

Resource Summary Report

Generated by T1D on Jul 28, 2026

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

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: 20260729T044212+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 652 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Sheppard DI, et al. (2025) N-Terminal domain homologs of the orange carotenoid protein increase quenching of cyanobacterial phycobilisomes. *Plant physiology*, 198(1).

Arzamasov AA, et al. (2025) Integrative genomic reconstruction reveals heterogeneity in carbohydrate utilization across human gut bifidobacteria. *Nature microbiology*, 10(8), 2031.

Wang C, et al. (2025) Integrated multi-omics to elucidate the interplay between rumen microorganisms and host metabolism in Hu sheep supplemented with herbal preparations. *mSphere*, 10(4), e0002425.

Chu S, et al. (2025) Exploring the effect of soybean fermentation broth (S-FB) on gut microbes of lipopolysaccharide (LPS)-infected loach (*Misgurnus anguillicaudatus*) using 16S rRNA sequencing. *Frontiers in microbiology*, 16, 1551409.

Peng LL, et al. (2025) The altitudinal patterns of global human gut microbial diversity. *BMC microbiology*, 25(1), 267.

Grossman AS, et al. (2025) Bioinformatic discovery of type 11 secretion system (T11SS) cargo across the Proteobacteria. *Microbial genomics*, 11(5).

Green EA, et al. (2025) Isolation and characterization of mollicute symbionts from a fungus-growing ant reveals high niche overlap leading to co-exclusion. *mBio*, 16(7), e0089325.

Cross K, et al. (2025) Microbiome metabolic capacity is buffered against phylotype losses by functional redundancy. *Applied and environmental microbiology*, 91(2), e0236824.

Kirchner MJ, et al. (2025) *Streptococcus hepaticus* sp. nov. isolated from the liver of domestic pigs (*Sus scrofa domestica*). *International journal of systematic and evolutionary microbiology*, 75(5).

Manjarrez-Paba G, et al. (2025) Decolorization of methyl orange and aniline red dyes by *Enterococcus hirae* isolated from beach sand. *Scientific reports*, 15(1), 33341.

Lemay-St-Denis C, et al. (2025) From Binding to Catalysis: Emergence of a Rudimentary Enzyme Conferring Intrinsic Antibiotic Resistance. *Molecular biology and evolution*, 42(10).

Mulligan C, et al. (2025) A Reassessment of the Coprostane Biomarker in the Ediacaran With Implications for Dickinsonia. *Geobiology*, 23(4), e70029.

Nadel O, et al. (2025) Viral NblA proteins negatively affect oceanic cyanobacterial photosynthesis. *Nature*, 648(8093), 434.

Chen SC, et al. (2025) Microbial iron oxide respiration coupled to sulfide oxidation. *Nature*, 646(8086), 925.

Zhao Y, et al. (2025) The gut methanotroph *Methylocystis intestini* modulates intestinal peristalsis and fat metabolism via reducing methane levels. *Nature communications*, 17(1), 2.

Novak V, et al. (2025) Breaking the reproducibility barrier with standardized protocols for plant-microbiome research. *PLoS biology*, 23(9), e3003358.

Timilsina S, et al. (2025) Diversification of an emerging bacterial plant pathogen; insights into the global spread of *Xanthomonas euvesicatoria* pv. *perforans*. *PLoS pathogens*, 21(4), e1013036.

Wall LA, et al. (2025) Acquired CRISPR spacers and rhamnose-glucose polysaccharide defects confer resistance to *Streptococcus mutans* phage ϕ APCM01. *bioRxiv : the preprint server for biology*.

Wöhlbrand L, et al. (2025) Key role of Desulfobacteraceae in C/S cycles of marine sediments is based on congeneric catabolic-regulatory networks. *Science advances*, 11(10), eads5631.

Sloboda S, et al. (2025) Methylation of foreign DNA overcomes the restriction barrier of *Flavobacterium psychrophilum* and allows efficient genetic manipulation. *Applied and environmental microbiology*, 91(2), e0144824.