

# Resource Summary Report

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## IMG System

RRID:SCR\_002965

Type: Tool

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### Proper Citation

IMG System (RRID:SCR\_002965)

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### Resource Information

**URL:** <http://img.jgi.doe.gov/cgi-bin/m/main.cgi>

**Proper Citation:** IMG System (RRID:SCR\_002965)

**Description:** Resource for analysis and annotation of genome and metagenome datasets in comprehensive comparative context. IMG provides users with tools for analyzing publicly available genome datasets and metagenome datasets.

**Abbreviations:** IMG, IMG/M

**Synonyms:** Integrated Microbial Genomes System

**Resource Type:** data or information resource, portal

**Defining Citation:** [PMID:17932063](#), [PMID:22086953](#)

**Keywords:** microbiome, microbial genetics, genome and metagenome datasets analysis, genome and metagenome datasets, genome, metagenomics, bio.tools, FASEB list

**Availability:** Free, Freely available

**Resource Name:** IMG System

**Resource ID:** SCR\_002965

**Alternate IDs:** nif-0000-03010, OMICS\_01478, SCR\_014605, biotools:img\_m

**Alternate URLs:** <http://img.jgi.doe.gov/m>, [https://bio.tools/img\\_m](https://bio.tools/img_m)

**Record Creation Time:** 20220129T080216+0000

**Record Last Update:** 20260829T182833+0000

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### Ratings and Alerts

No rating or validation information has been found for IMG System.

No alerts have been found for IMG System.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 212 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#).

Wang A, et al. (2026) Cross-species dissection of saline-related genes by genetically deciphering a euryhaline microalga *Chlorella* sp. *Nature communications*, 17(1), 1577.

Grant MA, et al. (2026) Influence of polyunsaturated fatty acids on *Aeromonas hydrophila*: sole carbon utilization, incorporation into membrane phospholipids, potentiation of cyclic lipopeptide activity, and other phenotypic impacts. *BMC microbiology*, 26(1).

Molina MC, et al. (2026) Functional characterization of a type I-F1 CRISPR-cas system from the clinical isolate *Shewanella xiamenensis* Sh95 reveals constitutive activity and plasmid-curing capability. *Scientific reports*, 16(1), 5409.

Lestin L, et al. (2025) Modulation of carbon-to-nitrogen ratio shapes the microbial ecology in a methanol-fed recirculating marine denitrifying reactor. *PeerJ*, 13, e20129.

Vargas BO, et al. (2025) Engineering *Saccharomyces Cerevisiae* With Novel Functional Xylose Isomerases From Rumen Microbiota for Enhanced Biofuel Production. *Biotechnology journal*, 20(6), e70050.

Cai Y, et al. (2025) Amino acid metabolism of the thermophilic acetogen *Thermacetogenium phaeum*. *PloS one*, 20(12), e0336914.

Timsina R, et al. (2025) Proteomic and metabolomic analysis reveals new insights into quaternary amine metabolism in *Citrobacter amalonaticus* CJ25. *mSphere*, 10(9), e0042125.

Dutkiewicz Z, et al. (2025) Proposal of *Patescibacterium danicum* gen. nov., sp. nov. in the ubiquitous bacterial phylum Patescibacteriota phyl. nov. *ISME communications*, 5(1), ycae147.

Teng ZJ, et al. (2025) Inositol phosphates as an overlooked phosphorous source in marine ecosystems. *The ISME journal*, 19(1).

George NA, et al. (2025) Discarded diversity: novel megaphages, auxiliary metabolic genes, and virally encoded CRISPR-Cas systems in landfills. *Virology journal*, 22(1), 370.

Li Y, et al. (2024) Thaumarchaeota from deep-sea methane seeps provide novel insights into their evolutionary history and ecological implications. *Microbiome*, 12(1), 197.

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.

George NA, et al. (2024) Discarded diversity: Novel megaphages, auxiliary metabolic genes, and virally encoded CRISPR-Cas systems in landfills. *bioRxiv : the preprint server for biology*.

Leunda-Esnaola A, et al. (2024) Harnessing the intragenomic variability of rRNA operons to improve differentiation of *Vibrio* species. *Scientific reports*, 14(1), 9908.

Palevich N, et al. (2024) Complete genome sequence of *Methanosphaera* sp. ISO3-F5, a rumen methylotrophic methanogen. *Microbiology resource announcements*, 13(4), e0004324.

O'Banion BS, et al. (2023) Plant myo-inositol transport influences bacterial colonization phenotypes. *Current biology : CB*, 33(15), 3111.

Jameson BD, et al. (2023) Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N<sub>2</sub>O cycling. *Communications biology*, 6(1), 212.

Botté ES, et al. (2023) Future ocean conditions induce necrosis, microbial dysbiosis and nutrient cycling imbalance in the reef sponge *Stylissa flabelliformis*. *ISME communications*, 3(1), 53.

Nieves-Mori6n M, et al. (2023) Heterologous expression of genes from a cyanobacterial endosymbiont highlights substrate exchanges with its diatom host. *PNAS nexus*, 2(6), pgad194.

P6rez-Losada M, et al. (2023) Nasal Bacteriomes of Patients with Asthma and Allergic Rhinitis Show Unique Composition, Structure, Function and Interactions. *Microorganisms*, 11(3).