Resource Summary Report

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IMG

RRID:SCR_007733
Type: Tool

Proper Citation

IMG (RRID:SCR_007733)

Resource Information

URL: http://img.jgi.doe.gov/

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Description: Datasets and tools for comparative analysis and annotation of all publicly available genomes from three domains of life in a uniquely integrated context. Plasmids that are not part of a specific microbial genome sequencing project and phage genomes are also included in order to increase its genomic context for comparative analysis. The user interface (see User Interface Map) allows navigating the microbial genome data space along its three key dimensions (genes, genomes, and functions), and groups together the main comparative analysis tools. Microbial genome data analysis in IMG usually starts with the definition of an analysis context in terms of selected genomes, functional annotations, and/or genes, followed by the individual or comparative analysis of genomes, functional annotations, or genes.

Abbreviations: IMG

Synonyms: Integrated Microbial Genomes

Resource Type: data or information resource, database

Keywords: genome, microorganism, annotation, bio.tools, FASEB list

Funding:

Resource Name: IMG

Resource ID: SCR_007733

Alternate IDs: nif-0000-03009, biotools:img

Alternate URLs: https://bio.tools/img

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250331T060725+0000

Ratings and Alerts

No rating or validation information has been found for IMG.

No alerts have been found for IMG.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 584 mentions in open access literature.

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

Farrell AA, et al. (2025) Bacterial Growth Temperature as a Horizontally Acquired Polygenic Trait. Genome biology and evolution, 17(1).

Wu D, et al. (2025) A metagenomic perspective on the microbial prokaryotic genome census. Science advances, 11(3), eadq2166.

Zhou P, et al. (2025) Development of SacB-based counterselection for efficient allelic exchange in Fusobacterium nucleatum. Microbiology spectrum, 13(1), e0206624.

Felipe Benites L, et al. (2024) Hot springs viruses at Yellowstone National Park have ancient origins and are adapted to thermophilic hosts. Communications biology, 7(1), 312.

Ren K, et al. (2024) Discovery and structural mechanism of DNA endonucleases guided by RAGATH-18-derived RNAs. Cell research, 34(5), 370.

Baruah N, et al. (2024) Biosynthesis of polyhydroxybutyrate by Methylorubrum extorquens DSM13060 is essential for intracellular colonization in plant endosymbiosis. Frontiers in plant science, 15, 1302705.

?auševi? S, et al. (2024) Niche availability and competitive loss by facilitation control proliferation of bacterial strains intended for soil microbiome interventions. Nature communications, 15(1), 2557.

Singha LP, et al. (2024) Functionally coherent transcriptional responses of Jatropha curcas and Pseudomonas fragi for rhizosphere mediated degradation of pyrene. Scientific reports, 14(1), 1014.

Uniacke-Lowe S, et al. (2024) Planococcus notacanthi sp. nov., isolated from the skin of a deep-sea snub-nosed spiny eel. International journal of systematic and evolutionary microbiology, 74(3).

Lillie IM, et al. (2024) Characterizing arginine, ornithine, and putrescine pathways in enteric pathobionts. MicrobiologyOpen, 13(2), e1408.

Scott KM, et al. (2024) Widespread dissolved inorganic carbon-modifying toolkits in genomes of autotrophic Bacteria and Archaea and how they are likely to bridge supply from the environment to demand by autotrophic pathways. Applied and environmental microbiology, 90(2), e0155723.

de la Fuente I, et al. (2024) Quorum sensing in bacteria: in silico protein analysis, ecophysiology, and reconstruction of their evolutionary history. BMC genomics, 25(1), 441.

Bowers RM, et al. (2024) scMicrobe PTA: near complete genomes from single bacterial cells. ISME communications, 4(1), ycae085.

Traglia GM, et al. (2024) Xanthomonas citri pv. eucalyptorum strain 4866-2_S43 (formerly X. axonopodis pv. eucalyptorum): the causal agent of bacterial leaf blight on eucalypts recovered in Argentina. Access microbiology, 6(10).

Jin T, et al. (2024) Effects of Klebsiella michiganensis LDS17 on Codonopsis pilosula growth, rhizosphere soil enzyme activities, and microflora, and genome-wide analysis of plant growth-promoting genes. Microbiology spectrum, 12(5), e0405623.

Walton JL, et al. (2024) Evidence for novel polycyclic aromatic hydrocarbon degradation pathways in culturable marine isolates. Microbiology spectrum, 12(1), e0340923.

Danov A, et al. (2024) Toxinome-the bacterial protein toxin database. mBio, 15(1), e0191123.

Bergmann L, et al. (2024) New dienelactone hydrolase from microalgae bacterial community-Antibiofilm activity against fish pathogens and potential applications for aquaculture. Scientific reports, 14(1), 377.

Chanda D, et al. (2024) Meta-analysis reveals obesity associated gut microbial alteration patterns and reproducible contributors of functional shift. Gut microbes, 16(1), 2304900.

Du X, et al. (2024) Proximity-based defensive mutualism between Streptomyces and Mesorhizobium by sharing and sequestering iron. The ISME journal, 18(1).