

Resource Summary Report

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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 phylogenetically-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: database, data or information resource

Defining Citation: [PMID:9847214](#)

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

Funding: Isis Pharmaceuticals ;
NIGMS GM52894

Resource Name: RNase P Database

Resource ID: SCR_006680

Alternate IDs: nif-0000-03403

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260805T044140+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 [dkNET](#) .

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.