Resource Summary Report

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Greengenes

RRID:SCR_002830
Type: Tool

Proper Citation

Greengenes (RRID:SCR_002830)

Resource Information

URL: http://greengenes.secondgenome.com/downloads

Proper Citation: Greengenes (RRID:SCR_002830)

Description: Database that provides access to the current and comprehensive 16S rRNA gene sequence alignment for browsing, blasting, probing, and downloading. The data and tools can assist the researcher in choosing phylogenetically specific probes, interpreting microarray results, and aligning/annotating novel sequences. The 16S rRNA gene database provides chimera screening, standard alignment, and taxonomic classification using multiple published taxonomies. ARB users can use Greengenes to update local databases., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: data or information resource, database

Defining Citation: PMID:16820507

Keywords: microbiome, rrna, 16s rrna, gene, dna, rna, chimera, alignment, taxonomic classification, taxonomy, FASEB list

Funding: Department of Energy contract DE-AC02-05CH11231

Availability: Free, Freely available

Resource Name: Greengenes

Resource ID: SCR_002830

Alternate IDs: OMICS_01512, r3d100010549, nif-0000-02927

Alternate URLs: http://greengenes.lbl.gov, https://doi.org/10.17616/R36C8G

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Record Creation Time: 20220129T080215+0000

Record Last Update: 20260919T195637+0000

Ratings and Alerts

No rating or validation information has been found for Greengenes.

No alerts have been found for Greengenes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3162 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Yu Q, et al. (2026) Gut microbiota-associated nutritional-immune status predicts prognosis in postoperative NSCLC patients. Gut microbes, 18(1), 2652460.

Cunningham-Oakes E, et al. (2026) Implementing portable, real-time 16S rRNA sequencing in the healthcare sector enhances antimicrobial stewardship. EBioMedicine, 129, 106317.

Shah UA, et al. (2026) A High-Fiber, Plant-Based Diet in Myeloma Precursor Disorders: Results from the NUTRIVENTION Clinical Trial and Preclinical Vk*MYC Model. Cancer discovery, 16(4), 697.

Zhang J, et al. (2026) Warming-induced unstable microbial community metabolically lowers straw-carbon sequestration in paddy soils. Journal of advanced research, 82, 33.

Terzo S, et al. (2026) Positive impact of indicaxanthin from Opuntia ficus-indica fruit on high-fat diet-induced neuronal damage and gut microbiota dysbiosis. Neural regeneration research, 21(1), 324.

Anggraeni AS, et al. (2026) Impact of chitosan supplementation on metabolomic profiles and microbial community dynamics in total mixed ration silage and rumen fluid. Animal bioscience, 39(3), 250178.

Liu SS, et al. (2026) Intratumoral microbiome evaluated progression and outcome of patients with HBV-associated hepatocellular carcinoma. Discover oncology, 17(1).

Senousy MA, et al. (2026) Dapagliflozin-intermittent fasting combination maximizes weight and metabolic regulation through AMPK/sirtuins/clock genes and gut microbiota signaling in high-fat diet-induced obesity: a novel anti-obesity approach. Cell & bioscience, 16(1).

Wang P, et al. (2026) Linkage of gut microbiota dysbiosis to chronic kidney disease in patients with graded proteinuria levels. Microbiology spectrum, 14(6), e0329425.

Abukhiran IM, et al. (2025) Mucosal Microbiome Markers of Complete Pathologic Response to Neoadjuvant Therapy in Rectal Carcinoma. Cancer research communications, 5(5), 756.

Dempsey E, et al. (2025) Protective Properties of the White Button Mushroom, Agaricus bisporus, in a Mouse Model of Colitis. Molecular nutrition & food research, e70133.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. Cancer discovery, 15(8), 1630.

Qin S, et al. (2025) Comparative efficacy of preventive vs. therapeutic resveratrol in modulating gut microbiota and alleviating inflammation in DSS-induced colitis. BMC immunology, 26(1), 42.

Yuan H, et al. (2025) Enterotype-stratified gut microbial signatures in MASLD and cirrhosis based on integrated microbiome data. Frontiers in microbiology, 16, 1568672.

Zhang F, et al. (2025) Different lysine-to-methionine ratios in a low-protein diet affect the microbiome and metabolome, influencing the jejunal barrier function in Tibetan sheep. Frontiers in microbiology, 16, 1441143.

Gong D, et al. (2025) The gastric microbiome altered by A4GNT deficiency in mice. Frontiers in microbiology, 16, 1541800.

Hsu WH, et al. (2025) Polystyrene nanoplastics disrupt the intestinal microenvironment by altering bacteria-host interactions through extracellular vesicle-delivered microRNAs. Nature communications, 16(1), 5026.

Sall I, et al. (2025) Dynamic flexibility of the murine gut microbiota to morphine disturbance enables escape from the stable dysbiosis associated with addiction-like behavior. bioRxiv : the preprint server for biology.

Lisenko KG, et al. (2025) Insect meals in cat diets and their effects on digestibility, physiology, and gut microbiota. Frontiers in veterinary science, 12, 1592625.

Aikepa D, et al. (2025) The Effects of Specific Gut Microbiota on Hyperuricemia - A Mendelian Randomization Analysis and Clinical Validation. Diabetes, metabolic syndrome and obesity : targets and therapy, 18, 1891.