

Resource Summary Report

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iMicrobe

RRID:SCR_017108

Type: Tool

Proper Citation

iMicrobe (RRID:SCR_017108)

Resource Information

URL: <https://www.imicrobe.us/>

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Description: Portal to provide integrated and federated system that interconnects diverse microbiome data sets, bioinformatics tools, and community resources. Built on guiding principles for FAIR data. Open source, community driven microbiome data marketplace and tool exchange for users to integrate their own data and tools with broader community. Partners with CyVerse and XSEDE.

Resource Type: data or information resource, organism-related portal, portal, topical portal

Keywords: microbiome, dataset, exchange, discovery, data

Funding: Gordon and Betty Moore Foundation ;
NSF

Availability: Free, Freely available

Resource Name: iMicrobe

Resource ID: SCR_017108

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260821T194104+0000

Ratings and Alerts

No rating or validation information has been found for iMicrobe.

No alerts have been found for iMicrobe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Zhuang GC, et al. (2026) Atmospheric deposition enhances marine methane production and emissions from global oceans. *Nature communications*, 17(1), 1811.

Koletti A, et al. (2024) Global omics study of *Tetraselmis chuii* reveals time-related metabolic adaptations upon oxidative stress. *Applied microbiology and biotechnology*, 108(1), 138.

Moromizato R, et al. (2024) Pyrenoid proteomics reveals independent evolution of the CO₂-concentrating organelle in chlorarachniophytes. *Proceedings of the National Academy of Sciences of the United States of America*, 121(10), e2318542121.

Montuori E, et al. (2023) Transcriptome Sequencing of the Diatom *Asterionellopsis thurstonii* and In Silico Identification of Enzymes Potentially Involved in the Synthesis of Bioactive Molecules. *Marine drugs*, 21(2).

Santoro D, et al. (2022) SPRISS: approximating frequent k-mers by sampling reads, and applications. *Bioinformatics (Oxford, England)*, 38(13), 3343.

Wang Q, et al. (2022) A Unique Set of Auxiliary Metabolic Genes Found in an Isolated Cyanophage Sheds New Light on Marine Phage-Host Interactions. *Microbiology spectrum*, 10(5), e0236722.

Hirakawa Y, et al. (2021) Characterization of a novel type of carbonic anhydrase that acts without metal cofactors. *BMC biology*, 19(1), 105.

Torres S, et al. (2021) Selection and validation of reference genes for quantitative real-time PCR in the green microalgae *Tetraselmis chuii*. *PloS one*, 16(1), e0245495.

Pyrih J, et al. (2021) The iron-sulfur scaffold protein HCF101 unveils the complexity of organellar evolution in SAR, Haptista and Cryptista. *BMC ecology and evolution*, 21(1), 46.

Cheng H, et al. (2021) Genome-wide identification of chitinase genes in *Thalassiosira pseudonana* and analysis of their expression under abiotic stresses. *BMC plant biology*, 21(1), 87.

Cho CH, et al. (2021) Phylogenetic analysis of ABCG subfamily proteins in plants: functional clustering and coevolution with ABCGs of pathogens. *Physiologia plantarum*, 172(3), 1422.

Lasek-Nesselquist E, et al. (2019) A Phylogenomic Approach to Clarifying the Relationship of Mesodinium within the Ciliophora: A Case Study in the Complexity of Mixed-Species Transcriptome Analyses. *Genome biology and evolution*, 11(11), 3218.

Hirakawa Y, et al. (2019) Organellar DNA Polymerases in Complex Plastid-Bearing Algae. *Biomolecules*, 9(4).

Balzano S, et al. (2019) Biosynthesis of Long Chain Alkyl Diols and Long Chain Alkenols in *Nannochloropsis* spp. (Eustigmatophyceae). *Plant & cell physiology*, 60(8), 1666.

Watts GS, et al. (2019) Identification and quantitation of clinically relevant microbes in patient samples: Comparison of three k-mer based classifiers for speed, accuracy, and sensitivity. *PLoS computational biology*, 15(11), e1006863.

Pan B, et al. (2019) Comparative Genomics Analysis of Ciliates Provides Insights on the Evolutionary History Within "Nassophorea-Synhymenia-Phyllopharyngea" Assemblage. *Frontiers in microbiology*, 10, 2819.

Nasko DJ, et al. (2019) CRISPR Spacers Indicate Preferential Matching of Specific Virioplankton Genes. *mBio*, 10(2).

Karp PD, et al. (2019) A Comparison of Microbial Genome Web Portals. *Frontiers in microbiology*, 10, 208.

Johnson LK, et al. (2019) Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. *GigaScience*, 8(4).

Kigundu G, et al. (2018) Hv 1 Proton Channels in Dinoflagellates: Not Just for Bioluminescence? *The Journal of eukaryotic microbiology*, 65(6), 928.