

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

rRNDB

RRID:SCR_007905

Type: Tool

Proper Citation

rRNDB (RRID:SCR_007905)

Resource Information

URL: <https://rrndb.umms.med.umich.edu>

Proper Citation: rRNDB (RRID:SCR_007905)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 19, 2016. It is a curated database that catalogs the numbers of genes that encode for 16S, 23S and 5S ribosomal RNAs in Bacteria and Archaea. Typically, a single copy of each of these genes is clustered into a rRNA operon, with as many as 15 rRNA operons present per genome. The genomic locus for any of the rRNA encoding genes is ?rrn? ? hence the name of this database. Because the number of genes encoding tRNAs is positively correlated with the number of rRNA-encoding genes (1), tRNA gene copy number is also cataloged in the rrnDB. Data are gathered both from sequenced genomes and from published articles that include estimates of the number of rRNA encoding genes.

Synonyms: rRNDB

Resource Type: data or information resource, database

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: rRNDB

Resource ID: SCR_007905

Old URLs: <http://ribosome.mmg.msu.edu/rrndb/index.php>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260912T200155+0000

Ratings and Alerts

No rating or validation information has been found for rRNDB.

No alerts have been found for rRNDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 101 mentions in open access literature.

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

Xu Y, et al. (2026) Performance, blood parameters, ruminal fermentation and microbial community of dairy cows supplemented with *Saccharomyces cerevisiae* fermentation product from dry-off to early lactation. *Journal of animal science*, 104.

Ye Z, et al. (2026) Bioenergy Cropping Reduces the Spatiotemporal Scaling of Soil Bacterial Biodiversity. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(29), e18964.

Liang Q, et al. (2026) Rapid de novo assembly of animal-microbe biofilter to mitigate seabed methane leakage. *National science review*, 13(12), nwag266.

Jiang F, et al. (2026) Post-defecation exposure alters gut microbiota of forest musk deer with implications for conservation metagenomics. *Applied microbiology and biotechnology*, 110(1), 53.

Selva A, et al. (2026) Microbiological Analysis Following Periodontal Treatment in Individuals with Bronchiectasis. *Microorganisms*, 14(5).

Laderriere V, et al. (2026) BactoTraits: a trait database for exploring functional diversity of bacterial communities. *Scientific data*, 13(1).

Bisaschi M, et al. (2025) Nanopore-based amplicon sequencing for rapid detection and identification of *Bacillus* spp. in plant-based products. *Frontiers in microbiology*, 16, 1701533.

Yan Y, et al. (2025) Soil Nutrient Enrichment Induces Trade-Offs in Bacterial Life-History Strategies Promoting Plant Productivity. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(45), e10066.

Srinivas M, et al. (2025) Evaluating the efficiency of 16S-ITS-23S operon sequencing for species level resolution in microbial communities. *Scientific reports*, 15(1), 2822.

He D, et al. (2025) Microbial life-history strategies and genomic traits between pristine and cropland soils. *mSystems*, 10(5), e0017825.

Sampson HR, et al. (2025) Air pollution modifies colonisation factors in beneficial symbiont *Snodgrassella* and disrupts the bumblebee gut microbiome. *NPJ biofilms and microbiomes*, 11(1), 2.

Fu W, et al. (2025) Industrial Trans Fatty Acids Promote the Development of Food Allergy in a Mouse Model. *Allergy, asthma & immunology research*, 17(2), 252.

Shi X, et al. (2025) Improving biocide evaluation using propidium monoazide (PMA) viability staining technique. *Scientific reports*, 16(1), 2535.

Dec M, et al. (2025) Prophage ϕ Er670 and Genomic Island GI_Er147 as Carriers of Resistance Genes in *Erysipelothrix rhusiopathiae* Strains. *International journal of molecular sciences*, 27(1).

Dyroff AI, et al. (2025) Comparison of RNA- and DNA-based 16S amplicon sequencing to find the optimal approach for the analysis of the uterine microbiome. *Scientific reports*, 15(1), 17037.

Li J, et al. (2025) Increased temperature enhances microbial-mediated lignin decomposition in river sediment. *Microbiome*, 13(1), 89.

Zhuang Y, et al. (2025) Core microbe *Bifidobacterium* in the hindgut of calves improves the growth phenotype of young hosts by regulating microbial functions and host metabolism. *Microbiome*, 13(1), 13.

Afzal MY, et al. (2025) Fast-growing *Bacillus sensu lato* rhizosphere populations are constrained by antagonistic *Pseudomonadota*, *Actinomycetota* and other *Bacillus sensu lato*. *bioRxiv : the preprint server for biology*.

Vályi P, et al. (2024) The oral microbiome of a family including Papillon-Lefèvre-syndrome patients and clinically healthy members. *BMC oral health*, 24(1), 158.

Dommann J, et al. (2024) A novel barcoded nanopore sequencing workflow of high-quality, full-length bacterial 16S amplicons for taxonomic annotation of bacterial isolates and complex microbial communities. *mSystems*, 9(10), e0085924.