

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

probeBase

RRID:SCR_003417

Type: Tool

Proper Citation

probeBase (RRID:SCR_003417)

Resource Information

URL: <http://www.microbial-ecology.net/probebase/>

Proper Citation: probeBase (RRID:SCR_003417)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on October 28, 2025. A database of probes and microbes that can be searched for target organisms, probe names, probe sequences, probe accession numbers, and references. The search target site function can assist in the development of new rRNA-targeted oligonucleotide probes for fluorescence in situ hybridization (FISH), while the match tool can be used to rapidly retrieve all published probes targeting your query sequences (e.g. from a rRNA gene clone library) without prior phylogenetic analysis. probeBase is hyperlinked with PubMed, RDP-II, and Greengenes to provide additional bibliographic information and up-to-date data on probe specificity. Ribosomal RNA (rRNA) targeted oligonucleotide probes are widely used for fluorescence in situ, dot blot, and microarray hybridization in culture-independent studies of microbial communities and for the identification of uncultured prokaryotes in clinical and environmental samples. probeBase is a comprehensive database containing published rRNA-targeted oligonucleotide probe sequences, DNA microarray layouts and associated information.

Synonyms: probeBase

Resource Type: data or information resource, database

Defining Citation: [PMID:17099228](#)

Keywords: FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: probeBase

Resource ID: SCR_003417

Alternate IDs: nif-0000-03340

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260905T133121+0000

Ratings and Alerts

No rating or validation information has been found for probeBase.

No alerts have been found for probeBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 77 mentions in open access literature.

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

Zhuang Y, et al. (2025) Mechanistic insights into endometriosis: roles of *Streptococcus agalactiae* and L-carnitine in lesion development and angiogenesis. *Angiogenesis*, 28(3), 38.

Sasaki-Higashimoto I, et al. (2025) Histopathological study of the localization/distribution of *Fusobacterium nucleatum* in esophageal cancer. *Pathology international*, 75(2), 82.

Suma HR, et al. (2025) Pleiotropic regulation of bacterial toxin production and Allee effect govern microbial predator-prey interactions. *ISME communications*, 5(1), ycaf031.

Mattelin V, et al. (2025) Integrating taxonomic and phenotypic information through FISH-enhanced flow cytometry for microbial community dynamics analysis. *Microbiology spectrum*, 13(8), e0197324.

Razavi S, et al. (2024) Gut microbiota composition and type 2 diabetes: Are these subjects linked Together? *Heliyon*, 10(20), e39464.

Juliyanti V, et al. (2024) Comparative analysis of root associated microbes in tropical cultivated and weedy rice (*Oryza* spp.) and temperate cultivated rice. *Scientific reports*, 14(1), 9656.

Mohammadzadeh N, et al. (2024) Impact of bariatric surgery on gut microbiota composition in obese patients compared to healthy controls. *AMB Express*, 14(1), 115.

Kendlbacher V, et al. (2024) *Zoothamnium mariella* sp. nov., a marine, colonial ciliate with an atypical growth pattern, and its ectosymbiont *Candidatus Fusimicrobium zoothamnicola* gen. nov., sp. nov. *PloS one*, 19(4), e0300758.

Inatomi T, et al. (2023) Ameliorating effect of probiotics in a rat model of chronic kidney disease. PloS one, 18(3), e0281745.

Kim YB, et al. (2023) In-depth metataxonomic investigation reveals low richness, high intervariability, and diverse phylotype candidates of archaea in the human urogenital tract. Scientific reports, 13(1), 11746.

Rohwer N, et al. (2023) Ketogenic Diet Has Moderate Effects on the Fecal Microbiota of Wild-Type Mice. Nutrients, 15(21).

Larsen IS, et al. (2023) *Bacillus velezensis* DSM 33864 reduces *Clostridioides difficile* colonization without disturbing commensal gut microbiota composition. Scientific reports, 13(1), 14941.

Hsueh CY, et al. (2022) A positive feed-forward loop between *Fusobacterium nucleatum* and ethanol metabolism reprogramming drives laryngeal cancer progression and metastasis. iScience, 25(2), 103829.

Jiménez-Pichardo R, et al. (2021) Innovative Control of Biofilms on Stainless Steel Surfaces Using Electrolyzed Water in the Dairy Industry. Foods (Basel, Switzerland), 10(1).

Nishimura H, et al. (2021) Role of the β -Catenin/REG I? Axis in the Proliferation of Sessile Serrated Adenoma/Polyps Associated with *Fusobacterium nucleatum*. Pathogens (Basel, Switzerland), 10(4).

Inatomi T, et al. (2021) Effects of probiotics on loperamide-induced constipation in rats. Scientific reports, 11(1), 24098.

Crognale S, et al. (2021) Direct Conversion of Food Waste Extract into Caproate: Metagenomics Assessment of Chain Elongation Process. Microorganisms, 9(2).

Sun Y, et al. (2021) Prenatal Maternal Stress Exacerbates Experimental Colitis of Offspring in Adulthood. Frontiers in immunology, 12, 700995.

Gagliano MC, et al. (2020) Microbial Community Drivers in Anaerobic Granulation at High Salinity. Frontiers in microbiology, 11, 235.

Serra V, et al. (2020) Morphology, ultrastructure, genomics, and phylogeny of *Euplotes vanleeuwenhoekii* sp. nov. and its ultra-reduced endosymbiont "*Candidatus Pinguicoccus supinus*" sp. nov. Scientific reports, 10(1), 20311.