

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 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: 20260905T133144+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 715 mentions in open access literature.

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

Novak LVF, et al. (2026) Sulfur disproportionation occurs globally across anoxic habitats and has multiple mechanisms of independent evolutionary origin. The ISME journal, 20(1).

Chaudhary A, et al. (2026) Metatranscriptomics-based investigation of bacterial community dynamics across a dissolved organic matter gradient in southern Lake Michigan. Applied and environmental microbiology, 92(4), e0026326.

Beals DG, et al. (2026) Genomic signatures in Variovorax enabling colonization of the Populus endosphere. mSystems, 11(2), e0160525.

Chambers LR, et al. (2026) A DNA damage-activated kinase controls bacterial immune pathway expression. bioRxiv : the preprint server for biology.

Langenfeld K, et al. (2026) Novel machine learning-based approach to identify viral biomarkers of human respiratory emissions from oral and nasal metagenomes. mSphere, 11(5), e0011326.

Leng H, et al. (2026) Comparative Genomic Insights into MatE Transporter Diversity and Habitat Adaptation of Archaea. Microorganisms, 14(3).

Ji R, et al. (2026) GdbMTB: a manually curated genomic database of magnetotactic bacteria. Database : the journal of biological databases and curation, 2026.

Su L, et al. (2026) Genomic adaptation strategies to habitat switching in Korarchaeota. Science advances, 12(2), eaea1035.

Rosenbaum FP, et al. (2026) Genomic and Transcriptomic Insights Into the Autotrophic Metabolism on H₂ + CO₂ or CO of the Thermophilic Acetogenic Model Organism Moorella thermoacetica. Environmental microbiology, 28(4), e70289.

Chaulagain D, et al. (2026) Rational assembly of synthetic marine biofilm community with chitinase production. Research square.

Ticer TD, et al. (2026) Intestinal mucus acts as a nutrient source and signal for Klebsiella pneumoniae. Microbiome research reports, 5(2), 9.

Chasapi MN, et al. (2026) metagRoot: a comprehensive database of protein families associated with plant root microbiomes. *Nucleic acids research*, 54(D1), D1733.

Han H, et al. (2026) Intestinal Epithelial Cell-derived Osteopontin Protects Against Metabolic Dysfunction-associated Steatohepatitis by Modulating Bile Acid Composition and the Gut Microbiome. *Cellular and molecular gastroenterology and hepatology*, 20(3), 101678.

Dmytrenko O, et al. (2026) RNA-triggered Cas12a3 cleaves tRNA tails to execute bacterial immunity. *Nature*, 649(8099), 1312.

Jasnauskaitė M, et al. (2026) Structure and mechanism of antiphage retron Eco2. *Nature structural & molecular biology*, 33(2), 330.

Oliveira-Filho ER, et al. (2026) Rethinking Suicide Thi4 Thiazole Synthases: Comparative Genomic Insights and Pilot Functional Evidence. *ACS omega*, 11(25), 36539.

Tang LX, et al. (2026) Biochemical characterization of a thermostable uricase from Tengchong hot spring and its urate-lowering therapeutic potential. *AMB Express*, 16(1), 12.

Porter NT, et al. (2026) A system for transferring large genetic loci in *Bacteroides* enables hemicellulose utilization in *Bacteroides thetaiotaomicron* and characterization of a locus from an uncultivated strain. *Applied and environmental microbiology*, 92(5), e0017626.

Shwartz D, et al. (2026) Genomic and structural analysis of major antigenic proteins' variability in the human relapsing fever spirochete *Borrelia persica*. *Current research in microbial sciences*, 10, 100598.

Liu Y, et al. (2026) Characterization of novel cellobiose 2-epimerases from *Teredinibacter haidensis* and *Cellvibrio japonicus*. *BMC biotechnology*, 26(1).