding in an Sm core domain: X-ray structure and functional analysis of an archaeal Sm protein complex. The EMBO journal, 20(9), 2293.