

Resource Summary Report

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FunGene

RRID:SCR_018749

Type: Tool

Proper Citation

FunGene (RRID:SCR_018749)

Resource Information

URL: <http://fungene.cme.msu.edu/>

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Description: Functional gene pipeline and repository. Functional gene repository provides collections of genes in interactive platform, while functional gene pipeline offers suite of tools for functional gene amplicon processing and analysis. Together they enable key steps in functional gene based microbial community analysis, from target selection and primer analysis to amplicon processing and ecological discovery.

Synonyms: FunGene Pipeline

Resource Type: analysis service resource, data or information resource, data repository, database, production service resource, service resource, software resource, software toolkit, storage service resource

Defining Citation: [PMID:24101916](#)

Keywords: Gene processing, microbial ecology, functional genes, amplification primers, phylogeny, biogeochemical cycles, amplicon analysis, ecological discovery, microbial community

Funding: NIDDK UH3 DK083993;
NIEHS ;
NIEHS P42 ES004911;
Office of Science U.S. Department of Energy ;
USDA National Institute of Food and Agriculture

Availability: Free, Freely available

Resource Name: FunGene

Resource ID: SCR_018749

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260829T182612+0000

Ratings and Alerts

No rating or validation information has been found for FunGene.

No alerts have been found for FunGene.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Wang J, et al. (2026) Earthworm gut microbiome promotes biodegradation of albendazole in soil. Crop health, 4(1).

He K, et al. (2026) Environmental Preferences and Functional Variations of Methanotrophs in Northeast Qinghai-Tibet Plateau Wetlands. Environmental microbiology reports, 18(3), e70352.

Kuang C, et al. (2025) Particle associated denitrification in coastal aquaculture water. BMC microbiology, 25(1), 396.

Phan HV, et al. (2025) Active bacteria driving N2O mitigation and dissimilatory nitrate reduction to ammonium in ammonia recovery bioreactors. The ISME journal, 19(1).

Zhang S, et al. (2025) Roles of core nosZ denitrifiers in enhancing denitrification activity under long-term rice straw retention. Frontiers in plant science, 16, 1541202.

He K, et al. (2025) Coexistence networks of soil methanogens are closely tied to methane generation in wetlands on the northeastern of the Qinghai-Tibet Plateau. Frontiers in microbiology, 16, 1616051.

Yang J, et al. (2025) Effect of dietary Dendrobium nobile Lindl. On production performance, immune function and caecal microbiota of Chishui black-bone hens. Scientific reports, 15(1), 9745.

Liu J, et al. (2025) Soil nifH-harboring community assemblage varies across pecan cultivars. Frontiers in microbiology, 16, 1716240.

Xiang H, et al. (2025) Spatiotemporal distribution and potential functions of N2O-reducing bacteria in the waters of the Pearl River Estuary. BMC microbiology, 25(1), 323.

Yang X, et al. (2024) Unraveling the important role of comammox *Nitrospira* to nitrification in the coastal aquaculture system. *Frontiers in microbiology*, 15, 1355859.

Fu M, et al. (2024) The Spatial Dynamics of Diazotrophs in the Forefield of Three Tibetan Glaciers. *Microbial ecology*, 87(1), 138.

Zhang CJ, et al. (2024) Anaerobic hydrocarbon biodegradation by alkylotrophic methanogens in deep oil reservoirs. *The ISME journal*, 18(1).

Brzeszcz J, et al. (2024) Bacteria degrading both n-alkanes and aromatic hydrocarbons are prevalent in soils. *Environmental science and pollution research international*, 31(4), 5668.

Rong X, et al. (2024) Biocrusts Mediate the Niche Distribution and Diversity of Ammonia-Oxidizing Microorganisms in the Gurbantunggut Desert, Northwestern China. *Microbial ecology*, 87(1), 148.

Dikeocha IJ, et al. (2023) Investigation into the Potential Role of *Propionibacterium freudenreichii* in Prevention of Colorectal Cancer and Its Effects on the Diversity of Gut Microbiota in Rats. *International journal of molecular sciences*, 24(9).

Rymer TL, et al. (2023) The effects of antibiotics and illness on gut microbial composition in the fawn-footed mosaic-tailed rat (*Melomys cervinipes*). *PloS one*, 18(2), e0281533.

Johnston J, et al. (2023) Ammonia-Oxidizing Bacteria Maintain Abundance but Lower *amoA*-Gene Expression during Cold Temperature Nitrification Failure in a Full-Scale Municipal Wastewater Treatment Plant. *Microbiology spectrum*, 11(2), e0257122.

He C, et al. (2023) Dynamics of Endophytic Fungal Communities Associated with Cultivated Medicinal Plants in Farmland Ecosystem. *Journal of fungi (Basel, Switzerland)*, 9(12).

Zhou G, et al. (2023) Synergistic effects of diazotrophs and arbuscular mycorrhizal fungi on soil biological nitrogen fixation after three decades of fertilization. *iMeta*, 2(1), e81.

Jordan D, et al. (2023) Salinity Impacts the Functional *mcrA* and *dsrA* Gene Abundances in Everglades Marshes. *Microorganisms*, 11(5).