

# The Ribonuclease P Database

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## ABSTRACT

**Ribonuclease P is responsible for the 5'-maturation of tRNA precursors. Ribonuclease P is a ribonucleo-protein, and in bacteria 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, available via the World Wide Web (<http://www.mbio.ncsu.edu/RNaseP/home.html>).**

## INTRODUCTION

Ribonuclease P is the ribonucleoprotein endonuclease that cleaves transfer RNA precursors, removing 5' precursor sequences and generating the mature 5' terminus of the tRNA (see ref. 1 for a review). RNase P is also implicated in the processing of other RNA precursors. In bacteria, in which RNase P is best understood, the holoenzyme consists of two subunits, an RNA of ~400 nt and a protein of ~120 amino acids (2). The RNA is the catalytic subunit of the enzyme; the bacterial RNase P RNA subunit alone is catalytically proficient, at high ionic strength *in vitro* (3). In the last few years, the number and diversity of RNase P RNA sequences available has increased dramatically.

On a yearly basis since 1991, RNase P RNA sequence alignments and secondary structures have been compiled and distributed in an informal publication, 'The Book of P', providing a single source for comparative information. In 1994 the Ribonuclease P Sequence Database was established as an electronic means of distributing the Book of P and in its eighth release (described here) is a well-established and widely-used World Wide Web resource.

## DESCRIPTION

The Ribonuclease P Sequence Database is a compilation of RNase P sequences, sequence alignments, secondary structures, three-dimensional models, and accessory information available electronically via the World Wide Web (Fig. 1 see below for details on accessing the database). The hypertext format of the database makes access to its various components straightforward. The database primarily contains information on bacterial and archaeal RNase P, focusing on the RNA subunit of the enzyme, although information is also included on the eucaryal and organellar RNase P RNAs and proteins. The database is updated

as additional sequences and structural information becomes available.

The RNase P RNA and protein sequences in the database are available from lists arranged phylogenetically as individual sequences or as alignments in GenBank format. Secondary structures of each RNA are presented in Graphic Interchange Format (GIFs) and can be downloaded either as level 1 Postscript (.ps) or Adobe Acrobat (.pdf) files. Models of the three-dimensional structure of the RNA are provided in Protein Database (PDB) format and as Quicktime movies. Accessory information, such as reference structures, phylogenetic trees, computer programs, and reference listings are also made available as part of the database.

## AVAILABILITY

The Ribonuclease P Database is accessible using any World Wide Web browser (e.g., Netscape Navigator, Microsoft Explorer) at the URL <http://www.mbio.ncsu.edu/RNaseP/home.html>. A CD-ROM copy of the RNase P Database is available for those without access to the World Wide Web. The administrator of the Ribonuclease P database (JWB) can be contacted by electronic mail ([jwbrown@mbio.ncsu.edu](mailto:jwbrown@mbio.ncsu.edu)) or by mail at the address given above. Users of the Ribonuclease P Database should cite this publication.

## PLEA FOR HELP

Users of the Ribonuclease P database are encouraged to provide corrections, new information, or other materials for inclusion in the database; unpublished information will be held confidential (via username and password protection) at the author's request. Help is especially needed for expansion of the data made available on the eukaryotic RNase P enzymes.

## ACKNOWLEDGEMENT

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## REFERENCES

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- 3 Guerrier-Takada, C., Gardiner, K., Marsh, T., Pace, N. and Altman, S. (1983) *Cell*, **35**, 849–857.



# The RNase P Database

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The Ribonuclease P Sequence Database is a compilation of RNase P sequences, sequence alignments, secondary structures, three-dimensional models, and accessory information. The database primarily contains information on the bacterial and archaeal enzymes, focusing on the RNA subunit. Some information is also included on the eucaryal and organellar RNase P RNAs. The database is updated as additional sequences and structural information becomes available.

**Information & resources:**

- [About the RNase P Database](#)
- [Cite this reference](#)
- [General background on RNase P](#)
- [RNase P bibliography](#)
- [Computer software](#)
- [Related Worldwide Web sites](#)

**The RNA subunit:**

- [Individual sequences and structures](#)
- [Sequence alignments](#)
- [Three-dimensional models](#)
- [Standard 'discussion' figures](#)

**The protein subunit:**

- [Individual sequences](#)
- [Alignment of bacterial sequences](#)

**Secondary structure survey**

Cast your vote, and/or make comments on several alternative representations of the RNase P RNA secondary structure.

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**Figure 1.** The Ribonuclease P Database home page. The appearance of the Ribonuclease P Database home page is shown as it appears in graphics-capable World Wide Web browser (Netscape Navigator, in this case). Links to the various sections of the Ribonuclease P Database are shown in blue.