

Resource Summary Report

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5S Ribosomal RNA Database

RRID:SCR_007545

Type: Tool

Proper Citation

5S Ribosomal RNA Database (RRID:SCR_007545)

Resource Information

URL: <http://biobases.ibch.poznan.pl/5SData/>

Proper Citation: 5S Ribosomal RNA Database (RRID:SCR_007545)

Description: A database on nucleotide sequences of 5S rRNAs and their genes. The database contains 1985 primary structures of 5S rRNA and 5S rDNA, and was last updated in 2002, according to the website. They include 60 archaeobacterial, 470 eubacterial, 63 plastid, nine mitochondrial and 1383 eukaryotic sequences. The nucleotide sequences of the 5S rRNAs or 5S rDNAs are divided according to the taxonomic position of the source organisms. The sequences for particular organisms can be retrieved as single files using a taxonomic browser or in multiple sequence structural alignments. The multiple sequence alignments of 5S ribosomal RNAs can be downloaded in TAB-delimited and FASTA formats.

Abbreviations: 5S Ribosomal RNA Database

Resource Type: data or information resource, database

Defining Citation: [PMID:10592212](#)

Keywords: eubacteria, eukaryote, archaeobacteria, mitochondrion, model rna molecule, nucleotide sequence database, ribosome, plastid, ribosomal rna, sequence alignment, rna-protein interaction, rna, rna structure, 5s rna, gene, 5s rdna, mitochondria, sequence, alignment

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Resource Name: 5S Ribosomal RNA Database

Resource ID: SCR_007545

Alternate IDs: nif-0000-02526

Old URLs: <http://rose.man.poznan.pl/5SData/index.html>

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133140+0000

Ratings and Alerts

No rating or validation information has been found for 5S Ribosomal RNA Database.

No alerts have been found for 5S Ribosomal RNA Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Sun F, et al. (2021) Menzerath-Altmann's Law of Syntax in RNA Accretion History. Life (Basel, Switzerland), 11(6).

Dollive S, et al. (2012) A tool kit for quantifying eukaryotic rRNA gene sequences from human microbiome samples. Genome biology, 13(7), R60.

Thiaucourt F, et al. (2011) Mycoplasma mycoides, from "mycoides Small Colony" to "capri". A microevolutionary perspective. BMC genomics, 12, 114.

Claesson MJ, et al. (2010) Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. Nucleic acids research, 38(22), e200.

Smit S, et al. (2009) RNA structure prediction from evolutionary patterns of nucleotide composition. Nucleic acids research, 37(5), 1378.

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