

Resource Summary Report

Generated by [nidm-terms](#) on Sep 1, 2026

SILVA

RRID:SCR_006423

Type: Tool

Proper Citation

SILVA (RRID:SCR_006423)

Resource Information

URL: <https://www.arb-silva.de>

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Description: High quality ribosomal RNA databases providing comprehensive, quality checked and regularly updated datasets of aligned small (16S/18S, SSU) and large subunit (23S/28S, LSU) ribosomal RNA (rRNA) sequences for all three domains of life (Bacteria, Archaea and Eukarya). Supplementary services include a rRNA gene aligner, online tools for probe and primer evaluation and optimized browsing, searching and downloading on the website. The extensively curated SILVA taxonomy and the new non-redundant SILVA datasets provide an ideal reference for high-throughput classification of data from next-generation sequencing approaches. Alignment tool, SINA, is available for download as well as available for use online.

Synonyms: SILVA rRNA database, SILVA - high quality ribosomal RNA databases

Resource Type: data or information resource, database

Defining Citation: [PMID:23193283](#), [PMID:24293649](#), [PMID:17947321](#)

Keywords: ribosomal rna, gene sequence, gene, sequence, alignment, taxonomy, 16s, 18s, 23s, 28s, phylogeny, probe, primer, alignment service, fish, arb, ribocon, geoblast, bio.tools

Funding: German Collection of Microorganisms and Cell Cultures

Resource Name: SILVA

Resource ID: SCR_006423

Alternate IDs: biotools:silva, OMICS_01514, nif-0000-03464, r3d100011323, rid_000103

Alternate URLs: <https://bio.tools/silva>, <https://doi.org/10.17616/R3FP60>

License URLs: <https://www.arb-silva.de/footer/privacy-statement/>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260829T182940+0000

Ratings and Alerts

No rating or validation information has been found for SILVA.

No alerts have been found for SILVA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15971 mentions in open access literature.

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

Fan K, et al. (2026) Monitored food intake in early pregnancy modulates the maternal microbiome in the obese BPH/5 mouse model of superimposed preeclampsia. *Physiological genomics*, 58(3), 144.

Liu YY, et al. (2026) Assessing whether rectal swabs reflect appendiceal microbiota profiles in acute appendicitis: a 16S rRNA-based comparative study. *Gut pathogens*, 18(1), 10.

Apgar M, et al. (2026) Dietary fiber reduces mortality from secondary sepsis in a murine model of *Clostridioides difficile* infection. *iScience*, 29(4), 115258.

Hutchison B, et al. (2026) Dysbiosis in the Gut-Liver Axis Is Associated With Low Bone Mass During Murine Cholestasis. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(6), e71667.

Yin S, et al. (2026) Association of Intratumoral Microbiota with Prognosis in Head and Neck Squamous Cell Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1799.

Yang J, et al. (2026) Age and sex-dependent tumor microbiome programs shape pancreatic cancer prognosis. *iScience*, 29(7), 116542.

Sun Z, et al. (2026) Intrapartum caesarean delivery and childhood BMI trajectories in relation to the infant gut microbiome in the VDAART prospective birth cohort. *EBioMedicine*, 129, 106347.

Deng S, et al. (2026) Repurposing of the Macrolide Antibiotic Clarithromycin for the Prevention of Lung Cancer. *Molecular cancer therapeutics*, 25(2), 283.

Hussain U, et al. (2026) Microbial communities in semi-mature oak trees are resilient to drought, nutrient limitation, and pathogen challenge. *Cell host & microbe*, 34(2), 344.

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. *Cell host & microbe*, 34(5), 844.

Rizk NM, et al. (2026) Microbial community assembly and pathogen signatures in groundwater and tap water systems in greater Cairo, Egypt. *The Journal of the Egyptian Public Health Association*, 101(1).

Kim S, et al. (2026) Gut microbiota transfer from autoimmune dry eye mice imprints stereotypic B cell receptor repertoires in the lacrimal gland and induces disease. *Frontiers in immunology*, 17, 1827057.

Takahashi H, et al. (2026) Testosterone deficiency synergistically exacerbates fructose-induced hepatic steatosis through gut microbiota and pyruvate in mice. *American journal of physiology. Endocrinology and metabolism*, 330(2), E233.

Zhou Z, et al. (2026) Integrative analysis of the mouse cecal microbiome across diet, age, and weight in the diverse BXD population. *Microbiome*, 14(1).

Hasegawa K, et al. (2026) Age-related decline in nuclear envelope LINC complex drives neuronal aging via axon initial segment dysfunction. *EMBO reports*, 27(13), 3788.

Wang Y, et al. (2026) Kaempferol drives genotype-specific microbiota Bacillaceae to enhance nitrogen acquisition in rapeseed. *Journal of advanced research*, 82, 127.

Choi H, et al. (2026) Investigation of nutritional and functional roles of ??-mannanase on intestinal health and growth performance of nursery pigs fed low-cost formulated diets with high phytase inclusion. *Journal of animal science*, 104.

Selhorst P, et al. (2026) Sensitive, flexible, and affordable serum RNA sequencing for pathogen detection on the Oxford Nanopore platform. *BMC genomics*, 27(1), 188.

Napier E, et al. (2026) Lung microbial dysregulation and TNF inhibition contribute to worsened nontuberculous mycobacterial lung disease. *Research square*.

Wu CY, et al. (2026) Role of Core Microbiome Shifts in Octocoral Litophyton Under Diurnal Temperature Fluctuations. *Microbial ecology*, 89(1).