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, storage service resource, production service resource, database, software resource, service resource, data repository, software toolkit

Defining Citation: PMID:24101916

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

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

Availability: Free, Freely available

Resource Name: FunGene

Resource ID: SCR_018749

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250425T060321+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 38 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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

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.

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).

Villena-Alemany C, et al. (2023) Diversity dynamics of aerobic anoxygenic phototrophic bacteria in a freshwater lake. Environmental microbiology reports, 15(1), 60.

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.

Cholet F, et al. (2022) Ecological Observations Based on Functional Gene Sequencing Are Sensitive to the Amplicon Processing Method. mSphere, 7(4), e0032422.

He C, et al. (2022) Dual inoculation of dark septate endophytes and Trichoderma viride drives plant performance and rhizosphere microbiome adaptations of Astragalus mongholicus to drought. Environmental microbiology, 24(1), 324.

Jiang C, et al. (2022) The inhibitory effects of sunlight on nitrogen removal in riverine overlying water with suspended particles. Chemosphere, 295, 133941.

Piwosz K, et al. (2022) Photoheterotrophy by aerobic anoxygenic bacteria modulates carbon fluxes in a freshwater lake. The ISME journal, 16(4), 1046.

Liu Z, et al. (2022) Deterministic Factors Determine the Comammox Community Composition in the Pearl River Estuary Ecosystem. Microbiology spectrum, 10(4), e0101622.

Pinto M, et al. (2022) Microbial Consortiums of Putative Degraders of Low-Density Polyethylene-Associated Compounds in the Ocean. mSystems, 7(2), e0141521.

Li W, et al. (2022) Tracking the diversity and interaction of methanogens in the energy recovery process of a full-scale wastewater treatment plant. Environmental research, 211, 113010.

Linsong H, et al. (2022) Bioaugmentation with methanogenic culture to improve methane production from chicken manure in batch anaerobic digestion. Chemosphere, 303(Pt 3), 135127.

Oshiki M, et al. (2022) N2O Reduction by Gemmatimonas aurantiaca and Potential Involvement of Gemmatimonadetes Bacteria in N2O Reduction in Agricultural Soils. Microbes and environments, 37(2).

Mallott EK, et al. (2022) Butyrate Production Pathway Abundances Are Similar in Human and Nonhuman Primate Gut Microbiomes. Molecular biology and evolution, 39(1).

Takizawa S, et al. (2021) Characteristics of various fibrolytic isozyme activities in the rumen microbial communities of Japanese Black and Holstein Friesian cattle under different conditions. Animal science journal = Nihon chikusan Gakkaiho, 92(1), e13653.